AI-Driven Predictive Modeling for COVID-19 Case Trends: An Ensemble Learning Approach

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ABSTRACT

Pandemics and epidemics present major challenges to global health and economies, as underscored by the COVID-19 pandemic, which has highlighted the critical need for advanced predictive analytics to support informed decision-making and efficient resource allocation. In this context, Artificial Intelligence (AI) and Machine Learning (ML) have emerged as powerful tools for forecasting pandemic trends. This study investigates various ML regression techniques to predict COVID-19 case trends using real-world data from the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (JHU), covering the period from January 22, 2020, to September 3, 2023. The regression models evaluated include Linear Regression, Support Vector Regression (SVR), Random Forest, Gradient Boosting, AdaBoost, and a Stacking Model, with performance assessed using Mean Absolute Error (MAE), Mean Squared Error (MSE), and R^2 Score. Results reveal that the Stacking Model achieved the highest accuracy, with the lowest MAE (49,182,280), lowest MSE (3.32e+15), and best R^2 Score (-2.669640), outperforming all other models. Random Forest and Gradient Boosting also performed well with R^2 Scores of -4.857282 and -4.863941, respectively, while SVR proved unsuitable with an R^2 Score of -265.084156. These findings underscore the superior performance of ensemble learning techniques, particularly Stacking, Random Forest, and Gradient Boosting, in predicting COVID-19 trends and emphasize the importance of selecting appropriate regression models to enhance the reliability of epidemiological forecasting.

Keywords: Machine Learning, Prediction, Epidemic, Pandemic, COVID-19, Regression, Random Forest, Gradient Boosting, Stacking Model.

INTRODUCTION

Epidemics and pandemics have historically posed significant threats to global public health, economic stability, and societal well-being. The outbreak of infectious diseases has been documented as early as 429 BC, with recurring instances of large-scale disease transmission across different periods. The 1918 Spanish Flu remains one of the deadliest pandemics in recorded history, followed by other major outbreaks such as Ebola (2018), Dengue Fever (2019–2020), Swine Flu (2015), and Yellow Fever (2016) [1][2].

Epidemics arise when infectious diseases spread rapidly within a specific region, while pandemics extend their reach globally. Historically, transmission pathways have included human-to-human contact, vector-borne transmission, and zoonotic spillovers from animals to humans. With globalization and increasing human mobility, the frequency and intensity of epidemics have increased, necessitating improved surveillance and predictive modeling techniques [4][5].

The COVID-19 pandemic, first reported in Wuhan, China, in December 2019, led to unprecedented global disruption.

Table 1 provides a comparative summary of major recent disease outbreaks, detailing the estimated number of cases and deaths in millions. Notably, the Spanish Flu of 1918 had the highest mortality, with 50 million deaths out of 500 million cases, while COVID-19 recorded the highest number of estimated cases at 770 million, with 7 million deaths [6].

Table 1. Summary of Major Recent Outbreaks [1] – [7]

Disease	Year	Estimated Cases (Millions)	Estimated Deaths (Millions)
Spanish Flu	1918	500	50
Swine Flu	2015	1.4	0.2
Yellow Fever	2016	0.2	0.045
Ebola	2018	0.03	0.011
Dengue Fever	2019	0.4	0.02
COVID-19	2020	774	7

Figure 1, below visually represents this data through a bar chart, highlighting the relative scale and impact of each outbreak. The chart clearly illustrates the disproportionate burden of certain diseases, emphasizing the global health significance of large-scale pandemics like COVID-19 and the Spanish Flu.

