

Modeling and Projecting Malaria Incidence in Somalia: A Dual-Approach Framework Combining Statistical Forecast Accuracy with Mechanistic Epidemiological Insight

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Abstract

Malaria remains a major public health challenge in Somalia, where evidence-based decision-making is complicated by the need to balance predictive accuracy with epidemiological interpretability. This study evaluates a dual-approach modeling framework by comparing the forecasting performance of eight statistical time-series models with a mechanistic Susceptible–Infected–Recovered–Susceptible (SIRS) model using annual malaria incidence data from 2000 to 2022. The objective was to assess both out-of-sample predictive accuracy and the ability of each approach to generate actionable epidemiological insight. A clear trade-off between accuracy and interpretability was observed. Among the statistical models, the Autoregressive Fractionally Integrated Moving Average (ARFIMA) model demonstrated superior forecasting performance, achieving a Mean Absolute Percentage Error (MAPE) of 7.44% on a hold-out test set. In contrast, the SIRS model exhibited lower predictive accuracy (MAPE = 24.15%) but provided important mechanistic insight into malaria transmission dynamics. The model estimated a basic reproduction number (R_0) of 1.19 and identified transmission and recovery rates as key parameters influencing epidemic behavior. These findings indicate that statistical and mechanistic models serve complementary roles rather than competing purposes. The results support the use of accurate statistical models, such as ARFIMA, for short-term operational forecasting and resource allocation, alongside mechanistic models, such as SIRS, for long-term strategic planning and intervention prioritization. This integrated framework offers a more robust and context-appropriate evidence base for malaria control and planning in Somalia.

Keywords: Malaria, Somalia, Time Series Forecasting, Mechanistic Models, Statistical Models, SIRS, Arfima, Public Health

1. Introduction

Malaria remains a major public health challenge globally, with the overwhelming burden concentrated in sub-Saharan Africa, where the majority of cases and deaths continue to occur (World Health Organization, 2022) [1]. The disease is caused by Plasmodium parasites and transmitted by female Anopheles mosquitoes, with transmission intensity shaped by interactions among human hosts, mosquito vectors, parasites, and the surrounding environment. Despite notable progress in malaria control over the past two decades, transmission persists in many African countries, particularly in fragile and conflict-affected settings. Malaria transmission dynamics are inherently complex and influenced by climatic variability, vector ecology, population immunity, and the effectiveness of control interventions. Temperature and rainfall play a central role by affecting

mosquito survival, breeding, and parasite development, thereby constraining where and when malaria transmission can occur [2]. Understanding these interacting drivers over time is essential for designing effective control strategies and anticipating future disease trends, especially in settings with unstable transmission.

Mathematical modeling has long played a central role in malaria epidemiology by providing a quantitative framework for understanding transmission mechanisms and evaluating intervention scenarios. Classical compartmental models, beginning with the seminal work of Kermack and McKendrick, established the theoretical foundations of infectious disease dynamics[3]. Subsequent malaria-specific models incorporated vector–host interactions and intervention effects, improving biological realism and

policy relevance. However, purely mechanistic models often require detailed and high-quality data, which may be unavailable in low-resource or conflict-affected settings. In parallel, statistical time-series models have been widely used to analyze malaria incidence data and generate short-to medium-term forecasts. These approaches are effective in capturing temporal dependence and longmemory properties in epidemiological data and have demonstrated strong predictive performance in malaria applications [4]. Advanced time-series frameworks, including fractional differencing models, allow for flexible representation of long-range dependence that may characterize malaria incidence trends [5,6,7]. Nevertheless, purely statistical models typically lack explicit biological interpretation, limiting their ability to explain why transmission patterns change.

Somalia represents a particularly challenging context for malaria modeling. Prolonged conflict, population displacement, and limitations in routine surveillance have constrained data availability and hindered comprehensive epidemiological analysis. In particular, inconsistencies in routine reporting and the absence of reliable high-frequency surveillance data necessitate the use of annual incidence series as the most stable and consistently available representation of malaria trends over time. As a result, Somalia remains under-represented in the malaria modeling literature, and regional studies often rely on generalized assumptions or data from neighboring countries that may not accurately reflect local transmission dynamics. To address this gap, this study develops a dual-approach modeling framework that integrates a mechanistic Susceptible–Infected–Recovered–Susceptible (SIRS) model with an Autoregressive Fractionally Integrated Moving Average (ARFIMA) time-series approach. By combining epidemiological structure with statistical forecasting capability, the proposed framework aims to capture both the biological processes underlying malaria transmission and the temporal characteristics of observed incidence data. The model is calibrated using annual malaria incidence data for Somalia obtained from internationally recognized sources and evaluated based on out-of-sample forecasting performance.

This complementary framework is intended to enhance understanding of malaria dynamics in Somalia while supporting evidence-based planning for malaria control in data-limited settings. By explicitly balancing predictive accuracy and mechanistic insight, the approach provides a more robust analytical basis for both short-term operational forecasting and long-term strategic decision-making in malaria control.

1.1. Main Objective of the Paper

The main objective of this study is to develop and evaluate a dual-approach framework for malaria analysis and forecasting in Somalia by systematically comparing the performance, predictive accuracy, and practical utility of multiple statistical time-series models (ARIMA, ETS, BATS, TBATS, Theta, ARFIMA, ARNN, and ANN-MLP) with a

mechanistic Susceptible–Infected–Recovered–Susceptible (SIRS) model. Specifically, the study aims to assess the suitability of statistical models for short-term malaria incidence forecasting, while developing and calibrating a simplified SIRS model to elucidate core malaria transmission dynamics, estimate key epidemiological parameters such as the basic reproduction number (R_0), and evaluate sensitivity to changes in transmission-related parameters. Through a direct comparative analysis, the study proposes an integrated framework that highlights the complementary roles of statistical and mechanistic models in supporting evidence-based public health planning and decision-making in Somalia.

2. Materials and Methods

2.1. Study Area, Research Design & Data Source

This study focused on Somalia, a country in the Horn of Africa characterized by a complex interplay of environmental, socio-economic, and political factors influencing malaria transmission. A quantitative, longitudinal research design was employed, utilizing a hybrid Susceptible–Infected–Recovered–Susceptible (SIRS) - Autoregressive Fractionally Integrated Moving Average (ARFIMA) mathematical model and time series analysis. The model was developed, parameterized, and validated using secondary annual malaria incidence rates for Somalia (per 1,000 population at risk) from 2000 to 2022, obtained from the World Health Organization and Our World in Data (<https://ourworldindata.org/malaria>). This approach aimed to leverage the mechanistic insights of the SIRS model with the statistical forecasting capabilities of the ARFIMA model to provide insights relevant for Somalia's national malaria eradication strategy.

