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**i - J a M C S I I X**  
**2023**

# **EXTENDED ABSTRACT BOOK**

**Publication Date: 30 March 2024**

**ISBN: 978-967-15337-0-3**

<https://jamcsiix.uitm.edu.my>



# i - J a M C S I I X 2023

INTERNATIONAL JASIN MULTIMEDIA & COMPUTER SCIENCE INVENTION AND  
INNOVATION EXHIBITION (I-JaMCSIIX) 2023

**EXTENDED ABSTRACT**

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ISBN: 978-967-15337-0-3

i-JaMCSIIX

Universiti Teknologi MARA Cawangan Melaka Kampus Jasin 77300, Merlimau, Melaka

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# Forecasting the Number of Schistosomiasis Cases (Snail Fever) in Napu, Central Sulawesi, Using the Auto Regressive Integrated Moving Average (ARIMA) Method

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**Abstract**— Schistosomiasis is the second deadliest parasitic disease after malaria. In Indonesia, schistosomiasis is caused by the trematode worm *Schistosoma japonicum* which is endemic in three regions in Central Sulawesi, namely the Lindu Plateau, Napu Plateau and Bada Plateau. A global public health perspective states that schistosomiasis is a water-based disease and is considered a neglected tropical disease, until now schistosomiasis interventions continue to increase. The aim of this study was to forecast the number of schistosomiasis patients in the Napu region of Poso District and provide a scientific contribution to planning for the prevention and control of this disease. The results showed that the forecasting that has been done shows a very worrying trend regarding the number of schistosomiasis cases in the Napu Region. In 2023, the number of cases reached 392. However, a more significant increase occurred in 2024, where the number of cases jumped to 472. Even more concerning, forecasts for 2025 indicate that the number of cases could reach 588. This is a very serious sign and should be a major concern in efforts to prevent and control this disease in the region. The efforts that can be made to eliminate schistosomiasis are as follows: Providing mass treatment, controlling snail population as the vector of schistosomiasis transmission, providing education about the dangers of schistosomiasis, and improving access to clean water.

**Keywords**— Forecasting, Schistosomiasis, Tropical Disease, *Schistosoma Japonicum*

## I. INTRODUCTION

Schistosomiasis is the second most deadly parasitic disease after malaria. This disease causes economic losses and public health problems in many developing countries [1]. Schistosomiasis or commonly known as snail fever is an infectious disease caused by worm parasites belonging to the genus *Schistosoma* [2]. This disease is found in tropical and subtropical areas [3]. In Indonesia, cases of schistosomiasis are only found in the Lindu, Napu and Bada highlands, Central Sulawesi. The target for schistosomiasis eradication is to reduce the prevalence of schistosomiasis to below 1%. Control efforts undertaken include mass treatment, snail eradication,

In Indonesia, Schistosomiasis is often found in the Bada, Napu and Lindu highlands and is spread in 28 villages in Poso and Sigi Regencies. Schistosomiasis in Central Sulawesi is caused by the worm *S. japonicum* with an intermediate host, namely the snail *Oncomelania hupensis lindoensis*. Schistosomiasis transmission requires snails as an intermediate host, in Indonesia the intermediate snail for schistosomiasis is the *Oncomelania hupensis lindoensis* snail. The transmission of schistosomiasis in Indonesia is as follows: *S. japonicum* eggs are excreted with the sufferer's feces, then in the water they hatch into miracidium which will penetrate the body of the *O. hupensis lindoensis* snail [1].

Suggests that knowledge and education are factors that can influence behavior [4]. Most schistosomiasis sufferers are residents whose daily activities are inseparable from water. One of the reasons for the increase in the number of Schistosomiasis sufferers in society is the frequent contact of sufferers with water or entering water contaminated with *Schistosoma* parasites.

This disease will continue to exist (re-emerging disease) in individuals who always move in watery places such as garden areas and rice fields without using personal protective equipment such as boots.

From 2017 to 2019, WHO supported an annual mass preventive medication (POPM) program implemented in affected villages, providing free weight-adjusted single doses of praziquantel. POPM coverage rates varied during this period, with figures of 79% in 2017, 92% in 2018, and 88% in 2019. The implementation of POPM resulted in a significant reduction in the prevalence of schistosomiasis in humans to reach 0.1% in 2019. However, in 2021 and 2022, the prevalence rate began to increase until it reached 1.45%. This increase was caused by a shift in public health resources and focus on the COVID-19 pandemic [5].

Forecasting the number of schistosomiasis cases is an important thing to do because it provides information for the government regarding the number of schistosomiasis cases in a region, especially the Napu Valley, in planning programs and determining policies to deal with this disease. The increase in the number of schistosomiasis cases will have an impact on people's welfare, especially health. Appropriate and structured planning by the government is very necessary to overcome the transmission of this disease so that the adverse impacts that may occur due to the transmission of schistosomiasis can be anticipated and managed properly.