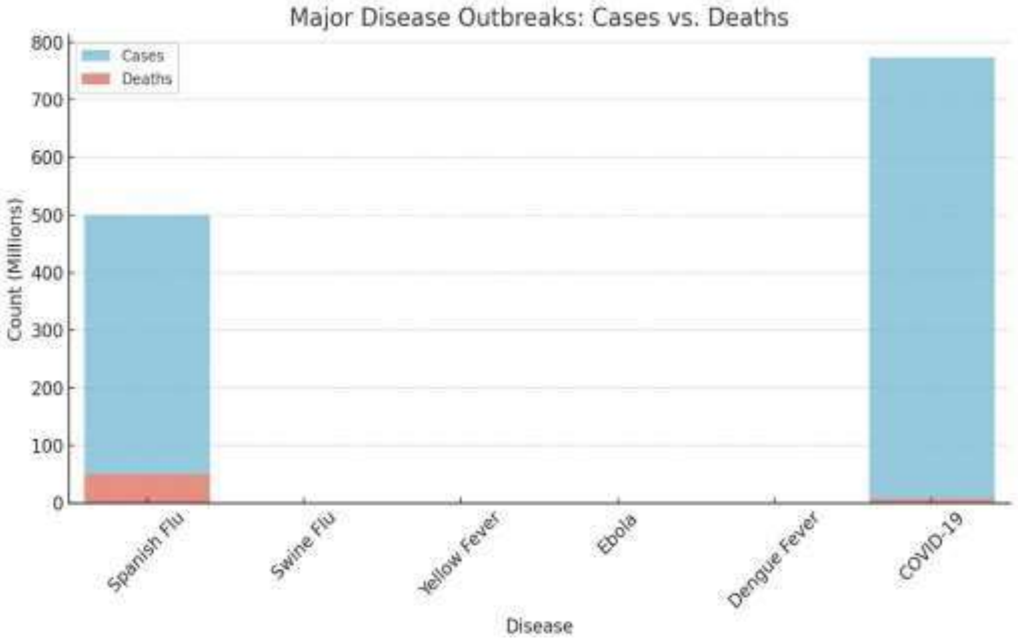

Figure 1: Bar chart comparing major disease outbreaks in terms of cases and deaths.

Building upon this context of historical outbreaks and their impacts, related work is presented in the section below, highlighting prior research efforts in disease prediction and the application of machine learning techniques in epidemiological modeling.

LITERATURE REVIEW

The prediction of disease outbreaks has been an area of significant research, especially with the increasing availability of large-scale epidemiological, environmental, and social media data. The use of machine learning (ML) techniques has revolutionized disease surveillance by improving accuracy, timeliness, and automation of outbreak prediction. A variety of ML models, including traditional statistical methods, supervised learning, deep learning, and hybrid approaches, have been applied to forecast disease spread, identify risk factors, and optimize intervention strategies. Recent studies [1], [2] have highlighted the role of global travel networks and urbanization in accelerating epidemic and pandemic spread. Improved surveillance systems, such as those leveraging real-time data analytics and AI-driven forecasting models, have been instrumental in early outbreak detection and response [3]. The COVID-19 pandemic has particularly underscored the need for robust predictive models to mitigate transmission risks and enhance preparedness [4]. Advanced ML approaches have demonstrated success in identifying high-risk populations and informing public health policies [5]. Furthermore, integration of genomic sequencing with epidemiological data has provided valuable insights into pathogen evolution and transmission dynamics [6], [7]. Early disease forecasting models primarily relied on statistical approaches, including autoregressive integrated moving average (ARIMA), seasonal ARIMA (SARIMA), and logistic regression. These models have been widely used for time-series forecasting of infectious diseases like influenza, dengue, and COVID-19 [8], [9]. Regression models, particularly logistic regression, are commonly employed for classification tasks where the objective is to predict disease presence or absence based on specific features. Linear regression, on the other hand, has been applied to predict case counts over time, often combined with epidemiological models like SEIR (Susceptible-Exposed-Infectious-Recovered) to improve forecasting accuracy [10]. Supervised ML models, such as Support Vector Machines (SVMs), Decision Trees, and Random Forests, have been utilized for disease prediction. SVM, particularly with polynomial and Gaussian kernels, has been effective in classifying disease outbreak risks based on multi-dimensional feature sets [11], [12]. Random Forest, an ensemble-based method, has demonstrated robust predictive performance in handling high-dimensional epidemiological data [12]. Moreover, k-Nearest Neighbors (KNN) and Naïve Bayes classifiers have been applied in outbreak detection, leveraging historical case data and environmental factors to improve predictions [13]. Recent studies have integrated real-time social media and web-based data sources to enhance disease forecasting. Twitter-based surveillance models have been developed to track outbreaks like H1N1 and COVID-19 by analyzing user-generated content and sentiment trends [14]. Similarly, search engine queries have been explored as early indicators of disease prevalence, providing insights into potential outbreaks before official case reports are available [15]. With advancements in computational power, machine learning and deep learning models have shown remarkable potential in disease forecasting. Feature-based time-series classification approaches have emerged as effective tools for predicting disease outbreaks by analyzing sequential data patterns extracted from diverse sources [16]. Additionally, univariate and multivariate time series forecasting methods have been extensively utilized for modeling and predicting COVID-19 trends and other infectious diseases [18]. Hybrid models that combine Convolutional Neural Networks (CNNs) and Recurrent Neural Networks (RNNs), such as Long Short-Term Memory (LSTM) networks, have demonstrated enhanced capability in capturing both spatial and temporal patterns of disease spread [22]. Beyond supervised learning, reinforcement learning (RL) techniques have been explored for optimizing intervention strategies during epidemics. These models dynamically learn from past outbreaks to devise adaptive control policies that account for healthcare system constraints [20]. Moreover, dynamic graph neural networks (DGNNs) have been developed to model complex spatiotemporal interactions across regions, enabling more accurate and scalable outbreak predictions [21].The integration of the Internet of Medical Things (IoMT) with AI has significantly improved real-time outbreak detection. These systems leverage data from wearable devices, environmental sensors, and electronic health records to provide timely alerts for potential outbreaks [19], [23]. Complementing this, cloud-based AI frameworks offer scalable infrastructure for running large-scale epidemiological simulations, further enhancing the efficiency and responsiveness of public health systems [24].

