Africa and Myanmar Using Machine Learning
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Abstract—HIV/AIDS is one of the deadliest infectious complex and include population, economy, behavior, and
diseases in the world, causing nearly one **diseases in the world, causing nearly one million deaths**
Machin Yang, Xin Chang
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 IAENG International Journal of Computer Science

Epidemiological Insights and Forecasting of

HIV/AIDS Mortality: A Case Study of South

Africa and Myanmar Using Machine Learning

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an **death, especially in regions like South Africa. In the Asian South Africa. In the Asia PERENT AND PERENT AND SET AS A set of the deadliest infectious**
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diseases in the world, causing nearly one million deaths

annually. In some countries, HIV/AIDS is the leading cause of

death, especially in regions like South Afric *Abstract*—HIV/AIDS is one of the deadliest infectious environment. In recentions and all the several year annually. In some countries, HIV/AIDS is the leading cause of deaths, Greey System Tleadin, especially in regions l ansite that the counter of the distance in the exameles in the world, causing nearly one million deaths Autoregressive Integration annually. In some countries, HIV/AIDS is the leading cause of models, Grey System T
death, **and Myanmar.** The LR model's predictions were doner to the for HIV incidence rates in the Asian collocal control of HIV/AIDS-related deaths. This study utilized data on the GM (1,1) model to fit HIV/AIDS-related deaths. T annuary. In some countries, the V/ADDS of the reading cause of the CBC (Stey System region, Myanmar is also a high-prevalence area for HIV/AIDS-related deaths. This study utilized data on ternd of HIV incidence HIV/AIDS-re **treadurity in Fegorial Material and Science in Altimata in the Asian experimental and filly in ourworldindata.org/HIV/AIDS. LR, SVM, RF and XGBoost and HIV/AIDS-related deaths from 1990 to 2019, sourced from the GM (1,1) comtains and my animal is also a mign-prevalence area in the GM (1,1) model to fit burworldindata.org/HIV/AIDS. LR, SVM, RF and XGBoost Province, with a relative models were introduced to predict the four-year mortality m for WADS-related deaths.** This study unified data on
ourworldindata.org/HIV/AIDS. LR, SVM, RF and XGBoost
models were introduced to predict the four-year mortality
trends in South Africa and Myanmar. Model performance was **INTEONIGTION**
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 INSTERNATE: THE **INDEX CONSTANT CONSTANT CONSTANT CONSTANT CONSTANT PHOTORS**
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 In the series predi moutes were introduced to predict the four-year mortanty

evaluated using metrics including RMSE, MAE, MSE, MAPE,

evaluated using metrics including RMSE, MAE, MSE, MAPE,

and Pinball. By fitting and forecasting mortality Example 10. Increasing mortality data from the

int was observed that the LR model

int was observed that the LR model

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odels in predicting trends in South Africa dis

R model's predictions were closer to the

for stu several years, it was observed that the LR model

equations to predict the term delst in predicting trends in South Africa disease[1]. Yang et in Myanmar. The LR model's predictions were closer to the for HIV incidence re

trends in these regions, offers insights for epidemiological

control, and helps of remultes to combat this epidemic.

formulate policies to combat this epidemic.
 Halex Terms—HIV/AIDS mortality, Time series prediction, control, and helps other countries take preventive measures and

formulate policies to combat this epidemic.
 and the Terms—HIV/AIDS mortality, Time series prediction,
 Belidemiological insights, Machine learnin
 Beli normulate poncies to combat this epidemic.
 Hepdemiological insights, Machine learnin
 Epidemiological insights, Machine learnin
 Hepdemiological insights, Machine learnin
 Hepdemiological insights, Machine learnin Index Terms—HIV/AIDS mortality, Time series prediction, 89.60%, respectively. An et al.

Epidemiological insights, Machine learnin

(Backpropagation Artificial N

I. INTRODUCTION predict HIV in Dalian City.

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Epidemiological insights, Machine learnin

I. INTRODUCTION

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 EVAIDS, which stands for Acquired Immunodeficiency

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From the considerable work on us

Syndrome, is a highly fatal infectious disease caused by

Ir et al. [16] used a multilaye

the Human Immunodeficiency Virus infection [1] (the predict the I. INTRODUCTION considerable work on Similar and Myanmar is a highly fatal infectious disease caused by and the Human Immunodeficiency Virus infection [1] (the predict the time series durable work on a summar infection HIV **IV/AIDS**, which stands for Acquired Immunodeficienc

Syndrome, is a highly fatal infectious disease caused t

the Human Immunodeficiency Virus infection [1] (th

abbreviation HIV is used below). Globally, the total numb
 TV/AIDs, which stands for Acquired imminodelene to $\frac{1}{2}$ for the HIV during the Human Imminodelene current of the predict the time series during the breviation HIV is used below). Globally, the total number COVID-19 p estimated increase of 3.3 million cases annually, and the

ghest burden in the African region[2]-[4]. It has become a

disruptions coul

bolal public health issue[5]-[8]. Interestingly, there are

casualties.

mificant dis ghest burden in the African region[2]-[4]. It has become a

bolal public health issue[5]-[8]. Interestingly, there are

estualities.

mificant disparities in the HIV burden in Africa, with the

However, there is curre

boglobal public health issue[5]-[8]. Interestingly, there are casualties.

significant disparities in the HIV burden in Africa, with the However, there is curre

sub-Saharan African region alone accounting for the trend of H Significant disparities in the HIV burden in Africa, with the
sub-Saharan African region alone accounting for the trend of HIV-rel
approximately 70% of all global HIV cases[9], [10]. four different model
Myanmar is one of Sub-Saharan African region alone accounting for the trend of Happroximately 70% of all global HIV cases[9], [10].

Myanmar is one of the countries in Southeast Asia severely death counts. Infected by the HIV epidemic[11].

The Tactors Influencing the prevalence trends of

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This work was supported by National Natural Science Fe

China under Grant 12001425, Natural Science Basic Research

yangwenbin-007@163.com).
X. Chang is a postgraduate of the School of Computer Science &

Frormed other models in predicting trends in South Africa disease [1]. Yang et al. [13] used
 Myanmar. The LR model's predictions were closer to the for HIV incidence rates in China
 In ductomes. This study aids in un Myanmar. The LR model's predictions were closer to the

in ductomes. This study aids in understanding mortality

in these regions, offers insights for epidemiological

ol, and helps other countries take preventive measure actual outcomes. This study aids in understanding mortality

average absolute percentage

control, and helps other countries take preventive measures and

calibration, and to predict the H

formulate policies to combat thi \sum Machine Learning
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complex and include population, economy, behavior, and
environment. In recent years, scholars have used
Autoregressive Integrated Moving Average (ARIMA)
models, Grey System Theo (Backpropagation) neural network models to predict models (Backpropagation) neural network models (Backpropagation) neural network models (GM (1,1)), and BP (Backpropagation) neural network models to predict the trend of H **EXECT:**

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environment. In recent years, scholars have used

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models, Grey System Theory models (GM (1,1)), **EXECTICS**

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models, Grey System Theory models (GM (1,1)), and BP
(Backpropagation environment. In recent years, scholars have used
Autoregressive Integrated Moving Average (ARIMA)
models, Grey System Theory models (GM (1,1)), and BP
(Backpropagation) neural network models to predict the
trend of HIV inc Autoregressive Integrated Moving Average (ARIMA)
models, Grey System Theory models (GM (1,1)), and BP
(Backpropagation) neural network models to predict the
trend of HIV incidence. For example, Liang et al. [12] used
the G models, Grey System Theory models (GM (1,1)), and BP
(Backpropagation) neural network models to predict the
trend of HIV incidence. For example, Liang et al. [12] used
the GM (1,1) model to fit the HIV incidence rate in Ji (Backpropagation) neural network models to predict the
trend of HIV incidence. For example, Liang et al. [12] used
the GM (1,1) model to fit the HIV incidence rate in Jiangsu
Province, with a relative error of 23.89%. The trend of HIV incidence. For example, Liang et al. [12] used
the GM (1,1) model to fit the HIV incidence rate in Jiangsu
Province, with a relative error of 23.89%. The GM (1,1)
model is the simplest form of this model, and the GM (1,1) model to fit the HIV incidence rate in Jiangsu
Province, with a relative error of 23.89%. The GM (1,1)
model is the simplest form of this model, and the basic steps
in establishing it are to first accumulate i Province, with a relative error of 23.89%. The GM (1,1)
model is the simplest form of this model, and the basic steps
in establishing it are to first accumulate irregular raw data
into regular data sequences and then estab model is the simplest form of this model, and the basic steps
in establishing it are to first accumulate irregular raw data
into regular data sequences and then establish differential
equations to predict future developmen in establishing it are to first accumulate irregular raw data
into regular data sequences and then establish differential
equations to predict future development trends of the
disease[1]. Yang et al. [13] used ARIMA to est into regular data sequences and then establish differential
equations to predict future development trends of the
disease[1]. Yang et al. [13] used ARIMA to establish a model
for HIV incidence rates in China from 2000 to equations to predict future development trends of the disease[1]. Yang et al. [13] used ARIMA to establish a model
for HIV incidence rates in China from 2000 to 2014, with an
average absolute percentage error of 19.90%. Wu disease[1]. Yang et al. [13] used ARIMA to establish a model
for HIV incidence rates in China from 2000 to 2014, with an
average absolute percentage error of 19.90%. Wu et al. [14]
used Backpropagation Artificial Neural Ne for HIV incidence rates in China from 2000 to 2014, with an
average absolute percentage error of 19.90%. Wu et al. [14]
used Backpropagation Artificial Neural Networks (BP-ANN)
as a model to predict the HIV prevalence rate average absolute percentage error of 19.90%. Wu et al. [14]
used Backpropagation Artificial Neural Networks (BP-ANN)
as a model to predict the HIV prevalence rate, with training,
calibration, and testing accuracies of 93.9 used Backpropagation Artificial Neural Networks (BP-ANN)
as a model to predict the HIV prevalence rate, with training,
calibration, and testing accuracies of 93.94%, 88.48%, and
89.60%, respectively. An et al. [15] establi as a model to predict the HIV prevalence rate, with training,
calibration, and testing accuracies of 93.94%, 88.48%, and
89.60%, respectively. An et al. [15] established a two-stage
Empirical Mode Decomposition (EMD) - BPN calibration, and testing accuracies of 93.94%, 88.48%, and
89.60%, respectively. An et al. [15] established a two-stage
Empirical Mode Decomposition (EMD) - BPNN
(Backpropagation Artificial Neural Network) model to
predict casualties. npirical Mode Decomposition (EMD) - BPNN
ackpropagation Artificial Neural Network) model to
edict HIV in Dalian City. Recently, there has been
msiderable work on using machine learning for
idemiological dynamics prediction (Backpropagation Artificial Neural Network) model to
predict HIV in Dalian City. Recently, there has been
considerable work on using machine learning for
epidemiological dynamics prediction. For instance[17]-[19],
Jr et al predict HIV in Dalian City. Recently, there has been considerable work on using machine learning for epidemiological dynamics prediction. For instance[17]-[19], Jr et al. [16] used a multilayer perceptron neural network to considerable work on using machine learning for
epidemiological dynamics prediction. For instance[17]-[19],
Jr et al. [16] used a multilayer perceptron neural network to
predict the time series during the nationwide outbre IV/AIDS, which stands for Acquired Immunodeficiency epidemiological dynamics prediction. For instance[17]-[19],
Syndrome, is a highly fatal infectious disease caused by Jr et al. [16] used a multilayer perceptron neural ne

Brownmar Affican region alone accounting for the trend of HIV-relat
proximately 70% of all global HIV cases[9], [10]. four different models
cated by the HIV epidemic[11]. The factors influencing the prevalence trends of HI approximately 70% of all global HIV cases[9], [10].