2.2. Data Preprocessing

To evaluate the forecasting accuracy of the models, the time series data was partitioned into a training set and a test set. The training set, comprising data from 2000 to 2017 ($n_{\text{train}} = 18$), was used for model estimation. The subsequent 5 years of data, from 2018 to 2022 ($n_{\text{test}} = 5$), served as the test set (hold-out set) for out-of-sample forecast evaluation. This partitioning was performed using the `ts_split` function from the `TSstudio` package in R.

2.3. Stationarity Testing and Differencing

Time series data often needs to be stationary for effective modelling, particularly for ARFIMA -family models. Stationarity implies that the mean, variance, and autocorrelation structure do not change over time. The Augmented Dickey-Fuller (ADF) test and the Phillips-Perron (PP) test were employed to check for the presence of unit roots in the training data, which would indicate non-stationarity [5,6]. The null hypothesis (H_0) for both tests is that the series has a unit root (is non-stationary), while the alternative hypothesis (H_1) is that the series is stationary. If non-stationarity was detected ($p\text{-value} > 0.05$), differencing was considered. The `ndiffs` function from the `forecast` package was also used to estimate the number of differences required to achieve stationarity. For the ARIMA model, the `auto.arima`

function automatically determines the appropriate level of differencing.

2.4. Time Series Model Development

The study employs a range of univariate time series modeling techniques to forecast the malaria incidence in Somalia. These techniques include

2.4.1. ARIMA Model

ARIMA (Autoregressive Integrated Moving Average) is a widely used time-series forecasting model that combines autoregressive (AR), differencing (I), and moving average (MA) components. It is effective in capturing both autoregressive dependence and short-term shock propagation in time-series data. The general ARIMA (p, d, q) model is expressed as:

$$(1 - \phi_1 L - \phi_2 L^2 - \dots - \phi_p L^p)(1 - L)^d y_t = (1 + \theta_1 L + \theta_2 L^2 + \dots + \theta_q L^q) \varepsilon_t \quad (1)$$

where y_t denotes the malaria incidence time series, L is the lag operator, ϕ_i and θ_i are the autoregressive and moving average parameters, respectively. The parameter p represents the order of the autoregressive component, d is the degree of differencing required to achieve stationarity, and q denotes the order of the moving-average component. ARIMA models were fitted using the `auto.arima()` function from the forecast package in R. This function automatically selects optimal values of p , d , and q based on information criteria. Model selection was guided by the Akaike Information Criterion (AIC), with the final model chosen as the one minimizing AIC. The automated procedure follows the Hyndman-Khandakar algorithm, which combines unit-root testing, stepwise model selection, and likelihood optimization. Model adequacy was assessed using standardized residual plots, residual autocorrelation function (ACF) diagnostics, and the Ljung-Box test to confirm the absence of remaining serial correlation [14].

2.4.2. ARFIMA Model

The Autoregressive Fractionally Integrated Moving Average (ARFIMA) model extends the ARIMA framework by allowing the differencing parameter to take fractional values, thereby accommodating long-range dependence or long-memory behaviour in time-series data. This feature is particularly relevant for epidemiological series such as malaria incidence, where persistence and gradual structural evolution may be present. The ARFIMA (p, d, q) model can be written as:

$$(1 - \phi_1 L - \phi_2 L^2 - \dots - \phi_p L^p)(1 - L)^d y_t = (1 + \theta_1 L + \theta_2 L^2 + \dots + \theta_q L^q) \varepsilon_t \quad (2)$$

where d is a fractional differencing parameter capturing long-memory dynamics, while the remaining terms retain their standard ARIMA interpretation. ARFIMA models were estimated to evaluate whether allowing fractional integration improves forecasting performance relative to integer-differenced ARIMA models.

2.4.3. Theta Model

The Theta model is a parsimonious forecasting method that decomposes a time series into long-term trend and short-term curvature components. It has been shown to perform competitively across a wide range of forecasting applications. The model assumes that future values of the time series are governed by a combination of a local level and a drift term. The forecasting equation for the Theta model is given by:

$$y_{t+1} = (1 + \theta)y_t + \mu + \varepsilon_{t+1} \quad (3)$$

where y_t is the observed time series, θ controls the curvature of the series, μ is a drift parameter, and ε_{t+1} represents the error term. In this study, the Theta model was applied to assess its suitability for capturing medium-term malaria incidence trends.

2.4.4. ETS Model

The Error-Trend-Seasonality (ETS) model provides a flexible state-space framework for time-series forecasting by decomposing observations into error (E), trend (T), and seasonal (S) components. These components may be additive (A), multiplicative (M), or absent (N), yielding a broad class of potential model structures. The ETS observation and state equations are expressed as:

$$y_t = w(x_{t-1}) + r(x_{t-1})\varepsilon_t \quad (4)$$

$$x_t = f(x_{t-1}) + g(x_{t-1})\varepsilon_t \quad (5)$$

where x_t denotes the unobserved state vector and ε_t is Gaussian white noise. ETS models were implemented using the `ets()` function from the forecast package and evaluated for their ability to capture trend behavior in malaria incidence [8].

2.4.5. NNAR Model

The Neural Network Autoregressive (NNAR) model combines lagged values of the time series with a feed-forward neural network architecture. It is capable of capturing both linear and nonlinear relationships that may not be adequately represented by traditional statistical models.

The NNAR model is expressed as:

$$y_t = \omega_0 + \sum_{j=1}^q \omega_j g(\omega_{0j} + \sum_{i=1}^p \omega_{ij} y_{t-i}) + e_t \quad (6)$$

where y_{t-i} are lagged inputs, $g(\cdot)$ is an activation function, and the ω 's denote network weights. NNAR models were fitted using the `nnetar()` function, which automatically selects lag length and network size [9].

2.4.5. TBATS Model

The TBATS (Trigonometric seasonality, Box-Cox transformation, ARMA errors, Trend, and Seasonality) model is designed to handle complex seasonal patterns and non-constant variance in time-series data. The general TBATS

formulation is:

$$y_t^{(\omega)} = l_{t-1} + \phi b_{t-1} + \sum_{i=1}^T s_{t-m_i}^{(i)} + d_t \quad (7)$$

where $y_t^{(\omega)}$ denotes the Box-Cox transformed observation, l_t is the local level, b_t is the trend, $s_t^{(i)}$ represents seasonal components, and d_t follows an ARMA process. TBATS models were estimated using the `tbats()` function [10].

