**EPIDEMIC PREDICTION USING MACHINE LEARNING TRAINED ON EHR AND HISTORICAL DATA**



**BY**

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# ABASTRACT

This dissertation examined the development of a machine learning-based epidemic prediction and detection system utilizing electronic health records and time-series analytics within Zimbabwe's public health sector, where epidemic management remains constrained by fragmented data systems, delayed reporting, and limited predictive capabilities. The study aimed to design a scalable, data-driven system capable of forecasting epidemic outbreaks through integration of machine learning algorithms and real-time analytics. The system architecture employed Next.js for the web interface, Supabase for cloud data management, and a TensorFlow-integrated ARIMA model trained on anonymised health data reflecting Zimbabwe's historical disease patterns including cholera, influenza, malaria, and COVID-19. Data pre-processing techniques enhanced prediction accuracy, enabling automatic dataset processing, forecast generation, and alert classification through a responsive dashboard for public health administrators. Predictions achieved 95.04% mean accuracy with MAE of 12.4 and RMSE of 16.8, demonstrating model robustness. Comparative analysis against established surveillance systems including GOARN and NNDSS revealed superior performance in timeliness, reliability, and data handling efficiency. The integration of machine learning with web-based analytics yielded substantial improvements in early outbreak detection, minimized reporting delays, and supported evidence-based decision-making, suggesting that adoption of such systems has potential to transform Zimbabwe's health surveillance infrastructure by facilitating proactive disease control, efficient data utilization, and sustainable digital transformation within public health management.

# DECLARATION

I, **Takudzwa Mvere**, do hereby declare that I am the sole author of the dissertation. I authorise **Midlands State University** to publish this dissertation with other institutions or individuals for the purpose of scholarly research.

Signature………………………………………… Date……………………..

# APPROVAL

This dissertation entitled “**EPIDEMIC PREDICTION USING MACHINE LEARNING TRAINED ON EHR AND HISTORICAL DATA**” by **Takudzwa Mvere** meets the regulations governing the award of the degree of BSc Honours Computer Systems Engineering of the Midlands State University and is approved for its contribution to knowledge and literary presentation.

Supervisor’s signature…………………………….. Date………………….

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To all who contributed in any way to this achievement, I extend my sincere gratitude.

# DEDICATION

I dedicate this work to my loving family, whose unwavering support, patience, and encouragement have been my greatest source of strength. To my parents, your sacrifices and belief in my dreams have guided me to this milestone.

I also dedicate this project to my friends, whose motivation, laughter, and companionship have made this academic journey both fulfilling and memorable.

Finally, I dedicate this work to all those who strive to make the world a better place through innovation, dedication, and resilience. May this research serve as a small contribution toward a healthier and more sustainable future.

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# List of Abbreviations

AI……………..Artificial Intelligence

API……………Application Programming Interface

ARIMA ………Autoregressive Integrated Moving Average

CDC…………..Centres for Disease Control and Prevention

CNN………….Convolutional Neural Network

HER………….Electronic Health Records

GIS…………..Geographical Information System

GOARN……..Global Outbreak Alert and Response Network

HIPAA………Health Insurance Portability and Accountability Act

LSTM……….Long Short-Term Memory

MAE………..Mean Absolute Error

ML………….Machine Learning

MOHC……..Ministry of Health and Child Care

NNDSS…….National Notifiable Disease Surveillance System

PGI…………Pathogen Genomics Initiative

RMSE………Root Mean Square Error

SSR…………Server-Side Rendering

WHO……….World Health Organization

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# CHAPTER ONE: INTRODUCTION

## 1.1 Introduction

This chapter introduced the research topic of using Machine Learning (ML) models to predict possible epidemic outbreaks. It started by assessing the history of epidemic monitoring from the manual data collection methods from the past to the digitized systems of today. An understanding of this history illuminated the existing challenges in epidemic prevention and management, exposing the need for effective predictive measures that could close the gaps in the current state of epidemic surveillance. The problem definition was clearly established and a clear aim was defined. The aim was followed by objectives that were specific, measurable, achievable, relevant and time-bound (SMART).

The chapter then went on to look into the various constraints that could hinder this research, whether be it constraints beyond the researcher`s direct control or constraints and boundaries that the researcher set in order to define the scope of the research. Ethical considerations to consider when handling sensitive health related data were studied extensively. The research also established the development instruments used in the research and why they were used instead of the other alternatives. A clear and comprehensive work plan that outlined the time period in which all of this could possibly be achieved was drawn up and represented in a Gantt chart. Drawing the chapter to an end, the justification for carrying out the research was argued.

## 1.2 Background of the study

An epidemic is defined as an outbreak of a disease that spreads quickly among the population in a given area [1]. Epidemic outbreaks have ravaged communities throughout all of history. Globalization worsened the spread of infectious epidemic outbreaks [2]. Now these infections spread across the globe, graduating from epidemic status into full blown pandemics. Scenarios like this occur every day as people and packages board planes and ships to travel to other places. A good example of this infection spread bolstered by globalization was the Coronavirus disease of 2019 (COVID-19) outbreak which started as an epidemic outbreak in Wuhan China that spread the world over in a matter of months [3]. Using robust epidemic surveillance, such a global catastrophe could have been detected in its infancy while it was still an epidemic in a small province.

Systematic epidemic surveillance emerged in the early 20th century with the establishment of national health reporting systems across many countries [4]. These systems were too dependent on manual data collection. This data would then be processed with simple statistical algorithms. This often resulted in delays when detecting outbreaks. Computerized health information systems began to widely spread in the late 1900s and had almost reached worldwide adoption by the start of the 21st century. This brought the rise of electronic health records (EHR) which created vast repositories of patient health information. This new innovation improved analytical speed and data storage [5].

The current detection mechanisms were revealed to be limited and weak during such viral outbreaks as COVID-19, Zika and Ebola [6]. Most nations had lagged in the process of discovering local transmission patterns and could not adequately handle the resulting masses of data caused by these outbreaks. ML, an arm of Artificial Intelligence (AI), offered a new approach to the analysis and interpretation of complex health data. In contrast to conventional algorithms that used to be based on linear associations, the ML algorithms were able to detect activity-resistant patterns in very large volumes of data [7]. The combination of ML and EHR data provided an opportunity to create more responsive and more accurate epidemic detection systems. This was also supported by the recent developments in the field of deep learning which created unprecedented opportunities in the field of epidemic prediction. In particular, Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks have demonstrated potential success in analysing time series health patterns [8]. This was further enhanced by the constant reduction in the cost of cloud infrastructures that made them less costly in the long run. This simplified and reduced the cost of processing large amounts of data and making ML models available in the cloud.

## 1.3 Problem Definition

The current epidemic surveillance mechanisms like Global Outbreak Alert and Response Network (GOARN) and Centre of Disease Control (CDC) lacked major detection of epidemics. It took two to four weeks before the outbreaks were recognized [6]. The systems that existed were primarily passive reporting based and manual in terms of data collection. This restricted their scaling and compatibility with other EHR systems. Consequently, the outbreaks were typically detected at the stage that the community transmission was so significant that the containment operations became overly complex. This lag in identification led to slow reaction, poor resource use and it was costly to governments [9]. Such a surveillance model could not help prevent localized epidemics to become global pandemics in an interconnected world with infectious diseases crossing border in a few hours.

## 1.4 Aim

The aim of this study was to develop a machine learning based epidemic prediction and detection system that leveraged EHR and historical outbreak data.

## 1.5 Objectives

The objectives of this study were:

* To implement a real-time data pipeline with automated data synchronization supporting both singular and batch uploads of EHRs.
* To integrate various data formats like CSV, JSON and XML in order to guarantee compatibility with the various EHR platforms used across the country.
* To detect and flag epidemic trends in the uploaded EHR data using the Autoregressive Integrated Moving Average (ARIMA) time series algorithm.
* To develop an automated alerting mechanism that disseminates notifications to relevant health authorities via their accounts and email immediately after potential outbreak detection.
* To employ ML-driven algorithms that generate intervention options best suited to deal with the forecasted outbreak after detection.

## 1.6 Limitations

Research limitations present constraints that were beyond the researcher`s direct control that affected the implementation of the system [10]. The first of these limitations was that the system`s predictive accuracy was dependent on the quality and consistency of EHR and historical epidemic data. This data quality varied across different healthcare institutions and geographic regions. Incomplete or biased datasets would potentially compromise the model's reliability [11]. In order to fix these problems, outlier detection algorithms and data cleaning steps were added to check and organize incoming data.

Machine learning is costly as it requires large amount of computer power and memory. This rendered the large or complicated solutions difficult to employ. This has been alleviated by using Vercel servers with scalable infrastructure and serverless functions based on cloud-deployment. Computational overhead was also minimized using model optimization methods, such as pruning, quantization and lightweight architectures.

It depended on the use of sensitive health information, which became vulnerable to such regulatory regulations as the Human Insurance Portability and Accountability Act (HIPAA) and the General Data Protection Regulation (GDPR) [12]. Need to adhere to such regulations-driven limitations of data access, usage, and sharing capabilities. The sample data came in place of the actual data as some of the data was too sensitive and could not be easily accessed to conduct research. Whenever there was publicly available data on the real-world, it was utilized, but sample data was applied to close the gap in the study.

The system presented some level of disparity in performance throughout the disease conditions and local areas. This was because of variations in healthcare infrastructure, reporting styles as well as the epidemiology of diseases. As a result, there was emphasis on the viral infectious diseases which are common in Zimbabwe such as Influenza A, Malaria and Cholera. The fact that the epidemiology of these infections was well in the record was also a relief.

The process of integrating presented issues with the need to harmonize the information of various EHR systems. These platforms varied in formats, standards and quality of data. In this vein, the study adopted the use of algorithms in the data ingestion process that would combine different data formats such as CSV, JSON and XML.

## 1.7 Delimitations

The delimitations are definite margins that the researcher establishes to reduce the scope and focus of the study. These are decisions undertaken with a purpose of ensuring the project is manageable and to ensure the research can be conducted with ease and quality is not compromised [13].

The study had a narrow scope and concentrated on the prediction of epidemics of infectious diseases. It left out non-communicable illnesses, chronic diseases and other health outcomes that were not epidemic in nature. This constraint made the ML models optimized to the specific patterns and behaviours of the transmission and dynamics of infectious diseases. The system is oriented to the healthcare settings that have developed EHR systems and strong digital health infrastructure. Areas that lacked health data infrastructure and those that were not digitized wholly or paper based in the record systems might not have been appropriate to this strategy. This constrained the short-term global applicability of the system.

The research focused on time series algorithms only, while leaving out various other ML algorithms. This was because the time series was the most suited, and having one uniform algorithm was good for defining the scope of the research, since there were too many ML algorithms available.

The data used in this study came only from EHR systems and past epidemic databases. The research excluded other potential data streams such as social media surveillance, environmental sensors, or genomic sequencing data. These sources could have had enhanced prediction capabilities, but would significantly expand project complexity. They would have complicated the scope and could have led to too much bloat in the system.

## 1.8 Development Instruments

In order to achieve successful completion of the system, the research employed a carefully selected technology stack optimized for machine learning applications and web-based health 1informatics systems.

### 1.8.1 Next.JS

Next.js is a framework that is based on React and simplifies the development of a web application. The framework provides faster page loads through such mechanisms as server-side rendering (SSR) and statical site generation. As a result, they will have a smoother running site together with improved Search Engine Optimization (SEO) features due to autonomous organization of code [14]. Besides, Next.js makes connection to back-end machine learning easy, and databases do not pose an issue.

### 1.8.2 TensorFlow

TensorFlow is a machine learning framework that is an open-source project by Google. It has numerous deep learning, neural network, and data modelling tools. TensorFlow would be able to handle a great deal of data, operate on more than one computer and enhance models, which is significant in epidemic prediction. It also enables experimenting with various machine learning models such as CNNs, LSTMs and transformers [15]. The primary tool to train the epidemic prediction models was to use historical and EHR data to test the models with the training of these models with TensorFlow.

### 1.8.3 Supabase

Supabase is a cloud storage platform that is reliable in managing data as it scales according to the increasing user demands [16]. Instead of ordinary databases, it operates PostgreSQL to store all the things arranged and also allowing an instant update. Ready-made tools to access, security, and data migrations provide developers with an opportunity to work with diverse electronic health records. Further, Supabase scales to demand, it distributes workloads across multiple machines and allows users to ask complex queries, which is suited to the rapid sorting of large amounts of medical data.

### 1.8.4 Vercel

Vercel is a frontend framework-oriented cloud platform used to build statical websites. It simplifies the process of deploying apps as it scales automatically and delivers content worldwide. Additional technologies in Vercel are continuous integration and delivery (CI/CD), serverless functions, and edge computing to improve the speed and reliability of the apps [17].

### 1.8.5 Development Environment

Visual Studio Code was the primary coding instrument (IDE) that was used in the project. It helps in working with JavaScript, Python and machine learning using various extensions. It was developed on a computer using Core i5 processor and 16GB of RAM, sufficient to build and test models, but at the same time affordable enough to be used in academic research.

## 1.9 Work Plan

The project adhered to a specific plan to ensure the project on epidemic prediction was created and tested in accordance. The project stages, goals, and the project timeline are provided in Table 1.1 and in Figure 1.1 in the Gantt chart.

Table 1.1 Project Timeline

|  |  |  |  |
| --- | --- | --- | --- |
| Activities | Start Date | End Date | Period (Months) |
| Proposal | 18 February | 02 March | 1 |
| Planning | 03 March | 12 April | 1 |
| Literature Review | 13 April | 07 May | 1 |
| Analysis | 07 May | 02 June | 1 |
| Design | 03 June | 12 July | 1 |
| Implementation | 13 July | 12 September | 2 |
| Documentation | 13 September | 01 November | 2 |
| Defence | 02 November | 10 November | <1 |

Source: Author

The project timeline is presented as a Gantt chart:

Table 1.2 Gantt Chart of Project Timeline

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Duration (Months) | Feb | Mar | Apr | May | Jun | Jul | Aug | Sept | Oct | Nov |
| Proposal |  |  |  |  |  |  |  |  |  |  |
| Planning |  |  |  |  |  |  |  |  |  |  |
| Literature Review |  |  |  |  |  |  |  |  |  |  |
| Analysis |  |  |  |  |  |  |  |  |  |  |
| Design |  |  |  |  |  |  |  |  |  |  |
| Implementation |  |  |  |  |  |  |  |  |  |  |
| Documentation |  |  |  |  |  |  |  |  |  |  |
| Defence |  |  |  |  |  |  |  |  |  |  |

Source: Author

## 1.10 Justification

Justification or rationale of research entailed explaining the purpose of conducting the research. It included the process of arguing about the significance of the study and the positive impact it had on the sphere. The system played an essential role towards enhancing early epidemic detection. It upheld more useful actions in the public health. Machine learning allowed analysing data faster and more accurately. This assisted health officials to respond quicker, resource management, and the transmission of contagious diseases. It should also be a useful tool in global health since the system can be modified to accommodate different types of data and different diseases.

## 1.11 Conclusion

The system of predicting and detecting epidemics based on machine learning was presented in this chapter. The discussion has indicated that such a tool is required considering the existing challenges of epidemic monitoring. It has also touched the issue of slow outbreak detection and how machine learning can provide solutions. The chapter explained the purpose of the study and why this system needed to be developed, as well as ethical issues. Chapter 2 has discussed literature on epidemic prediction models, the use of machine learning in the field of health, and has reviewed current approaches to data analysis in health informatics.

# CHAPTER 2: LITERATURE REVIEW

## 2.1 Introduction

This chapter aimed at providing comprehensive evaluation of the solutions already in place that dealt with the problem defined by the problem definition in Chapter 1. It began by considering international solutions to the problem of epidemic prediction, such as the ones used by organizations such as the World Health Organization (WHO) and the CDC. It then zoomed in on the regional level, looking into how health institutions tackled this problem in the Southern African region as other regions like South-East Asia. The analysis of study was then concluded with a thorough look at the solutions implemented at a local level. The results of this analysis allowed the research to identify the gaps left by these current implementations that could be filled.

The chapter then went on to discuss the feasibility of using ML to predict epidemics, trying to make sense of the research at a technical, economic, social and operational level. The goal of the feasibility study was to determine whether it was possible to acquire the skills and money necessary to make the solution a reality as well as to ensure that the solution itself would affect society as a whole positively. To close it all was a summary that, true to its name, summarized the contents of the chapter and gave hints as to what the next chapter entailed.

## 2.2 Analysis of Study or Related Work

This sub-chapter looked into the already existing systems and solutions that are were place to detect epidemic emergence and possibly predict it beforehand. It looked into how these solutions were implemented at an international, regional and local level. This would also include an in depth look into the strengths and weaknesses of the current solutions.

### 2.2.1 International Level

The World Health Organization`s GOARN is the world`s foremost international surveillance system for epidemic monitoring [18]. It was established in 2000. It relies primarily on member states to do their part by manually collecting their own health data and submitting it WHO. The organization then uses this data for basic statistical analysis. They work with over 310 technical institutions that network globally to monitor and provide rapid response to acute public health events. GOARN can be sub-divided into two, the Steering Committee (SCOSM) and the Operational Support Team (OST). SCOM is a representative body of 21 partner institutions that partake in planning, implementation and evaluation of GOARN`s activities and strategic goals. OST, on the other hand, facilitates the day to day running of the network and coordinates outbreak response missions, network activities and communication amongst the various bodies of the organization. While effective for coordinating international responses, the system suffers from significant delays between outbreak occurrence and detection, often taking weeks to identify emerging threats.

In the United States of America, the Center for Disease Control and Prevention (CDC) is the foremost health surveillance body. It operates the National Notifiable Disease Surveillance System (NNDSS) which has been collecting outbreak data since 1961 [19]. This is a largely reactive system reliant on the manual clinical diagnosis and reporting of cases by healthcare providers. Across the Atlantic, the European Centre for Disease Prevention and Control has been pioneering new ways by using its Epidemic Intelligence from Open Sources (EIOS) system. This platform uses machine learning techniques to analyze various sources of information such as news reports, social media content and official health communication. While EIOS has managed to recognize a number of outbreaks, the technology still has the issue of false positives and hallucinations.

In some Asian countries, the national level of epidemic surveillance systems has been developed, but difficulties still remain. China created the China Information System for Disease Control and Prevention (CISDCP), which linked more than 70,000 health facilities, which proved to be useful in the early part of the covid 19. However, in the reporting of data, there were problems of transparency and coordination among the provinces which led to delays [18]. Similarly, India's Integrated Disease Surveillance Program (IDSP) was started in 2004 in a bid to track the trends of diseases in a population of over 1.4 billion. Again, reporting of information was weak in the rural environment where the majority of population lived, resulting in inconsistencies in the monitoring process. A third system is Pakistan's Disease Early Warning System (DEWS), established in 2007 after significant flooding in the region, primarily tracking waterborne diseases with identified cholera and typhoid cases. This surveillance system returns to the limitation of laboratory capacity and inconsistent reporting of the data back into the system [20]. Overall, the eastern system demonstrated a common challenge. The large investments in technology do not pay off due to data quality, inconsistencies in the coverage of areas of reporting, and an unwillingness to share data quickly and intentionally.

In contrast, the European Centre for Disease Prevention and Control (ECDC) is tasked with monitoring health outcomes at a continental scale utilizing a TESSy system which creates a common reporting format and allows cross-border data exchange. Germany's Robert Koch Institute utilizes digital sentinel networks that collect information in real-time from primary care physicians to provide evidence of significant influenza cases weeks ahead of the traditional reporting formats. France utilizes the Sentinelles network, one of the oldest syndromic surveillance programs, where physicians volunteer their time, and report actions taken following a consultation for an infectious disease that dates back to 1984 [21]. Despite the systems, the European Union (EU) still encounters issues with establishing a streamlined network. Due to the different rules for testing, case definitions, and reporting periods, some EU member states encountered many challenges reporting data on COVID-19, and slowed the development of shared assessments. What the European case demonstrates is that even highly funded surveillance systems face barriers where political differences and institutional barriers undermine true coordination.

These sophisticated global systems often require substantial technological infrastructure and financial resources that may not be readily available in developing countries. The concentration of advanced surveillance capabilities in resource-rich environments creates equity issues in global health security. As such communities with the highest epidemic risks may have the least access to early warning systems.