In forecasting there are methods that can be used, one of which is the Autoregressive Integrated Moving Average Method or known as the ARIMA Method. Auto Regressive Integrative Moving Average (ARIMA) is a method developed by George Box and Gwilym Jenkins so that their name is often synonymous with the Box-Jenkins method which is applied for data analysis and forecasting time series data. The ARIMA model has high strength and flexibility in analyzing various time series data and the resulting forecast values are more accurate [6].

In this research, the ARIMA method will be applied to describe a suitable model for predicting the number of cases of schistosomiasis transmission in the Napu Valley, Poso Regency in 2023 - 2025 using the ARIMA method and predicting the number of cases of schistosomiasis transmission in the Napu Valley, Poso Regency in 2023 - 2025 using ARIMA method, so accurate prediction results are needed to provide a reference and picture that can be used as a basis for government policy in anticipating an explosion in the number of schistosomiasis cases which will certainly have a negative impact on various sectors of life.

## II. MATERIALS

In this study, the case taken is a well-known disease called Schistosomiasis. The samples used in this study came from the Lindu Plateau, Napu Plateau and Bada Plateau, but the data used came from secondary data published by the Central Sulawesi Provincial Health Office, Indonesia. This institution is a data source that provides and organizes government affairs in the health sector. The data taken for this research is also included as quantitative data that can be calculated with numbers and writing the results of the research using tables, statistical analysis, and graphs so that the results are clear and unambiguous. Therefore, the data generated from this case is data from a year-to-year period to see the development of Schistosomiasis significantly per year.

This data is a time series data taken from 2007 to 2022 which is the number of Schistosomiasis cases per year. With this data, we can predict the value of schistosomiasis cases in the Lindu Plateau, Napu Plateau and Bada Plateau. The number of past years' cases of Schistosomiasis is used to forecast fluctuations in the number of Schistosomiasis cases 3 years in the future. This will be useful for residents and the local government in dealing with future spikes in schistosomiasis cases. The variables of this data also consist of two columns, namely year and number of cases per year. Although this data only consists of two columns, ignoring the independent data and using the past data of the dependent variable will result in accurate short-term forecasting. This is very suitable in this case where the data is from a time series used in short-term forecasting.

The method used in determining the model, performing forecasting, and determining software that is more accurate in the data processing stage is the ARIMA time series method using Rstudio software. The use of Rstudio software in this study provides easy access in analyzing data using the ARIMA method and provides more accurate research results with various features available.

## III. METHODS

### A. Data Description

The data used in this research is annual data on the number of schistosomiasis cases in the Napu Valley, Poso district for 2007-2022. Data on the number of schistosomiasis cases was obtained from the Central Sulawesi provincial Health Service Profile.

### B. Data Analysis Step

- Model Identification

The first step in time series modeling ARIMA is identifying the data on the variables used. The aim of identification is to find out whether the data used meets the assumptions of stationary in the variance and stationary in the mean. Model identification is carried out by making a Time-Series plot. Time series plots will help in determining data patterns and trends in the observation series. The identification process is carried out using variance and mean stationarity.

- Estimating Model Parameters (Estimation)

Model parameter estimation is an estimate of model parameters so that the temporary model obtained can be used in the parameters. This step is carried out to determine the estimated values of the ARIMA model parameters. The estimated parameters must be tested so that their significance in the model is known. The parameter estimation process is carried out to find the best model to be used and obtain results with the smallest error values. At this stage, the analysis technique is carried out. The mathematics is relatively complex, so the researchers used R Studio 4.2.3 software.

- Diagnostic Checking

The diagnosis stage of this model is used to detect whether the estimated data obtained is suitable for use in forecasting or not suitable for use in forecasting. In this case, by detecting residual correlation between lags.

- Selection of the best ARIMA models

Based on estimates and checking the best model that has been carried out on the number of schistosomiasis cases in the Napu valley, Poso district, the next step is to determine the best ARIMA model that is suitable for use in forecasting trials. The model used is the ARIMA model (p, d, q) with the following general equation [7]:

$$Z_t = \theta_0 + (1 + \theta_1)z_{t-1} + (\theta_2 - \theta_1)z_{t-2} + \dots + (\theta_p - \theta_{p-1})z_{t-p} - \theta_{p+1}z_{t-p-1} + a_t - \theta_1 a_{t-1} - \dots - \theta_q a_{t-q} \quad (1)$$

Similarity with the Backshift operator:

$$(1 - \theta_1 B - \theta_2 B^2 - \dots - \theta_p B^p)(1 - B)^d Z_t = \theta_0 + (1 - \theta_1 B - \theta_2 B^2 - \dots - \theta_q B^q) a_t$$

$$\theta_p(B)(1 - B)^d Z_t = \theta_0 + \theta_q(B) a_t \quad (2)$$

Information :

- $Z_t$  = Data on time t, t = 1, 2, 3, ..., n
- $B$  = Backshift operator
- $(1 - B)^d Z_t$  = Time series stationary at the second differentiation  $d$
- $a_t$  = Error in period t, t = 1, 2, 3, ..., n
- $p$  = Orders (AR)
- $d$  = Order differentiation
- $q$  = Orders (MA)

- Forecasting

The final step is to forecast with the best model that is significant and meets the assumptions.