Despite the significant progress in ML-based disease outbreak prediction, several challenges remain. Data quality and availability continue to be major concerns, as real-world epidemiological data often suffer from reporting delays, inconsistencies, and underreporting. Addressing these issues requires the development of data augmentation techniques, imputation strategies, and federated learning models that can learn from decentralized data sources while preserving privacy. Another challenge is model interpretability, particularly in deep learning applications. While neural networks provide high accuracy, their "black-box" nature limits their adoption in epidemiology and healthcare decision-making. Future research should focus on explainable AI (XAI) techniques that enhance transparency and provide actionable insights for public health professionals. Additionally, integrating multi-source data—including clinical records, genomic data, environmental factors, and mobility patterns—remains an open research area. Developing robust data fusion frameworks that can process heterogeneous data streams will be crucial for improving disease prediction accuracy. Finally, the use of transfer learning and continual learning models is gaining attention for epidemic forecasting. These approaches enable models trained on historical outbreaks to adapt to new and emerging diseases, reducing the need for retraining from scratch. As new diseases emerge, adaptive learning mechanisms will be essential for maintaining accurate and reliable predictions. Problem statement and methodology The dataset used in this study was obtained from the official GitHub repository of the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (CSSE-JHU). The repository provides daily updates on confirmed cases, deaths, and recoveries across multiple countries and regions. The dataset is widely used in epidemiological studies and is maintained by CSSE-JHU to ensure its authenticity and reliability.

The rapid and widespread transmission of infectious diseases such as COVID-19 highlights the urgent need for effective predictive tools that can aid in early outbreak detection and healthcare resource planning. Traditional epidemiological models, while useful, often fall short in adapting to real-time data and complex, nonlinear patterns inherent in disease spread. This research addresses the challenge of accurately forecasting the cumulative number of confirmed COVID-19 cases over time using machine learning (ML) approaches. Specifically, the study evaluates and compares the performance of six ML models—Stacking, Random Forest, Gradient Boosting, AdaBoost, Linear Regression, and Support Vector Regression (SVR)—to identify the most effective model for predicting global case trends and supporting data-driven decision-making in public health.