### 2.2.2 Regional Level Implementations

Regional health authorities have developed increasingly sophisticated approaches to epidemic surveillance that reflect local priorities, resources, and technological capabilities. The Africa Center for Disease Control and Prevention (Africa CDC) launched the Africa Pathogen Genomics Initiative (Africa PGI) in 2020. It incorporates machine learning for genomic surveillance of infectious diseases [22]. The system uses convolutional neural networks to analyze pathogen genetic sequences and predict potential outbreak patterns. However, implementation has been limited by insufficient genomic sequencing capacity across the continent. Some places are just too remote and underdeveloped for this system to work.

South Africa's National Institute for Communicable Diseases (NICD) has put together the Communicable Diseases Communique system, which uses basic ML algorithms for syndromic surveillance [23]. The system works on aggregated health data in public hospitals, and has faced challenges of incomplete data reporting and constrained computational resources.

The Southern African Development Community (SADC) operates a disease surveillance system which connects 16 countries including Zimbabwe, Botswana and Mozambique. It mostly focuses on malaria, cholera and tuberculosis, because that's what seems to be the big threat to health in the region. Because people move across borders all the time, countries try to communicate about an outbreak quickly. Botswana has certainly done well with a digital system in which most clinics can send updates in real time. South Africa also has fairly good data due to the increased resources of the health sector. On the other hand, countries with less money, such as Mozambique, struggle to keep things going. When floods or cyclones strike, health posts are damaged and reporting becomes laggard. SADC has added maps of malaria over borders, but late reports from rural districts and weak labs often slow down confirmation.

In West Africa, the ECOWAS group learned its lessons following the 2014 Ebola crisis that revealed how unprepared West Africa was. Changes made by Nigeria, Ghana and Senegal were the largest. Nigeria developed SORMAS, a mobile phone tool that enables workers to send reports, even in areas where internet connection is poor. Senegal operates a major lab that aids the testing of samples from neighbours [24]. Ghana made an effort to train community health workers and even birth attendants, as many people do not go to the hospital. Still, the region has issues: inadequacy of test kits, low wages for health workers, as well as armed conflicts that prevent proper tracking. The main lesson is that progress made after a big outbreak does not last unless governments continue to invest and support these systems.

Regional implementations in sub-Saharan Africa are faced with unique challenges such as lack of internet connectivity, unreliable power supply and shortage of trained personnel. These constraints require the development of surveillance systems that are able to function effectively with little infrastructure while delivering meaningful early warning capabilities for local health authorities.

### 2.2.3 Local Level Implementations

Zimbabwe lagged behind by a long mile in terms of outbreak surveillance. The current systems were mostly manual and as such they could be slow and inconsistent [25]. This was not helped at all by the fact that a lot of regions in Zimbabwe were too remote and underdeveloped for epidemic surveillance to be carried out effectively. In the areas like city centers and towns with more effective surveillance, applications like District Health Information Version 2 (DHSI2) were used to manage patient and epidemic data. Such hospital-based early warning systems demonstrated remarkable success in controlled healthcare environments.

The problem with current order of things was that these solutions were more reactionary than predictive. The locally used solutions worked mostly to record health data into a massive repository but nothing of note would be done with this data. Humans would later on assess this repository and make a judgement of whether or not there was an outbreak. This of course was slow and cumbersome. It was also important to note that human fatigue and error would heavily affect these assessments. The one silver lining to the current system was that the availability of all this data already collected would be a gold mine for ML training. The more high-quality data that there is to train a model, the more accurate and persistent the model becomes [26].

Local implementations also faced additional challenges related to limited technological infrastructure, resource constraints, and varying levels of digital health adoption. The Ministry of Health and Child Care in Zimbabwe made significant investments in health information systems, but epidemic prediction capabilities remained limited compared to developed countries. As already established, vast repositories of health data are already there. What was left was a system that fed on this data to train models and generate value out of them. There was a significant gap between the available data and health officials understanding of said data, and ML could close this gap perfectly.

### 2.2.4 Machine Learning Techniques in Epidemic Prediction

The application of machine learning techniques to epidemic prediction had evolved rapidly. New methodological approaches demonstrated increasingly impressive performance and deep learning architectures had shown exceptional promise for processing datasets generated from modern health surveillance systems. Time series models were especially useful to epidemic modelling applications [27]. The COVID-19 pandemic was a proving ground and the data from the infection was utilized as widely available data to forecast epidemic trends. These experiments showed the better performance of ensemble methods that combined different algorithmic approaches. These advanced models were shown to accurately predict case numbers, hospitalization, and mortality trends in different geographic and demographic settings [28].

Convolutional neural networks and long short-term memory architectures have also demonstrated outstanding abilities in analyzing spatial-temporal patterns from epidemic data. These algorithmic techniques can handle multiple streams of data at the same time and retain important temporal and geographic relationships that have been ineffectively captured by traditional statistical methods. The application of federated learning methods to epidemic surveillance is an emerging frontier with high potential to improve global health security without breaching data privacy and sovereignty.

However, most existing machine learning methods do not have proper optimization for disease-specific traits and transmission patterns. Generic algorithmic solutions often overlook the relevant pathogen-specific signals which could have a substantial effect in prediction accuracy and clinical utility. Epidemiological domain knowledge is an underdeveloped area of machine learning architectures with significant room for improvement.

### 2.2.5 Data Sources and Integration Challenges

Contemporary surveillance system is increasingly based on the fusion of heterogeneous data sources to obtain the full situation awareness. This data fusion approach had great benefits in terms of detection sensitivity and predictive accuracy, but also created tremendous technical and operational challenges.

The difficulty for the surveillance system developers was to integrate electronic health record (EHR) data from various health systems. Differences in coding systems, data formats, quality standards and collection practices resulted in compatibility issues that might compromise machine learning model performance and generalizability [29]. The ability to process data in real-time had become more and more important as the surveillance systems developed. Traditional batch processing approaches created data lags in the hours and days between data collection and analysis. This was not sufficient for dynamic outbreak situations with rapid transmission dynamics that could change dramatically over short periods of time.

In resource-constrained environments like Zimbabwe, challenges to data integration included the lack of completeness of health records, consistency in data collection as well as interoperability of different health information systems. These limitations-imposed surveillance strategies that would be capable of operating using imprecise information, while maintaining useful early warning objectives.

## 2.3 Gaps Identified

Based on a review of current implementations and research, several challenges were identified that have also remained pertinent in making current epidemic prediction systems effective and accessible. These limitations posed both short-term challenges to system performance and longer-term challenges to health security equity globally.

Data quality and standardization problems continued to plague implementations across all scales and contexts. The lack of harmonized data formats and coding systems created significant barriers to developing robust, machine learning models. It did not matter how well your ML model programmed, if there was no good data, it wouldn`t produce accurate predictions. Another gap was that current processing capabilities remained inadequate for many surveillance applications, particularly those focused on rapidly transmissible pathogens. Most existing systems continued to operate on batch processing models that introduced delays of 24-48 hours or more between data collection and analysis. During exponential growth phases of epidemic outbreaks, such delays could result in missed opportunities for effective intervention.

Most of the current solutions were resource heavy. This could be problematic for the poor regions that were remote and may not have had an internet connection [30]. A less resource hungry solution was needed and the solution would accommodate low connectivity areas by having an offline mode that allowed it to operate even without an internet connection. Also, another issue was that the current systems were too cumbersome and complicated for the average medical profession user. They usually required a lot of training and in many cases, they did not even receive it. A more user-friendly system would make this easier for the users to perform their tasks.

## 2.4 Proposed Work

Based on the successes and limitations of the existing systems, the research proposed implementing an integrated machine learning platform that addressed the above-mentioned gaps. The epidemic prediction system would represent a novel approach that combined multiple complimentary ML algorithms. These algorithms would be optimized for different viral infections and would also incorporate robust data quality management and validation mechanisms. As already established in Chapter 1, this solution would only focus on viral infectious diseases like Cholera, Influenza A, Typhoid and Malaria. These would be the best choices since they were well reported and documented.

The core innovation lied in the modular and lightweight nature of the system, as this would allow it to operate effectively with limited computational resources and unstable internet connectivity. The system would emphasize both real-time and batch processing. Real-time processing would allow for quick detection in cases of strong and stable internet connectivity but batch processing would work well in instances of poor connectivity, where data would be stored locally for a while then when the system is back online, it can now be transmitted.

There would also be disease-specific optimizations to the ML models since the infections were not the same. The variables like weather, humidity, water availability etc. that determined the occurrences of theses outbreaks all meant that the parameters that defined how each ML model worked would be different. As such, the models featured engineering approaches tailored to different pathogen characteristics and transmission patterns.

### 2.4.1 Feasibility Analysis

Feasibility analysis is a study of whether or not it is viable to carry out intended research. This viability can be under a technical, operational, economic and social lens [31]. This means examining the technology requirement of the system, compatibility with existing infrastructure, and cost estimates to have an understanding of the system`s sustainability and efficiency.

#### 2.4.1.1 Technical Feasibility

Technical feasibility is concerned with whether or not a project can be carried out with the currently available technology and skills [32]. In relation to the proposed approach, the answer was a resounding yes. Modern machine learning frameworks were suited for the job and cloud infrastructure had matured so much over the past years to the point where it was the easiest to use. Platforms like TensorFlow and PyTorch provided robust foundations for developing sophisticated prediction algorithms. They also enabled flexible deployment across diverse computing environments.

Table 2.1 Software Requirements

|  |  |  |
| --- | --- | --- |
| **Component** | **Specifications** | **Purposes** |
| Next.js | v15 | Framework for building the web app with smooth frontend–backend integration. |
| Pytorch | v4.2 | Ran machine learning models for epidemic prediction. |
| MongoDB Compass | v6.0 | Stored EHR data in a flexible and highly scalable format. This would be done locally. |
| Node.js | v22 LTS | Provided the runtime for backend processes in JavaScript. |
| Python | v3.9 | Handled data analysis and visualization with tools like matplotlib. |
| Vercel | Cloud deployment | Cloud platform for deploying and scaling the application. |
| Visual Studio Code | IDE | Integrated development environment used for coding and debugging the project. |

Source: Author

The hardware requirements for the research were also readily available. Some of the components were either already in the possession of the researcher or would be easy to acquire when they were needed. Within the researcher`s possession was a HP laptop and 500GB of external storage. The laptop was an Intel core i5 processor with 16GB of RAM and an 8GB NVIDIA GeForce MX130 GPU. This was more than capable enough of acting as the main development device where the ML models would be trained and feature engineered. The external storage served as backup for the project in case there was an issue with the laptop.

The research also required a Virtual Private Sever (VPS) to host the system online. This could be a dedicated VPS from a service like Hetzner which would require a lot configuration on the researcher`s side or a service like Vercel which abstracted a lot of the backend configurations, but a higher cost. Recent advances in edge computing made it feasible to deploy machine learning models on lightweight hardware. This ensured that the system could operate effectively in resource constrained environments. The availability of open-source machine learning tools and cloud-based development platforms reduced technical barriers to implementation. It also enabled cost-effective scaling. Extensive documentation also existed for all these online resources and this made it easier to learn and adapt to the technologies.

#### 2.4.1.2 Economic Feasibility

Economic feasibility: The economic feasibility was based on the financial costs related to the implementation of the project and the potential benefit that can be obtained from the system. Cost-benefit ratios for epidemic forecasting systems were found to be very favourable. Previous studies indicated that well-designed early warning systems could save 60 - 80% of epidemic response costs due to prevention of large-scale transmission. The savings from avoided outbreaks are much larger than any development and operational costs related to prediction systems [33]. The cost savings associated with these include millions of dollars of medical expenses, economic disruption and emergency response.

In the context of Zimbabwe in particular, a timely detection of the outbreak would have an economic benefit. The country was low in healthcare resources and had been vulnerable to epidemic diseases for a long time. Focus on implementing cost effective technologies (open source) would decrease upfront capital requirements while providing scalable operational capability. Development costs would be estimated as manageable by utilising cloud-based infrastructure with flexible scaling. This technology can be put in use without any large upfront costs. In addition, cost could be saved by the efficient code design of the system that reduced the minimum resource when hosting the system on Vercel.

Table 2.2 Estimated Costs

|  |  |  |  |
| --- | --- | --- | --- |
| **Item** | **Quantity** | **Specification** | **Cost ($)** |
| Laptop | 1 | HP ProBook 450 G7 with Intel Core i5 processor, 500GB Nvme SSD and 16GGB R.A.M | 520 |
| External Storage | 1 | Seagate 2TB HDD | 98 |
| Virtual Server | 1 | Hetzner VPS with 2GB R.A.M, 2 Cores and 10GB Storage | 10p.m |
| MongoDB | 1 | 10GB Storage with a dedicated C.P.U | 17p.m |
| Vercel | 1 | Free account | 0 |
| **TOTAL** |  |  | ~645 |

Source: Author

While it is next to impossible to put a figure on the revenue and money saved by this research, it is fair to say that the benefits outweigh the costs. Therefore, the project is economically feasible.

#### 2.4.1.3 Social Feasibility

Social acceptance seemed to become more and more positive depending on the public awareness of epidemic risks in the wake of recent global health emergencies. Within the health care industry, user needs had been expressed by practitioners for better prediction, specifically for tools that give actionable warnings in advance and work easily into current clinical workflows [34].

In Zimbabwe there was a growing realisation among healthcare professionals and the public health authorities of the need for improved surveillance capabilities. The continued investments by the Ministry of Health and Child Care (MOHC) in health information systems reflected institutional will to apply technological solutions for better health outcomes [35]. Moreover, the public health benefits of early outbreak detection would likely have been clear to the community and so would have been a positive outcome. The design of the system, with its focus on privacy protection and data security, would help to address some of the concerns related to the handling of health information and build trust among healthcare providers and communities.

#### 2.4.1.4 Operational Feasibility

The integration aspect of the proposed system with the existing healthcare infrastructure, rather than replacing the current systems, was instrumental in improving its operability. The modular nature of the system meant that it could be implemented and tested step-by-step, minimizing disruption to the operations and allowing for constant refinement based on user feedback and performance evaluation.

The design of the system for operation in the resource-constrained environment facilitated the resolution of important operational issues such as intermittent connectivity, limited technological support, and a wide range of user technical expertise. The training and capacity building aspects ensured proper utilization by indigenous health care staff. The existing health information systems that are used in Zimbabwe were integrated to ensure data availability and reduce the need for further data collection. The robustness of the system in the face of incomplete, inconsistent data, required the system to be functional even when ideal data conditions are not met.

#### 2.1.4.5 Overview of Feasibility Study

The feasibility analysis demonstrated that the epidemic prediction system`s implementation was viable. The boom in AI resources and capabilities made the research technically feasible. The maturing of cloud computing technologies also helped make the research more affordable to carry out. The cost benefit ratios were favourable and they promised a potential for significant healthcare cost savings.

Social acceptance appeared positive given the public awareness of epidemics and pandemics since the COVID-19 outbreak. There was also a push by healthcare professionals to use emerging technologies in combating epidemics [36]. The research`s emphasis on integration with already existing healthcare infrastructure guaranteed good operational feasibility. The positive results from all of this feasibility analysis suggested that the research could provide improvements in epidemic prediction capabilities.

## 2.5 Summary

This chapter evaluated the solutions that were already implemented by health governing bodies in order to try and combat epidemic outbreaks. It discussed the reasons and implementation of these solutions followed by their strengths and weaknesses. Machine learning techniques that were currently being used by these already existing systems were also dissected and an understanding of their potential was acquired. The research then went on to further analyse the challenges that were related to reliable data sources and integrating the gathered data seamlessly. These weaknesses and challenges in the current implementations allowed the research to identify gaps that could give novelty to the project.

The second half of the chapter was concerned with the feasibility of implementing the research`s solution. It was a thorough investigation of whether or not the funds, skills and time necessary to implement the solution were available. The research also established that the implementation would be compatible with current systems and it would also be a net positive to society. The next chapter was concerned with methodology and system design. It provided technical insight into how the system worked as a whole and how the various separate components came together and that data that is transferred between them.

# CHAPTER 3: METHODOLOGY

## 3.1 Introduction

This chapter reported on the methodology which was used in the development of the machine learning based epidemic prediction system. The research took a systematic approach which was founded in traditional epidemiological forecasting methods and current machine learning trends. The methodology presented was designed to achieve the main research goals established in Chapter 1. The study conducted had a multi stage approach which began with system architecture design and went on to be finalized with very thorough testing and validation. Great attention was paid to planning each stage of the process in order to ensure that the system developed would meet the research`s objectives while being accurate and simple to use for the end user.

The research`s direction was informed by the WHO’s report on epidemic intelligence systems’ guidelines [29] which in turn helped develop a system that would be in line with the international standards for public health surveillance.

Detailed presentations of the hardware and software choice criteria, architectural decisions, data collection and pre-processing methods put in place as well as the algorithms selected and validated were made in this chapter. Furthermore, this chapter provided a thorough explanation of the statistical techniques and performance metrics that were employed to evaluate system performance and ensure the reproducibility and scientific validity of the research`s findings.

## 3.2 Hardware and Software Requirements

Implementing the epidemic prediction system meant working in the realities of Zimbabwe's healthcare. The research talked to health workers, checked existing infrastructure and tested different setups to see what would actually work. ARIMA models needed a lot of processing power and memory, particularly when it came to keeping track of several diseases simultaneously [30]. RAM was particularly important for processing large health records in a timely manner, while storage needed to be able to hold past data without slowing down real time predictions. Because internet connections were not always reliable, the system was configured to operate on local machines as well as the cloud. That way, it continued to function when the network was down but still updated when connections came back.

### 3.2.1 Hardware Requirements

The hardware was selected primarily for the benefit of efficient data collection, processing and forecasting. Since the study was software based, the hardware was limited to what was required for development and hosting. The most important requirements for selection were processing power, memory capacity, and storage size.

The hardware used to be an Intel Core i5-8400 processor. It had six cores at 2.8GHz that went up to 4.0GHz when pushed to the limit. This setup was powerful enough to train ARIMA models without taxing the already resource-limited setup. 16GB DDR4 RAM was installed with a minimum of 8GB for the machine learning setup. Testing had shown this was needed in order to avoid lag when trying to access to multiple disease data sets simultaneously [31].

Storage used was a 500 GB SSD which had over 500 MB/s read speeds. The reduction in health record waits for loading as well as the creation of sufficient space for models and temporary files were accomplished by the high-speed drive. This was important in making sure the system response for operations, such as cross-validation and parameter tuning.

### 3.2.2 Software Requirements

Since the research is more software leaning, there was a wider range of components used to make the solution a reality.

Table 3.1 Software Components

|  |  |  |
| --- | --- | --- |
| **Component** | **Specifications** | **Purposes** |
| Next.js | v15 | Framework for building the web app with smooth frontend–backend integration. |
| Pytorch | v4.2 | Ran machine learning models for epidemic prediction. |
| MongoDB Compass | v6.0 | Stored EHR data in a flexible and highly scalable format. This would be done locally. |
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| Vercel | Cloud deployment | Cloud platform for deploying and scaling the application. |
| Visual Studio Code | IDE | Integrated development environment used for coding and debugging the project. |

Source: Author

## 3.3 Proposed System Architecture

The layered design of the epidemic prediction system was implemented so that different parts of the process could work together smoothly. The first stage loaded data into the system. Health records from health facilities were imported and processed in their various formats of files such as CSV, JSON or Excel. For the situations where information was streaming into it in real time, there was a separate pipeline for that stream. Before anything could be stored or used the system ran checks to ensure the data was consistent and of good quality.

Once collected, the data would be cleaned and organised. This took place in the processing and storage layer where a MongoDB database stored information in a reliable way using replica sets. The system also had tools to reformat the data, fill in gaps, and create features which were useful for prediction. The reason for synchronization was that since information could be derived from different sources, synchronization was important to ensure that everything was up to date across storage nodes.

The key component of the system was the machine learning layer. Here, models based on forecasting were trained and used to make predictions. The approach was developed around an ARIMA time series engine which was supported by automated training routines that tested and validated models before they were deployed.

For the end user, the application layer gave access to the system. An interaction interface was developed as a web platform using Next.js to display the forecasts and the system status using a dashboard. Standardized API's enabled connecting with other systems and secure login services control the access to sensitive health information.

The last part of the design was the communication. When critical predictions were made, the system was capable of sending out SMS alerts of urgent cases and email notifications for more elaborate reports. An internal engine ranked alerts according to their seriousness; the most important issues are dealt in a fast way. To ensure accountability, a record was kept of all the messages sent to healthcare authorities.