2.4.6. NNETAR / ARNN Model

NNETAR models use a feed-forward neural network with lagged values of the time series as inputs. A NNETAR(p, k) model includes p lagged inputs and k hidden neurons in a single hidden layer. The model was implemented using the `nnetar` function, which selects optimal lag length and network size based on information criteria [10]. Artificial Neural Network (ANN-MLP) A Multilayer Perceptron (MLP) is a feed-forward artificial neural network composed of input, hidden, and output layers. In this study, MLP models were estimated using the `mlp()` function from the `nnfor` package. Lagged malaria incidence values were used as inputs, and multiple repetitions were performed to mitigate convergence to local minima.

2.4.7. Model Evaluation

To assess model performance, the malaria incidence data for Somalia were divided into training and validation sets. Models were evaluated using the Mean Absolute Scaled Error (MASE), Symmetric Mean Absolute Percentage Error (SMAPE), and Mean Absolute Percentage Error (MAPE) to identify the most accurate forecasting approaches. Models with the lowest error values were considered best-performing and were subsequently used for forecasting. Comparative analysis across models enabled identification of temporal patterns and performance differences relevant to public health planning. The study evaluated ARIMA, ETS, Theta, NNAR, TBATS, ARFIMA, and hybrid modeling approaches to support evidence-based policy and decision-making.

2.5. Forecast and Model Performance

Forecast accuracy was assessed using scale-independent error metrics, including MASE, SMAPE, MAPE, and Theil's U statistic. MASE was emphasized due to its robustness and comparability across models, while MAPE and SMAPE were reported to facilitate interpretability and comparison with existing literature. These metrics enabled systematic comparison of both individual and hybrid models [10,11].

2.5.1. Mean Absolute Percentage Error (MAPE)

MAPE measures the average percentage deviation between observed and forecasted values and is defined as:

$$MAPE = \frac{1}{n} \sum_{t=1}^n \left| \frac{y_t - \hat{y}_t}{y_t} \right| \times 100 \quad (8)$$

where y_t denotes the observed malaria incidence at time t , $\hat{y}_t$ is the corresponding forecasted value, and n is the number of observations.

2.5.2. Mean Absolute Scaled Error (MASE)

MASE provides a scale-free measure of forecast accuracy by comparing model errors with those of a naïve benchmark forecast:

$$MASE = \frac{\frac{1}{n} \sum_{i=1}^n |y_i - \hat{y}_i|}{\frac{1}{n-1} \sum_{i=2}^n |y_i - y_{i-1}|} \quad (9)$$

Lower MASE values indicate superior predictive performance relative to the naïve model.

2.5.3. Symmetric Mean Absolute Percentage Error (SMAPE)

SMAPE quantifies forecast accuracy while accounting for the magnitude of both observed and predicted values:

$$SMAPE = \frac{1}{n} \sum_{i=1}^n \frac{2 |F_i - A_i|}{|F_i| + |A_i|} \times 100 \quad (10)$$

where F_i and A_i represent forecasted and actual values, respectively.

2.6. Theil's U Statistic

Theil's U statistic compares forecast accuracy against a naïve benchmark and is given by:

$$U = \frac{\sqrt{\frac{1}{n} \sum_{i=1}^n \left(\frac{y_i - \hat{y}_i}{y_i} \right)^2}}{\sqrt{\frac{1}{n} \sum_{i=1}^n \left(\frac{y_i - \bar{y}}{y_i} \right)^2}} \quad (11)$$

A value of $U < 1$ indicates that the forecasting model outperforms the naïve benchmark.

2.7. Mechanistic Model: Simplified SIRS

A simplified deterministic Susceptible–Infected–Recovered–Susceptible (SIRS) model was developed to examine malaria transmission dynamics. The model is governed by a system of ordinary differential equations describing transitions between epidemiological compartments [3]. Key parameters—including the transmission rate (β), recovery rate (γ), and waning immunity rate (α)—were estimated by fitting the model to historical incidence data (2000–2021). Model sensitivity was assessed by varying each parameter by $\pm 20\%$ to evaluate its influence on epidemic behavior.

2.8. Software

All analyses were conducted using R statistical software [12]. Key packages included *psych* for descriptive analysis, *tseries* for stationarity testing, *TSstudio* for data partitioning

and visualization, *forecast* for timeseries modeling, *Metrics* for accuracy evaluation, and *nnfor* for neural network-based forecasting.

3. Results

3.1. Data Description

3.2. Descriptive Statistics of the Data

In table 4.1, results of the time series of annual malaria cases in Somalia from 2000 to 2021 (N=22) had showed that it had a mean of 914,829 cases and a standard deviation of 324,368. The median was 927,482 cases. The number of cases ranged from a minimum of 411,167 to a maximum of 1,392,709.

Variable	# of Obs.(n)	mean	SD	Median	Trimmed Mean	MAD
Data	22	914829	324368	927482	921890	423117.7
Variable	Minimum	Maximum	Range	skewness	Kurtosis	SE
Data	411167	1392709	981542	- 0.16	-1.46	69155.54

Table 1: Descriptive Statistics of Malaria Incidence in Somalia (2000 To 2021)

3.3. Visual Representation of the Data

Figure 1 illustrated a visualization of the time series revealed a complex, non-linear trend. Cases were high in the early 2000s, peaking around 2005. This was followed by a steep and sustained decline until a nadir was reached around

2011-2012. From 2012 onwards, the data shows a period of resurgence and stabilization, with cases rising again but not to the levels seen in the early 2000s. No obvious seasonality is present in the annual data.



Figure 1: Time Series Diagram of Somalia Malaria Incidence

3.4. Data Stationary Testing (Stationarity Testing)

Stationarity tests performed on the training data (2000-2016) indicated that the series was non-stationary. Specifically, the Augmented Dickey-Fuller (ADF) test yielded a statistic of -2.1493 with a p-value of 0.5155, and the Phillips-Perron (PP) test resulted in a Z (alpha) statistic of -5.32 with a p-value of 0.7888. Since both p-values are significantly greater than the 0.05 threshold, the null hypothesis of non-stationarity could not be rejected. This conclusion was corroborated by the *ndiffs* function, which suggested that one order of differencing ($d=1$) was required to achieve stationarity, a key parameter that subsequently guided the ARIMA model selection.