Myanmar is one of the countries in Southeast Asia severely

affected by the HIV epidemic[11].

The factors influencing the prevalence trends of HIV are

Africa in 2019, Example the HIV epidemic[11].

Sected by the HIV epidemic prevalence trends of HIV are

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This work wa The factors influencing the prevalence trends of HIV are

The factors influencing the prevalence trends of HIV are

of Myanmar in 2019.

Africa and Myanmar,

This work was supported by National Natural Science Foundation o epidemiological dynamics prediction. For instance[17]-[19], Jr et al. [16] used a multilayer perceptron neural network to predict the time series during the nationwide outbreak of the COVID-19 pandemic. Although the full e Jr et al. [16] used a multilayer perceptron neural network to
predict the time series during the nationwide outbreak of the
COVID-19 pandemic. Although the full effects of
COVID-19 on HIV services and development are still predict the time series during the nationwide outbreak of the COVID-19 pandemic. Although the full effects of COVID-19 on HIV services and development are still unknown, there are predictions suggesting that such disruptio COVID-19 pandemic. Although the full effects of COVID-19 on HIV services and development are still unknown, there are predictions suggesting that such disruptions could lead to a significant increase in HIV-related casualt COVID-19 on HIV services and development are still
unknown, there are predictions suggesting that such
disruptions could lead to a significant increase in HIV-related
casualties.
However, there is currently limited researc unknown, there are predictions suggesting that such disruptions could lead to a significant increase in HIV-related casualties.

However, there is currently limited research on predicting the trend of HIV-related death cou disruptions could lead to a significant increase in HIV-related casualties.

However, there is currently limited research on predicting

the trend of HIV-related death counts. This study will use

four different models to casualties.

However, there is currently limited research on predicting

the trend of HIV-related death counts. This study will use

four different models to predict the trend of HIV-related

death counts. Figure 1 shows t However, there is currently limited research on predicting
the trend of HIV-related death counts. This study will use
four different models to predict the trend of HIV-related
death counts. Figure 1 shows the mortality rat the trend of HIV-related death counts. This study will use
four different models to predict the trend of HIV-related
death counts. Figure 1 shows the mortality rate map of South
Africa in 2019, while Figure 2 shows the mor four different models to predict the trend of HIV-related death counts. Figure 1 shows the mortality rate map of South Africa in 2019, while Figure 2 shows the mortality rate map of Myanmar in 2019. As seen from the figure

aid.

Myanmar was collected from the Our World in Data website

Neratal particle of the number of the number of the animal south Africa from 1990 to 2019

Neratal particle in the Our World in Data website

Myanmar was collected (HIV/AIDS - Our World in Data). This source provides

Alternative manner of the number of the number of deaths increased gradually

Figure 2. The mortality rate map of Myanmar in 2019 (The number of the number of deaths be No dialom 1,000 5,000 10,000 9000 10,000 90,000 90,000 90,000 90,000 90,000 90,000 90,000 90,000 90,000 90,000 100,000 Prophet of the number of deaths increased gradually from deaths from HIV per 100,000 people).

II. MATE Ne state and the mortality rate map of Myanmar in 2019 (The number of the number of deaths began to deaths from HIV per 100,000 people).

The data related to HIV cases in South Africa and Myanmar in 2019 (The number of dea Figure 2. The mortality rate map of Myanmar in 2019 (The number of the number of deaths began to
deaths from HIV per 100,000 people).

II. MATERIALS AND METHODS

A. Data Description

The data related to HIV cases in South deaths from HIV per 100,000 people).
 H. MATERIALS AND METHODS
 A. Data Description

The data related to HIV cases in South Africa and

Myanmar was collected from the Our World in Data website

(HIV/AIDS - Our World in II. MATERIALS AND METHODS

A. Data Description

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 A. Data Description

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 A. Data Description

The data related to HIV cases in South Africa and

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The data related to HIV cases in South Africa and
Myanmar was collected from the Our World in Data website
(HIV/AIDS - Our World in Data). This source provides
comprehensive information on all HIV-relat Figure 3 illustrates the actual trend of the number of deaths

The data related to HIV cases in South Africa and

IV/AIDS - Our World in Data). This source provides

myrrehensive information on all HIV-related data, such a The data related to HIV cases in South Africa and

Myanmar was collected from the Our World in Data website

(HIV/AIDS - Our World in Data). This source provides

deaths, confirmed cases, and laboratory testing data.

Curr Myanmar was collected from the Our World in Data website

(HIV/AIDS - Our World in Data). This source provides

comprehensive information on all HIV-related data, such as

deaths, confirmed cases, and laboratory testing d

IAENG International Journal of Computer Science and it can further facilitate the efficient allocation of medical increased in a J-shaped trend of a
period, after the end of aparticular influx of foreign many social issues **nal of Computer Science**

increased in a J-shaped trend from 1990 to 2006. During this

period, after the end of apartheid in South Africa, there was a

significant influx of foreign immigrants, which also brought

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significant influx of foreign immigrants, which also brought

many soc increased in a J-shaped trend from 1990 to 2006. During this
period, after the end of apartheid in South Africa, there was a
significant influx of foreign immigrants, which also brought
many social issues such as violence, increased in a J-shaped trend from 1990 to 2006. During this
period, after the end of apartheid in South Africa, there was a
significant influx of foreign immigrants, which also brought
many social issues such as violence, increased in a J-shaped trend from 1990 to 2006. During this
period, after the end of apartheid in South Africa, there was a
significant influx of foreign immigrants, which also brought
many social issues such as violence, period, after the end of apartheid in South Africa, there was a significant influx of foreign immigrants, which also brought many social issues such as violence, drug trafficking, and prostitution. This led to a sharp incr significant influx of foreign immigrants, which also brought
many social issues such as violence, drug trafficking, and
prostitution. This led to a sharp increase in HIV infections,
making South Africa one of the countries many social issues such as violence, drug trafficking, and
prostitution. This led to a sharp increase in HIV infections,
making South Africa one of the countries with the highest
HIV infection rates in the world. However, prostitution. This led to a sharp increase in HIV infections, making South Africa one of the countries with the highest HIV infection rates in the world. However, due to inadequate healthcare resources, the country couldn' making South Africa one of the countries with the highest HIV infection rates in the world. However, due to inadequate healthcare resources, the country couldn't meet the demands of a large number of infected individuals, HIV infection rates in the world. However, due to inadequate healthcare resources, the country couldn't meet the demands of a large number of infected individuals, resulting in an increasing number of deaths due to HIV. Ho healthcare resources, the country couldn't meet the of a large number of infected individuals, resu increasing number of deaths due to HIV. How 2006 onwards, the number of deaths started to decrease. This decline is attrib

Example to the standard Constrainer
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 Commonly used kernel function
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 Commonly used kernel function
 C Example 1.5 South Africa Deathed Cases
 Example 1.5 South Africa Deathed Cases
 Example 1.5 Comparison 2003
 Example 1.6 The results of the tend in the number of deaths caused by the deplications in prediction

Fi **because South Africa is one of the countries with the highest** inction (RBF),
 because it can handle c

Figure 5. Comparison of the trend in the number of deaths caused by the

Figure 5. Comparison of the trend in the Figure 5. Comparison of the tend of the number of deaths dual basis tunction (KBF), and

Figure 5. Comparison of the trend in the number of deaths caused by the

Figure 5. Comparison of the trend in the number of deaths c Figure 5. Comparison of the trend in the number of deaths cause of the sease it can handle completed because to the HIV virus in South Africa and Myanmar form 1990 to 2019.

Figure 5 comparison of the trend in the number Figure 5. Comparison of the trend in the number of deaths clusted by the

HIV virus in South Africa and Myanmar from 1990 to 2019.

Hivar is south Africa and Myanmar from 1990 to 2019 between South Africa

and Myanmar. Fi Figure 5. Comparison of the trend in the number of deaths caused by the

HIV virus in South Africa and Myanmar from 1990 to 2019.

Eigure 5 compares the trends in the number of deaths due

to the HIV virus in objet

to th HIV virus in South Africa and Myanmar from 1990 to 2019.

Figure 5 compares the trends in the number of deaths due

small-sample test data. The obto the HIV virus from 1990 to 2019 between South Africa and Myanmar

in \frac Figure 5 compares the trends in the number of deaths due

to the HIV virus from 1990 to 2019 between South Africa

and Myanmar. First, the data for South Africa and Myanmar

is is standardized to eliminate scale differenc to the HIV virus from 1990 to 2019 between South Africa min $\frac{1}{2} ||\omega||^2 + C \sum_{i=1}^{n} \xi_i$

and Myanmar. First, the data for South Africa and Myanmar

is standardized to eliminate scale differences. Then, from the

graphs and Myanmar. First, the data for South Africa and Myanmar

is standardized to eliminate scale differences. Then, from the

graphs, we can observe that the number of deaths in South

Africa is significantly higher than in patients. aphs, we can observe that the number of deaths in South

irica is significantly higher than in Myanmar. This is

penalty parameter (C

cause South Africa is one of the countries with the highest
 ω is the coefficient Africa is significantly higher than in Myanmar. This is
because South Africa is one of the countries with the highest ω is the coefficients of
HIV infection rates globally and has a large population of
the constant par because South Africa is one of the countries with the highest ω is the coefficients of the HIV infection rates globally and has a large population of the constant parameter of HIV-religion in South Africa may lead to i HIV infection rates globally and has a large population of

HIV-infected individuals. The high infection rate leads to

more HIV-related diseases and complications, contributing to

the higher number of deaths. Additional

HIV-infected individuals. The high infection rate leads to

more HIV-related diseases and complications, contributing to

antiretroviens in South Africa may lead to issues of true and the *i*-th trai

extension the *i*-th more HIV-related diseases and complications, contributing to
the higher number of deaths. Additionally, long-term use of
antiretroviral drugs in South Africa may lead to issues of drug
state of the *i*-th sample
state of the higher number of deaths. Additionally, long-term use of
antiretroviral drugs in South Africa may lead to issues of drug
mericularity and the solene resistance, which can affect the effectiveness of treatment.
The Rando antiretroviral drugs in South Africa may lead to issues of drug

resistance, which can affect the effectiveness of treatment

resistance, impacting the treatment outcomes for certain

considered in South Africa may also ex resistance, which can affect the effectiveness of treatment

Some regions in South Africa may also experience drug

resistance, impacting the treatment outcomes for certain

patients.