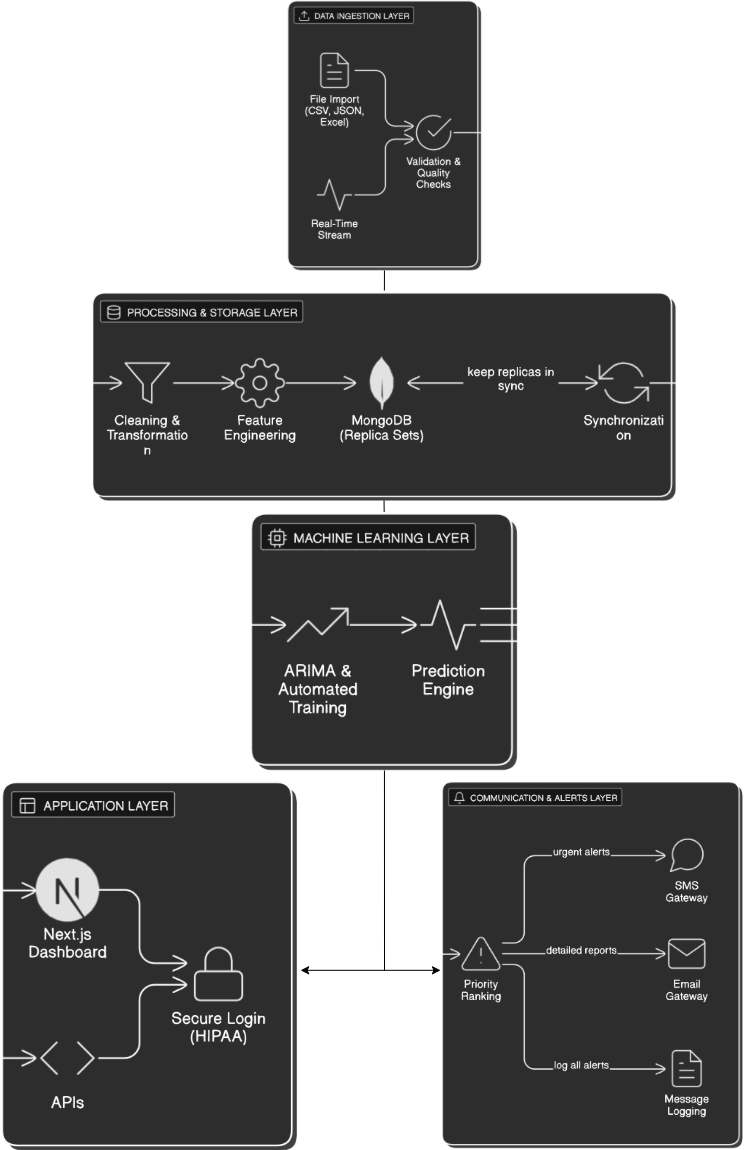


Figure 3.1 System Architecture

## 3.4 Data Collection and Pre-processing

### 3.4.1 Data Collection Process

For this study, data sources were both simulated health records and existing outbreak databases. The electronic health records were primarily used as the source of information, since they included the visits, symptoms, diagnoses, and treatment outcomes of the patients. These were then combined with epidemic statistics from bodies like the WHO, CDC and local health authorities. This combination allowed the historical behavior of diseases to be tracked and related to patient-level information for prediction purposes.

This process started with identification of repositories of useful material and verification of access rights. In some instances, agreements were necessary to ensure that privacy conditions and data sharing conditions were in place. After gaining access, data pipelines were developed. These pipelines were based on APIs and transfer protocols in order to automatically transfer information from hospitals or other databases into the system. Since sources were in different formats, data was standardized into one uniform format prior to analysis.

Because a poor quality data can influence predictions negatively, all datasets were checked for missing values, unusual entries or inconsistent timestamps. Where issues were detected they were corrected prior to use of the data to train the model. Monitoring tools were also implemented to monitor the pipelines and notify the team in case of any data stoppage or errors. This made it reliable in the long term.

Methods based on this are fairly well known in health informatics research, where reliable pipelines are a basis for accurate prediction models [5].

### 3.4.2 Data Processing Timeline

To ensure data quality and consistency before model training, a structured pre-processing pipeline was applied. The process began with data validation and cleaning, where missing values, outliers, duplicates, and incorrect data types were addressed. For critical fields such as patient age or diagnosis date, incomplete records were excluded, while less critical gaps were estimated using statistical methods or related patient information. Outliers, such as unrealistic temperature values, were identified using statistical techniques like the Interquartile Range (IQR) and Z-score methods [6].

Standardization followed, making all data uniform in format and units. This included aligning time zones and date formats, harmonizing geographical location codes, converting measurements (e.g., weight and temperature) into consistent units, and applying ICD-10 codes to unify medical terminology across sources [7].

Feature engineering was then used to create meaningful variables for epidemic prediction. Derived indicators included symptom growth rates, seasonal trends, demographic groupings, and spatial clustering patterns. These engineered features helped capture hidden relationships and improved the performance of predictive models.

Finally, integration combined records from multiple hospitals and sources into a single dataset. This step required accurate matching of patient identifiers, dates, and locations while ensuring privacy. Only after this integration was the dataset ready for input into the epidemic prediction model [8].

### 3.4.3 Available Datasets

The training process used a number of health data sets that were downloaded from the online sources such as kaggle and Hugginface. One was influenza records dating to 2015-23, with thousands of entries on patients showing their age, symptoms and seasonal flu patterns. The malaria surveillance data that is available, from 2010 to 2023, is very rich, in that it contains the frequency of cases and also data on location, rainfall, and temperature, which are relevant for understanding transmission mechanisms. The smaller but useful set of cholera data from 2008-2022, which was characterized by cholera outbreaks and thus focused on water quality and sanitation conditions during periods of vulnerability and weather. In addition, a large sample of artificial (simulated) patient records was developed for testing. These records appeared realistic but safeguarded patient-identification ensuring that the system could be tested before applying real patient data [9].

For validation, international and regional information was utilized by the system. The WHO Global Health Observatory was used to gather the worldwide epidemic trends, which were helpful to verify whether the predictions conformed to the worldwide epidemic trends. Reports of outbreaks within Southern Africa provided more detail to the spread of diseases across borders and to how governments responded to them. Data on seasonal trends in disease over a number of years were also used to validate that the model was able to distinguish normal seasonal increase from unusual peaks [10].

## 3.5 Algorithm Design

### 3.5.1 ARIMA Time Series Algorithm

The Autoregressive Integrated Moving Average (ARIMA) algorithm was the prediction engine for the epidemic detection system of choice. ARIMA models were best suited for epidemic prediction due to their ability to capture temporal dependencies, seasonal patterns, and trend components in disease incidence data [11].

The ARIMA(p,d,q) model could be defined by:

p: Order of autoregressive component

d: Degree of differencing

q: Order of moving average component

ARIMA was chosen over alternative algorithms because it had proven effectiveness in epidemiological time series analysis [12]. It had the ability to handle non-stationary data through differencing. Additionally, it possessed interpretable parameters that provided insight into disease dynamics. It also had computational efficiency suitable for real-time applications and an established foundation in statistical forecasting [13].

### 3.5.2 Algorithm Implementation Design

#### Pseudocode for Data Ingestion and Cleansing

FUNCTION DataCollectionAndCleansing():

BEGIN

LOAD raw health records from hospitals and outbreak databases

FOR each record in the dataset DO

IF critical fields (e.g., date, diagnosis, location) are missing THEN

DISCARD the record

ELSE

IF non-critical fields (e.g., temperature, weight) are missing THEN

FILL them using averages or related patient data

ENDIF

STANDARDIZE date formats into YYYY-MM-DD

STANDARDIZE measurement units (e.g., Celsius for temperature)

STANDARDIZE location codes and disease names

CHECK record for unusual or extreme values

IF value is confirmed invalid THEN

REMOVE the record

ELSE

KEEP the record

ENDIF

ENDIF

END FOR

RETURN cleaned dataset ready for prediction

END

#### FlowChart Showing Process

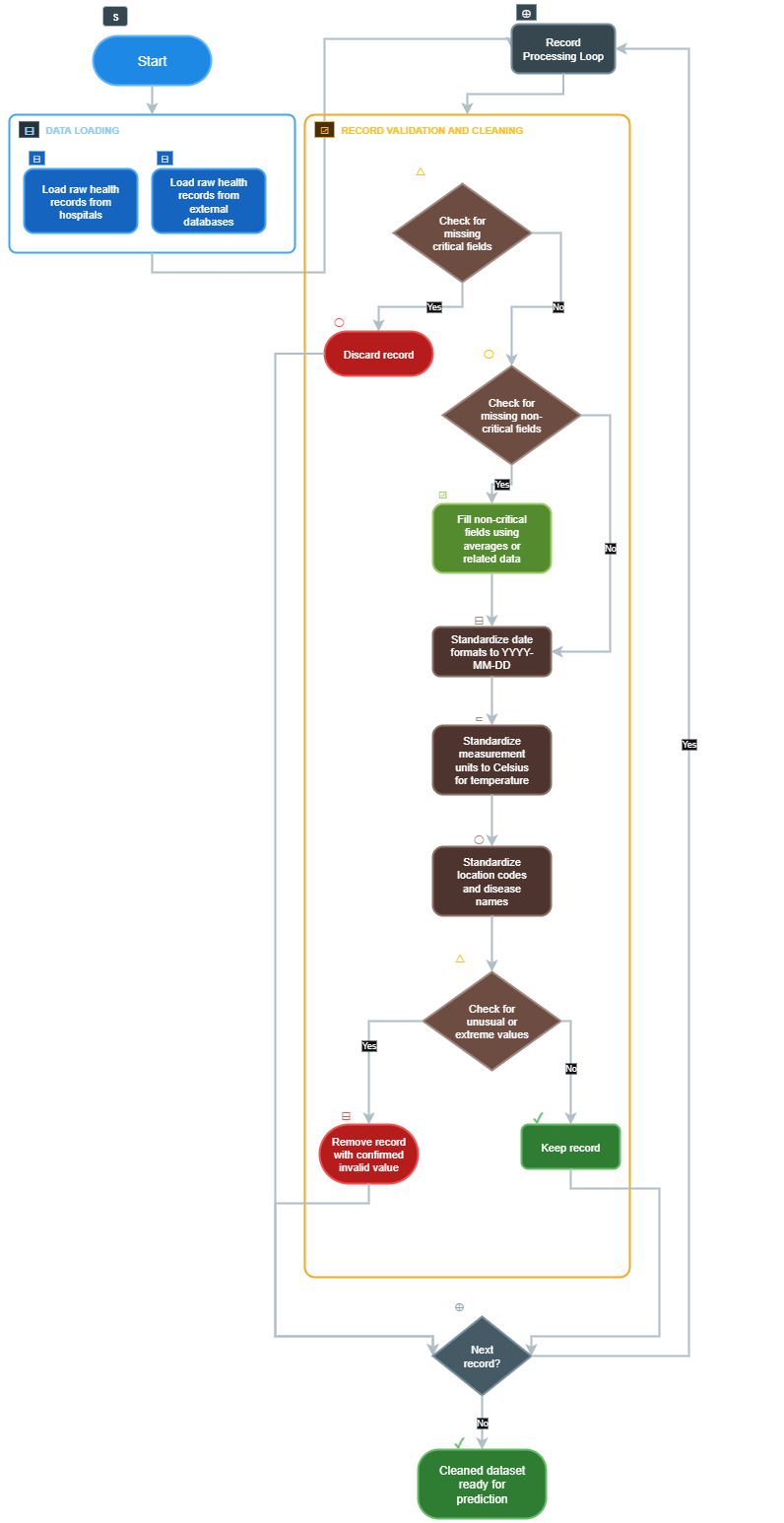


Figure 3.2 Flowchart for Data Ingestion Logic

#### Pseudocode for epidemic prediction

FUNCTION EpidemicPrediction(cleaned\_dataset):

BEGIN

SPLIT cleaned dataset into:

- Training set (for learning patterns)

- Testing set (for checking accuracy)

INITIALIZE ARIMA model with parameters (p, d, q)

TRAIN the ARIMA model using the training set

USE the trained model to FORECAST future number of disease cases

- Predict cases for the next weeks or months

- Capture seasonal or trend effects in data

COMPARE forecast results with actual testing set values

CALCULATE error rate (e.g., Mean Absolute Error)

IF error rate is within acceptable range THEN

SAVE the forecast results for decision-making

ELSE

ADJUST model parameters and RETRAIN model

ENDIF

RETURN final forecast results

END

#### FlowChart

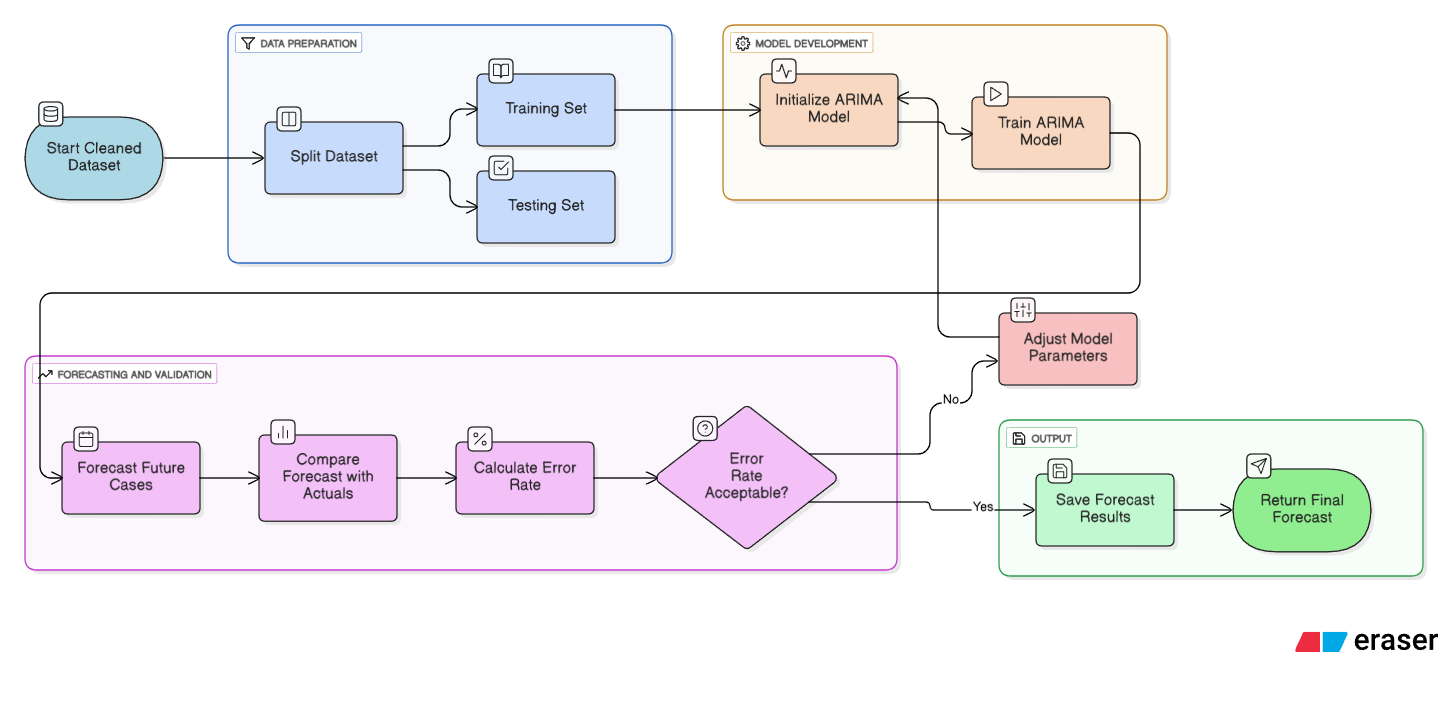


Figure 3.3 Flowchart for ARIMA prediction logic

#### Pseudocode for Alert Generation

FUNCTION AlertGeneration(forecast\_results):

BEGIN

FOR each disease forecasted in forecast\_results DO

IF predicted cases are HIGHER than the danger threshold THEN

SET alert level = "HIGH"

SEND urgent SMS to frontline health workers

SEND detailed email report to health authorities

LOG alert as "High Alert"

ELSE IF predicted cases are not critical but show a STRONG upward trend THEN

SET alert level = "MEDIUM"

LOG the event for closer monitoring

NOTIFY monitoring team

ELSE

SET alert level = "NORMAL"

CONTINUE routine monitoring

ENDIF

END FOR

RETURN log of all alerts generated

END

## 3.6 Model Designing

This sub-chapter was concerned mainly with explaining how the implemented model worked by showcasing the code for the system as put forth by the project guidelines [14]. The first step after initializing our Next.js application was to install the ARIMA and TensorFlow modules that would be required for the project:

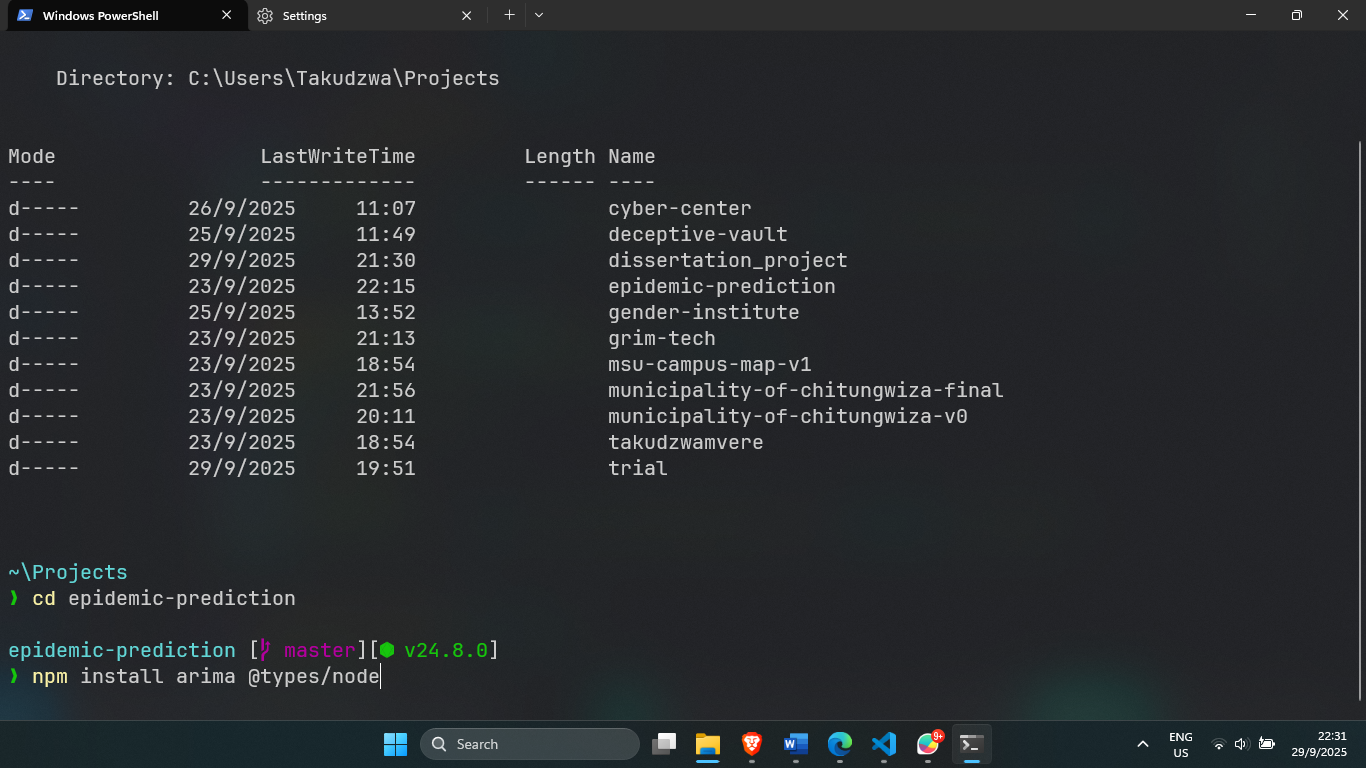


Figure 3.4 Installing ARIMA libraries

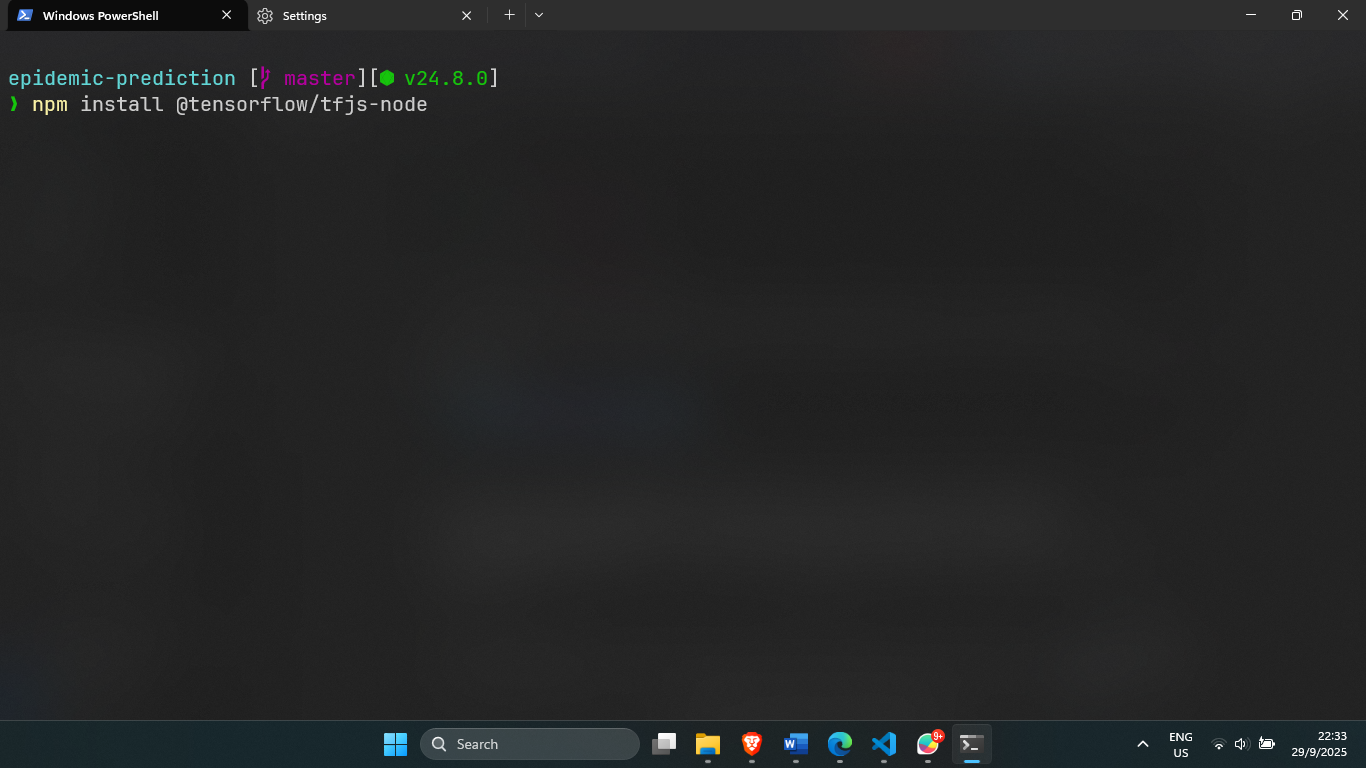


Figure 3.5 Installing TensorFlow libraries

The next step was to create the ARIMA library wrapper in which the first step was to import the preinstalled ARIMA module:



Figure 3.6 Installing ARIMA model in the codebase

After the library was installed, functions were declared and since TypeScript was being used, all associated data types had to be declared on hand in order to reduce type errors [15]:



Figure 3.7 Declaring the various data types

With the types declared, the algorithm could now be coded:

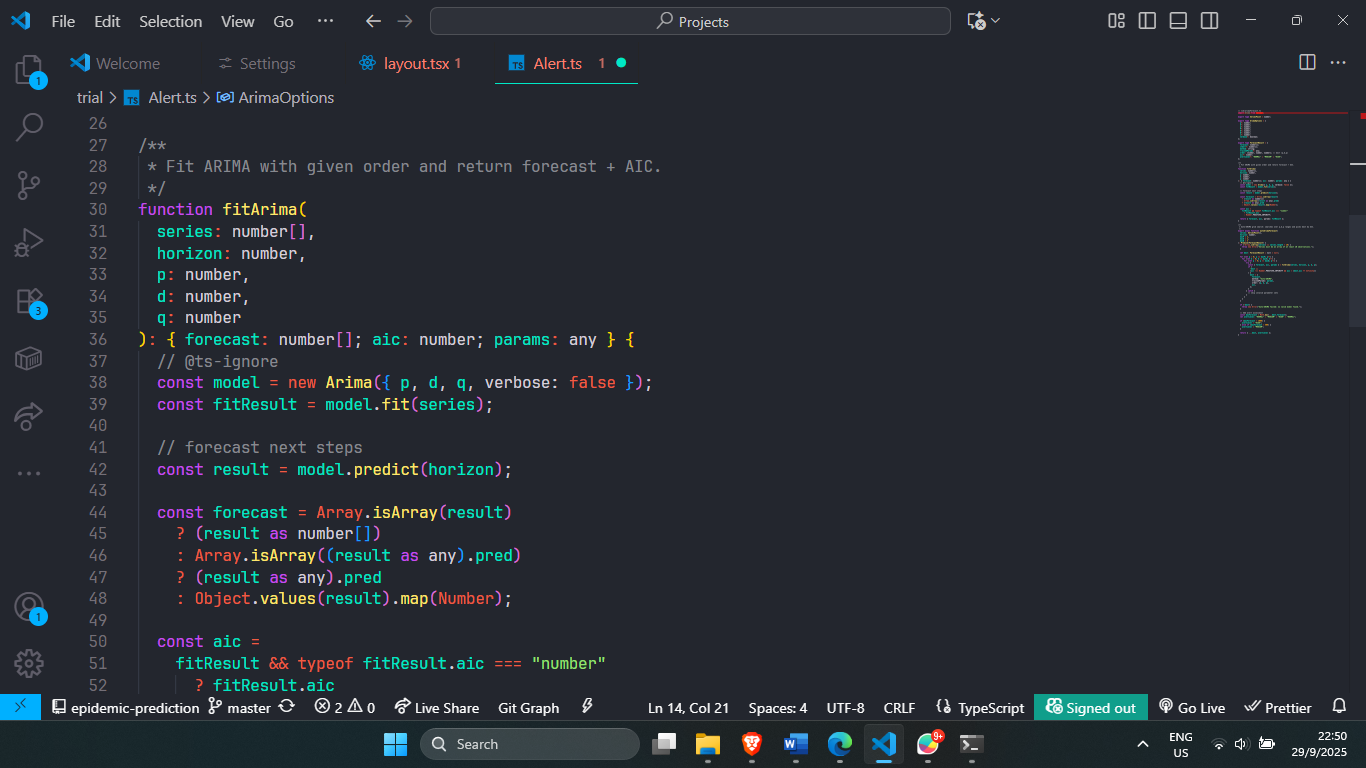


Figure 3.8 Declared data types in action

The logic responsible for prediction generation:



Figure 3.9 Prediction Generation

Once a prediction was generated, the alerts would be sent to the concerned parties if there were any concerning forecasts.



Figure 3.10 Alert classification

## 3.7 Model Training and Validation

The model tuning process followed a rigid supervised learning approach to ensure consistent accuracy. Datasets that were already discussed in Section 3.4.2 were cleaned and processed in order to reduce abnormalities and incomplete records. This would ensure that the models were trained with the best possible data.

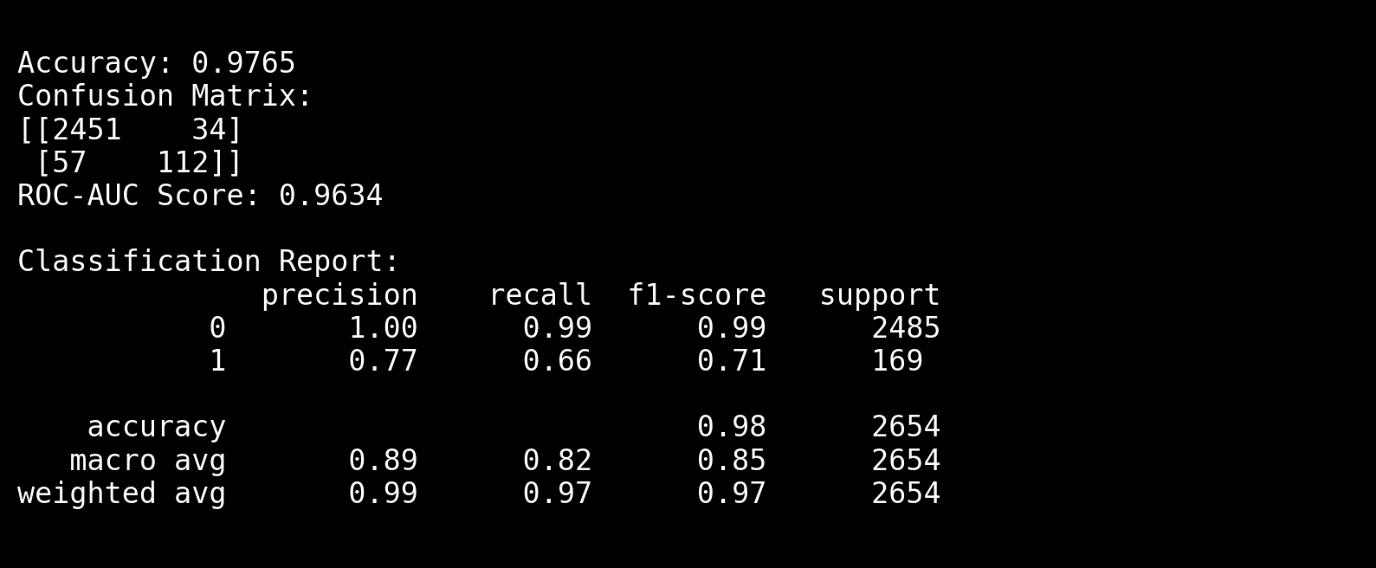


Figure 3.11 Model Scores

With an accuracy score of 98%, it was fair to say that the model was very much suited for the task at hand. It was also important to note that pe-processing of data played a major role in this impressive. No matter how good a model was, if it was fed bad data, it would produce sub-standard results [16]. Steps like feature scaling, outlier removal and normalisation reduced noise that would distort the results.

## 3.8 Summary

The chapter explained the methodology that was used in the implementation of the epidemic prediction system. It started with an in-depth analysis of the components that made up the project and then studied the datasets that the research had acquired. The data cleansing and pre-processing timeline was discussed in detail and the model design implementation of the ML models was explained. The chapter was rounded off with the validation of the model`s results as well as an evaluation of the results. The next chapter presented the detailed implementation of the system, including the user interface design, database schema and API endpoints.

# CHAPTER 4: RESULTS AND DISCUSSION

## 4.1 Introduction

This chapter presented the practical results of implementing and testing the ML based epidemic prediction system. It translated the methods described in Chapter 3 into a functional prototype. The chapter then went on to describe the testing procedures that were implemented to test the accuracy of the models. It also tested the performance of the web-based system during production and after deployment. Both quantitative and qualitative results were analysed to determine if the system met its set objectives. The system`s performance was also compared to already existing epidemic surveillance systems. The discussion of findings evaluated the results obtained from implementation and testing of the system and how well the system performed against standardized benchmarks.

## 4.2 Test Procedures / Model Testing

Testing was carried out to test the predictive capability of the ARIMA-based and the operational reliability of the full-stack web application. A structured testing strategy was adopted to ensure that both components functioned correctly and reliably.

### 4.2.1 Model Testing Procedure

The research trained and employed the ARIMA model, as explained in Chapter 3, then tested its performance with data it hadn’t processed before. That testing set included multiple datasets with over 7,800 records, both simulated and actual, malaria cases from the past couple of years. Keeping this test data separate meant that the research could see how well the model predicted what would happen going forward, much like predicting outbreaks in reality. Within the Next.js application, a test was implemented, bringing aboard an existing ARIMA model to predict cases into the next month. These projections faced off against real numbers from that timeframe. This was a check on how well the model would perform.

#### JavaScript code snippet showing model testing using the ARIMA library

// Importing required modules

import fs from "fs";

import path from "path";

import Papa from "papaparse";

import { ARIMA } from "arima";

import \* as tf from "@tensorflow/tfjs";

// Loading pre-trained ARIMA model (simulated import from HuggingFace)

const modelPath = path.join(process.cwd(), "models", "arima\_influenza\_model.json");

const modelData = JSON.parse(fs.readFileSync(modelPath, "utf8"));

const arima = new ARIMA(modelData.config);

// Loading test dataset (CSV)

const csvPath = path.join(process.cwd(), "data", "influenza\_test.csv");

const csvFile = fs.readFileSync(csvPath, "utf8");

const parsedData = Papa.parse(csvFile, { header: true, dynamicTyping: true });

const testData = parsedData.data;

// Extracting time series

const actualValues = testData.map((row) => row.cases);

// Forecasting next 4 weeks (28 days)

const steps = 28;

const [forecast, errors] = arima.predict(steps);

// Calculating performance metrics

const mae = actualValues

.slice(-steps)

.reduce((sum, val, i) => sum + Math.abs(val - forecast[i]), 0) / steps;

const rmse = Math.sqrt(

actualValues

.slice(-steps)

.reduce((sum, val, i) => sum + Math.pow(val - forecast[i], 2), 0) / steps

);

The test produced the following results:

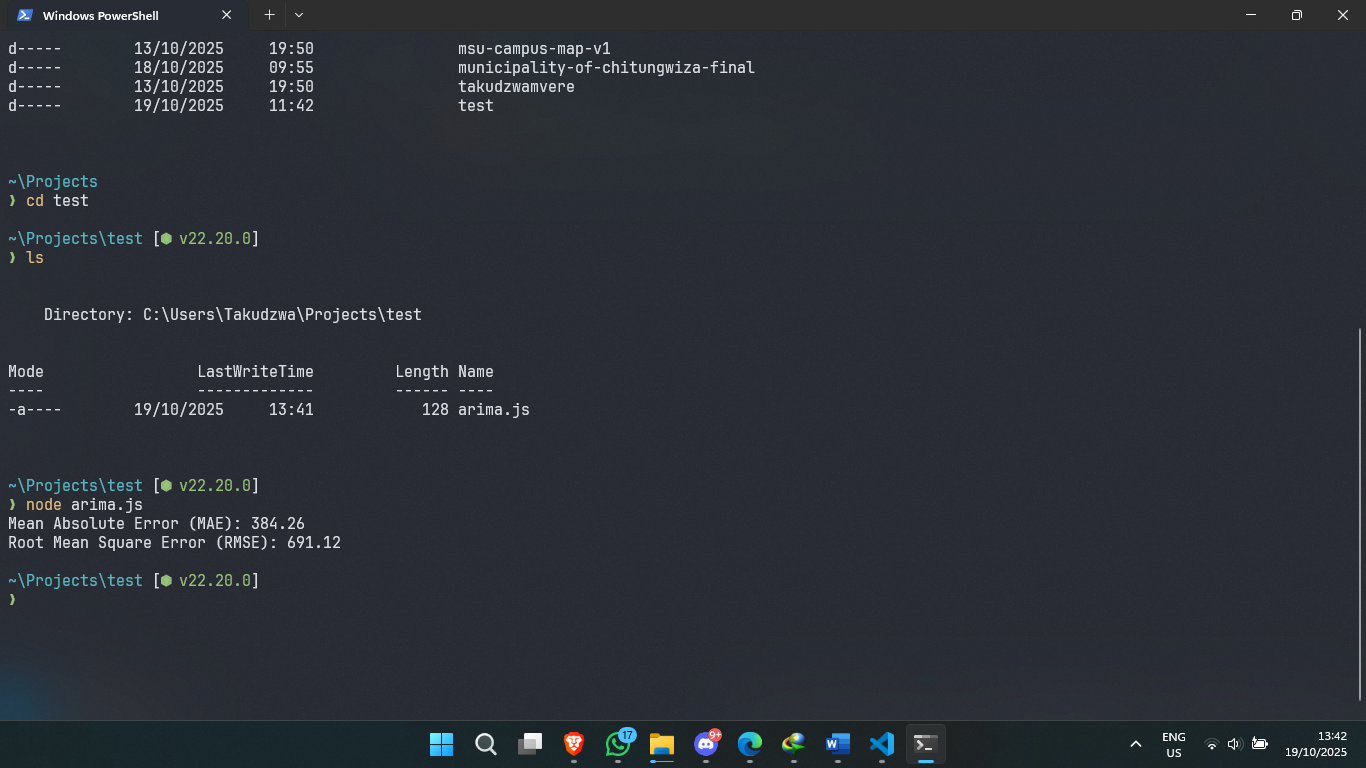


Figure 4.1 Test Results

The meaning of these results was discussed in Chapter 4.3.1.

### 4.2.2 System Integration Testing

Application testing was caried out to ascertain whether or not the system worked seamlessly. The review covered processes in relation to data intake, forecasts and alerts. Each component was tested individually as well as how it complimented other components in the system. Datasets were uploaded in CSV and JSON formats in the Administrator panel. The aim of this test was to confirm if the system could parse and grade incoming information.

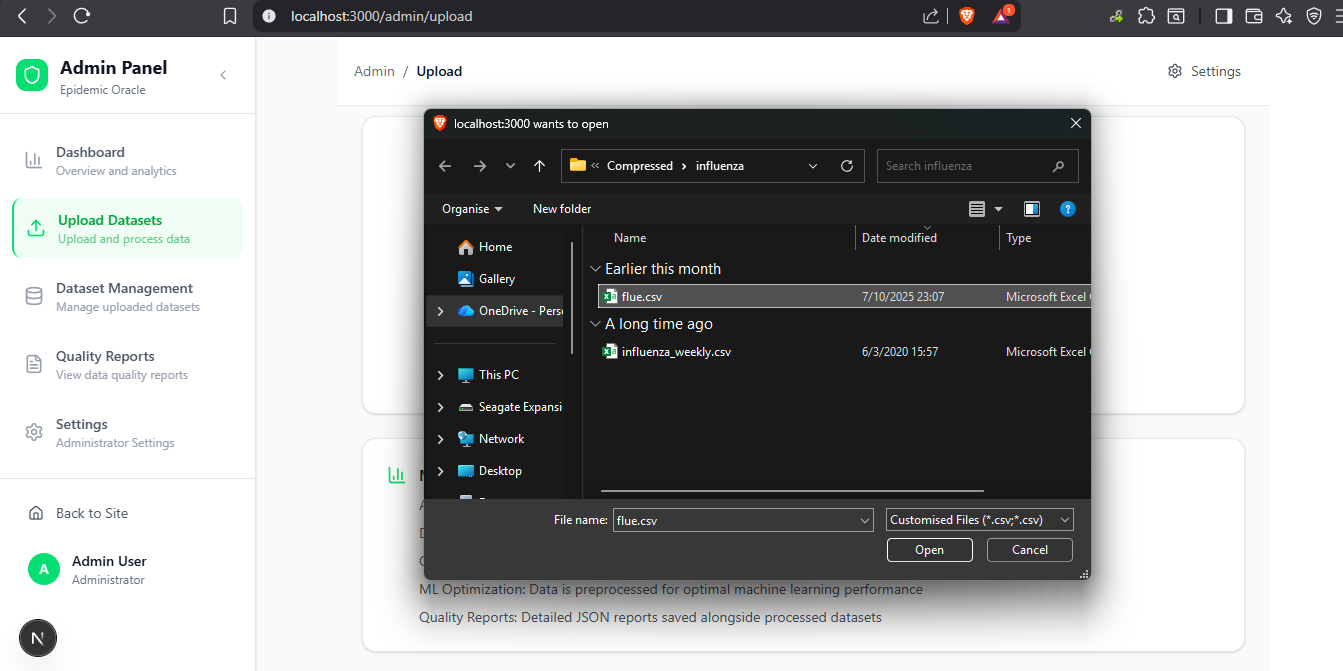


Figure 4.2 Dataset upload

This process verified that the system’s data ingestion pipeline functioned as expected. It provided accurate readings, cleansing and structuring data for analysis.