EXPERIMENTATION & RESULTS

In this experiment, we evaluated six different machine learning models to predict the global cumulative confirmed COVID-19 cases over time: Stacking Model, Random Forest, Gradient Boosting, AdaBoost, Linear Regression, and Support Vector Regression (SVR). The methodology followed in this analysis, as illustrated in Figure 2, aimed to assess the predictive accuracy of these models using three different evaluation metrics.

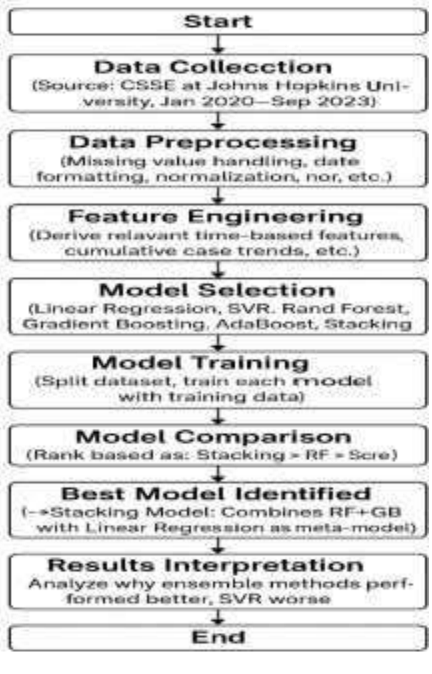

Figure 2: Methodology Implemented

The goal of this analysis was to assess the predictive accuracy of various models using three key performance metrics. The first metric, Mean Absolute Error (MAE), measures the average magnitude of errors in predictions, treating all errors equally without considering their direction. It calculates the average of the absolute differences between predicted and actual values. A lower MAE indicates that the model's predictions are closer to the actual outcomes on average, highlighting better accuracy. The second metric, Mean Squared Error (MSE), is similar to MAE but with a crucial difference: MSE squares the error terms before averaging. This squaring process amplifies the impact of larger errors, making MSE more sensitive to outliers. A lower MSE suggests that the model has fewer and smaller prediction errors, whereas a higher MSE reflects greater variation and larger errors in predictions. Finally, the R^2 Score (Coefficient of Determination) evaluates how well the model’s predictions align with actual outcomes. An R^2 score closer to 1 indicates that the model is able to explain a significant portion of the variation in the data, reflecting strong predictive power. On the other hand, negative R^2 values suggest that the model performs poorly, often worse than a simple horizontal line that predicts the mean value. These metrics combined provide a comprehensive understanding of a model's predictive accuracy and its ability to capture the underlying trends in the data.

Model Performance Table:

The table 2 below shows the MAE, MSE, and R^2 Score for each of the models tested:

Table 2: Model performance

Model	**MAE**	**MSE**	**R^2 Score**
Stacking Model	4.918228e+07	3.324972e+15	-2.669640
Random Forest	6.634053e+07	5.307141e+15	-4.857282
Gradient Boosting	6.638599e+07	5.313175e+15	-4.863941
Linear Regression	8.329432e+07	7.109429e+15	-6.846396
AdaBoost	9.562474e+07	1.005017e+16	-10.091972
Support Vector Regression	4.900881e+08	2.410924e+17	-265.084156

The Stacking Model demonstrates the best performance overall. With a Mean Absolute Error (MAE) of 4.92e+07, it predicts global cumulative confirmed COVID-19 cases with relatively high accuracy compared to the other models. Its Mean Squared Error (MSE) of 3.32e+15 is the lowest among all models, reinforcing its strong overall performance. However, the model's R^2 score of -2.67 indicates that its predictive power is still suboptimal, which is expected when dealing with volatile data like COVID-19 trends, but it still outperforms many other models in this case. The Stacking Model combines predictions from multiple base models using a meta-model. The equation for the final prediction ŷ is:

$$\hat{y} = g(f_1(x), f_2(x), \ldots, f_n(x))$$

Where:

- **$f_1(x), f_2(x), \ldots, f_n(x)$ are the predictions from the base models.**

- **g is the meta-model that combines these predictions.**

For this study, with Random Forest and Gradient Boosting as base models and Linear Regression as the meta-model, the equation becomes:

$$\hat{y} = \text{LinearRegression}(\text{RandomForestRegressor}(x), \text{GradientBoostingRegressor}(x))$$