The other hand, Myanmar has a smaller Some regions in South Africa may also experience drug

resistance, impacting the treatment outcomes for certain

emsemble algorithm constraines.

Moreover, Myanmar has a smaller population,

the number of decision tree

wh resistance, impacting the treatment outcomes for certain
patients.
On the other hand, Myanmar has a smaller population,
which means fewer potential transmission pathways.
Moreover, Myanmar's culture, religion, and social s The other hand, Myanmar has a smaller population, the num

inch means fewer potential transmission pathways.

Ioreover, Myanmar's culture, religion, and social structure

and reg algorith

and reg are a represented and con EXEL STAR FURE REGENSION of the User and the state of the Menastropoleal in the speed and control of HIV. Certain cultured and regression tasks.

The parterns of infection and tracture and several and regression tasks.

Th Moreover, Myanmar's culture, religion, and social structure

may influence the spread and control of HIV. Certain cultural

may influence the spread and control of HIV. Certain cultural

influencing the patterns of infecti the speed and control of HIV. Certain cultural

may influence the spread and control of HIV. Certain cultural

and social factors can affect people's behavior and attitudes,

influencing the patterns of infection and trea

and social factors can affect people's behavior and attitudes,

influencing the patterns of infection and treatment.

International organizations, non-governmental organizations,

and cooperation from other countries may influencing the patterns of infection and treatment.

International organizations, non-governmental organizations, tree, a randomly selected proport

and cooperation from other countries may have played a uddel building, International organizations, non-governmental organizations,

International organizations, non-governmental organizations,

tree, a randomly select

and cooperation from other countries may have played a

model building, w and cooperation from other countries may have played a
positive role in HIV control in Myanmar by providing
positive role in HIV control in Myanmar by providing
classification. For each sat
technical support, drug supplies From the linear expections and the linear regression containing the MGRoost model
transfer since the NGRoost models and the resources, helping and the results to reduce the number of deaths.
 B. LR, SVM, RF and XGBoost mo Exercised unions are the model is pertically that the model is a supervised element of the least support, λ and the resources, helping combines the results from model to reduce the number of deaths.

B. LR, SVM, RF and to reduce the number of deaths.

B. LR, SVM, RF and XGBoost models

Linear regression (LR) [24] is a method that transforms multiple trees.

input variables through a linear combination to predict the The XGBoost models
 evaluation of the model of the model of the model of the transforms predictions, and in regression B . LR, SVM, RF and XGBoost models the model in the set set of the model in the model in the star equivalent term combina B. LR, SVM, RF and XGBoost models

predicted values on the test se

Linear regression (LR) [24] is a method that transforms multiple trees.

input variables through a linear combination to predict the TR XGBoost model [20 Linear regression (LR) [24] is a method that transforms multiple trees.
input variables through a linear combination to predict the The XGBoost model [20]-
target value. Linear regression offers advantages such as algorit input variables through a linear combination to predict the The XGBoost model larget value. Linear regression offers advantages such as signithm based on decision
simplicity in form, ease of modeling, and embodies science target value. Linear regression offers advantages such as algorithm based on decision t
simplicity in form, ease of modeling, and embodies science. By using an internal a
fundamental concepts in machine learning. Specific simplicity in form, ease of modeling, and embodies
science. By using an fundamental concepts in machine learning. Specifically, it results from multiple in
constructs one or multiple models to describe the relationship
he

**Support Vector Machine (SVM) [25] is a powerful
pervised machine learning model primarily used for
ssification and regression tasks. SVM aims to find the
timal hyperplane that best separates different classes in a
the dim nal of Computer Science**

Support Vector Machine (SVM) [25] is a powerful

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Support Vector Machine (SVM) [25] is a powerful

supervised machine learning model primarily used for

classification and regression tasks. SVM aims to find the

optimal hyperplane that best sepa **Example 18 Computer Science**

Support Vector Machine (SVM) [25] is a powerful

supervised machine learning model primarily used for

classification and regression tasks. SVM aims to find the

optimal hyperplane that best Support Vector Machine (SVM) [25] is a powerful supervised machine learning model primarily used for classification and regression tasks. SVM aims to find the optimal hyperplane that best separates different classes in a h Support Vector Machine (SVM) [25] is a powerful supervised machine learning model primarily used for classification and regression tasks. SVM aims to find the optimal hyperplane that best separates different classes in a h Support Vector Machine (SVM) [25] is a powerful supervised machine learning model primarily used for classification and regression tasks. SVM aims to find the optimal hyperplane that best separates different classes in a h supervised machine learning model primarily used for classification and regression tasks. SVM aims to find the optimal hyperplane that best separates different classes in a high-dimensional feature space. 'Support vectors' classification and regression tasks. SVM aims to find the
optimal hyperplane that best separates different classes in a
high-dimensional feature space. 'Support vectors' are the data
points closest to the decision boundar optimal hyperplane that best separates different classes in a
high-dimensional feature space. 'Support vectors' are the data
points closest to the decision boundary. The effectiveness of
SVM lies in its ability to handle high-dimensional feature space. 'Support vectors' are the data
points closest to the decision boundary. The effectiveness of
SVM lies in its ability to handle complex data relationships
and generalize well to new, unseen periorinance can be infinienced by the choce of kenter
functions and hyperparameters, which require careful tuning.
Commonly used kernel functions include linear, polynomial,
radial basis function (RBF), and sigmoid kerne functions and nyperparameters, which require eare
and hamis. Commonly used kernel functions include linear, polynomial,
radial basis function (RBF), and sigmoid kernels. SVM finds
because it can handle complex data relati

$$
\min \frac{1}{2} ||\omega||^2 + C \sum_{i=1}^n \xi_i, s.t. y_i (\omega^T x_i + b) \ge 1 - \xi_i \quad (1)
$$

$$
\xi_i \ge 0, i = 1, 2, \cdots, n,
$$

countinuity sisted action (RBF), and sigmoid kernels. SVM finds
wide applications in prediction and classification tasks
because it can handle complex data relationships and
generalize well to new data. SVM models perform wide applications in prediction and classification tasks
because it can handle complex data relationships and
generalize well to new data. SVM models perform well in
classifying numerical samples and are suitable for
smal where uppreciations in Processor in the complex data relationships and generalize well to new data. SVM models perform well in classifying numerical samples and are suitable for small-sample test data. The objective funct classifying numerical samples and are suitable for
small-sample test data. The objective function is as follows:
 $\min \frac{1}{2} ||\omega||^2 + C \sum_{i=1}^n \xi_i, s.t.y_i(\omega^T x_i + b) \ge 1 - \xi_i$ (1)
 $\xi_i \ge 0, i = 1, 2, \dots, n$,
where *n* represents the n aall-sample test data. The objective function is as follows:
 $\min \frac{1}{2} ||\omega||^2 + C \sum_{i=1}^n \xi_i, s.t. y_i (\omega^T x_i + b) \ge 1 - \xi_i$ (1)
 $\xi_i \ge 0, i = 1, 2, \dots, n$,

here *n* represents the number of test samples; *C* is the

nalty paramete min $\frac{1}{2} ||\omega||^2 + C \sum_{i=1}^n \xi_i$, $s.t.\mathcal{Y}_i(\omega^T x_i + b) \ge 1 - \xi_i$ (1)
 $\xi_i \ge 0, i = 1, 2, \dots, n$,

where *n* represents the number of test samples; *C* is the

penalty parameter $(C > 0)$; ξ represents the slack variable,
 $\$ min $\frac{1}{2}||\omega|| + C \sum_{i=1} \xi_i, s.t.y_i(\omega \cdot x_i + b) \ge 1 - \xi_i$ (1)
 $\xi_i \ge 0, i = 1, 2, \dots, n$,

where *n* represents the number of test samples; *C* is the

penalty parameter $(C > 0)$; ξ represents the slack variable,
 ω is the co

 $\xi_i \geq 0, i = 1, 2, \dots, n$,
where *n* represents the number of test samples; *C* is the
penalty parameter $(C > 0)$; ξ represents the slack variable,
 ω is the coefficients of the separating hyperplane, and *b* is
the con where *n* represents the number of test samples; *C* is the penalty parameter $(C > 0)$; ξ represents the slack variable, ω is the coefficients of the separating hyperplane, and *b* is the constant parameter of the se where *n* represents the number of test samples; C is the penalty parameter $(C > 0)$; ξ represents the slack variable, ω is the coefficients of the separating hyperplane, and *b* is the constant parameter of the sepa behavity parameter $(C > 0)$; ζ represents the slack variable,
 ω is the coefficients of the separating hyperplane, and *b* is

the constant parameter of the separating hyperplane. Both of

these parameters need to b ω is the coefficients of the separating hyperplane, and b is
the constant parameter of the separating hyperplane. Both of
these parameters need to be obtained through model training.
 x_i represents the *i*-th traini the constant parameter of the separating hyperplane. Both of
these parameters need to be obtained through model training.
 x_i represents the *i*-th training sample, and y_i represents the
state of the *i*-th sample corr these parameters need to be obtained through model training.
 x_i represents the *i*-th training sample, and y_i represents the

state of the *i*-th sample corresponding to the path node.

The Random Forest algorithm [2 x_i represents the *i*-th training sample, and y_i represents the state of the *i*-th sample corresponding to the path node.
The Random Forest algorithm [26] is an improvement and extension of the decision tree algorith state of the *i*-th sample corresponding to the path node.
The Random Forest algorithm [26] is an improvement and
extension of the decision tree algorithm. It's a type of
ensemble algorithm constructed based on the princip The Random Forest algorithm [26] is an improvement and
extension of the decision tree algorithm. It's a type of
ensemble algorithm constructed based on the principles of
statistical sampling. Two key parameters in this alg extension of the decision tree algorithm. It's a type of
ensemble algorithm constructed based on the principles of
statistical sampling. Two key parameters in this algorithm are
the number of decision trees built and the n ensemble algorithm constructed based on the principles of statistical sampling. Two key parameters in this algorithm are the number of decision trees built and the number of features considered in each individual tree. The statistical sampling. Two key parameters in this algorithm are
the number of decision trees built and the number of features
considered in each individual tree. The Random Forest
algorithm can achieve favorable results for the number of decision trees built and the number of features
considered in each individual tree. The Random Forest
algorithm can achieve favorable results for both classification
and regression tasks. By utilizing resampl considered in each individual tree. The Ra
algorithm can achieve favorable results for both
and regression tasks. By utilizing resampli
samples are drawn from the original dataset, and
generates its own independent decisio gorithm can achieve favorable results for both classification
d regression tasks. By utilizing resampling, multiple
mples are drawn from the original dataset, and each sample
nerates its own independent decision tree. In e and regression tasks. By utilizing resampling, multiple samples are drawn from the original dataset, and each sample generates its own independent decision tree. In each decision tree, a randomly selected proportion of the samples are drawn from the original dataset, and each sample
generates its own independent decision tree. In each decision
tree, a randomly selected proportion of the data is used for
model building, while the remaining da generates its own independent decision tree. In each decision
tree, a randomly selected proportion of the data is used for
model building, while the remaining data is used for
validation. For each sample in the test set, t