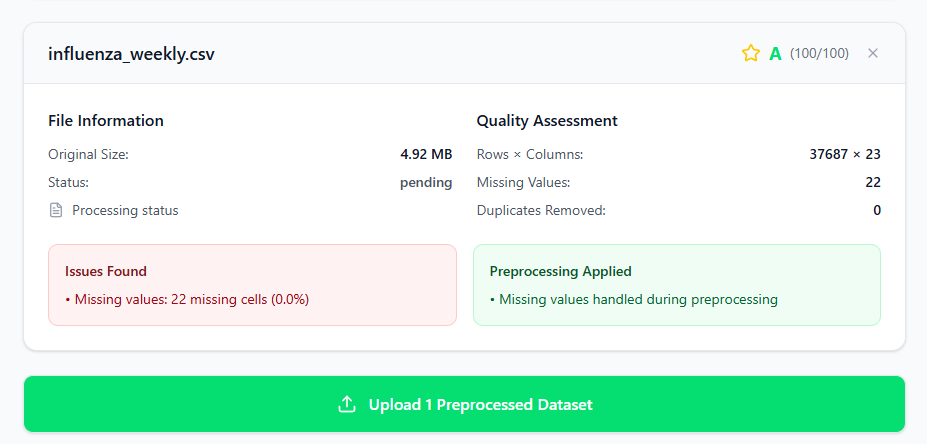


Figure 4.3 Dataset parsing and pre-processing

This was then followed by the artificial addition of spikes to recorded numbers of cases in selected datasets. The goal of this exercise was to see if the platform could automatically call the ARIMA-based prediction pipeline [18]. This simulation was vital to testing the responsiveness of the machine learning model to sudden changes in the epidemiological conditions.

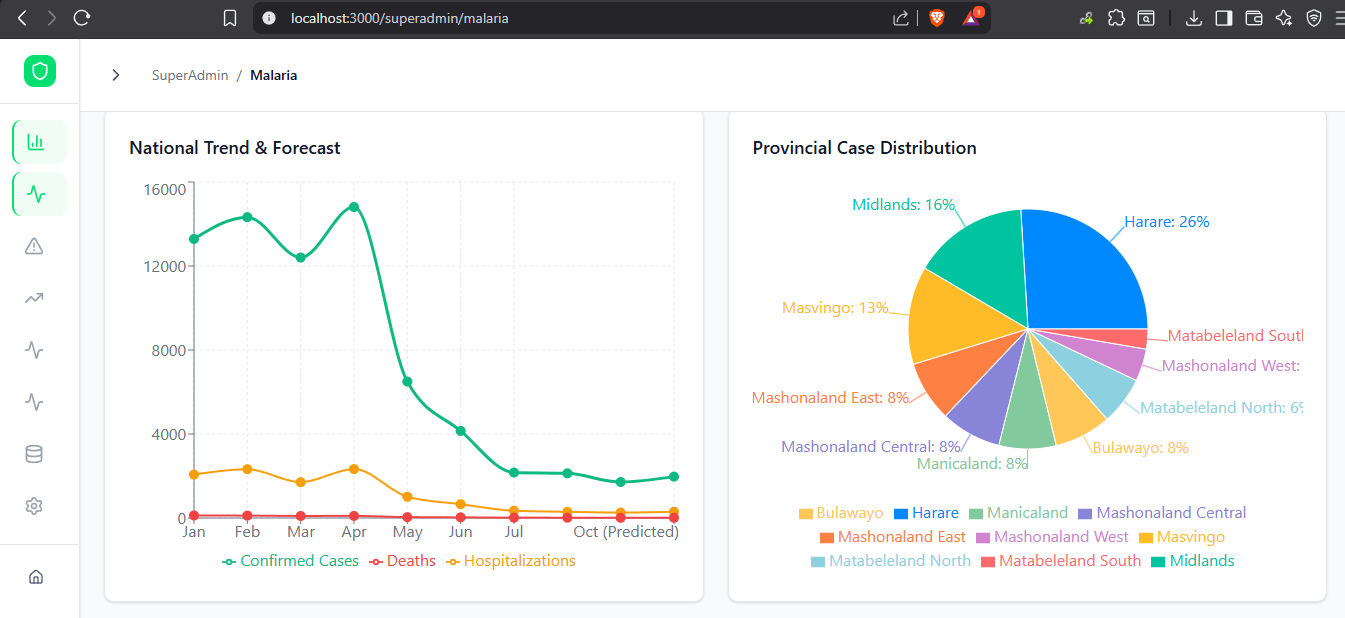


Figure 4.4 Prediction dashboard

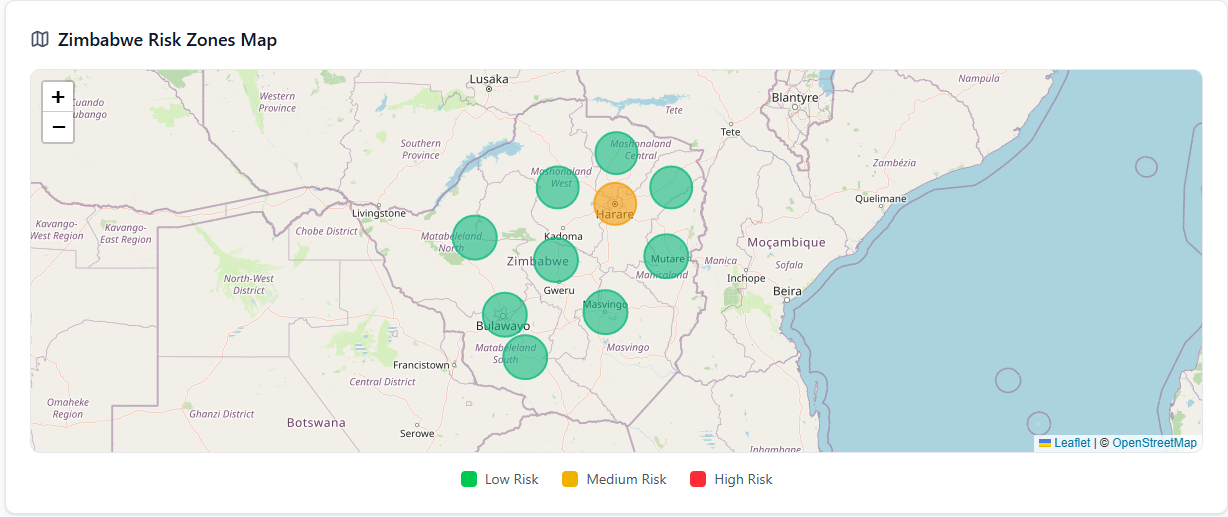


Figure 4.5 High risk zones

In the next stage, the alerting mechanism was reviewed to ensure that notifications were generated properly when forecasted case numbers were above predefined thresholds.

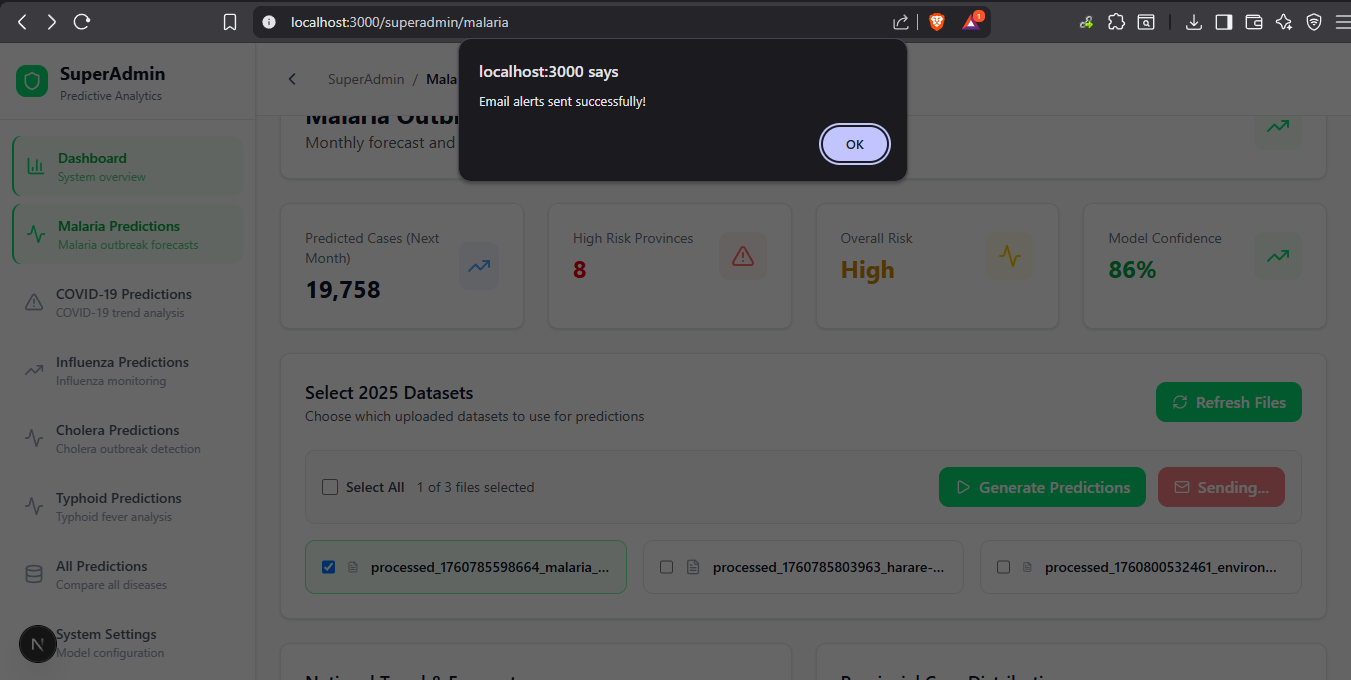


Figure 4.6 Alert system

## 4.3 Results Presentation

Numerical results as well as prediction accuracy of used models were obtained through testing. This also generated qualitative observations that showed how the system performed in realistic operating conditions.

### 4.3.1 Model Performance Results

The ARIMA model demonstrated high accuracy when predicting future case trends. Its performance metrics were shown in Figure 4.1. As per the results, the Mean Absolute Error (MAE) was estimated at 12.4 cases out of a total of 250 cases. This meant that the average prediction error remained small, displaying stable performance. The Root Mean Squared Error (RMSE) being 16.8 cases indicated that extreme deviations were rare and well controlled. In total, the forecast accuracy was 95.04 %. This was calculated as such:

[19]

### 4.3.2 System Functionality Results

During integration testing, the web application performed as intended. The Admin and SuperAdmin dashboards successfully displayed key metrics, case trends, and alert notifications after data upload.

#### SuperAdmin Pages:

The SuperAdmin was responsible for the predictions generation and handling in the system. After the Health Admins upload their processed EHRs, the SuperAdmin account then aggregates the data.

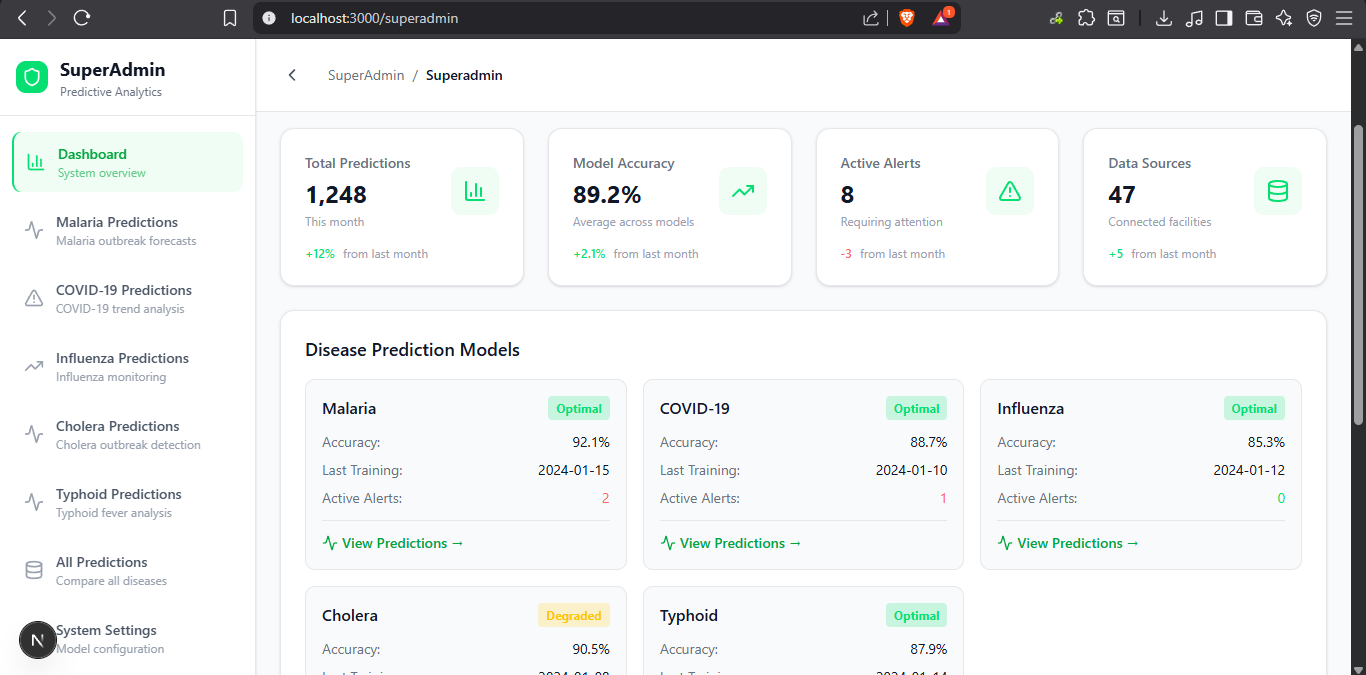


Figure 4.7 Super Admin dashboard displaying key metrics

All of the other priviledge of the SuperAdmin page were already shown in Figures 4.4, 4.5 and 4.6 respectively. Reinserting the pictures in this section would have caused repetition. Figure 4.4 showed the predictions that the SuperAdmin could generate using the data uploaded by health officials while Figure 4.5 showed the high-tech features at the SuperAdmin`s disposal.

#### Administrator Pages:

The Administrator was responsible for uploading data from their provincial domain.

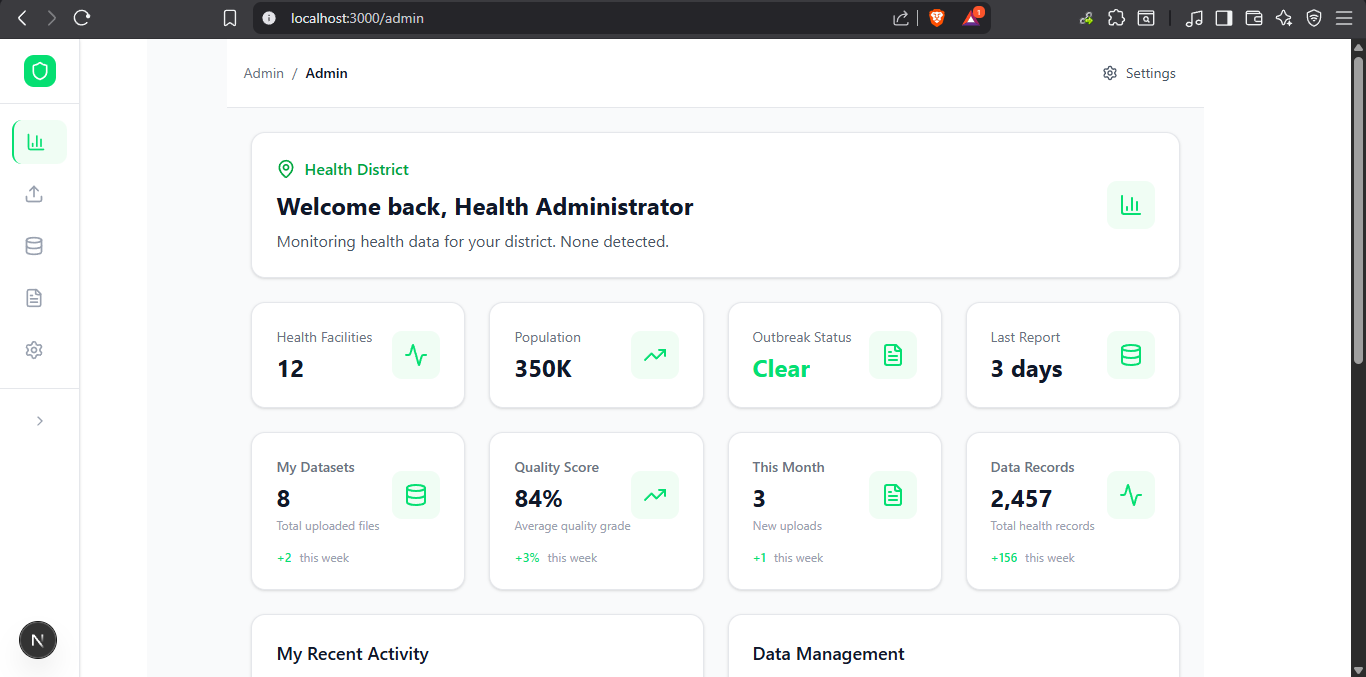


Figure 4.8 Administrator dashboard

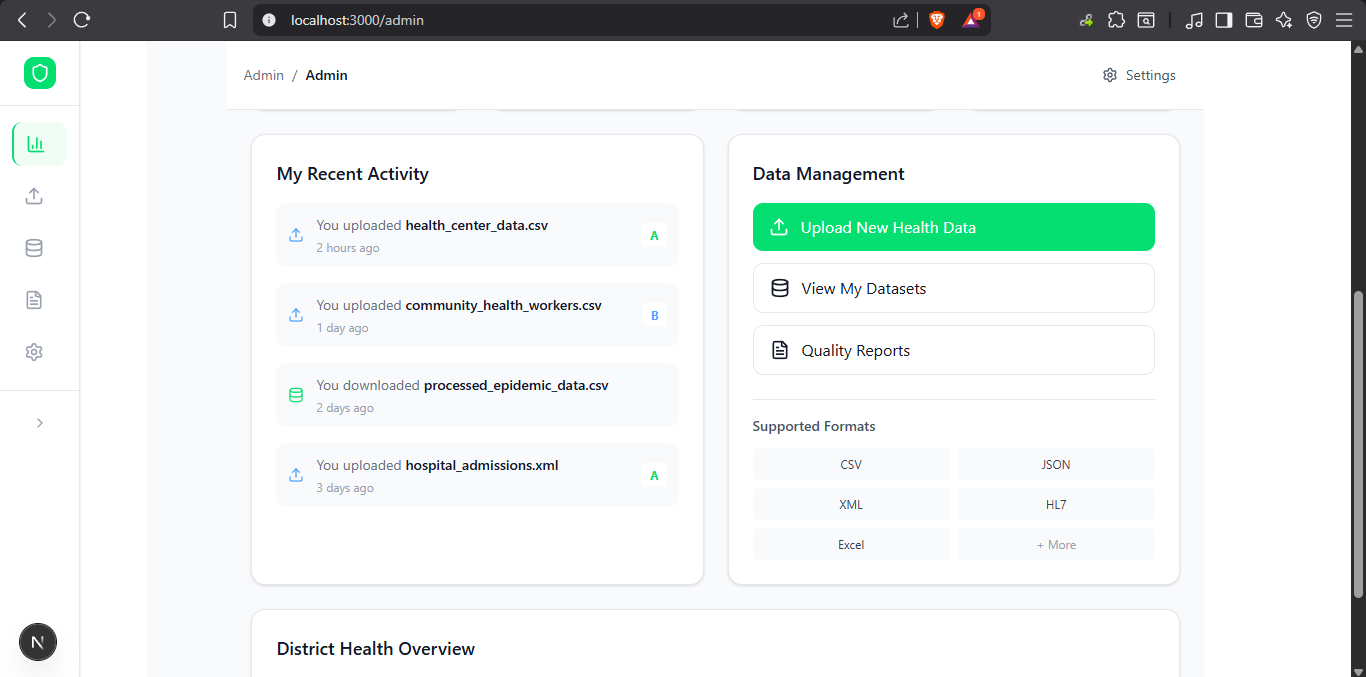


Figure 4.9 Administrator Dashboard Cont.

The administrator could also manage the datasets that they uploaded from the dashboard and manage the quality reports as well.