3.5. Time Series Model Fitting, Evaluation and Diagnostics

The eight time series models were fitted to the training data. The *auto.arima* function, after an exhaustive search, selected an ARIMA (1, 1, 0) model as the best fit, with an AICc of

428.48. Diagnostic checking of these model's residuals via the Ljung-Box test ($Q^* = 1.4222$, $p\text{-value} = 0.7003$) showed no evidence of significant remaining autocorrelation, indicating the model was adequate for the data. The other models were fitted as described in the methodology, including an ETS (M, N, N) model, a BATS model, and various neural network configurations.

3.6. Forecasting Performance on the Test Set (2017-2021)

The eight fitted models were used to generate a 5-year forecast, which was then compared against the actual data in the test set. Table 4.3 summarizes the performance metrics of all models. The results clearly indicate that the ARFIMA model was the superior statistical forecasting model. It achieved the lowest error across every key metric (MAE, MASE, MAPE, Theil's U, SMAPE) and was the only model with a Theil's U statistic below 1, signifying that it outperformed a simple naive forecast. The ARIMA (1,1,0) model was

the second-best performer, though its error metrics were considerably higher than ARFIMA's. The ETS, BATS, and TBATS models performed moderately but were clearly inferior to the ARIMA-family models. The Theta, ANN-MLP, and ARNN models performed very poorly, with extremely high error metrics, demonstrating their unsuitability for

forecasting this particular time series. Visual inspection of the forecast plots confirmed these quantitative findings. The ARFIMA forecast tracked the test data most closely. In contrast, the neural network models (ARNN and MLP) produced forecasts that deviated substantially from the actual values, highlighting their poor performance.

Model	MASE	MAPE (%)	Theil's U	SMAPE
ARFIMA	74,939	7.44	0.94	0.0784
ARIMA(1,1,0)	109,647	10.89	1.31	0.1176
ETS(M,N,N)	126,073	12.51	1.50	0.1370
TBATS	129,158	12.80	1.54	0.1406
Theta	201,166	20.04	2.34	0.2320
ANN-MLP	239,130	23.80	2.79	0.2854
ARNN	433,822	44.41	4.63	0.5954

Note: Best performance for each metric is bolded.

Table 2: Comparative Forecasting Accuracy of Models on the Test Set

3.7. Visual Comparison of Forecasts

Figure 2 Presents the Forecasts from All Eight Models Overlaid on the Original Time Series, with the Test Period highlighted.

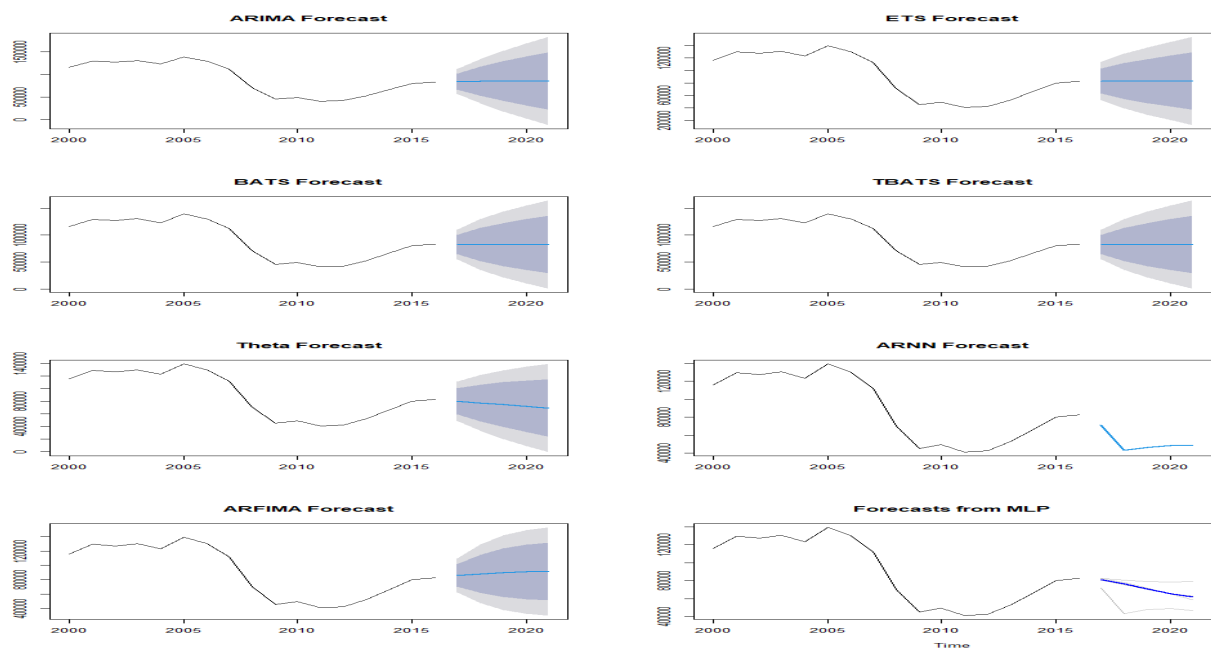


Figure 2: Forecasts from 8 Single Time Series Models

Visually, the forecasts from ETS, ARFIMA, BATS, and TBATS appear to track the test data more closely than the other models. The ARIMA model's forecast shows a slight decline, underestimating the actual values in the test period. The Theta, NNETAR, and MLP models show forecasts that deviate more substantially from the actual test data points, consistent with their poorer quantitative performance metrics. The NNETAR and MLP forecasts, in particular, show a flatter trajectory that does not capture the nuances of the test data. The prediction intervals for most models widen over the forecast horizon, reflecting increasing uncertainty.

3.8. Visual Model Diagnostic Checking Test

The provided Figure 3 displays a visual model diagnostic checking test for an ARIMA(1,1,0) model. The top plot shows the residuals over time, revealing no obvious patterns, which is a good sign. The bottom-left plot presents the Autocorrelation Function (ACF) of the residuals; ideally, all lags should fall within the blue dashed lines, indicating no significant autocorrelation, which largely holds true here. The bottom-right plot is a histogram of the residuals, overlaid with a normal distribution curve, suggesting that the residuals are approximately normally distributed around

zero. Together, these plots indicate that the ARIMA(1,1,0) model appears to adequately capture the underlying patterns in the data, as the residuals behave like white noise.