tree, a randomly selected proportion of the data is used for model building, while the remaining data is used for validation. For each sample in the test set, the model combines the results from multiple decision trees. In model building, while the remaining data is used for validation. For each sample in the test set, the model combines the results from multiple decision trees. In classification problems, it uses majority voting to make pre validation. For each sample in the test set, the model
combines the results from multiple decision trees. In
classification problems, it uses majority voting to make
predictions, and in regression problems, it calculates t combines the results from multiple decision trees. In classification problems, it uses majority voting to make predictions, and in regression problems, it calculates the predicted values on the test set by averaging the re classification problems, it uses majority voting to make
predictions, and in regression problems, it calculates the
predicted values on the test set by averaging the results from
multiple trees.
The XGBoost model [20]-[22 predictions, and in regression problems, it calculates the
predicted values on the test set by averaging the results from
multiple trees.
The XGBoost model [20]-[22] is a machine learning
algorithm based on decision trees predicted values on the test set by averaging the results from
multiple trees.
The XGBoost model [20]-[22] is a machine learning
algorithm based on decision trees, widely used in data
science. By using an internal algorit algorithm based on decision trees, widely used in data
science. By using an internal algorithm that combines the
results from multiple individual trees, XGBoost can generate
accurate predictions[23]. Additionally, this mo science. By using an internal algorithm that combines the
results from multiple individual trees, XGBoost can generate
accurate predictions[23]. Additionally, this model provides
rankings for input features. Furthermore,

$$
Y' = \sum_{i=1}^{n} (y_i, \hat{y}^{(t-1)} + f_t(x_i)) + \Omega(f_t),
$$
 (2)

the feature vector and label of the *i* -th instance, $\hat{v}^{(t-1)}$

IAENG International Journal of Computer Science
represents the prediction of the *i* -th instance at the $(t-1)$ -th data, while Figure 7 represents the predictive
iteration, f_t represents the new tree that classifies t **IAENG International Journal of Computer Scie**
represents the prediction of the *i* -th instance at the $(t-1)$ -th data, while Figure 7 repres
iteration, f_t represents the new tree that classifies the *i* -th testing dat **IAENG International Journal of Computer Science**
represents the prediction of the *i*-th instance at the $(t-1)$ -th data, while Figure 7 represents
iteration, f_i represents the new tree that classifies the *i*-th testin **IAENG International Journal of Convertises**
represents the prediction of the *i*-th instance at the $(t-1)$ -th data, while
iteration, f_t represents the new tree that classifies the *i*-th testing dat
instance using x_i **IAENG International Journ**
presents the prediction of the *i*-th instance at the $(t-1)$ -th deration, f_t represents the new tree that classifies the *i*-th the stance using x_t , and represents the regularization term t **TAENG International Journal of Computer Scien**

DENG International Journal of Computer Scien

The presents the prediction of the *i*-th instance at the $(t-1)$ -th data, while Figure 7 represent

testing data. The blue cur **IAENG International Journal of Computer**

represents the prediction of the *i*-th instance at the $(t-1)$ -th data, while Figure 7 re

iteration, f_i represents the new tree that classifies the *i*-th testing data. The bl **IAENG International Journal of Computer Science**

represents the prediction of the *i*-th instance at the $(t-1)$ -th data, while Figure 7 represents the

iteration, f_i represents the new tree that classifies the *i*-th represents the prediction of the *i*-th instance at
iteration, f_t represents the new tree that class
instance using x_t , and represents the regulariza
penalizes the complexity of the new tree.
C. Models performance me between the prediction of the *i*-th instance at the $(t-1)$ -th data, while

tration, f_i represents the new tree that classifies the *i*-th testing da

tance using x_i , and represents the regularization term that

maliz

stance using x_i , and represents the regularization term that
nalizes the complexity of the new tree.
 C. Models performance measures

To evaluate the performance of each of the models

entioned above, commonly used ac To evaluate the performance of each of the models

entioned above, commonly used accuracy measurement

thods were applied. The performance functions are as
 $\frac{1}{2}$

Mean Absolute Percentage Error (MAPE):
 $MAPE = \frac{100\%}{$

$$
MAPE = \frac{100\%}{N} \sum_{i=1}^{n} \frac{|\tilde{\omega}_i - \omega_i|}{\omega_i};
$$
 (3) of each model
represents the a

$$
MAE = \frac{1}{N} \sum_{i=1}^{n} |\tilde{\omega}_i - \omega_i|;
$$
 (4) the Linear Regression
represents the XGF

Mean Absolute Percentage Error (MAPE):
\n
$$
MAPE = \frac{100\%}{N} \sum_{i=1}^{n} \frac{|\tilde{\omega}_{i} - \omega_{i}|}{\omega_{i}};
$$
\nMean absolute error (MAE):
\nMean absolute error (MAE):
\n
$$
MAE = \frac{1}{N} \sum_{i=1}^{n} |\tilde{\omega}_{i} - \omega_{i}|;
$$
\n(3) of each model's
\nSVM model's
\nRandom Forest r
\nRandom Forest r
\nRoot mean square error (RMSE):
\n
$$
RMSE = \sqrt{\frac{1}{N} \sum_{i=1}^{n} (\omega_{i} - \tilde{\omega}_{i})^{2}};
$$
\n(4) the Linear Regres
\nresults are more
\nRegression mode
\nand XGBoost model
\nthe evaluation me
\nof 18.3070%, and
\nthe evaluation me

$$
MSE = \frac{1}{N} \sum_{i=1}^{n} (\omega_i - \tilde{\omega}_i)^2;
$$
 (6) of 0.0374, an MSE of 18.3070%, and a

Pinball:

$$
L_{\tau}(y, z) = \begin{cases} (\omega_i - \tilde{\omega}_i)\tau, & \omega_i \ge \tilde{\omega}_i, \\ (\omega_i - \tilde{\omega}_i)(1 - \tau), & \omega_i < \tilde{\omega}_i. \end{cases}
$$
 7
(7) Forest, and XGBoost are shown in T
results of deaths in Myanmar, the L
0.0202, an MSE of 0.0005, an PMS

 $RMSE = \sqrt{\frac{1}{N} \sum_{i=1}^{N} (\omega_i - \tilde{\omega}_i)^2$;

Mean Square Error (MSE):

The prediction results

mod XGBoost model.

Massenglands in South Africa she is south Africa she in South Africa she in South Africa she is small:

Pinball mentous above; contained by increase the controller intended by different models for So-

menthods were applied. The performance functions are as $\frac{1}{9 \text{ shows the coupling}}$.

Mann Absolute Percentage Error (MAPE):

Mann Absolute Per Mean Square Error (MSE):

leads in South Africa show the

levaluation metrics of the other

l $MSE = \frac{1}{N} \sum_{i=1}^{n} (\omega_i - \tilde{\omega}_i)^2;$ (6) of 0.0374, an MSE of 0.00

Pinball:

Pinball:
 $L_r(y,z) = \begin{cases} (\omega_i - \tilde{\omega}_i) \tau, & \omega_i \ge \tilde{\omega}_i, \\ (\omega_i - \tilde{\omega}_i)(1-\tau), & \omega_i < \tilde{\omega}_i. \end{cases}$ (7) prediction results evaluat

In these above equation $MSE = \frac{1}{N} \sum_{i=1}^{N} (\omega_i - \omega_i)$;

(6) 618.3070%, and a Pinbal

the evaluation metrics of the sealuation coulds the eva Pinball:
 $L_r(y,z) = \begin{cases} (\omega_i - \tilde{\omega}_i)\tau, & \omega_i \ge \tilde{\omega}_i, \\ (\omega_i - \tilde{\omega}_i)(1-\tau), & \omega_i < \tilde{\omega}_i. \end{cases}$ prediction results evaluation metrics of the other

in these above equations (3)-(7), N, ω_i and $\tilde{\omega}_i$ represent 18.75849%, and Findial!
 $L_r(y,z) = \begin{cases} (\omega_i - \tilde{\omega}_i)\tau, & \omega_i \ge \tilde{\omega}_i, \\ (\omega_i - \tilde{\omega}_i)(1-\tau), & \omega_i < \tilde{\omega}_i. \end{cases}$ Forest, and XGBoost are shown

The mumber of observations, actual values, and predicted of deaths in Myanmar, the

In these above equa $L_r(y,z) = \begin{cases} (\omega_i - \tilde{\omega}_i)\tau, & \omega_i \geq \tilde{\omega}_i, \\ (\omega_i - \tilde{\omega}_i)(1-\tau), & \omega_i < \tilde{\omega}_i. \end{cases}$ Forest, and XGBoost are shown in
the number of observations (3)-(7), N, ω_i and $\tilde{\omega}_i$ represent 18.7549%, and a Pinball of 0.01
the numbe $L_r(y, z) = \begin{cases} (\omega_i - \tilde{\omega}_i)(1-\tau), & \omega_i < \tilde{\omega}_i, \\ (\omega_i - \tilde{\omega}_i)(1-\tau), & \omega_i < \tilde{\omega}_i, \\ (\omega_i - \tilde{\omega}_i)(1-\tau), & \omega_i < \tilde{\omega}_i \end{cases}$ results of deaths in Myanmar,
In these above equations (3)-(7), N, ω_i and $\tilde{\omega}_i$ represent 0.0203, an MSE o ($(\omega_i - \omega_i)(1 - \epsilon)$, $\omega_i \times \omega_i$,

In these above equations (3)-(7), N, ω_i and $\tilde{\omega}_i$ represent 18.7549%, and a Pinball of 0.0

the number of observations, actual values, and predicted other three models. The evaluat

v In these above equations (3)-(7), N , ω_i and $\tilde{\omega}_i$ represent 18.7549% , and a Pinball of
the number of observations, actual values, and predicted other three models. The eva
values, respectively, while $\omega_i - \tilde{\$ the number of observations, actual values, and predicted other three models. The values, respectively, while $\omega_i - \tilde{\omega}_i$ represents the error results of other models abetween predicted values and actual values. MAE is t and mathematic of observations, actuan values, and predicted
values, respectively, while $\omega_i - \tilde{\omega}_i$ represents the error
between prediction errors between predicted values and actual values. MAE is the
artifinetic mean values, respectively, while $\omega_i - \omega_i$ represents the error
between prediction results
between predicted values and actual values. MAE is the
arithmetic mean of the absolute errors between predicted
of 18.3070%, and a Pinb between predicted values and actual values. MAE is the
arithmetic mean of the absolute errors between predicted
of 0.
values and true values, providing the average of absolute
of 1?
prediction errors. MSE is a loss functio the metic mean of the absolute errors between predicted

dof 0.0374, an MSE of 0.0014

dediction errors. MSE is a loss function used to measure the

dediction errors. MSE is a loss function used to measure the

unrespected values and true values, providing the average of absolute

prediction errors. MSE is a loss function used to measure the

error between predicted values and true values. RMSE is the prediction results evaluation in

square an squared error and is often used to

i between predicted values and true

ssed as a percentage and represents the

i actual values and predicted values,

age absolute percentage difference

redicted values. Pinball is al Examples the differences between predicted values and true

In the range error between actual values and represents the 0.0203, an MSE of 0.0005, an R

In the range error between actual values and predicted values.