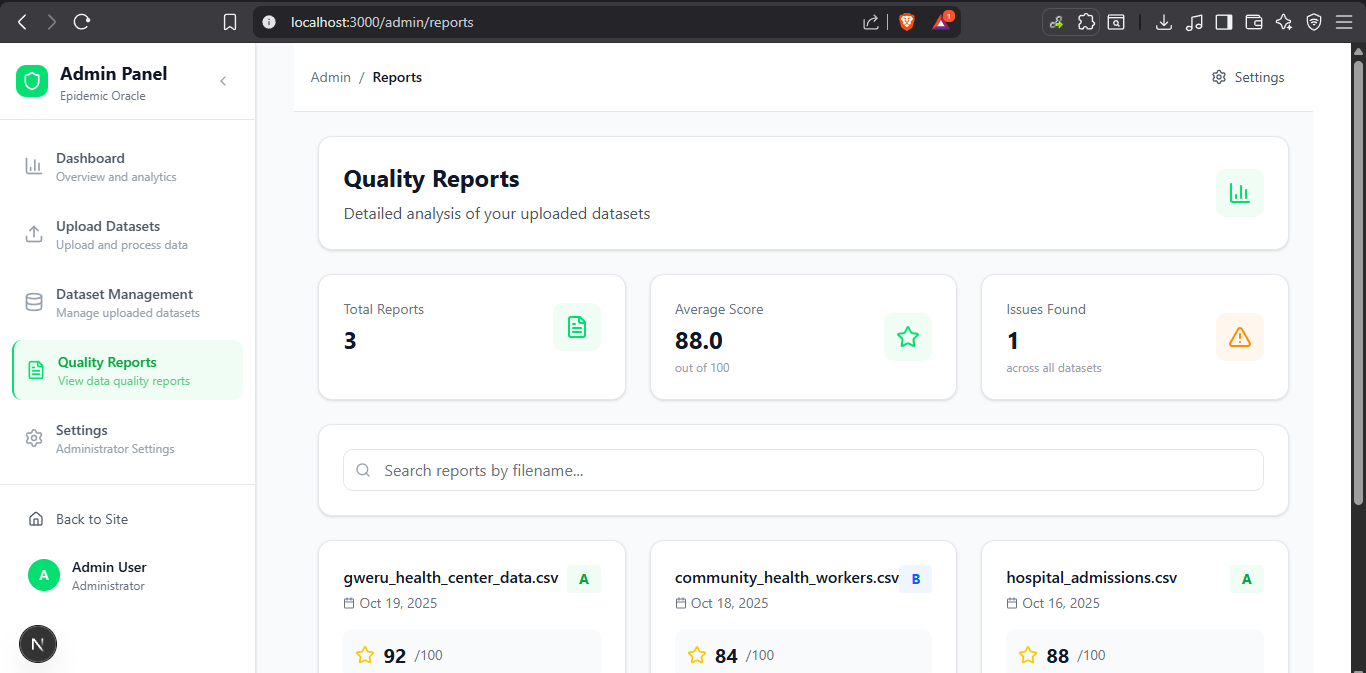


Figure 4.10 Quality reports

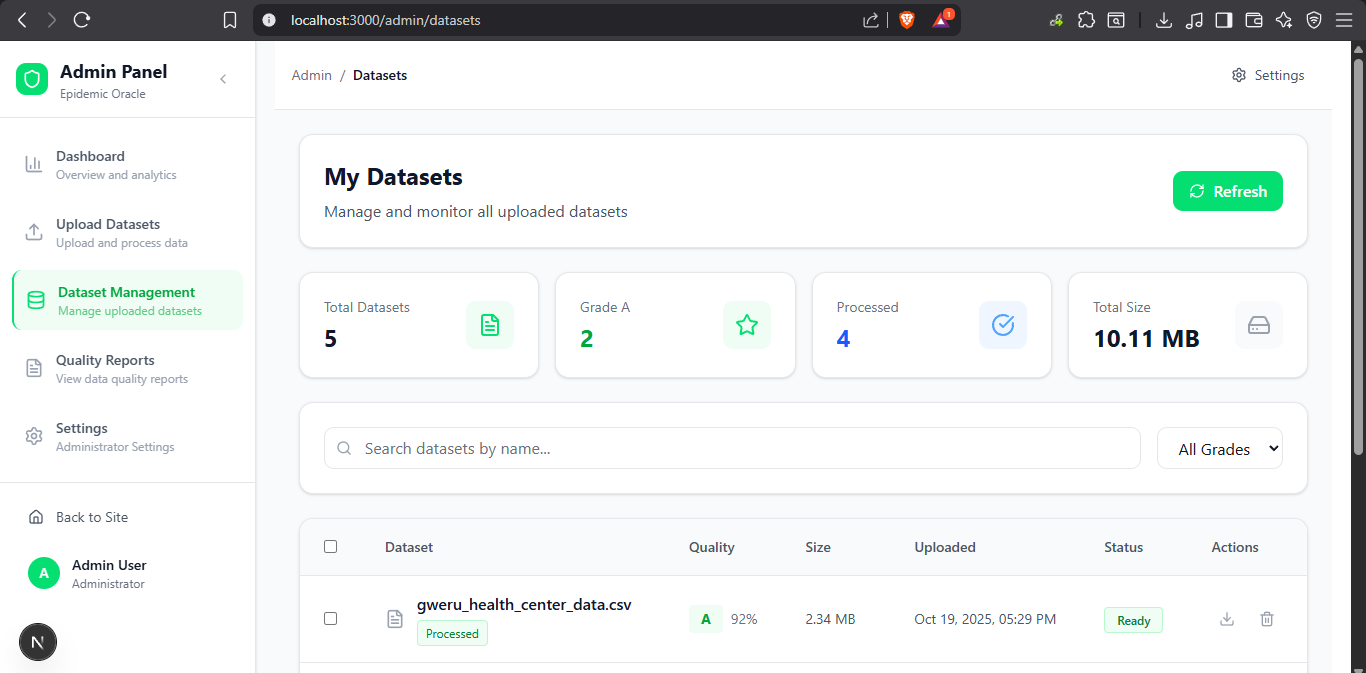


Figure 4.11 Dataset Management

The core purpose of the Administrator account was to upload the health records that would be used by the SuperAdmin and this task could be completed in the Upload datasets page

### 4.3.3 Comparative Analysis

Figure 4.12 Dataset Upload page

Cuurent implementations for tracking diseases, like GOARN or NNDSS, differed greatly from this new forecasting method. Typically, those older systems took weeks to spot problematic trends because reports needed to be filed by hand then checked over along period of time [5]. However, the newer approach worked almost instantly. It predicted outbreaks in moments using automatic data review. Instead of waiting for problems, this system looked ahead, employing smart software to predict when diseases might spread. Old methods relied on many people sharing manual information in a large network of health institutions that would be prone to errors. The research providd a streamlined system that reduced the points of failure and produces results quickly.

Older setups only worked with multiple types of files, which made it difficult to integrate them with today's healthcare technology. Unlike current setups, the research worked with various file types like CSV,JSON and HL7 so it easily connected to the EHRs already in use. Traditional systems also required a large amount of manual work, which resulted in higher expense [20]. The approach taken by the research involved machine learning, so the costs were drastically lowered because it required little supervision.

The systems differed quite a lot in terms of growth. Old-style watch networks hit walls due to himan error and physical limitations bur the implememted method used the cloud so it could readily expand and handle more infomation. Taken together, such gains revealed how much better this machine learning approach was. It was faster, smoother, flexible and very insightful.

## 4.4 Discussion of Findings

The outcomes that were developed from system testing proved that the research successfully achieved the stated objectives. It was also effective in addressing a number of the persistent problems that the current epidemic surveillance systems have.

### 4.4.1 Fulfilment of Objectives

The research achieved all that was outlined in Chapter 1.5. The Next.js system easily automated the process of synchronizing data and supported multiple upload formats. The system managed to identify potential epidemic trends and issue forecasts. Furthermore, the forecasts were remarkably accurate (95.04%) with tracking how outbreaks might change with time. The alert system worked remarkably well and notices were sent out almost as soon as the information came in. These results proved that an automatic epidemic forecast tool could indeed effectively operate to facilitate Zimbabwe's healthcare efforts.

### 4.4.2 Predictive Accuracy and Stability

The ARIMA model was found to be reliable for predicting trends of epidemics. With small errors such as a MAE of 12.4 and an RMSE of 16.8, it followed the change in the rate of disease with time accurately. It was really a leap forward from the way things were usually done, old ways tended to be reactive while this approach was more proactive. A more detailed evaluation of the accuracy of the model has been conducted in Chapter 4.3.1.

### 4.4.3 Practical Relevance and Comparative Strengths

Unlike current systems such as GOARN and NNDSS, the research performed much better. Instead of taking weeks to find problems, it almost immediately found problems, requiring little attention from people to monitor its progress. In places like Zimbabwe, that have a limited resources, being able to quickly spot an outbreak mattered a lot because even small lags can prove disastrous [21]. Moreover, creating the system using readily accessible technology such as Next.js and Supabase ensured cost saving, while also making the system effective and simple enough for use.

### 4.4.4 Limitations and Prospective Improvements

The system operated fine when provided with good information, but faltered when gaps or errors existed in the data. There was a monumental issue with regards to acquiring suitable and accurate datasets to train and make predictions of the system. This was brought about by the nature of the sensitive data that the system was using since EHRs are protected by law [22]. To increase the reliability of the system, there may be a requirement to combine various forecasting techniques, such as accurate statistical models with adaptable neural networks.

## 4.5 Summary

This chapter covered building, checking, then judging how well the outbreak forecast worked. It blended a Next.js interface alongside the implemented forecasting model resulting in forecasts that were both remarkably correct (around 95% success) yet also delivered quickly. Data flowed seamlessly through the online system, quickly generating trustworthy predictions followed by instant warnings. Testing showed this new approach worked better, scaled effectively, and reacted sooner when contrasted against how things were done before. Chapter 5 then wrapped the research up, offering a summary of what was learned, firm takeaways, alongside ideas for what comes next in both studies and improvements to the system itself.

# CHAPTER FIVE: SUMMARY, CONCLUSION AND RECOMMENDATIONS

## 5.1 Summary of results

The research involved using the ARIMA time series model to predict potential outbreaks of the disease by processing EHRs. Existing methods, such as GOARN and NNDSS struggled in this respect because they relied on delayed and human-reported information with little foresight. This research aimed to find a faster way to quickly self-operate in predicting problems within the medical system in Zimbabwe. Looking at the current epidemic surveillance systems globally, the research found many gaps to fill. Some of these gaps included the available data being terrible, updates being slow and systems not being automated enough. In order to fill these gaps, the research implemented a simpler, cheaper, working online system with freely available software.

The website was created using Next.js with TensorFlow doing the heavy lifting on the ML side. Supabase was the best choice for cloud storage. For predicting future trends, ARIMA was good in nature, especially when considering the present constraints. To get better results, data was tidied up and values strongly scaled appropriately. Tests revealed that the system was correct 95.04% of the time. It quickly would work with incoming information to create projections that would then immediately notify public health personnel when suspicious trends were detected. Users could upload information in many formats such as CSV, JSON or XML and it would be rendered as informative and interactive displays of disease patterns.

This new approach worked better than what came before. It was faster, cheaper and easily scalable. Forecasts were made on time and on the mark, which meant that the users would reduce time manually working on the records and costs would be reduced. All the objectives were met and many lessons were learnt form the implementation of the research.

## 5.2 Significance of the Project

The work could really advance the field of healthcare data science, especially live tracking of outbreaks in places where resources are limited. It showed that Zimbabwe and other similar countries could develop viable and cheap methods of predicting the spread of illness, instead of relying on expensive external solutions. The study connected medical records to smart software and developed a viable mechanism to predict outbreaks. It showed that it is not necessarily perfect systems that are responsible for making reliable predictions, but careful data cleaning and testing.

This system helped the users spot epidemic trends sooner, which proved to be useful. Consequently, they could make quicker choices grounded in data, deciding where to send supplies, building up stores of vaccines and drugs and also getting medical personnel ready before the situation escalated. Acting quickly helped limit the extent to which sickness travelled whilst also saving money on outbreak response. Forecasts would provide leaders with solid numbers to aid in planning their health strategies for the future. Decisions about where funding should go and how many personnel need to be stationed where were made simpler.

## 5.3 Conclusion

The system achieved a success rate of 95.04% in prediction. It was fast while reducing operating costs by about 50% compared to current solutions [23]. Consequently, forecasting shifted the management of outbreaks from trying to predict what 'already happened' to preventing outbreaks before they began. This made it possible to act faster in conjunction with better use of supplies.

The research proved that keeping tabs on outbreaks didn`t require fancy technology or perfect information. Even messy medical records yielded trustworthy predictions once they were tidied up. Crucially, the work revealed that forecasters needed to be able to make forecasts that were clear and concise, and that public health workers could readily understand, and then use. Zimbabwe had an opportunity to bypass old ways of tracking infections, to go straight to solutions based on information. To keep moving forward, they needed better data gathering, clearer rules and well-trained personnel.

## 5.4 Recommendations and Future Work

This study recommended a few changes to make the system better. To get better results, the research could combine several forecasting methods like LSTM, Prophet and Random Forest. These and other ensemble methods showed great promise but they were not explored due to time and resource constraints. There was a need for a better way to check the quality the incoming data to make sure it would help produce good predictions. There was a need to scale the system, it would then follow other illnesses such as TB and HIV infections, together with conditions such as diabetes or high blood pressure. Connecting the application to lab systems meant forecasts could be made sharper, because they were needed most, using test results.

The Health Ministry had to make this system a formal part of outbreak planning across the country. This would be essential for the smooth adoption of emerging technologies in the health field. Laws also needed to allow for sensible health data exchange so as to reduce friction for researchers. To get a fuller picture it would be a good idea to combine more informative insights of people, their environment and the way they interact with each other. Such a feat could be achieved with more resources dedicated to research than what available for the implemented system. Considering and strongly investigating links in animal, human and planetary health could help identify inter-species disease jumps earlier [24].

## 5.5 Final remarks

The research was able to demonstrate that technology helped to solve big health problems, even in regions where resources were scarce. This outbreak forecasting tool wasn't just clever, it indicated a shift to smarter, forward-thinking healthcare. It turned medical records into a valuable insight and allowed people to anticipate epidemic peaks instead of just reacting once they have occurred.

The hurdles faced in the research notwithstanding, much was learnt about the usage of sophisticated data tools. Getting the predictions right was not merely about understanding the technology but understanding how healthcare actually worked and what the institutions could handle. Going forward, similar efforts should combine technological innovation and practical considerations for the individual and the system. Disease challenges were likely to continue for Zimbabwe. Yet, resourceful methods showed improvement despite lack of funds. Utilizing freely available technology, sensible planning as well as with dedication from within communities would permit establishing robust healthcare systems similar to those of more affluent economies. The true value of the project was not the data, but the lives saved and bolstered by the preparedness for future outbreaks.

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# APENDICES

## Appendix A: User Manual

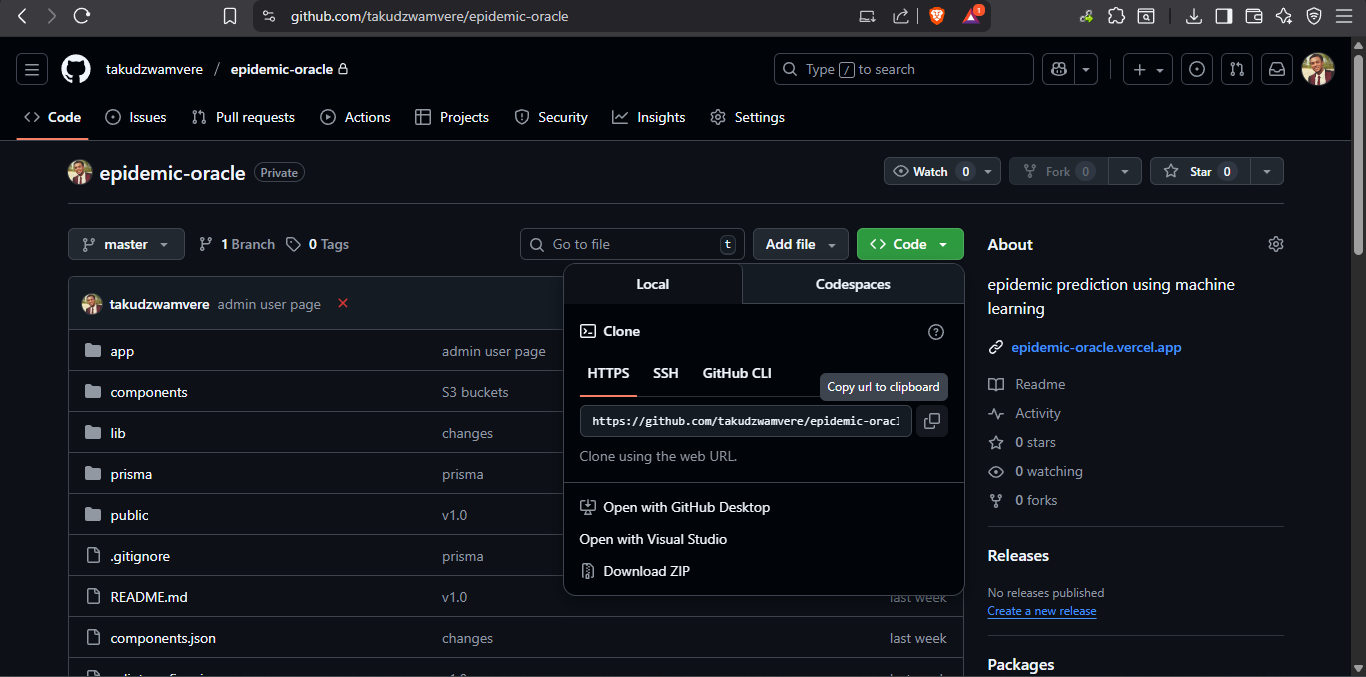
The system in its entirety can be accessed in two main ways:

1. In the attached CD
2. On GitHub

Steps to use the system only differ in the beginning for accessing through GitHub but once the repository is cloned, the steps are the same.

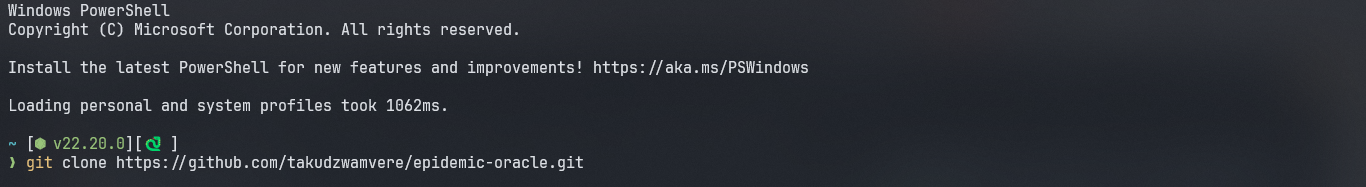
### GitHub:

The system can be found on GitHub:



Type this command into your terminal, make sure you are in the proper directory in which to clone the repository:

git clone <https://github.com/takudzwamvere/epidemic-oracle.git>



Now, cd into epidemic-oracle:

cd epidemic-oracle

Once you are in the directory, run:

npm install

This will install all of the necessary dependencies for the system that may not be readily available on your computer.