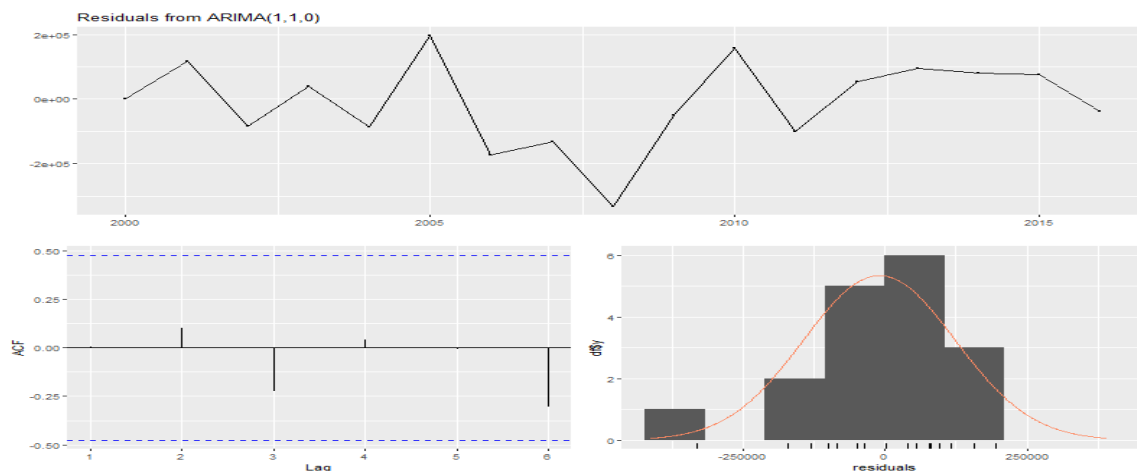


Figure 3: Arima Model Residual Diagnostic Plot

3.9. Analysis of Malaria Dynamics Using a Simplified SIRS Model

This section details the development and interpretation of a Susceptible-Infected-Recovered-Susceptible (SIRS) epidemiological model to analyze and forecast malaria cases. The analysis is based on a time-series dataset of reported infections, as shown in Figure 4. The historical

data reveals a complex pattern, with an initial rise in cases peaking around 2005, followed by a sharp decline until 2010, and a subsequent period of resurgence. To capture the core dynamics of this outbreak, a simplified SIRS model was employed, focusing on the interplay between transmissions, recovery, and waning immunity, while omitting long-term vital dynamics like births and deaths.



Note: This figure illustrates the historical data used for model calibration, showing the number of active infected individuals per year

Figure 4: Reported Infected Cases over Time

3.10. Model Calibration and Fit

The SIRS model was calibrated by fitting it to the historical data to estimate three key epidemiological parameters. The optimization process yielded the parameter values that best describe the observed trend, which are detailed in Table 4.4. The model estimates a transmission rate (β) of 1.21, a

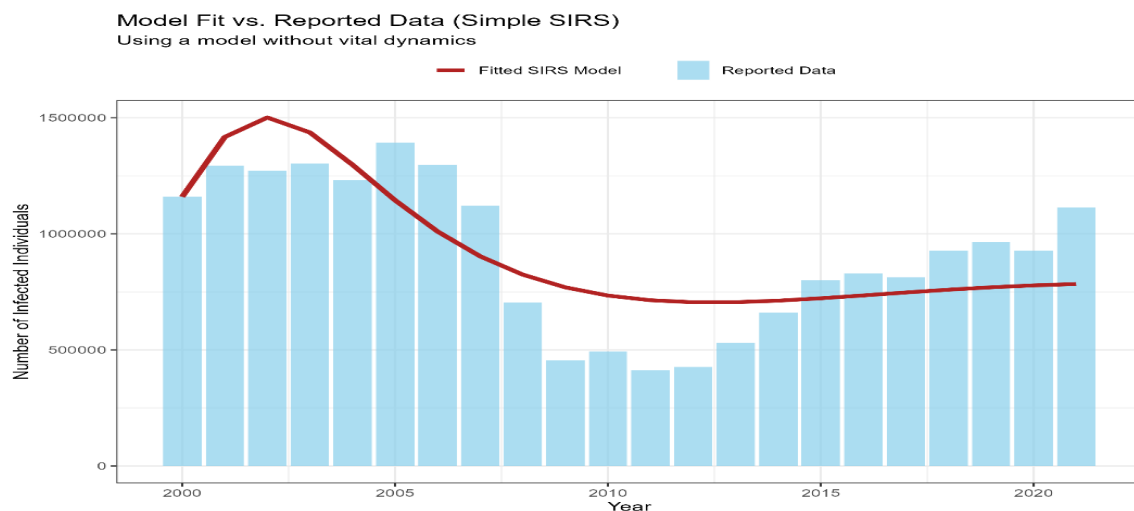
recovery rate (γ) of 0.77, and a waning immunity rate (α) of 0.25. These values imply an average infectious period of approximately 1.3 years ($1/\gamma$) and an average duration of immunity of about 4 years ($1/\alpha$) before an individual becomes susceptible again.

Parameter	Symbol	Estimate Value	Interpretation
Transmission Rate	β	1.2114	The rate at which susceptible individuals become infected.
Recovery Rate	γ	0.7680	The rate at which infected individuals recover.
Waning Immunity Rate	α	0.2481	The rate at which recovered individuals lose immunity.

Table 3: Estimated Parameters for the Simplified SIRS Model

The performance of the calibrated model is visualized in Figure 5. The model successfully captures the broad arc of the epidemic: the initial rise, the peak, the subsequent decline, and the eventual stabilization towards an endemic level.

However, the smooth curve of the deterministic model does not capture the significant year-to-year volatility present in the reported data, particularly the sharp drop after 2005 and the fluctuations in the later years.



Note: This figure compares the infected cases predicted by the fitted SIRS model (red line) against the actual reported data (blue bars).

Figure 5: Model Fit vs. Reported Data (Simple SIRS)

To quantify the model's accuracy, several error metrics were calculated in Table 4.5. The Mean Absolute Percentage Error (MAPE) of 24.15% indicates that the model's predictions are, on average, within about 24% of the actual values.

This confirms the visual assessment: the model provides a reasonable approximation of the overall trend but has moderate error due to its inability to replicate the finer-grained fluctuations.