In the

accurate.

calculating the average absolute percentage difference of the three models. The evaluation function used to evaluate the accuracy of quantile forecasts, the LR model is often models are show where τ represents the targe Solution use the coural and predicted values. Pinball is also a loss

fresults of other models are shown

function used to vealuate the accuracy of quantile forceasts,

where τ represents the target quantile.

When MAPE The LR model is often the secure of the accuracy of quantile forecasts,

where Terresting the area equantile.

When MAPE, RMSE, MAE, MSE, and Pinball values

are considered more that of other models. The operator

accurate where T represents the target quantile.

When MAPE, RMSE, MAE, MSE, and Pinball values

approach zero, the prediction results are considered more

that of other models. The overacurate.

III. RESULTS

III. RESULTS

III. RE When MAPE, RMSE, MAE, MSE, and Pinball values
approach zero, the prediction results are considered more
that of other models. The
accurate. Africa is not linear model performs better
accurate. Africa is not linear model pe

nal of Computer Science

data, while Figure 7 represents the predictions for Myanmar's

testing data. The blue curve represents the data from the

testing set, and the red curve represents the predicted data

using diffe **nal of Computer Science**

data, while Figure 7 represents the predictions for Myanmar's

testing data. The blue curve represents the data from the

testing set, and the red curve represents the predicted data

using diffe **nal of Computer Science**

data, while Figure 7 represents the predictions for Myanmar's

testing data. The blue curve represents the data from the

testing set, and the red curve represents the predicted data

using diffe **nal of Computer Science**

data, while Figure 7 represents the predictions for Myanmar's

testing data. The blue curve represents the data from the

testing set, and the red curve represents the predicted data

using diffe **nal of Computer Science**
data, while Figure 7 represents the predictions for Myanmar's
testing data. The blue curve represents the data from the
testing set, and the red curve represents the predicted data
using different **nal of Computer Science**
data, while Figure 7 represents the predictions for Myanmar's
testing data. The blue curve represents the data from the
testing set, and the red curve represents the predicted data
using different **nal of Computer Science**

data, while Figure 7 represents the prediction

testing data. The blue curve represents the

testing set, and the red curve represents the

using different models. The learning results

figures. **If of Computer Science**
 Example 8 Figure 7 represents the predictions for Myanmar's
 Example 8 and the red curve represents the data from the
 Example 8 and the red curve represents the predicted data
 Example 18 nal of Computer Science
data, while Figure 7 represents the predictions for Myanmar's
testing data. The blue curve represents the data from the
testing set, and the red curve represents the predicted data
using different **The comparison for Computer Science**
 Example 19 shows the comparist the predictions for Myanmar's
 Example 18 data. The blue curve represents the data from the
 Example of the comparistion for Myanmar's
 Example 1

IAENG International Journal of Computer Science

The *i*-th instance at the $(t-1)$ -th data, while Figure 7 represents the predictions for Myanm

new tree that classifies the *i*-th testing data. The blue curve represent nce at the $(t-1)$ -th data, while Figure 7 reprections if the interval interval intervalses the *i*-th testing data. The blue conductions term that the reduction of the models three models. Figure 8 presents a predicted by $N \left(\frac{N}{n-1} \right)$ *o_i* σ represents the actual test data, the orange 1 **Example 12**
 Example 16 Computer Science

tance at the $(t-1)$ -th data, while Figure 7 represents the predictions

tat classifies the *i*-th testing data. The blue curve represents the

regularization term that using di $=\frac{100\%}{N}\sum_{i=1}^{n} \frac{|\tilde{\omega}_i - \omega_i|}{\omega_i}$; (3) data for HTV-related dealing, providing a more intuitive view EXIG International Journal of Computer Science

the instance at the $(t-1)$ -th data, while Figure 7 represents the predictions for Myan

the retar data from the testing data. The blue curve represents the data from

the re Examples the LR models

figures. From Figures

the LR model yields be

each of the models

figures. From Figures

three models.

Figure 8 presents

predicted by different

innce functions are as

predicted by different
 represents the XGBoost model's predictions. The comparison **IG International Journal of Computer Science**

Instance at the $(t-1)$ -th data, while Figure 7 represents the predictio

that classifies the *i*-th testing data. The blue curve represents the

regularization term that tes **IAENG International Journal of Computer Science**

the *i*-th instance at the (*t*-1)-th data, while Figure 7 represents the predictions for Myanmar's

new tree that classifies the *i*-th testing data. The blue curve repr **NG International Journal of Computer Science**

instance at the $(t-1)$ -th data, while Figure 7 represents the predictions for Myanma

instance at the $(t-1)$ -th data, while Figure 7 represents the predictions for Myanma

t *i i* and XGBoost model.
The prediction results for the number of HIV-related **5 International Journal of Computer Science**

stance at the $(i-1)$ -th data, while Figure 7 represents the prediction

that classifies the i -th testing data. The blue curve represents the

gegularization term that using **IAENG International Journal of Computer Science**

f the *i*-th instance at the $(n-1)$ -th data, while Figure 7 represents the predictions for Myanmar's

respective that elsistifies the *i*-th testing data. The blue curve Instance at the two-the material to the time that with the red atternation of the experiment in the tect of each of the model is the time set, and the red curve represents the predicted data from the regularization term t $\left(\frac{\delta_i - \omega_i}{\omega_i}\right)$; and the UN-related deal
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we tree that classifies the *i*-th testing data. The blue curve represents the data from the
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testing data. The blue curve represents the data from the
testing set, and the red curve represents the predicted data
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testing data. The blue curve represents the data from the
testing set, and the red curve represents the predicted data
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testing data. The blue curve represents the data from the
testing set, and the red curve represents the predicted data
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figures. From Figures 6 and 7, we can roughly observe that
the LR model yields better predictions c using different models. The learning results are shown in the figures. From Figures 6 and 7, we can roughly observe that the LR model yields better predictions compared to the other three models. Figure 8 presents a compar figures. From Figures 6 and 7, we can roughly observe that
the LR model yields better predictions compared to the other
three models.
Figure 8 presents a comparison of the death trends
predicted by different models for Sou the LR model yields better predictions compared to the other
three models.
Figure 8 presents a comparison of the death trends
predicted by different models for South Africa, while Figure
9 shows the comparison for Myanmar. three models.

Figure 8 presents a comparison of the death trends

predicted by different models for South Africa, while Figure

9 shows the comparison for Myanmar. These figures display

the predictions of all four models Figure 8 presents a comparison of the death trends
predicted by different models for South Africa, while Figure
9 shows the comparison for Myanmar. These figures display
the predictions of all four models alongside the act predicted by different models for South Africa, while Figure
9 shows the comparison for Myanmar. These figures display
the predictions of all four models alongside the actual test
data for HIV-related deaths, providing a m 9 shows the comparison for Myanmar. These figures
the predictions of all four models alongside the ac
data for HIV-related deaths, providing a more intuiti
of each model's prediction performance. The bi
represents the actu e predictions of all four models alongside the actual test
ta for HIV-related deaths, providing a more intuitive view
each model's prediction performance. The blue line
presents the actual test data, the orange line repres data for HIV-related deaths, providing a more intuitive view
of each model's prediction performance. The blue line
represents the actual test data, the orange line represents the
SVM model's predictions, the green line rep of each model's prediction performance. The blue line
represents the actual test data, the orange line represents the
SVM model's predictions, the green line represents the
Random Forest model's predictions, the red line r represents the actual test data, the orange line represents the
SVM model's predictions, the green line represents the
Random Forest model's predictions, the red line represents
the Linear Regression model's predictions, a

of 18.3070%, and a Pinball of 0.0187, which are better than the evaluation metrics of the other three models. The specific AE):
 $\frac{1}{N} = \frac{1}{N} \sum_{i=1}^{n} |\tilde{\omega}_i - \omega_i|$;
 $\overline{\zeta} = \sqrt{\frac{1}{N} \sum_{i=1}^{n} (\omega_i - \tilde{\omega}_i)^2}$;
 $\overline{\zeta} = \frac{1}{N} \sum_{i=1}^{n} (\omega_i - \tilde{\omega}_i)^2$;
 $\overline{\zeta} = \frac{1}{N} \sum_{i=1}^{n} (\omega_i - \tilde{\omega}_i)^2$;
 $\overline{\zeta} = \frac{1}{N} \sum_{i=1}^{n} (\omega_i - \tilde{\omega}_i)^2$; = $\frac{1}{N} \sum_{i=1}^{n} |\tilde{\omega}_i - \omega_i|$;

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Mean Square Error (MSE):

MSE = $\frac{1}{N}\sum_{i=1}^{n} (\omega_i - \tilde{\omega}_i)^2$;

MSE = $\frac{1}{N}\sum_{i=1}^{n} (\omega_i - \tilde{\omega}_i)^2$ SVM model's predictions, the green line represents the Random Forest model's predictions, the red line represents the Linear Regression model's predictions, and the purple line represents the XGBoost model's predictions. T Random Forest model's predictions, the red line represents
the Linear Regression model's predictions, and the purple line
represents the XGBoost model's predictions. The comparison
results are more clearly displayed here, the Linear Regression model's predictions, and the purple line
represents the XGBoost model's predictions. The comparison
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Regression model having predictions closest represents the XGBoost model's predictions. The comparison
results are more clearly displayed here, with the Linear
Regression model having predictions closest to the actual
values, followed by the SVM model, Random Forest results are more clearly displayed here, with the Linear
Regression model having predictions closest to the actual
values, followed by the SVM model, Random Forest model,
and XGBoost model.
The prediction results for the n Regression model having predictions closest to the actual
values, followed by the SVM model, Random Forest model,
and XGBoost model.
The prediction results for the number of HIV-related
deaths in South Africa show that the values, followed by the SVM model, Random Forest model,
and XGBoost model.
The prediction results for the number of HIV-related
deaths in South Africa show that the LR model has an MAE
of 0.0374, an MSE of 0.0014, an RMSE and XGBoost model.
The prediction results for the number of HIV-related
deaths in South Africa show that the LR model has an MAE
of 0.0374, an MSE of 0.0014, an RMSE of 0.0383, an MAPE
of 18.3070%, and a Pinball of 0.0187, The prediction results for the number of HIV-related
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18.3070%, and a Pinball of 0.0187, which are better than
e ev deaths in South Africa show that the LR model has an MAE
of 0.0374, an MSE of 0.0014, an RMSE of 0.0383, an MAPE
of 18.3070%, and a Pinball of 0.0187, which are better than
the evaluation metrics of the other three models. of 0.0374, an MSE of 0.0014, an RMSE of 0.0383, an MAPE
of 18.3070%, and a Pinball of 0.0187, which are better than
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prediction results evaluation metrics for S of 18.3070%, and a Pinball of 0.0187, which are better than
the evaluation metrics of the other three models. The specific
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Forest, and XGBoost are shown in Table I.