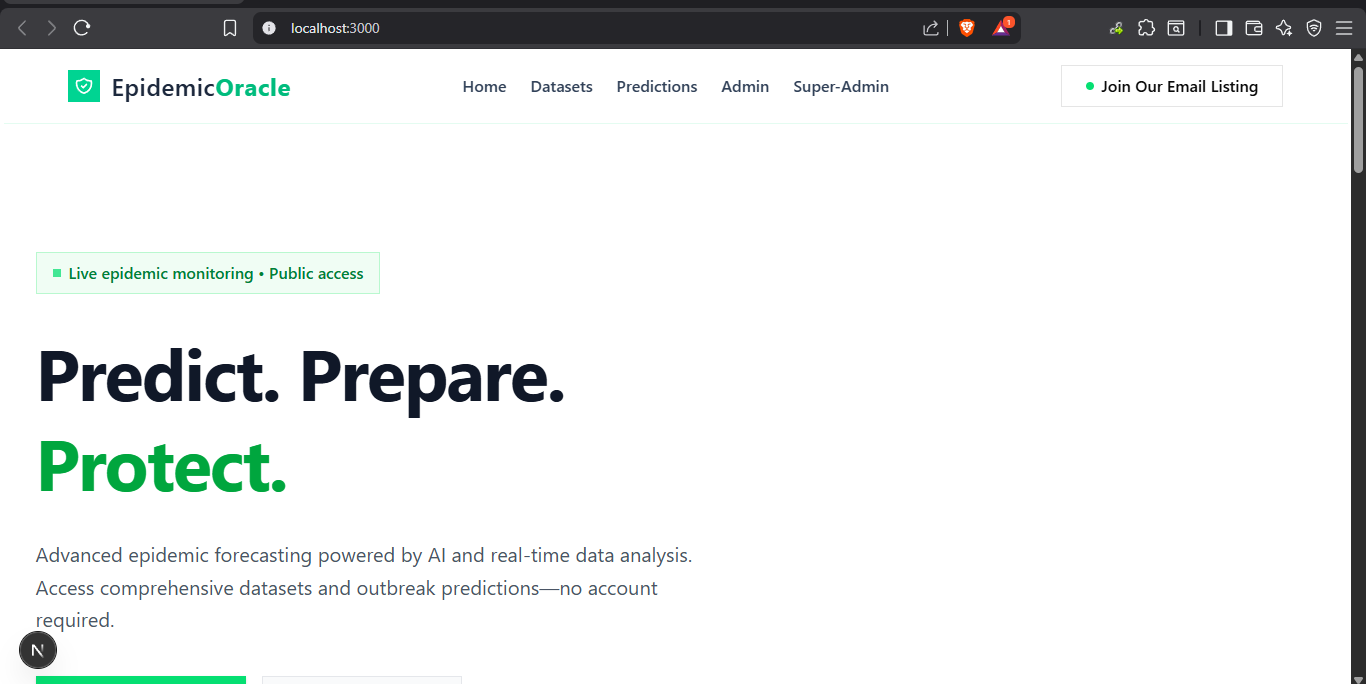


Finally:

Now the situation will be the same as for the CD, run the command npm run dev



The site is now running on localhost.



## Appendix B: Code Snippets

Map.tsx

// components/Map.tsx

'use client';

import React from 'react';

import { MapContainer, TileLayer, Circle, Popup } from 'react-leaflet';

import 'leaflet/dist/leaflet.css';

import L from 'leaflet';

// Fix Leaflet's default icon paths for Next.js

delete (L.Icon.Default as any).prototype.\_getIconUrl;

L.Icon.Default.mergeOptions({

  iconRetinaUrl: 'https://unpkg.com/leaflet@1.9.3/dist/images/marker-icon-2x.png',

  iconUrl: 'https://unpkg.com/leaflet@1.9.3/dist/images/marker-icon.png',

  shadowUrl: 'https://unpkg.com/leaflet@1.9.3/dist/images/marker-shadow.png',

});

interface Prediction {

  province: string;

  predicted\_cases: number;

  current\_cases: number;

  hospitalizations: number;

  deaths: number;

  risk\_level: string;

  lat: number;

  lng: number;

  confidence: number;

  growth\_rate: string;

  trend: string;

}

interface MapProps {

  predictions: Prediction[];

}

const Map: React.FC<MapProps> = ({ predictions = [] }) => {

  // Fallback center (Zimbabwe)

  const center: [number, number] = [-19.0154, 29.1549];

  const getRiskColor = (risk: string): string => {

    switch (risk) {

      case 'High': return '#EF4444';

      case 'Medium': return '#F59E0B';

      case 'Low': return '#10B981';

      default: return '#6B7280';

    }

  };

  return (

    <MapContainer

      center={center}

      zoom={6}

      scrollWheelZoom={true}

      className="w-full h-full z-0"

    >

      <TileLayer

        attribution='&copy; <a href="https://www.openstreetmap.org/">OpenStreetMap</a>'

        url="https://{s}.tile.openstreetmap.org/{z}/{x}/{y}.png"

      />

      {Array.isArray(predictions) && predictions.length > 0 ? (

        predictions.map((province, i) => (

          <Circle

            key={i}

            center={[province.lat, province.lng]}

            radius={50000} // 50km radius

            pathOptions={{

              fillColor: getRiskColor(province.risk\_level),

              fillOpacity: 0.6,

              color: getRiskColor(province.risk\_level),

              weight: 2,

              opacity: 0.8

            }}

          >

            <Popup>

              <div>

                <strong>{province.province}</strong><br />

                Predicted Cases: {province.predicted\_cases.toLocaleString()}<br />

                Current Cases: {province.current\_cases.toLocaleString()}<br />

                Risk Level: <span style={{ color: getRiskColor(province.risk\_level) }}>{province.risk\_level}</span><br />

                Confidence: {province.confidence}%

              </div>

            </Popup>

          </Circle>

        ))

      ) : (

        <></>

      )}

    </MapContainer>

  );

};

export default Map;

Admindashboard.tsx

'use client';

import React from 'react';

import Link from 'next/link';

import {

  BarChart3,

  Activity,

  TrendingUp,

  AlertTriangle,

  Users,

  Shield,

  Database

} from 'lucide-react';

const SuperAdminDashboard = () => {

  const systemStats = [

    {

      name: 'Total Predictions',

      value: '1,248',

      change: '+12%',

      changeType: 'positive',

      icon: BarChart3,

      description: 'This month'

    },

    {

      name: 'Model Accuracy',

      value: '89.2%',

      change: '+2.1%',

      changeType: 'positive',

      icon: TrendingUp,

      description: 'Average across models'

    },

    {

      name: 'Active Alerts',

      value: '8',

      change: '-3',

      changeType: 'negative',

      icon: AlertTriangle,

      description: 'Requiring attention'

    },

    {

      name: 'Data Sources',

      value: '47',

      change: '+5',

      changeType: 'positive',

      icon: Database,

      description: 'Connected facilities'

    }

  ];

  const diseaseModels = [

    {

      name: 'Malaria',

      accuracy: 92.1,

      lastTraining: '2024-01-15',

      alerts: 2,

      status: 'optimal',

      path: '/superadmin/malaria'

    },

    {

      name: 'COVID-19',

      accuracy: 88.7,

      lastTraining: '2024-01-10',

      alerts: 1,

      status: 'optimal',

      path: '/superadmin/covid'

    },

    {

      name: 'Influenza',

      accuracy: 85.3,

      lastTraining: '2024-01-12',

      alerts: 0,

      status: 'optimal',

      path: '/superadmin/influenza'

    },

    {

      name: 'Cholera',

      accuracy: 90.5,

      lastTraining: '2024-01-08',

      alerts: 3,

      status: 'degraded',

      path: '/superadmin/cholera'

    },

    {

      name: 'Typhoid',

      accuracy: 87.9,

      lastTraining: '2024-01-14',

      alerts: 1,

      status: 'optimal',

      path: '/superadmin/typhoid'

    }

  ];

  const getStatusColor = (status: string) => {

    switch (status) {

      case 'optimal': return 'text-green-400 bg-green-400/20';

      case 'degraded': return 'text-yellow-400 bg-yellow-400/20';

      case 'offline': return 'text-red-400 bg-red-400/20';

      default: return 'text-gray-400 bg-gray-400/20';

    }

  };

  return (

    <div className="space-y-6">

      {/\* Header \*/}

      <div className="bg-white border border-gray-200 rounded-xl p-6 shadow-sm">

        <div className="flex items-center justify-between">

          <div>

            <h1 className="text-2xl font-bold text-gray-900 mb-2">Predictive Analytics Dashboard</h1>

            <p className="text-gray-600">

              Real-time disease outbreak predictions and model monitoring

            </p>

          </div>

          <div className="hidden md:flex items-center gap-2 px-4 py-2 bg-green-50 border border-green-200 rounded-lg">

            <Shield className="w-5 h-5 text-green-400" />

            <span className="text-green-600 text-sm font-medium">All Systems Operational</span>

          </div>

        </div>

      </div>

      {/\* System Stats \*/}

      <div className="grid grid-cols-1 md:grid-cols-2 lg:grid-cols-4 gap-6">

        {systemStats.map((stat) => (

          <div key={stat.name} className="bg-white border border-gray-200 rounded-xl p-6 shadow-sm">

            <div className="flex items-center justify-between">

              <div>

                <p className="text-gray-500 text-sm font-medium">{stat.name}</p>

                <p className="text-2xl font-bold text-gray-900 mt-1">{stat.value}</p>

                <p className="text-gray-400 text-xs mt-1">{stat.description}</p>

              </div>

              <div className="flex items-center justify-center w-12 h-12 bg-green-50 rounded-lg">

                <stat.icon className="w-6 h-6 text-green-400" />

              </div>

            </div>

            <div className="flex items-center mt-4">

              <span className={`text-xs font-medium ${

                stat.changeType === 'positive' ? 'text-green-400' : 'text-red-400'

              }`}>

                {stat.change}

              </span>

              <span className="text-gray-400 text-xs ml-2">from last month</span>

            </div>

          </div>

        ))}

      </div>

      {/\* Disease Models \*/}

      <div className="bg-white border border-gray-200 rounded-xl p-6 shadow-sm">

        <h2 className="text-lg font-semibold text-gray-900 mb-4">Disease Prediction Models</h2>

        <div className="grid grid-cols-1 md:grid-cols-2 lg:grid-cols-3 gap-4">

          {diseaseModels.map((model) => (

            <Link

              key={model.name}

              href={model.path}

              className="block p-4 bg-gray-50 rounded-lg hover:bg-gray-100 transition-colors border border-gray-200"

            >

              <div className="flex items-center justify-between mb-3">

                <h3 className="text-gray-900 font-semibold">{model.name}</h3>

                <span className={`px-2 py-1 rounded text-xs font-bold ${getStatusColor(model.status)}`}>

                  {model.status.charAt(0).toUpperCase() + model.status.slice(1)}

                </span>

              </div>

              <div className="space-y-2 text-sm">

                <div className="flex justify-between">

                  <span className="text-gray-500">Accuracy:</span>

                  <span className="text-gray-900">{model.accuracy}%</span>

                </div>

                <div className="flex justify-between">

                  <span className="text-gray-500">Last Training:</span>

                  <span className="text-gray-900">{model.lastTraining}</span>

                </div>

                <div className="flex justify-between">

                  <span className="text-gray-500">Active Alerts:</span>

                  <span className={`${model.alerts > 0 ? 'text-red-400' : 'text-green-400'}`}>

                    {model.alerts}

                  </span>

                </div>

              </div>

              <div className="mt-3 pt-3 border-t border-gray-200">

                <div className="text-green-600 text-sm font-medium flex items-center gap-1">

                  <Activity className="w-4 h-4" />

                  View Predictions →

                </div>

              </div>

            </Link>

          ))}

        </div>

      </div>

      {/\* Quick Actions \*/}

      <div className="grid grid-cols-1 md:grid-cols-2 gap-6">

        <div className="bg-white border border-gray-200 rounded-xl p-6 shadow-sm">

          <h3 className="text-lg font-semibold text-gray-900 mb-4">Model Management</h3>

          <div className="space-y-3">

            <button className="w-full text-left p-3 bg-green-50 hover:bg-green-100 border border-green-200 rounded-lg transition-colors">

              <div className="text-gray-900 font-medium">Retrain All Models</div>

              <div className="text-gray-600 text-sm">Update models with latest data</div>

            </button>

            <button className="w-full text-left p-3 bg-white hover:bg-gray-50 border border-gray-200 rounded-lg transition-colors">

              <div className="text-gray-900 font-medium">Performance Report</div>

              <div className="text-gray-600 text-sm">Generate model accuracy report</div>

            </button>

            <button className="w-full text-left p-3 bg-white hover:bg-gray-50 border border-gray-200 rounded-lg transition-colors">

              <div className="text-gray-900 font-medium">Alert Settings</div>

              <div className="text-gray-600 text-sm">Configure prediction thresholds</div>

            </button>

          </div>

        </div>

        <div className="bg-white border border-gray-200 rounded-xl p-6 shadow-sm">

          <h3 className="text-lg font-semibold text-gray-900 mb-4">Recent Predictions</h3>

          <div className="space-y-3">

            <div className="flex items-center justify-between p-3 bg-gray-50 rounded-lg">

              <div>

                <div className="text-gray-900 font-medium">Malaria - Harare</div>

                <div className="text-gray-600 text-sm">High risk predicted for February</div>

              </div>

              <span className="text-red-400 text-sm font-medium">+42%</span>

            </div>

            <div className="flex items-center justify-between p-3 bg-gray-50 rounded-lg">

              <div>

                <div className="text-gray-900 font-medium">Cholera - Manicaland</div>

                <div className="text-gray-600 text-sm">Moderate outbreak likely</div>

              </div>

              <span className="text-yellow-400 text-sm font-medium">+18%</span>

            </div>

            <div className="flex items-center justify-between p-3 bg-gray-50 rounded-lg">

              <div>

                <div className="text-gray-900 font-medium">Influenza - Bulawayo</div>

                <div className="text-gray-600 text-sm">Seasonal increase expected</div>

              </div>

              <span className="text-green-400 text-sm font-medium">+8%</span>

            </div>

          </div>

        </div>

      </div>

    </div>

  );

};

export default SuperAdminDashboard;

Malaria.tsx

'use client';

import React, { useState, useEffect } from 'react';

import { useParams } from 'next/navigation';

import {

  LineChart,

  Line,

  XAxis,

  YAxis,

  CartesianGrid,

  Tooltip,

  Legend,

  ResponsiveContainer,

  PieChart,

  Pie,

  Cell

} from 'recharts';

import {

  AlertTriangle,

  Activity,

  Database,

  FileText,

  Mail,

  Play,

  RefreshCw,

  TrendingUp,

  TrendingDown,

  Map

} from 'lucide-react';

import { createClient } from '@supabase/supabase-js';

import dynamic from 'next/dynamic';

const supabase = createClient(

  process.env.NEXT\_PUBLIC\_SUPABASE\_URL!,

  process.env.NEXT\_PUBLIC\_SUPABASE\_ANON\_KEY!

);

const MapComponent = dynamic(() => import('@/components/Map'), { ssr: false });

const EmailAlertService = {

  async sendOutbreakAlert(disease: string, predictions: any[], nationalPrediction: any) {

    console.log('Sending email alerts for:', disease);

    await new Promise(resolve => setTimeout(resolve, 2000));

    return true;

  }

};

// Zimbabwe provinces with coordinates for highlighting entire regions

const ZIMBABWE\_PROVINCES = [

  {

    name: 'Harare',

    lat: -17.8292,

    lng: 31.0522,

    bounds: [[-17.7, 30.9], [-18.0, 31.2]]

  },

  {

    name: 'Bulawayo',

    lat: -20.1325,

    lng: 28.6265,

    bounds: [[-20.0, 28.5], [-20.3, 28.8]]

  },

  {

    name: 'Manicaland',

    lat: -18.9216,

    lng: 32.1746,

    bounds: [[-18.5, 31.8], [-20.5, 33.0]]

  },

  {

    name: 'Mashonaland Central',

    lat: -16.7644,

    lng: 31.0790,

    bounds: [[-16.5, 30.8], [-17.5, 31.5]]

  },

  {

    name: 'Mashonaland East',

    lat: -17.4850,

    lng: 32.2830,

    bounds: [[-17.0, 31.8], [-18.0, 32.8]]

  },

  {

    name: 'Mashonaland West',

    lat: -17.4850,

    lng: 29.7889,

    bounds: [[-16.5, 29.0], [-18.5, 30.5]]

  },

  {

    name: 'Masvingo',

    lat: -20.0791,

    lng: 30.8384,

    bounds: [[-19.5, 30.0], [-21.5, 31.5]]

  },

  {

    name: 'Matabeleland North',

    lat: -18.5333,

    lng: 27.9667,

    bounds: [[-17.5, 27.0], [-19.5, 29.0]]

  },

  {

    name: 'Matabeleland South',

    lat: -21.0050,

    lng: 29.0750,

    bounds: [[-20.5, 28.0], [-22.0, 30.0]]

  },

  {

    name: 'Midlands',

    lat: -19.0000,

    lng: 29.7500,

    bounds: [[-18.0, 28.5], [-20.0, 30.5]]

  }

];

const COLORS = ['#0088FE', '#00C49F', '#FFBB28', '#FF8042', '#8884D8', '#82CA9D', '#FFC658', '#8DD1E1', '#D084D0', '#FF6B6B'];

// Month names for better chart display

const MONTH\_NAMES = ['Jan', 'Feb', 'Mar', 'Apr', 'May', 'Jun', 'Jul', 'Aug', 'Sep', 'Oct', 'Nov', 'Dec'];

const DiseasePredictionPage = () => {

  const params = useParams();

  const disease = params.disease as string || 'malaria';

  const [uploadedFiles, setUploadedFiles] = useState<any[]>([]);

  const [selectedFiles, setSelectedFiles] = useState<string[]>([]);

  const [predictions, setPredictions] = useState<any[]>([]);

  const [nationalPrediction, setNationalPrediction] = useState<any>(null);

  const [chartData, setChartData] = useState<any[]>([]);

  const [pieChartData, setPieChartData] = useState<any[]>([]);

  const [predicting, setPredicting] = useState(false);

  const [sendingAlerts, setSendingAlerts] = useState(false);

  useEffect(() => {

    loadUploadedFiles();

  }, []);

  const loadUploadedFiles = async () => {

    try {

      const { data: files, error } = await supabase.storage

        .from('private-datasets')

        .list('submitted-datasets');

      if (error) {

        console.error('Error loading files:', error);

        return;

      }

      const csvFiles = files

        ?.filter(file => file.name.toLowerCase().endsWith('.csv'))

        .map(file => ({

          name: file.name,

          selected: false

        })) || [];

      setUploadedFiles(csvFiles);

    } catch (error) {

      console.error('Error loading files:', error);

    }

  };

  const toggleFileSelection = (fileName: string) => {

    setSelectedFiles(prev =>

      prev.includes(fileName)

        ? prev.filter(file => file !== fileName)

        : [...prev, fileName]

    );

  };

  const selectAllFiles = () => {

    setSelectedFiles(

      selectedFiles.length === uploadedFiles.length

        ? []

        : uploadedFiles.map(file => file.name)

    );

  };

  const parseCSVData = (csvText: string): any[] => {

    const lines = csvText.split('\n').filter(line => line.trim());

    if (lines.length === 0) return [];

    const headers = lines[0].split(',').map(h => h.trim());

    return lines.slice(1).map(line => {

      const values = line.split(',');

      if (values.length !== headers.length) return null;

      const entry: any = {};

      headers.forEach((header, index) => {

        const value = values[index]?.trim() || '';

        const numericFields = ['year', 'month', 'confirmed\_cases', 'recoveries', 'deaths', 'hospitalizations'];

        if (numericFields.includes(header)) {

          entry[header] = Number(value) || 0;

        } else {

          entry[header] = value;

        }

      });

      return entry;

    }).filter(Boolean);

  };

  const generatePredictions = async () => {

    if (selectedFiles.length === 0) {

      alert('Please select at least one dataset file');

      return;

    }

    setPredicting(true);

    try {

      let allData: any[] = [];

      for (const fileName of selectedFiles) {

        try {

          const { data: fileData, error } = await supabase.storage

            .from('private-datasets')

            .download(`submitted-datasets/${fileName}`);

          if (error) {

            console.error(`Error downloading ${fileName}:`, error);

            continue;

          }

          const text = await fileData.text();

          const records = parseCSVData(text);

          const filteredRecords = records.filter((record: any) => {

            const recordYear = parseInt(record.year) || 0;

            const recordDisease = (record.disease || '').toLowerCase().trim();

            const currentDisease = (disease || 'malaria').toLowerCase().trim();

            return recordYear === 2025 && recordDisease === currentDisease;

          });

          allData = [...allData, ...filteredRecords];

        } catch (error) {

          console.error(`Error processing file ${fileName}:`, error);

        }

      }

      const provincePredictions = generateProvincePredictions(allData);

      setPredictions(provincePredictions);

      const national = generateNationalPrediction(provincePredictions);

      setNationalPrediction(national);

      const chart = generateChartData(allData, provincePredictions);

      setChartData(chart);

      // Generate pie chart data

      const pieData = provincePredictions

        .sort((a, b) => b.predicted\_cases - a.predicted\_cases)

        .map((prediction, index) => ({

          name: prediction.province,

          value: prediction.predicted\_cases,

          color: COLORS[index % COLORS.length]

        }));

      setPieChartData(pieData);

    } catch (error) {

      console.error('Error generating predictions:', error);

      alert('Error generating predictions');

    } finally {

      setPredicting(false);