The Random Forest model shows a slightly higher MAE of 6.63e+07, which suggests its predictions are less accurate on average than the Stacking Model. Its MSE of 5.31e+15 is also higher, pointing to greater variation in prediction errors. The model's R² score of -4.86, while still negative, shows a better performance than AdaBoost and Support Vector Regression (SVR), although further improvements could be made with hyperparameter tuning and additional feature engineering. Gradient Boosting shares similar performance to Random Forest, with an MAE of 6.64e+07 and an MSE of 5.31e+15, indicating comparable prediction accuracy and error variation. Its R² score also mirrors Random Forest at -4.86, suggesting that it is similarly underperforming but may benefit from further optimization. In contrast, Linear Regression performs the worst among the more sophisticated models, with an MAE of 8.33e+07, signifying less accurate predictions. Its MSE of 7.11e+15 is also higher, indicating larger prediction errors. The R² score of -6.85 further confirms its inability to capture the non-linear trends inherent in COVID-19 case progression, highlighting its unsuitability for this type of data. AdaBoost shows poor performance with the highest MAE of 9.56e+07, indicating a tendency to make larger errors on average. Its MSE of 1.01e+16 is the highest among all models, reflecting its struggles with outliers and large prediction errors. The R² score of -10.09 reveals its poor fit, likely due to overfitting or underfitting, common problems in models overly sensitive to data noise. Finally, Support Vector Regression (SVR) performs the worst overall. With the highest MAE of 4.90e+08 and the largest MSE of 2.41e+17, SVR's predictions are farthest from the actual values. Its R² score of -265.08 is significantly worse than all the other models, suggesting that it has failed to capture any meaningful patterns in the data and may have been overfitted to noise. In summary, the Stacking Model offers the best performance across multiple metrics, but none of the models are perfect, with significant room for improvement, particularly in terms of predictive accuracy for COVID-19 trends. To further evaluate the performance of the implemented regression models in predicting COVID-19 trends, the following tables—Table 4, Table 5, and Table 6—present a comparative ranking of the models based on key evaluation metrics: R² Score, Mean Absolute Error (MAE), and Mean Squared Error (MSE), respectively. These rankings provide a comprehensive view of each model's predictive accuracy and robustness.

Table 3 Ranked Models Based on R² Score:

Rank	Model	R² Score	MAE	MSE
1	**Stacking Model**	-2.669640	4.918228e+07	3.324972e+15
2	**Random Forest**	-4.857282	6.634053e+07	5.307141e+15
3	**Gradient Boosting**	-4.863941	6.638599e+07	5.313175e+15
4	**Linear Regression**	-6.846396	8.329432e+07	7.109429e+15
5	**AdaBoost**	-10.091972	9.562474e+07	1.005017e+16
6	**Support Vector Regression**	-265.084156	4.900881e+08	2.410924e+17

Table 4 Ranked Models Based on MAE (Lower is Better):

Rank	Model	MAE	R² Score	MSE
1	**Stacking Model**	4.918228e+07	-2.669640	3.324972e+15
2	**Random Forest**	6.634053e+07	-4.857282	5.307141e+15
3	**Gradient Boosting**	6.638599e+07	-4.863941	5.313175e+15
4	**Linear Regression**	8.329432e+07	-6.846396	7.109429e+15
5	**AdaBoost**	9.562474e+07	-10.091972	1.005017e+16
6	**Support Vector Regression**	4.900881e+08	-265.084156	2.410924e+17

Table 5 Ranked Models Based on MSE (Lower is Better):

Rank	Model	MSE	R² Score	MAE
1	**Stacking Model**	3.324972e+15	-2.669640	4.918228e+07
2	**Random Forest**	5.307141e+15	-4.857282	6.634053e+07
3	**Gradient Boosting**	5.313175e+15	-4.863941	6.638599e+07
4	**Linear Regression**	7.109429e+15	-6.846396	8.329432e+07