the evaluation metrics of the other three models. The specific
prediction results evaluation metrics for SVM, LR, Random
Forest, and XGBoost are shown in Table I. For the prediction
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Forest, and XGBoost are shown in Table I. For the prediction
results of deaths in Myanmar, the LR model has an MAE of
0.0203, an MSE of 0.0005, an RMSE of 0.0219, a Forest, and XGBoost are shown in Table I. For the prediction
results of deaths in Myanmar, the LR model has an MAE of
0.0203, an MSE of 0.0005, an RMSE of 0.0219, a MAPE of
18.7549%, and a Pinball of 0.0101, which is super results of deaths in Myanmar, the LR model has an MAE of 0.0203, an MSE of 0.0005, an RMSE of 0.0219, a MAPE of 18.7549%, and a Pinball of 0.0101, which is superior to the other three models. The evaluation metrics for the 0.0203, an MSE of 0.0005, an RMSE of 0.0219, a MAPE of 18.7549%, and a Pinball of 0.0101, which is superior to the other three models. The evaluation metrics for the prediction results of other models are shown in Table I 18.7549%, and a Pinball of 0.0101, which is superior to the other three models. The evaluation metrics for the prediction results of other models are shown in Table II. The prediction results for the number of HIV-related other three models. The evaluation metrics for the prediction
results of other models are shown in Table II.
The prediction results for the number of HIV-related
deaths in South Africa show that the LR model has an MAE
of results of other models are shown in Table II.
The prediction results for the number of HIV-related
deaths in South Africa show that the LR model has an MAE
of 0.0374, an MSE of 0.0014, an RMSE of 0.0383, an MAPE
of 18.307 The prediction results for the number of HIV-related
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0.0374, an MSE of 0.0014, an RMSE of 0.0383, an MAPE
18.3070%, and a Pinball of 0.0187, which are better than
e ev deaths in South Africa show that the LR model has an MAE
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of 18.3070%, and a Pinball of 0.0187, which are better than
the evaluation metrics of the other three models. of 0.0374, an MSE of 0.0014, an RMSE of 0.0383, an MAPE
of 18.3070%, and a Pinball of 0.0187, which are better than
the evaluation metrics of the other three models. The specific
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the evaluation metrics of the other three models. The specific
prediction results evaluation metrics for SVM, LR, Random
Forest, and XGBoost are shown in Table I.

values. MAPE is expressed as a percentage and represents the

average error between actual values and predicted values, $\frac{18.7549\%}{18.7549\%}$, and a Pinball of C

between actual and predicted values. Pinball is also a average error between actual values and predicted values,

calculating the average absolute percentage difference

between actual and predicted values. Pinball is also a loss

function used to evaluate the accuracy of qua the evaluation metrics of the other three models. The specific
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Forest, and XGBoost are shown in Table I. For the prediction
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Forest, and XGBoost are shown in Table I. For the prediction
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0.0203, an MSE of 0.0005, an RMSE of 0.0219, a Forest, and XGBoost are shown in Table I. For the prediction
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0.0203, an MSE of 0.0005, an RMSE of 0.0219, a MAPE of
18.7549%, and a Pinball of 0.0101, which is super results of deaths in Myanmar, the LR model has an MAE of 0.0203, an MSE of 0.0005, an RMSE of 0.0219, a MAPE of 18.7549%, and a Pinball of 0.0101, which is superior to the other three models. The evaluation metrics for the 0.0203, an MSE of 0.0005, an RMSE of 0.0219, a MAPE of 18.7549%, and a Pinball of 0.0101, which is superior to the other three models. The evaluation metrics for the prediction results of other models are shown in Table I 18.7549%, and a Pinball of 0.0101, which is superior to the other three models. The evaluation metrics for the prediction results of other models are shown in Table II. The LR model is often used as a baseline model for co other three models. The evaluation metrics for the prediction
results of other models are shown in Table II.
The LR model is often used as a baseline model for
comparison with other more complex models. In some cases,
the results of other models are shown in Table II.
The LR model is often used as a baseline model for
comparison with other more complex models. In some cases,
the performance of a linear model may unexpectedly surpass
that of The LR model is often used as a baseline model for comparison with other more complex models. In some cases, the performance of a linear model may unexpectedly surpass that of other models. The overall trend of HIV in Sout comparison with other more complex models. In some cases, the performance of a linear model may unexpectedly surpass that of other models. The overall trend of HIV in South Africa is not linear, but the prediction results

Example 10
 Example Predictions
 For example Predictions
 $\frac{1}{2019}$
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Figure 9. Comparison of different learning models in predicting death

trends in Myanmar.

Figure 9. Comparison of different learning models **Example Predictions**
 Example Predictions

Figure 9. Comparison of different learning models in predicting death

Figure 9. Comparison of different learning models in predicting death

trends in Myanmar.

IV. DISCUSSIO Figure 9. Comparison of different learning models in predicting death

Figure 9. Comparison of different learning models in predicting death

Trends in Myanmar.

The decline is separal downward trend, though the decline i Figure 9. Comparison of different learning models in predicting death

trends in Myanmar.

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IV. DISCUSSION

Figure 10 presents the trend prediction of HIV mortality in

SOUM Africa from 2020 to 2023. The blu Figure 9. Comparison of different learning models in predicting death

trends in Myanmar.

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IV. DISCUSSION

Eigure 10 presents the trend prediction of HIV mortality in

South Africa from 2 Example 10 presents the trend prediction of HIV mortality in

Example 10 presents the trend prediction of HIV mortality in

South Africa from 2020 to 2023. The blue line represents

South Africa from 2020 to 2023. The blu representing the estimated minimum. The data is sourced Figure 10 presents the trend prediction of HIV mortality in

South Africa from 2020 to 2023. The blue line represents

historical actual data, while the red line indicates future

forecast data. It shows that over the next Figure 10 presents the trend prediction of HIV mortality in

South Africa from 2020 to 2023. The blue line represents

historical actual data, while the red line indicates future

forecast data. It shows that over the next Figure 10 presents the trend prediction of HIV mortality in

South Africa from 2020 to 2023. The blue line represents

Inistorical actual data, while the red line indicates future

forceast data. It shows that over the ne South Africa from 2020 to 2023. The blue line represents

historical actual data, while the red line indicates future

forecast data. It shows that over the next four years,

exhibiting a general downward trend, though the historical actual data, while the red line indicates future
forecast data. It shows that over the next four years, the
annual number of deaths is expected to decrease year by year,
relatively slow. The figure also provides forecast data. It shows that over the next four years, the

annual number of deaths is expected to decrease year by year,

exhibiting a general downward trend, though the decline is

relatively slow. The figure also provid annual number of deaths is expected to decrease year by year,

exhibiting a general downward trend, though the decline is

relatively slow. The figure also provides the estimated range

ostimated maximum number of deaths a exhibiting a general downward trend, though the decline is

relatively slow. The figure also provides the estimated range

estimated maximum number of deaths and the green line

representing the estimated minimum. The data relatively slow. The figure also provides the estimated ra
of HIV deaths, with the yellow line representing
estimated maximum number of deaths and the green
representing the estimated minimum. The data is sout
from the AID HIV deaths, with the yellow line representing the

imated maximum number of deaths and the green line

oresenting the estimated minimum. The data is sourced

to the end of 2022. Figure 11 depicts the trend prediction

HIV estimated maximum number of deaths and the green line

representing the estimated minimum. The data is sourced

from the AIDSinfo website, with the forecast data extending

of the end of 2022. Figure 11 depicts the trend p representing the estimated minimum. The data is sourced
from the AIDSinfo website, with the forecast data extending
up to the end of 2022. Figure 11 depicts the trend prediction
of HIV mortality in Myanmar from 2020 to 202 From the AIDSinfo website, with the forecast data extending
up to the end of 2022. Figure 11 depicts the trend prediction
of HIV mortality in Myanmar from 2020 to 2023, with the
blue line illustrating historical actual dat up to the end of 2022. Figure 11 depicts the trend prediction
of HIV mortality in Myanmar from 2020 to 2023, with the
blue line illustrating historical actual data, the red line future
forceast data, the yellow line the es and the mortality in Myanmar from 2020 to 2023, with the

blue line illustrating historical actual data, the red line future

forecast data, the yellow line the estimated maximum number

of deaths, and the green line the e

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mortality estimates. However, due to a large base of infected

individuals and the time required for treatment to become

widely accessible, this study's predictions based on actual

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morothility rates show a slight deviation from official estimates,
although the overall trend remains sim Widely accessible, this study's predictions based on actual
mortality rates show a slight deviation from official estimates,
although the overall trend remains similarly positive. For
Myanmar, the study's forecast data fal ge, and increased investments in THV dealinent in
yanmar have led to a gradual and slow decrease in death
es, falling back within the estimated range. Under the
rrent conditions of disease prevention measures, social
viron Model model of the forecasts, the growing forecast
ge, and increased investments in HIV treatment in
anmar have led to a gradual and slow decrease in death
respectively. The method of disease prevention measures, social
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line).

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 Example 11. Death toll trend forces are proper and HTM befoldere. Eximal HTM be Figure 11. Dead to 1995

Pindicted Data

Pindicted Comes for Myanmar until 2023 (red line).

In this study, we **1995 2020**
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In this study, we introduced machine learning models,

INS services in Myanmar. To train and test the models used for our research,

Myanmar. To tr Fig. 11. Study, we introduced machine learning models, [12] Y. Liang, Y. Wang, L. Zhine including SVM, LR, Random Forest, and XGBoost, to AIDS, gonorrhea, and sy predict the trends in HIV-induced deaths in South Africa an In this study, we introduced manemic learning modes,

including SVM, LR, Random Forest, and XGBoost, to

including SVM, LR, Random Forest, and SGBoost, to

predict the trends in HIV-induced deaths in South Africa and

Mya Incularing SVM, LR, Random Forest, and XGBOost, to

Indel,"Journal of Nantong Universed the trends in HIV-induced deaths in South Africa and

Myanmar. To train and test the models used for our research,

the swe utilized d preduct the trends in Fit v-induced dealas in Solut Airica and

We utilized data up to the year 2019. The models used for our research,

we utilized data up to the year 2019. The models end ployed in

this work are data-dr Inven approaches, and we assessed our

sing MAE, MSE, RMSE, MAPE, and

models we developed, we forecasted the

for the next four years. Our findings

ore rational allocation of HIV medical

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resources, prioritizing assistance in countries with

persistently high death rates. For instance, this can enhance

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resources, prioritizing assistance in countries with

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in the Philippines Using Doutstre?", International Journal Mater?", persistently high death rates. For instance, this can enhance

antiretroviral therapy programs in regions with high mortality

and therapy and the more area implementing prevailed delivery. This can aid
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antises, ensuring their accessibility and delivery. This can aid

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prov rates, ensuring their accessibility and delivery. This can aid [17] C. Mweenba, P. Hangoma, I.