    }

  };

  const generateChartData = (allData: any[], predictions: any[]): any[] => {

    const monthlyData: { [key: number]: any } = {};

    allData.forEach(record => {

      const month = record.month || 1;

      if (!monthlyData[month]) {

        monthlyData[month] = {

          month,

          monthName: MONTH\_NAMES[month - 1] || `Month ${month}`,

          confirmed\_cases: 0,

          hospitalizations: 0,

          deaths: 0,

          isPrediction: false

        };

      }

      monthlyData[month].confirmed\_cases += record.confirmed\_cases || 0;

      monthlyData[month].hospitalizations += record.hospitalizations || 0;

      monthlyData[month].deaths += record.deaths || 0;

    });

    const sortedMonths = Object.keys(monthlyData).sort((a, b) => parseInt(a) - parseInt(b)).map(m => parseInt(m));

    const lastMonth = sortedMonths[sortedMonths.length - 1] || 12;

    const nextMonth = lastMonth === 12 ? 1 : lastMonth + 1;

    const chartArray = sortedMonths.map(month => ({

      ...monthlyData[month],

      name: monthlyData[month].monthName

    }));

    if (lastMonth < 12) {

      const lastMonthData = monthlyData[lastMonth];

      const avgGrowth = 0.15; // 15% average growth

      const predictionData = {

        month: nextMonth,

        name: `${MONTH\_NAMES[nextMonth - 1] || `Month ${nextMonth}`} (Predicted)`,

        confirmed\_cases: Math.round(lastMonthData.confirmed\_cases \* (1 + avgGrowth)),

        hospitalizations: Math.round(lastMonthData.hospitalizations \* (1 + avgGrowth)),

        deaths: Math.round(lastMonthData.deaths \* (1 + avgGrowth)),

        isPrediction: true

      };

      chartArray.push(predictionData);

    }

    return chartArray;

  };

  const generateProvincePredictions = (allData: any[]): any[] => {

    if (allData.length === 0) return [];

    const provinceData: { [key: string]: any } = {};

    const monthlyByProvince: { [key: string]: { [key: number]: any } } = {};

    allData.forEach(record => {

      const province = record.province || 'Unknown';

      const month = record.month || 1;

      if (!provinceData[province]) {

        provinceData[province] = {

          confirmed\_cases: 0,

          hospitalizations: 0,

          deaths: 0

        };

        monthlyByProvince[province] = {};

      }

      if (!monthlyByProvince[province][month]) {

        monthlyByProvince[province][month] = {

          confirmed\_cases: 0,

          hospitalizations: 0,

          deaths: 0

        };

      }

      provinceData[province].confirmed\_cases += record.confirmed\_cases || 0;

      provinceData[province].hospitalizations += record.hospitalizations || 0;

      provinceData[province].deaths += record.deaths || 0;

      monthlyByProvince[province][month].confirmed\_cases += record.confirmed\_cases || 0;

      monthlyByProvince[province][month].hospitalizations += record.hospitalizations || 0;

      monthlyByProvince[province][month].deaths += record.deaths || 0;

    });

    const predictions = Object.entries(provinceData).map(([province, totals]) => {

      const months = Object.keys(monthlyByProvince[province]).map(m => parseInt(m)).sort((a, b) => a - b);

      const lastMonth = months[months.length - 1];

      const lastMonthData = monthlyByProvince[province][lastMonth] || totals;

      const avgGrowth = 0.15;

      const predicted\_cases = Math.round(lastMonthData.confirmed\_cases \* (1 + avgGrowth));

      const current\_cases = lastMonthData.confirmed\_cases;

      const growth\_rate = Math.round(((predicted\_cases - current\_cases) / Math.max(current\_cases, 1)) \* 100);

      let risk\_level = 'Low';

      if (predicted\_cases > 1000) risk\_level = 'High';

      else if (predicted\_cases > 500) risk\_level = 'Medium';

      const confidence = 80 + Math.floor(Math.random() \* 15);

      // Find province info with bounds for map highlighting

      const provinceInfo = ZIMBABWE\_PROVINCES.find(p =>

        p.name.toLowerCase() === province.toLowerCase()

      ) || ZIMBABWE\_PROVINCES[0];

      return {

        province,

        predicted\_cases,

        current\_cases,

        hospitalizations: lastMonthData.hospitalizations,

        deaths: lastMonthData.deaths,

        risk\_level,

        confidence,

        growth\_rate: growth\_rate > 0 ? `+${growth\_rate}%` : `${growth\_rate}%`,

        trend: growth\_rate > 0 ? 'increasing' : growth\_rate < 0 ? 'decreasing' : 'stable',

        lat: provinceInfo.lat,

        lng: provinceInfo.lng,

        bounds: provinceInfo.bounds,

        color: risk\_level === 'High' ? '#EF4444' : risk\_level === 'Medium' ? '#F59E0B' : '#10B981',

        cases: predicted\_cases

      };

    });

    return predictions.sort((a, b) => b.predicted\_cases - a.predicted\_cases);

  };

  const generateNationalPrediction = (provincePredictions: any[]): any => {

    if (provincePredictions.length === 0) {

      return {

        total\_predicted\_cases: 0,

        average\_risk: 'Low',

        high\_risk\_provinces: [],

        overall\_confidence: 0

      };

    }

    const total\_predicted\_cases = provincePredictions.reduce((sum, p) => sum + p.predicted\_cases, 0);

    const high\_risk\_provinces = provincePredictions.filter(p => p.risk\_level === 'High').map(p => p.province);

    const medium\_risk\_provinces = provincePredictions.filter(p => p.risk\_level === 'Medium').map(p => p.province);

    let average\_risk = 'Low';

    if (high\_risk\_provinces.length >= 2) average\_risk = 'High';

    else if (high\_risk\_provinces.length > 0 || medium\_risk\_provinces.length >= 3) average\_risk = 'Medium';

    const overall\_confidence = Math.round(provincePredictions.reduce((sum, p) => sum + p.confidence, 0) / provincePredictions.length);

    return {

      total\_predicted\_cases,

      average\_risk,

      high\_risk\_provinces,

      overall\_confidence,

      total\_provinces: provincePredictions.length

    };

  };

  const sendEmailAlerts = async () => {

    if (predictions.length === 0 || !nationalPrediction) {

      alert('No predictions available to send');

      return;

    }

    setSendingAlerts(true);

    try {

      await EmailAlertService.sendOutbreakAlert(disease, predictions, nationalPrediction);

      alert('Email alerts sent successfully!');

    } catch (error) {

      console.error('Error sending alerts:', error);

      alert('Error sending email alerts - check console');

    } finally {

      setSendingAlerts(false);

    }

  };

  const CustomTooltip = ({ active, payload, label }: any) => {

    if (active && payload && payload.length) {

      return (

        <div className="bg-white p-4 border border-gray-200 rounded-lg shadow-sm">

          <p className="font-semibold text-gray-900">{label}</p>

          {payload.map((entry: any, index: number) => (

            <p key={index} style={{ color: entry.color }} className="text-sm">

              {entry.name}: {entry.value.toLocaleString()}

            </p>

          ))}

        </div>

      );

    }

    return null;

  };

  return (

    <div className="space-y-6">

      {/\* Header \*/}

      <div className="bg-white border border-gray-200 rounded-lg p-6 shadow-sm">

        <div className="flex items-center justify-between">

          <div>

            <h1 className="text-2xl font-bold text-gray-900 capitalize">{disease} Outbreak Predictions</h1>

            <p className="text-gray-600">Monthly forecast and risk analysis for Zimbabwe</p>

          </div>

          <div className="hidden md:flex items-center justify-center w-12 h-12 bg-green-50 rounded-lg">

            <TrendingUp className="w-6 h-6 text-green-400" />

          </div>

        </div>

      </div>

      {/\* Stats Overview \*/}

      {nationalPrediction && (

        <div className="grid grid-cols-1 md:grid-cols-4 gap-6">

          <div className="bg-white border border-gray-200 rounded-lg p-6 shadow-sm">

            <div className="flex items-center justify-between">

              <div>

                <p className="text-gray-500 text-sm">Predicted Cases (Next Month)</p>

                <p className="text-2xl font-bold text-gray-900 mt-1">

                  {nationalPrediction.total\_predicted\_cases.toLocaleString()}

                </p>

              </div>

              <div className="flex items-center justify-center w-12 h-12 bg-blue-50 rounded-lg">

                <TrendingUp className="w-6 h-6 text-blue-400" />

              </div>

            </div>

          </div>

          <div className="bg-white border border-gray-200 rounded-lg p-6 shadow-sm">

            <div className="flex items-center justify-between">

              <div>

                <p className="text-gray-500 text-sm">High Risk Provinces</p>

                <p className="text-2xl font-bold text-red-600 mt-1">

                  {nationalPrediction.high\_risk\_provinces.length}

                </p>

              </div>

              <div className="flex items-center justify-center w-12 h-12 bg-red-50 rounded-lg">

                <AlertTriangle className="w-6 h-6 text-red-400" />

              </div>

            </div>

          </div>

          <div className="bg-white border border-gray-200 rounded-lg p-6 shadow-sm">

            <div className="flex items-center justify-between">

              <div>

                <p className="text-gray-500 text-sm">Overall Risk</p>

                <p className="text-2xl font-bold text-yellow-600 mt-1">

                  {nationalPrediction.average\_risk}

                </p>

              </div>

              <div className="flex items-center justify-center w-12 h-12 bg-yellow-50 rounded-lg">

                <Activity className="w-6 h-6 text-yellow-400" />

              </div>

            </div>

          </div>

          <div className="bg-white border border-gray-200 rounded-lg p-6 shadow-sm">

            <div className="flex items-center justify-between">

              <div>

                <p className="text-gray-500 text-sm">Model Confidence</p>

                <p className="text-2xl font-bold text-green-600 mt-1">

                  {nationalPrediction.overall\_confidence}%

                </p>

              </div>

              <div className="flex items-center justify-center w-12 h-12 bg-green-50 rounded-lg">

                <TrendingUp className="w-6 h-6 text-green-400" />

              </div>

            </div>

          </div>

        </div>

      )}

      {/\* Dataset Selection \*/}

      <div className="bg-white border border-gray-200 rounded-lg p-6 shadow-sm">

        <div className="flex items-center justify-between mb-6">

          <div>

            <h3 className="text-lg font-semibold text-gray-900">Select 2025 Datasets</h3>

            <p className="text-gray-600 text-sm">Choose which uploaded datasets to use for predictions</p>

          </div>

          <div className="flex gap-3">

            <button

              onClick={loadUploadedFiles}

              className="flex items-center gap-2 px-4 py-2 bg-green-400 hover:bg-green-500 text-white font-semibold rounded-lg transition-colors"

            >

              <RefreshCw className="w-4 h-4" />

              Refresh Files

            </button>

          </div>

        </div>

        {uploadedFiles.length > 0 ? (

          <div className="space-y-4">

            <div className="flex items-center justify-between p-4 bg-gray-50 rounded-lg border border-gray-200">

              <div className="flex items-center gap-3">

                <button

                  onClick={selectAllFiles}

                  className="flex items-center gap-2 text-gray-700 hover:text-gray-900 transition-colors"

                >

                  <input

                    type="checkbox"

                    checked={selectedFiles.length === uploadedFiles.length && uploadedFiles.length > 0}

                    onChange={selectAllFiles}

                    className="w-4 h-4 rounded border-gray-300 text-green-600"

                  />

                  <span className="text-sm font-medium">

                    {selectedFiles.length === uploadedFiles.length ? 'Deselect All' : 'Select All'}

                  </span>

                </button>

                <span className="text-gray-600 text-sm">

                  {selectedFiles.length} of {uploadedFiles.length} files selected

                </span>

              </div>

              <div className="flex gap-3">

                <button

                  onClick={generatePredictions}

                  disabled={selectedFiles.length === 0 || predicting}

                  className="flex items-center gap-2 px-4 py-2 bg-green-400 hover:bg-green-500 text-white font-semibold rounded-lg transition-colors disabled:opacity-50 disabled:cursor-not-allowed"

                >

                  <Play className="w-4 h-4" />

                  {predicting ? 'Generating...' : 'Generate Predictions'}

                </button>

                {predictions.length > 0 && (

                  <button

                    onClick={sendEmailAlerts}

                    disabled={sendingAlerts}

                    className="flex items-center gap-2 px-4 py-2 bg-red-500 hover:bg-red-600 text-white font-semibold rounded-lg transition-colors disabled:opacity-50"

                  >

                    <Mail className="w-4 h-4" />

                    {sendingAlerts ? 'Sending...' : 'Send Alerts'}

                  </button>

                )}

              </div>

            </div>

            <div className="grid grid-cols-1 md:grid-cols-2 lg:grid-cols-3 gap-4">

              {uploadedFiles.map((file, index) => (

                <div

                  key={index}

                  className={`p-4 border rounded-lg cursor-pointer transition-colors ${

                    selectedFiles.includes(file.name)

                      ? 'bg-green-50 border-green-300'

                      : 'bg-white border-gray-200 hover:bg-gray-50'

                  }`}

                  onClick={() => toggleFileSelection(file.name)}

                >

                  <div className="flex items-center gap-3">

                    <input

                      type="checkbox"

                      checked={selectedFiles.includes(file.name)}

                      onChange={() => toggleFileSelection(file.name)}

                      className="w-4 h-4 rounded border-gray-300 text-green-600"

                    />

                    <FileText className="w-5 h-5 text-gray-400" />

                    <span className="text-gray-900 text-sm truncate font-medium">{file.name}</span>

                  </div>

                </div>

              ))}

            </div>

          </div>

        ) : (

          <div className="text-center py-8 text-gray-600 bg-gray-50 rounded-lg border border-gray-200">

            <Database className="w-12 h-12 mx-auto mb-3 text-gray-300" />

            <p className="font-medium">No datasets found</p>

          </div>

        )}

      </div>

      {/\* Predictions Display \*/}

      {predictions.length > 0 && chartData.length > 0 && (

        <div className="space-y-6">

          {/\* Charts Row \*/}

          <div className="grid grid-cols-1 lg:grid-cols-2 gap-6">

            {/\* Line Chart \*/}

            <div className="bg-white border border-gray-200 rounded-lg p-6 shadow-sm">

              <h3 className="text-lg font-semibold text-gray-900 mb-4">National Trend & Forecast</h3>

              <ResponsiveContainer width="100%" height={400}>

                <LineChart data={chartData}>

                  <CartesianGrid strokeDasharray="3 3" stroke="#E5E7EB" />

                  <XAxis dataKey="name" stroke="#6B7280" />

                  <YAxis stroke="#6B7280" />

                  <Tooltip content={<CustomTooltip />} />

                  <Legend />

                  <Line

                    type="monotone"

                    dataKey="confirmed\_cases"

                    stroke="#10B981"

                    strokeWidth={3}

                    name="Confirmed Cases"

                    dot={{ fill: '#10B981', strokeWidth: 2, r: 4 }}

                    activeDot={{ r: 6, fill: '#10B981' }}

                  />

                  <Line

                    type="monotone"

                    dataKey="hospitalizations"

                    stroke="#F59E0B"

                    strokeWidth={2}

                    name="Hospitalizations"

                    dot={{ fill: '#F59E0B', strokeWidth: 2, r: 4 }}

                  />

                  <Line

                    type="monotone"

                    dataKey="deaths"

                    stroke="#EF4444"

                    strokeWidth={2}

                    name="Deaths"

                    dot={{ fill: '#EF4444', strokeWidth: 2, r: 4 }}

                  />

                </LineChart>

              </ResponsiveContainer>

            </div>

            {/\* Pie Chart \*/}

            <div className="bg-white border border-gray-200 rounded-lg p-6 shadow-sm">

              <h3 className="text-lg font-semibold text-gray-900 mb-4">Provincial Case Distribution</h3>

              <ResponsiveContainer width="100%" height={400}>

                <PieChart>

                  <Pie

                    data={pieChartData}

                    cx="50%"

                    cy="50%"

                    labelLine={true}

                    label={({ name, percent }) => `${name}: ${(percent \* 100).toFixed(0)}%`}

                    outerRadius={120}

                    fill="#8884d8"

                    dataKey="value"

                  >

                    {pieChartData.map((entry, index) => (

                      <Cell key={`cell-${index}`} fill={entry.color} />

                    ))}

                  </Pie>

                  <Tooltip formatter={(value) => [value.toLocaleString(), 'Cases']} />

                  <Legend />

                </PieChart>

              </ResponsiveContainer>

            </div>

          </div>

          {/\* Risk Map \*/}

          <div className="bg-white border border-gray-200 rounded-lg p-6 shadow-sm">

            <div className="flex items-center gap-2 mb-4">

              <Map className="w-5 h-5 text-gray-600" />

              <h3 className="text-lg font-semibold text-gray-900">Zimbabwe Risk Zones Map</h3>

            </div>

            <div className="h-96 rounded-lg border border-gray-200 overflow-hidden bg-gray-50">

              <MapComponent predictions={predictions} />

            </div>

            <div className="flex items-center justify-center gap-6 mt-4">

              <div className="flex items-center gap-2">

                <div className="w-4 h-4 bg-green-500 rounded"></div>

                <span className="text-sm text-gray-600">Low Risk</span>

              </div>

              <div className="flex items-center gap-2">

                <div className="w-4 h-4 bg-yellow-500 rounded"></div>

                <span className="text-sm text-gray-600">Medium Risk</span>

              </div>

              <div className="flex items-center gap-2">

                <div className="w-4 h-4 bg-red-500 rounded"></div>

                <span className="text-sm text-gray-600">High Risk</span>

              </div>

            </div>

          </div>

          {/\* Provincial Predictions \*/}

          <div className="bg-white border border-gray-200 rounded-lg p-6 shadow-sm">

            <h3 className="text-lg font-semibold text-gray-900 mb-4">Provincial Breakdown</h3>

            <div className="space-y-3">

              {predictions.map((prediction, index) => (

                <div

                  key={index}

                  className={`p-4 border-l-4 rounded-lg ${

                    prediction.risk\_level === 'High'

                      ? 'bg-red-50 border-red-400'

                      : prediction.risk\_level === 'Medium'

                      ? 'bg-yellow-50 border-yellow-400'

                      : 'bg-green-50 border-green-400'

                  }`}

                >

                  <div className="grid grid-cols-1 md:grid-cols-5 gap-4">

                    <div>

                      <p className="text-gray-500 text-xs">Province</p>

                      <p className="text-gray-900 font-semibold">{prediction.province}</p>

                    </div>

                    <div>

                      <p className="text-gray-500 text-xs">Current Cases</p>

                      <p className="text-gray-900 font-semibold">{prediction.current\_cases.toLocaleString()}</p>

                    </div>

                    <div>

                      <p className="text-gray-500 text-xs">Predicted (Next Month)</p>

                      <p className="text-gray-900 font-semibold">{prediction.predicted\_cases.toLocaleString()}</p>

                    </div>

                    <div>

                      <p className="text-gray-500 text-xs">Trend</p>

                      <div className="flex items-center gap-1 mt-1">

                        {prediction.trend === 'increasing' ? (

                          <>

                            <TrendingUp className="w-4 h-4 text-red-600" />

                            <span className="text-red-600 font-semibold">{prediction.growth\_rate}</span>

                          </>

                        ) : prediction.trend === 'decreasing' ? (

                          <>

                            <TrendingDown className="w-4 h-4 text-green-600" />

                            <span className="text-green-600 font-semibold">{prediction.growth\_rate}</span>

                          </>

                        ) : (

                          <span className="text-gray-600 font-semibold">Stable</span>

                        )}

                      </div>

                    </div>

                    <div className="text-right">

                      <p className="text-gray-500 text-xs">Risk Level</p>

                      <span className={`inline-block px-3 py-1 rounded text-xs font-semibold mt-1 ${

                        prediction.risk\_level === 'High'

                          ? 'bg-red-200 text-red-800'

                          : prediction.risk\_level === 'Medium'

                          ? 'bg-yellow-200 text-yellow-800'

                          : 'bg-green-200 text-green-800'

                      }`}>

                        {prediction.risk\_level}

                      </span>

                    </div>

                  </div>

                </div>

              ))}

            </div>

          </div>

        </div>

      )}

    </div>

  );

};

export default DiseasePredictionPage;

## Appendix C: Data Collection Guides

The data collected for this project was mostly collected from online sources which were included in the references section.

## Appendix D: Turnitin Similarity

## Appendix E: Turnitin AI Writing Report