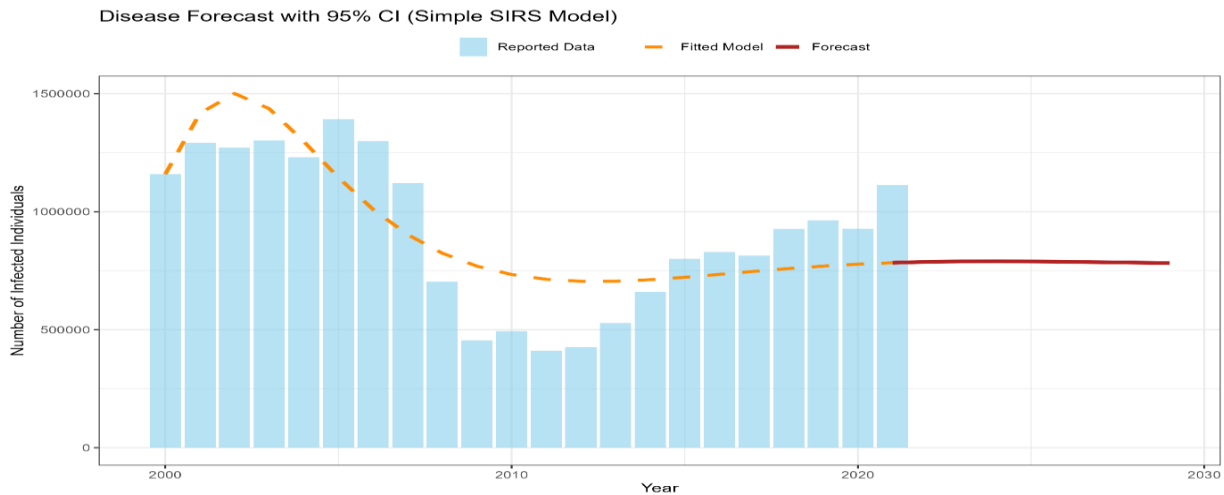
Metric	Abbreviation	Value	Interpretation
Mean Absolute Error	MASE	176,137.24	The average absolute difference between predicted and actual cases.
Mean Absolute Percentage Error	MAPE	24.15%	The average percentage difference between predicted and actual cases.

Table 4: Model Fit Evaluation Metrics

3.11. Disease Dynamics and Forecasting

A key insight from the model is the Basic Reproduction Number (R_0), which was calculated to be 1.19. Since this value is greater than 1, it indicates that, on average, each infected individual will transmit the disease to more than one other person in a fully susceptible population. This confirms that the underlying conditions are sufficient for the disease to spread and become endemic. Using the final state of the fitted model as a starting point, a forecast was generated

for the next eight years (2022-2029), as shown in Figure 6. The forecast predicts that the number of infected individuals will remain relatively stable, hovering just below 800,000 cases per year with a very slight downward trend. The 95% confidence interval (the red shaded area) is extremely narrow, suggesting the model is highly certain about this stable trajectory. This high certainty is a characteristic of the deterministic model and may not reflect the potential for real-world volatility.



Note: This plot shows the historical data (bars), the model fit (dashed orange line), and the 8-year forecast (solid red line) with its 95% confidence interval (shaded ribbon).

Figure 6: Disease Forecast with 95% CI (Simple SIRS Model)

The specific values for the forecast of the SIERS model are provided in Table 4.6, detailing the median prediction and the narrow bounds of the confidence interval.

Year	Lower 95% CI	Median Forecast	Median Forecast
2022	787,663.8	787,664.0	787,664.2
2023	789,579.9	789,580.2	789,580.5
2024	789,986.8	789,987.2	789,987.6
2025	789,987.6	789,987.6	789,987.6
2026	789,987.6	789,987.6	789,987.6
2027	786,166.7	786,167.1	786,167.5
2028	784,334.4	784,334.8	784,335.1
2029	782,611.2	782,611.5	782,611.9

Table 5: Forecast of Infected Cases with 95% Confidence Interval (CI)

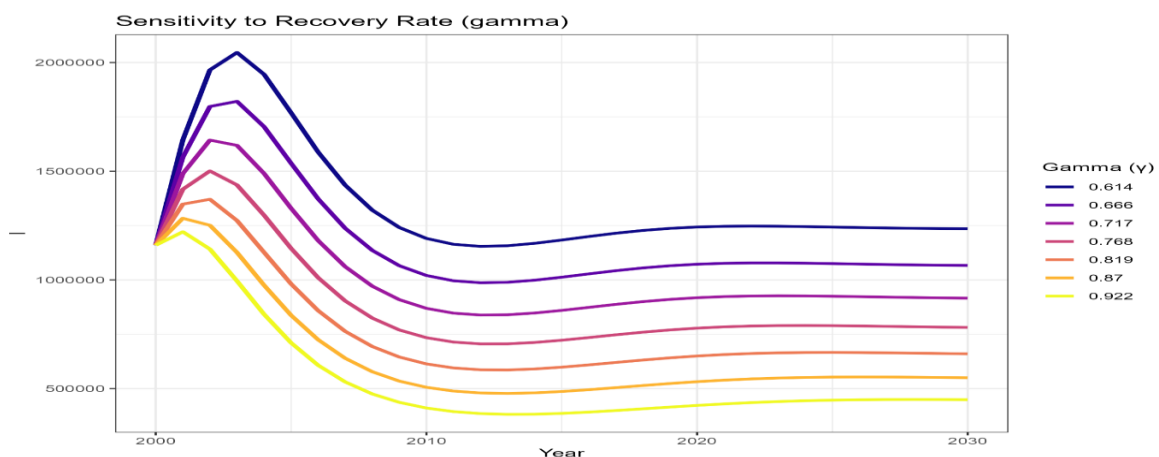


Figure 7: Sensitivity to Transmission Rate (Beta)

Figure 7: This graph illustrates the sensitivity of an epidemic model to the transmission rate, beta (β), over a 30-year period. It demonstrates a clear, positive correlation between the transmission rate and the number of infected individuals (I). Higher beta values (represented by warmer colors like yellow and green) result in a more severe epidemic, characterized by a significantly higher and earlier peak

in infections around the early 2000s. Moreover, a higher transmission rate also leads to a higher long-term endemic level of infection, as seen in the sustained separation of the curves towards the year 2030. This indicates that even small changes in the transmission rate have a substantial impact on both the short-term severity and the long-term burden of the disease.