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epidemic and formulating policies to reduce mortality rates.

[18] Y. Wang, Z. Yan, D. Wang, "Prece epidemic and formulating policies to reduce mortality rates.

[18] Y. Wang, Z. Yan, D. Wang,
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Myanmar, has a relatively small amount of data, covering

Myanmar, has a relatively small amount of data, covering

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Myanmar, has a relatively small amount of data, covering

Myanmar, has a relatively small amount of data, covering

only the mortality data from 1990 to 2019. Official Myanmar, nas a relatively small amount of data, covering

and on ot provide mortality data from 2020 to the present.

do not provide mortality data from 2020 to the present.

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However, we can indirectly corroborate our predictive results

However, we can indirectly corroborate our predictive results

However, we can indirectly corroborate our predict do not provide mortality data rom 2020 to the present.

However, we can indirectly corroborate our predictive results

through the estimated mortality data range provided by

the model, showing that the LR model performs b Although the overall trend of HIV in South Africa is not

linear, some local areas of the data exhibit linear relationships,

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inear models may better fit the data within these areas.

With the in expection and solely the data exhibit linear relations

inear models may better fit the data within thes

in the overall smaller data volume, linear models a

y to achieve robust results. If a larger datase

lable, a no and linear models may better fit the data within these areas.

With the overall smaller data volume, linear models are more

likely to achieve robust results. If a larger dataset were

likely to achieve robust results. If From the overall smaller data volume, linear models are more

in the overall smaller data volume, linear models are more

y to achieve robust results. If a larger dataset were

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y to achieve robust results. If a larger data

lable, a non-linear trend might emerge, po

ing to better predictive performance from mo

dom Forest, Support Vector Regress 23 Global HIV & AIDS statistics - Fact sheet, UNAIDS, 2022.

43 Kath, A. The more statistic in the statistic of the statistical field in the statistical conduction of our server of the statistical CDM and CH and CH and the available, a non-linear trend might emerge, potentially

leading to better predictive performance from models like

Random Forest, Support Vector Regression, and XGBoost.

REFERENCES

Tail 2, pp. 1273-1279, 1993.

SI12, pp ing to better predictive performance from models like

dom Forest, Support Vector Regression, and XGBoost.

Tain, C. Chen, X.

REFERENCES

R. A. Weiss, "How does HIV cause AIDS?," Science, vol. 260, no. a for urban land us

REFERENCES

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- **of Computer Science**

International Journal of Environmental Research and Public Health,

vol. 19, no. 13, pp. 8125, 2022.

T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national

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vol. 19, no. 13, pp. 8125, 2022.
T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and na
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International Journal of Environmental Research and Public Health,

vol. 19, no. 13, pp. 8125, 2022.

[5] T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national

incidence, preval **of Computer Science**
International Journal of Environmental Research and Public Health,
vol. 19, no. 13, pp. 8125, 2022.
T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national
incidence, prevalence, and mo **of Computer Science**

International Journal of Environmental Research and Public Health,

vol. 19, no. 13, pp. 8125, 2022.

T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national

incidence, prevalence, an **of Computer Science**
International Journal of Environmental Research and Public Health,
vol. 19, no. 13, pp. 8125, 2022.
T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national
incidence, prevalence, and mo **of Computer Science**

International Journal of Environmental Research and Public Health,

vol. 19, no. 13, pp. 8125, 2022.

T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national

incidence, prevalence, an [6] "Global Burden of Disease Collaborative Network. Global Burden of **Or Computer Science**

International Journal of Environmental Research and Public Health,

vol. 19, no. 13, pp. 8125, 2022.

T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national

incidence, prevalence, an International Journal of Environmental Research and Public Health,
vol. 19, no. 13, pp. 8125, 2022.
T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national
incidence, prevalence, and mortality of HIV, 1980-2 International Journal of Environmental Research and Public Health,
vol. 19, no. 13, pp. 8125, 2022.

[5] T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national

incidence, prevalence, and mortality of HIV, International Journal of Environmental Research and Public Health, vol. 19, no. 13, pp. 8125, 2022.
T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national incidence, prevalence, and mortality of HIV, 1980-2 International Journal of Environmental Research and Public Health,
vol. 19, no. 13, pp. 8125, 2022.
T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national
incidence, prevalence, and mortality of HIV, 1980-2 vol. 19, no. 13, pp. 8125, 2022.

[5] T. D. Frank, A. Carter, D. Jahagirdar, "Global, regional, and national

incidence, prevalence, and mortality of HIV, 1980-2017, and forecasts

to 2030, for 195 countries and territorie T. D. Frank, A. Carter, D. Jahagurdar, "Global, regional, and national
incidence, prevalence, and mortality of HIV, 1980-2017, and forecasts
to 2030, for 195 countries and territories: A systematic analysis for the
Global
-
- 2021.
Y. Yang, S. Mao, Y. Xue, "Prediction on the incidence rate of AIDS in incidence, prevalence, and mortality of HIV, 1980-2017, and forecasts
to 2030, for 195 countries and territories: A systematic analysis for the
Global Burden of Diseases, Injuries, and Risk Factors Study 2017,"
Lancet HIV, to 2030, for 195 countries and territories: A systematic analy
Global Burden of Diseases, Injuries, and Risk Factors Studence HIV, vol. 6, no. 12, pp. e831-e859, 2019.
(6) "Global Burden of Disease Collaborative Network. G Global Burden of Diseases, Injuries, and Risk Factors Study 2017,"

Lancet HIV, vol. 6, no. 12, pp. e831-e859, 2019.

(Global Burden of Disease Collaborative Network. Global Burden of

Disease Study 2019 (GBD 2019) Results Lancet HIV, vol. 6, no. 12, pp. e831-e859, 2019.

"Global Burden of Disease Collaborative Network. Global Burden of

Disease Study 2019 (GBD 2019) Results, "Neattle, United States:

Institute for Health Metrics and Evaluat "Global Burden of Disease Collaborative Network. Global Burden of Disease Study 2019 (GBD 2019) Results," Seattle, United States: Institute for Health Metrics and Evaluation (IHME), 2021.

P. Haldar, S. Reza-Paul, R. A. Da Disease Study 2019 (GBD 2019) Results," Seattle, United States:

Institute for Health Metrics and Evaluation (IHME), 2021.

[7] P. Haldar, S. Reza-Paul, R. A. Daniel, "A rapid review of pre-exposure

prophylaxis for HIV in Institute for Health Metrics and Evaluation (IHME), 2021.

P. Haldar, S. Reza-Paul, R. A. Daniel, "A rapid review of pre-exposure

prophylaxis for HIV in the Asia-Pacific region: recommendations for

scale up and future di
-
-
-
-
- [7] P. Haldar, S. Reza-Paul, R. A. Daniel, "A rapid review of pre-exposure
prophylaxis for HIV in the Asia-Pacific region: recommendations for
scale up and future directions," Sexual Health, vol. 18, no. 1, pp. 31-40,
2021 prophylaxis for HIV in the Asia-Pacific region: recommendations for
scale up and future directions," Sexual Health, vol. 18, no. 1, pp. 31-40,
2021.
Y. Yang, S. Mao, Y. Xue, "Prediction on the incidence rate of AIDS in
Chi scale up and tuture directions," Sexual Health, vol. 18, no. 1, pp. 31-40,
2021.

Y. Yang, S. Mao, Y. Xue, "Prediction on the incidence rate of AIDS in

Y. Yang, S. Mao, Y. Xue, "Prediction on the incidence rate of AIDS in 2021.

Y. Yang, S. Mao, Y. Xue, "Prediction on the information of Health Statistics, vol. 31, pp. 952-954, 2014 UNAIDS, AIDSinfo, 2022.

UNAIDS, AIDSinfo, 2022.

UNAIDS, AIDSinfo, 2022.

T. Rehle, L. Johnson, T. Hallett, " [8] Y. Yang, S. Mao, Y. Xue, "Prediction on the incidence rate of AIDS in China with GM(1, 1) and trend extrapolation model," Chinese Journal of Health Statistics, vol. 31, pp. 952-954, 2014.

[9] UNAIDS, AIDSinfo, 2022.
 China with GM(1, 1) and trend extrapolation model," Chinese Journal
of Health Statistics, vol. 31, pp. 952-954, 2014.
UNAIDS, AIDSinfo, 2022.
T. Rehle, L. Johnson, T. Hallett, "A Comparison of South African
National HIV In of Health Statistics, vol. 31, pp. 952-954, 2014.

[9] UNAIDS, AIDSinfo, 2022.

[10] T. Rehle, L. Johnson, T. Hallett, "A Comparison of South African

National HIV Incidence Estimates: A Critical Appraisal of Different

Me UNAIDS, AIDSinfo, 2022.

T. Rehle, L. Johnson, T. Hallett, "A Comparison of South African

National HIV Incidence Estimates: A Critical Appraisal of Different

National HIV Incidence Estimates: A Critical Appraisal of Diff T. Rehle, L. Johnson, T. Hallett, "A Comparison of Soutional HIV Incidence Estimates: A Critical Appraisal c
Methods," PLoS ONE, vol. 10, no. 7, pp. e0133255, 2015.
B. Williams, D. Baker, M. Bühler, "Increase coverage c
AI National HIV Incidence Estimates: A Critical Appraisal of Different

111 B. Williams, D. Baker, M. Bühler, "Increase coverage of HIV and

111 B. Williams, D. Baker, M. Bühler, "Increase coverage of HIV and

1121 Y. Liang, Methods," PLoS ONE, vol. 10, no. 7, pp. e0133255, 2015.

B. Williams, D. Baker, M. Bühler, "Increase coverage of HIV and

AIDS services in Myanmar," Conflict and Health, vol. 2, pp. 3, 2008.

A' Liang, Y. Wang, L. Zhai, "A B. Williams, D. Baker, M. Bühler, "Increase coverage of HIV and
AIDS services in Myanmar," Conflict and Health, vol. 2, pp. 3, 2008.
Y. Liang, Y. Wang, L. Zhai, "Analysis of forecasting the incidence of
AIDS, gonorrhea, an AlDS services in Myanmar," Conflict and Health, vol. 2, pp. 3, 2008.

[12] Y. Liang, Y. Wang, L. Zhai, "Analysis of forecasting the incidence of

AlDS, gonorrhea, and syphilis in Jiangsu Province with GM(1, 1)

model," Jou
-
-
-
- Y. Liang, Y. Wang, L. Zhai, "Analysis of forecasting the incidence of AIDS, gonorrhea, and syphilis in Jiangsu Province with GM(1, 1) model," Journal of Nantong University (Medical Sciences), vol. 1, pp. 21-24, 2013.
Q. Ya AIDS, gonorrhea, and syphilis in Jiangsu Province with GM(1, 1)

model," Journal of Nantong University (Medical Sciences), vol. 1, pp.