5	**AdaBoost**	1.005017e+16	-10.091972	9.562474e+07
6	**Support Vector Regression**	2.410924e+17	-265.084156	4.900881e+08

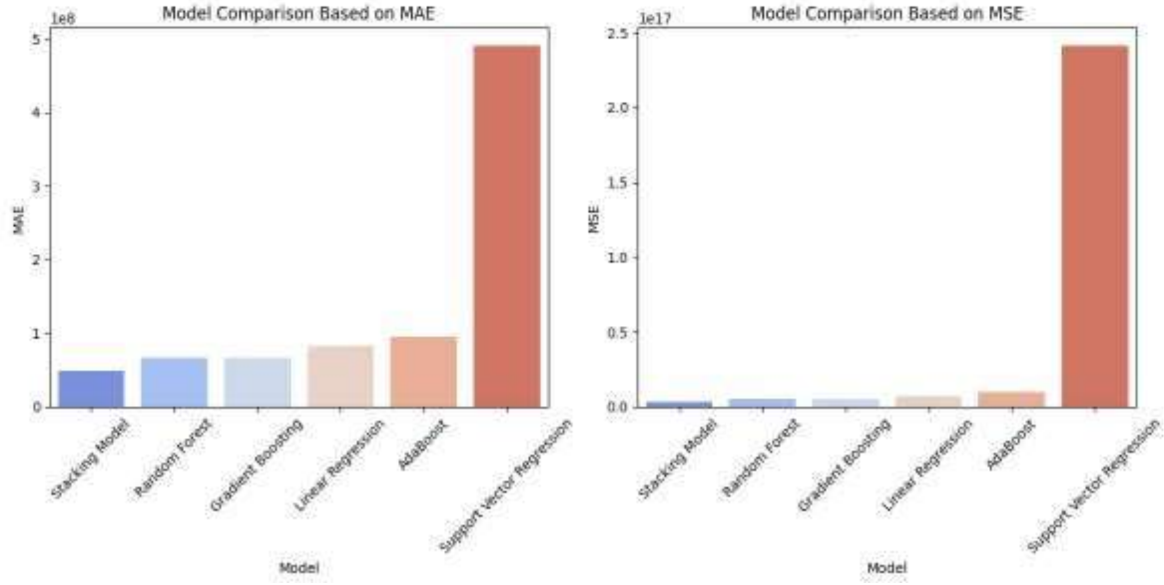

Figure 3: Models comparison based on MAE and MSE Score

The figure 3 illustrates a comparative analysis of six machine learning models—Stacking Model, Random Forest, Gradient Boosting, Linear Regression, AdaBoost, and Support Vector Regression (SVR)—based on Mean Absolute Error (MAE) and Mean Squared Error (MSE). The bar chart on the left shows that the Stacking Model achieved the lowest MAE, indicating superior performance in minimizing average prediction errors, followed closely by Random Forest and Gradient Boosting. In contrast, SVR recorded the highest MAE, reflecting poor predictive accuracy. The right chart, which compares the models based on MSE, reinforces these findings, with the Stacking Model again exhibiting the lowest error, while SVR displays a significantly higher MSE than all other models. These results highlight the effectiveness of ensemble-based models like Stacking in forecasting COVID-19 case trends.

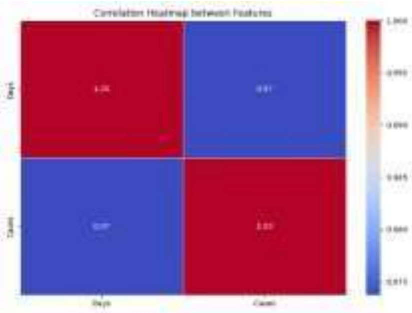

Figure 4: Correlation heatmap of features

The figure 4, heatmap illustrates the correlation between the two features: Days and Cases. It reveals a strong positive correlation of 0.97 between them, indicating that as the number of days increases, the cumulative number of confirmed COVID-19 cases also rises significantly. Both features show perfect self-correlation with a value of 1.00, as expected. This high correlation suggests a strong temporal trend in the data, which justifies the use of time-series forecasting models for predicting case progression over time.