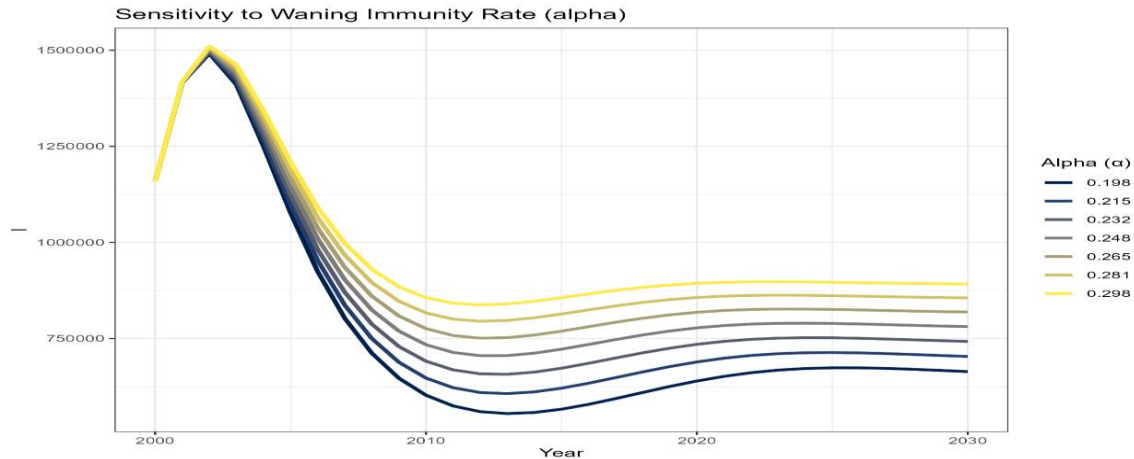


Figure 8: Sensitivity to Recovery Rate (Gamma)

Figure 8: This graph illustrates the sensitivity of an infection model to the recovery rate, represented by gamma (γ). It shows that a higher recovery rate leads to a more favourable outcome with fewer infected individuals over time. Specifically, lower gamma values (e.g., 0.614, dark blue line), which signify slower recovery, result in a much higher peak number of infections (over 2 million) and a higher stable

number of infections in the long term. Conversely, as the recovery rate increases (moving from blue to yellow lines), the initial peak of the outbreak is significantly lower, and the long-term endemic level of the infection is also substantially reduced, demonstrating that a faster recovery rate is critical in mitigating the overall impact of the disease.

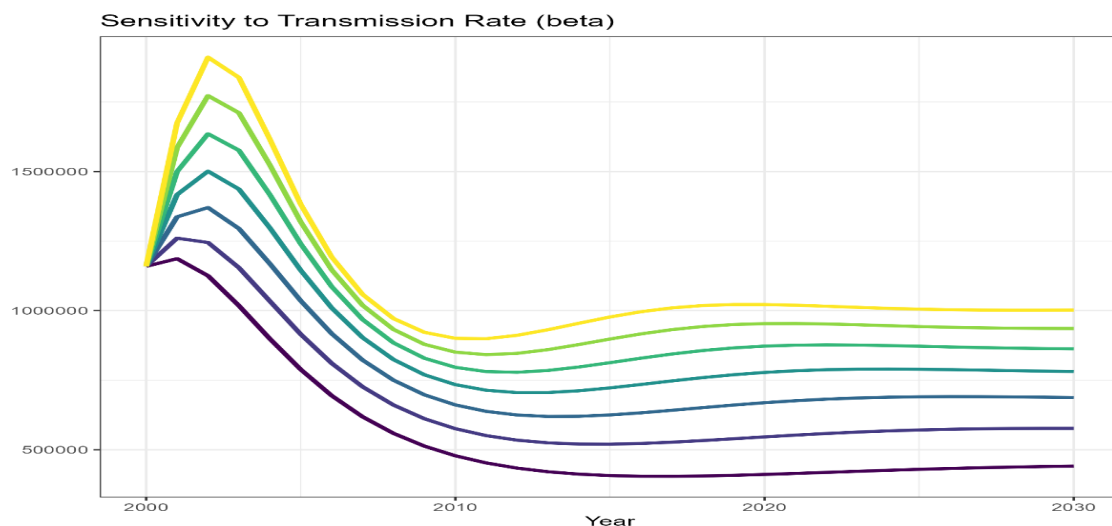


Figure 9: Sensitivity to Waning Immunity Rate (Alpha)

Figure 9 this graph illustrates the sensitivity of the number of infected individuals (I) to the waning immunity rate (alpha) over a 30-year period. All scenarios show an initial peak in infections around 2002, followed by a sharp decline and a subsequent stabilization at a new, endemic level. The key finding is that higher rates of waning immunity (higher alpha

values, represented by the brighter yellow lines) lead to a substantially higher number of infections in the long term. This demonstrates that the speed at which a population loses immunity is a critical factor in determining the sustained prevalence of the disease after an initial outbreak.

3.12. Comparative Analysis: SIRS vs. ARFIMA Model

Having identified the ARFIMA model as the best statistical forecasting tool and having a full analysis of the mechanistic SIRS model, we can now compare them on their performance,

insights, and utility. A direct comparison of the key error metrics reveals a significant difference in predictive accuracy on the historical data.

Metric	SIRS Model	ARFIMA Model
MAE	199,277	98,594
MASE	176,137	74,939
MAPE (%)	24.15%	7.44%

Table 6: Accuracy Metric Comparison Between Sirs and Arfima

The ARFIMA model is substantially more accurate in fitting the historical data, with error metrics that are less than half those of the SIRS model. The MAPE of 7.44% for ARFIMA indicates a high degree of predictive accuracy, whereas the 24.15% MAPE for the SIRS model suggests only a moderate fit. This is visually confirmed in Figure 5 (SIRS fit) and the ARFIMA forecast plot; the smooth deterministic curve of the SIRS model cannot capture the year-to-year volatility and sharp turning points that the data-driven ARFIMA model can. Despite its lower quantitative accuracy, the SIRS model provides invaluable epidemiological insights that the ARFIMA model cannot. **Mechanistic Understanding:** The SIRS model explains the why behind the epidemic's general shape. It quantifies the interplay between transmission (β), recovery (γ), and waning immunity (α). **Key Epidemiological Parameters:** It produced a Basic Reproduction Number (R_0) of 1.19, confirming that conditions are sufficient for the disease to be endemic. It also estimated an average infectious period of 1.3 years ($1/\gamma$) and an average duration of immunity of 4 years ($1/\alpha$). These are actionable insights for public health. **Intervention Simulation:** The sensitivity analysis (Figures 7, 8, 9) clearly shows that interventions targeting the transmission rate (β) and recovery rate (γ) would be most effective at reducing the peak of an outbreak. This helps prioritize public health strategies. The ARFIMA model, while highly accurate, is a statistical "black box." It excels at identifying and extrapolating temporal patterns but provides no understanding of the underlying biological or social drivers of those patterns. The two models produce fundamentally different types of forecasts. **SIRS Forecast:** Predicts a stable endemic equilibrium, with cases hovering just below 800,000 per year and an extremely narrow 95% confidence interval (Figure 6). This high certainty is an artifact of its deterministic nature and does not reflect real-world volatility. **ARFIMA Forecast:** Provides a more statistically robust forecast. While its point forecast may also show a trend, its 95% prediction intervals are much wider, realistically reflecting the uncertainty learned from the historical volatility of the data. This provides a better sense of the range of possible future outcomes. The SIRS and ARFIMA models are not competitors but are complementary tools. The SIRS model should be used for strategic planning to understand disease dynamics, identify key drivers, and simulate the potential impact of different types of interventions for- instance should we focus on treatment or prevention. While the ARFIMA model, due to its superior