21-24, 2013.

21. Yang, G. Guo, H. Chen, "Research on AIDS incidence prediction

based model," Journal of Nantong University (Medical Sciences), vol. 1, pp. 21-24, 2013.

21-24, 2013.

21-24, 2013.

based on ARIMA," China Medical Equipment, vol. 13, pp. 1-4, 2016.

S. Meakin, S. Abbott, N. Bosse, "BP-neural 21-24, 2013.

[13] Q. Yang, G. Guo, H. Chen, "Research on AIDS incidence prediction

based on ARIMA," China Medical Equipment, vol. 13, pp. 1-4, 2016.

[14] S. Meakin, S. Abbott, N. Bosse, "BP-neural network as a model of Q. Yang, G. Guo, H. Chen, "Research on AIDS incidence prediction
based on ARIMA," China Medical Equipment, vol. 13, pp. 1-4, 2016.
S. Meakin, S. Abbott, N. Bosse, "BP-neural network as a model of
predicting STD/AIDS preval based on ARIMA," China Medical Equipment, vol. 13, pp. 1-4, 2016.

S. Meakin, S. Abbott, N. Bosse, "BP-neural network as a model of

predicting STD/AIDS prevalence," Chinese Journal of AIDS & STD,

vol. 6, pp. 525-528, 200
-
- [14] S. Meakin, S. Abbott, N. Bosse, "BP-neural network as a model of
prodicting STD/AIDS prevalence," Chinese Journal of AIDS & STD,
vol. 6, pp. 525-528, 2007.
[15] Q. An, J. Wu, J. Meng, "Using the hybrid EMD-BPNN model predicting STD/AIDS prevalence," Chinese Journal of AIDS & STD,
vol. 6, pp. 525-528, 2007.
O. An, J. Wu, J. Meng, "Using the hybrid EMD-BPNN model to
predict the incidence of HIV in Dalian, Liaoning Province, China,
2004-2 vol. 6, pp. 525-528, 2007.

Q. An, J. Wu, J. Meng, "Using the hybrid EMD-BPNN model to

predict the incidence of HIV in Dalian, Liaoning Province, China,

2004-2018," BMC Infectious Diseases, vol. 22, no. 1, pp. 102, 2022. Q. An, J. Wu, J. Meng, "Using the hybr
predict the incidence of HIV in Dalian, I
2004-2018," BMC Infectious Diseases, vol.
S. A. Jr, G. B. De, R. Medina, "Time Series
in the Philippines Using Deep Learning: Eliant
Matter?, predict the incidence of HIV in Dalian, Liaoning Province, China,

2004-2018, "BMC Infectious Diseases, vol. 22, no. 1, pp. 102, 2022.

[16] S. A. Jr, G. B. De, R. Medina, "Time Series Forecasting of HIV/AIDS

in the Phili 2004-2018," BMC Infectious Diseases, vol. 22, no. 1, pp. 102, 2022.

S. A. Jr, G. B. De, R. Medina, "Time Series Forecasting of HIV/AIDS

in the Philippines Using Deep Learning: Does COVID-19 Epidemic

in the Philippines U S. A. Jr, G. B. De, R. Medina, "Time Series Forecasting of HIV/AIDS
in the Philippines Using Deep Learning: Does COVID-19 Epidemic
Matter?," International Journal of Emerging Technology and
Advanced Engineering, vol. 12, n In the Philippines Using Deep Learning: Does COVID-19 Epidemic

Matter?," International Journal of Emerging Technology and

Advanced Engineering, vol. 12, no. 9, pp. 144-157, 2022.

C. Mweemba, P. Hangoma, I. Fwemba, "Esti Matter?," International Journal of Emerging Technology and

19 C. Mweemba, P. Hangoma, I. Fwemba, "Estimating district HIV

prevalence in Zambia using small-area estimation methods (SAE),"

Population Health Metrics, vol. Advanced Engmeering, vol. 12, no. 9, pp. 144-157, 2022.

C. Mweemba, P. Hangoma, I. Fwemba, "Estimating district HIV

prevalence in Zambia using small-area estimation methods (SAE),"

Population Health Metrics, vol. 20, no C. Mweemba, P. Hangoma, I. Fwemba, "Estimating district HIV
prevalence in Zambia using small-area estimation methods (SAE),"
Population Health Metrics, vol. 20, no. 1, pp. 8, 2022.
Y. Wang, Z. Yan, D. Wang, "Prediction and prevalence in Zambia using small-area estimation methods (SAE),"
Population Health Metrics, vol. 20, no. 1, pp. 8, 2022.
Y. Wang, Z. Yan, D. Wang, "Prediction and analysis of COVID-19
daily new cases and cumulative cases: Population Health Metrics, vol. 20, no. 1, pp. 8, 2022.

[18] Y. Wang, Z. Yan, D. Wang, "Prediction and analysis of COVID-19

daily new cases and cumulative cases: times series forecasting and

machine learning models," BM
- Y. Wang, Z. Yan, D. Wang, "Prediction and analysis of COVID-19
daily new cases and cumulative cases: times series forecasting and
machine learning models," BMC Infectious Diseases, vol. 22, no. 1, pp.
495, 2022.
A. K. Gupt daily new cases and cumulative cases: times series forecasting and
machine learning models," BMC Infectious Diseases, vol. 22, no. 1, pp.
495, 2022.
A. K. Gupta, V. Singh, P. Mathur, "Prediction of COVID-19 pandemic
measur machine learning models," BMC Infectious Diseases, vol. 22, no. 1, pp.

495, 2022.

[19] A. K. Gupta, V. Singh, P. Mathur, "Prediction of COVID-19 pandemic

measuring criteria using support vector machine, prophet, and lin 495, 2022.
A. K. Gupta, V. Singh, P. Mathur, "Prediction of COVID-19 pandemic
measuring criteria using support vector machine, prophet, and linear
regression models in Indian scenario," Journal of Interdisciplinary
Mathema
- A. K. Gupta, V. Singh, P. Mathur, "Prediction of COVID-19 pandemic
measuring criteria using support vector machine, prophet, and linear
regression models in Indian scenario," Journal of Interdisciplinary
Mathematics, vol.
-
-
- measuring criteria using support vector machine, prophet, and linear
regression models in Indian scenario," Journal of Interdisciplinary
Mathematics, vol. 24, no. 1, pp. 89-108, 2021.
[20] K. Menguc, N. Aydin, A. Yilmaz, " regression models in Indian scenario," Journal of Interdisciplinary
Mathematics, vol. 24, no. 1, pp. 89-108, 2021.

K. Menguc, N. Aydin, A. Yilmaz, "A data-driven approach to

forecasting traffic speed classes using the Ex Mathematics, vol. 24, no. 1, pp. 89-108, 2021.

K. Menguc, N. Aydin, A. Yilmaz, "A data-driven approach to

forecasting traffic speed classes using the Extreme Gradient Boosting

algorithm and graph theory," Physica A: Sta K. Menguc, N. Aydın, A. Yılmaz, "A dai
forecasting traffic speed classes using the Extra
forecasting traffic speed classes using the Extra
algorithm and graph theory," Physica A: Statis
Applications, vol. 620, pp. 128738, forecasting traffic speed classes using the Extreme Gradient Boosting
algorithm and graph theory," Physica A: Statistical Mechanics and its
Applications, vol. 620, pp. 128738, 2023.
[21] J. Luo, Z. Zhang, Y. Fu, "Time seri algorithm and graph theory," Physica A: Statistical Mechanics and its
Applications, vol. 620, pp. 128738, 2023.
I. Luo, Z. Zhang, Y. Fu, "Time series prediction of COVID-19
Itansmission in America using LSTM and XGBoost al Applications, vol. 620, pp. 128738, 2023.

J. Luo, Z. Zhang, Y. Fu, "Time series prediction of COVID-19

transmission in America using LSTM and XGBoost algorithms,"

transmission in America using LSTM and XGBoost algorithm J. Luo, Z. Zhang, Y. Fu, "Time series prediction of COVID-19

transmission in America using LSTM and XGBoost algorithms,"

Results in Physics, vol. 27, pp. 104462, 2021.

Z. Fang, S. Yang, C. Lv, "Application of a data-dri transmission in America using LSTM and XGBoost algorithms,"

Results in Physics, vol. 27, pp. 104462, 2021.

2. Fang, S. Yang, C. Lv, "Application of a data-driven XGBoost model

for the prediction of COVID-19 in the USA: Results in Physics, vol. 27, pp. 104462, 2021.

Z. Fang, S. Yang, C. Lv, "Application of a data-driven XGBoost model

for the prediction of COVID-19 in the USA: a time-series study," BMJ

Open, vol. 12, no. 7, pp. e056685, Z. Fang, S. Yang, C. Lv, "Application of a data-driven XGBoost model
for the prediction of COVID-19 in the USA: a time-series study," BMJ
Open, vol. 12, no. 7, pp. 056685, 2022.
M. Mehta, J. Julaiti, P. Griffin, "Early Sta
-
-
- for the prediction of COVID-19 in the USA: a time-series study," BMJ

(23) M. Mehta, J. Julaiti, P. Griffin, "Early Stage Machine Learning Based

Prediction of US County Vulnerability to the COVID-19 Pandemic

(Preprint)," Open, vol. 12, no. 7, pp. e056685, 2022.

M. Mehta, J. Julaiti, P. Griffin, "Early Stage Machine Learning Based

Prediction of US County Vulnerability to the COVID-19 Pandemic

Prediction of US County Public Health and Sur M. Mehta, J. Julaiti, P. Griffin, "Early Stage Machine Learning Based
Prediction of US County Vulnerability to the COVID-19 Pandemic
(Preprint)," MIR Public Health and Surveillance, vol. 6, no. 3, pp.
e19446, 2020.
S. Rath Prediction of US County Vulnerability to the

(Preprint)," JMIR Public Health and Surveilla

e19446, 2020.

S. Rath, A. Tripathy, A. R. Tripathy, "Prediction

coronavirus disease (COVID-19) pandemic u

regression model," D
- (Preprint)," JMIR Public Health and Surveillance, vol. 6, no. 3, pp.

19446, 2020.

24] C. Rath, A. Tripathy, A. R. Tripathy, "Prediction of new active cases of

coronavirus disease (COVID-19) pandemic using a multiple lin el 9446, 2020.

S. Rath, A. Tripathy, A. R. Tripathy, "Prediction of new active cases of

coronavirus disease (COVID-19) pandemic using a multiple linear

regression model," Diabetes & Metabolic Syndrome: Clinical

Researc S. Rath, A. Tripathy, A. R. Tripathy, "Prediction of new active cases of coronavirus disease (COVID-19) pandemic using a multiple linear regression model," Diabetes & Metabolic Syndrome: Clinical Research & Reviews, vol. 1 coronavirus disease (COVID-19) pandemic usin regression model," Diabetes & Metabolic {Research & Reviews, vol. 14, no. 5, pp. 1467-147 Y. Tian, C. Chen, X. Chen, "Research on real-time of urban land use based on support ve