The figure 5 bar chart presents a comparison of various machine learning models based on their R² scores, which measure how well each model explains the variance in the actual COVID-19 case data. A higher R² score indicates better predictive performance. The Stacking Model, Random Forest, and Gradient Boosting exhibit relatively better R² values, closer to 0, implying modest predictive accuracy. In contrast, Support Vector Regression (SVR) yields a highly negative R² score (around -250), indicating a poor fit and that it performs worse than a simple mean prediction. Overall, ensemble models such as stacking and boosting show better generalization, while SVR fails to capture the underlying trend effectively.

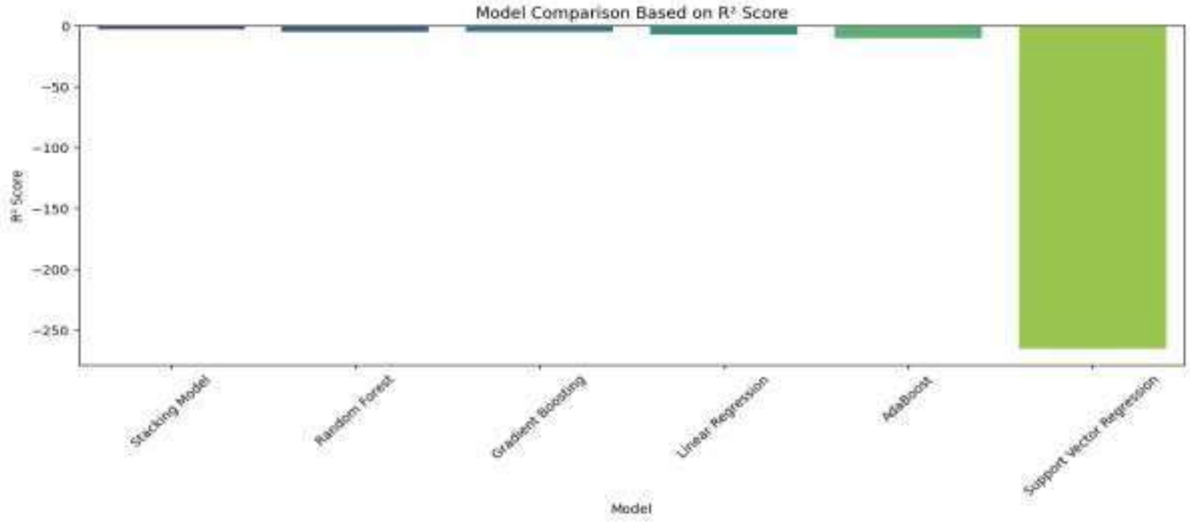

Figure 5: Models comparison based on R2 Score

Among the evaluated models, the Stacking Model consistently outperforms others across all metrics—achieving the lowest Mean Absolute Error (MAE: 4.92e+07), Mean Squared Error (MSE: 3.32e+15), and the least negative R² Score (-2.67). Although the negative R² indicates poor overall model fit, the Stacking Model remains the most accurate and reliable for predicting global cumulative COVID-19 cases. Random Forest and Gradient Boosting also show relatively strong performance but lag slightly behind the Stacking approach. In contrast, simpler models like Linear Regression and ensemble methods such as AdaBoost perform worse, likely due to their limited capacity to capture complex nonlinear patterns. Support Vector Regression (SVR) demonstrates the weakest results, with particularly high error rates and an extremely negative R², underscoring its unsuitability for this forecasting task.

CONCLUSION

This study assessed several machine learning models for predicting global COVID-19 trends using real-world data. The Stacking Model—leveraging Random Forest and Gradient Boosting—emerged as the most effective, despite the generally poor R² scores across all models. These results highlight the challenges of forecasting in highly dynamic environments such as pandemics. To improve predictive accuracy, future work should explore deeper feature engineering, data enrichment (e.g., vaccination rates, mobility trends, policy changes), and more advanced hybrid modeling techniques. Accurate forecasting remains critical for timely public health responses and strategic planning during global health crises.

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