accuracy, is the better tool for tactical and operational planning to generate the most likely short-term forecast for resource allocation, such as ordering medication and preparing hospital beds for the upcoming years. Combining the insights from both provides a much more powerful and comprehensive basis for public health decision-making.

4. Discussion

The findings of this study provide a nuanced perspective on applying different modelling philosophies to malaria forecasting in Somalia. The superior performance of the ARFIMA model suggests that annual malaria incidence in Somalia contains long-range dependence ("long memory"), where distant past observations retain meaningful correlation with current values. This property is consistent with the slow-changing decline and later resurgence observed in the series, and it explains why fractional differencing can outperform standard differencing in capturing persistence and gradual structural evolution in epidemiological time series [7,13]. While ARIMA models have been widely used for infectious disease forecasting, including malaria applications, the ARFIMA results here indicate that allowing fractional integration can provide improved short horizon predictive performance in settings where persistence dominates [4]. In contrast, the simplified deterministic SIRS model produced moderate fit (MAPE = 24.15%), which is expected given the model's structural simplicity relative to the complexity of malaria transmission. The SIRS framework is designed to represent average population-level dynamics and cannot reproduce year-to-year volatility embedded in routine surveillance data. This limitation is especially relevant for Somalia, where variability in ecological conditions, intervention coverage, population movement, and surveillance consistency can produce abrupt fluctuations that are difficult for a smooth deterministic model to match. Nonetheless, the mechanistic structure provides an interpretable explanation for the broad epidemic arc rise, peak, decline, and stabilization—consistent with foundational compartmental modelling principles [3].

Despite its lower predictive accuracy, the SIRS model offers key epidemiological insight that statistical models do not provide. The estimated basic reproduction number ($R_0 = 1.19$) indicates that transmission conditions are sufficient for persistence and endemicity in the absence of additional

control pressure. Furthermore, the sensitivity analysis highlights that parameters controlling transmission and recovery are influential drivers of epidemic magnitude, supporting the public health value of interventions that reduce transmission and improve case management. These interpretations align with the broader malaria control rationale that emphasizes vector control and effective treatment as central tools in reducing malaria burden (World Health Organization, 2022). Environmental drivers also remain critical: climatic variability, particularly rainfall and temperature, shapes mosquito ecology and parasite development, influencing transmission suitability over time [2].

The results also illustrate an important trade-off between accuracy and interpretability. The ARFIMA model provides strong short-term forecasting performance but remains primarily pattern-based and does not explain why incidence changes. By contrast, the SIRS model provides mechanistic “why” insight through parameters and dynamic structure, but its simplified form is less suited to capturing short-run noise in surveillance series. This supports a complementary modeling strategy: use ARFIMA for operational forecasting and near-term resource allocation, and use SIRS for strategic interpretation of transmission dynamics and intervention prioritization. Such a dual-approach framework is particularly valuable in data-limited settings, where decision-makers benefit from both accurate forecasts and interpretable epidemic drivers (World Health Organization, 2022) [3,4,15].

4.1. Recommendations

Based on the findings of this study, the following recommendations are proposed for public health authorities and stakeholders involved in malaria control in Somalia. **Operational Planning and Resource Allocation:** The results support the adoption of the ARFIMA model as the primary tool for short-term (1–3 year) forecasting of malaria incidence. Its superior predictive accuracy makes it particularly suitable for operational decision-making, including budgeting, procurement and distribution of antimalarial drugs and diagnostic supplies, and short-term planning of healthcare workforce requirements. Accurate near-term forecasts can improve preparedness and optimize the allocation of limited public health resources.

Strategic Policy and Intervention Design: For long-term strategic planning, it is recommended that the mechanistic SIRS model and its sensitivity analysis be used alongside statistical forecasts. The identification of transmission and recovery rates as key drivers of epidemic dynamics underscores the importance of maintaining a dual intervention focus: (i) reducing transmission through sustained vector control measures and community-based prevention strategies, and (ii) improving recovery through strengthened health systems that ensure timely diagnosis and access to effective treatment. This approach is consistent with established malaria control principles and supports evidence-based prioritization of interventions.

Data Collection and Surveillance Systems: The variability observed in the historical incidence data highlights the need to strengthen malaria surveillance systems in Somalia. Improving the consistency, completeness, and temporal resolution of surveillance data is strongly recommended. Transitioning from annual reporting to monthly or quarterly data collection would enable the application of models that capture seasonal dynamics and short-term fluctuations, thereby enhancing both forecasting accuracy and epidemiological interpretation. Strengthened surveillance would benefit both statistical and mechanistic modeling approaches and support more responsive malaria control planning.

5. Conclusion

This study addressed the challenge of modeling and forecasting malaria incidence in the complex and data limited context of Somalia. The findings demonstrate a clear trade-off between the high predictive accuracy of data-driven statistical models and the epidemiological interpretability offered by theory-driven mechanistic models. Among the approaches evaluated, the ARFIMA model proved most effective for short-term forecasting, while the simplified SIRS model provided valuable insight into the underlying transmission dynamics and key drivers of malaria persistence. A central contribution of this work is the demonstration that statistical and mechanistic models should be regarded as complementary rather than competing approaches. In the Somali context, the use of ARFIMA for operational forecasting and near-term resource planning, combined with the use of SIRS for strategic interpretation and long-term intervention planning, offers a robust and practical dual-model framework. By integrating forecasting accuracy with epidemiological insight, this approach strengthens evidence-based decision-making, supports more efficient allocation of limited public health resources, and contributes to more effective and sustainable malaria control efforts in Somalia.

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