#### IV. RESULTS AND FINDINGS

##### A. Result

The data used in this analysis is the number of snail fever cases in Napu, Poso District, from 2007 to 2022. The data was obtained from the Health Office of Central Sulawesi Province. Before conducting ARIMA analysis, the first step is to conduct time series analysis with the aim of forecasting values in the coming years. The time series plot of the actual data shows that the number of people with snail fever in the Napu region, Poso District, from 2007 to 2022 has fluctuated over the time span..

##### B. Findings

First, in ARIMA time series modeling, the first step is to identify the model against the actual data. This identification is done using time series plots to observe the emerging patterns. The model identification process involves two important aspects, namely stationarity in variance and stationarity in the mean of the data. To test stationarity in variance, the Box-Cox transformation method is used. If the value of  $\lambda$  (lambda) in the Box-Cox transformation is equal to 1, then the data is considered stationary in variance. The analysis results using the Box-Cox method show that the data has a value of  $\lambda = 1$ , so it can be concluded that the data is stationary in variance. Furthermore, stationarity in the average data is tested using the *Augmented Dickey-Fuller* (ADF) test or better known as the *ADF test*. The results of the analysis with the ADF test at a significance level of 10% ( $\alpha = 0.1$ ) resulted in a *p-value* of 0.4594. A *p-value* greater than 0.1 indicates that the data is not stationary in average, so it is necessary to perform a differencing process on the actual data. Differencing is done 3 times to achieve stationarity in the average, and the results obtained a *p-value* smaller than 0.1.

Second, in estimating the prediction model based on the results of the ACF (*Autocorrelation Function*) and PACF (*Partial Autocorrelation Function*) plot analysis after *differencing* three times. From the results of the analysis, it can be seen that the partial autocorrelation value at lag 1 is outside the dashed boundary. With this result, we can identify the initial model for this time series as ARIMA (1,3,1). In addition, there are several other possible models that can be considered, such as ARIMA(1,3,0), ARIMA(0,3,1), ARIMA(2,1,0), ARIMA(2,2,0), ARIMA(2,3,0), ARIMA(2,1,1), ARIMA(2,2,1), and ARIMA(2,3,1). From the fitting results, it is found that the ARIMA (2,3,0) model has the lowest AIC (Akaike Information Criterion) value compared to other ARIMA models. The ARIMA (2,3,0) model is the model chosen for forecasting future data.

Third, in detecting the overall estimation data obtained is feasible to use in forecasting by detecting the residual correlation between lags. The results of the Box-Ljung test conducted on the residuals of the time series model on the number of snail fever cases in the Napu region show a *p-value* of 0.2589 with a degree of freedom (*df*) of 2. Using a significance level of 5%, it can be concluded that the *p-value* of the Box-Ljung test is 0.2589, greater than the 5% significance level (0.05), indicating that there is no significant correlation between the residuals at certain lags in the time series model.

Fifth, forecasting was carried out for the next three consecutive years, from 2023 to 2025. The forecasting results show an increase, as shown in the following graph:

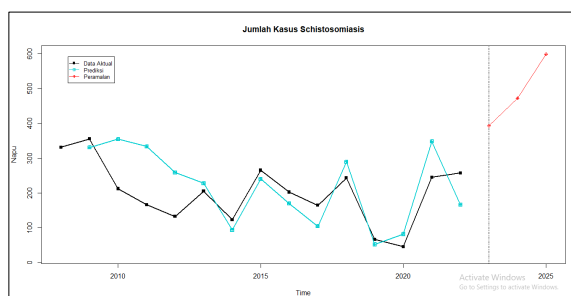


Fig. 1. Plot Forecasting The Number of Schistosomiasis.

The forecast results for the number of cases of snail fever sufferers in the Napu area, Poso Regency, for 2023 are 392, for 2024 it is 472, and for 2025 it is 599. These results indicate that in the next three years, there will be a significant increase in number of cases of snail fever sufferers.

## V. CONCLUSIONS

Based on the results of the analysis and discussion carried out in the previous chapter, the following conclusions can be obtained:

1. Forecasting the number of cases of schistosomiasis transmission in Napu, Poso Regency in 2023 - 2025 using the ARIMA method, the best ARIMA model was obtained based on the goodness of the model and the fulfillment of the assumptions to be used, namely the ARIMA model (2,3,0).
2. The forecast results for the number of cases of schistosomiasis transmission in Napu, Poso Regency in 2023 are estimated to reach around 392 people, in 2024 it is estimated that the number of cases will reach around 472 people, and in 2025 it is estimated that the number of cases will reach around 588 people. Based on forecast results using RStudio software, it was obtained that the number of cases of schistosomiasis transmission in Napu, Poso Regency over the next three years will experience an increase in population every year.

## ACKNOWLEDGMENT

In the name of Allah, the Most Gracious, The most merciful. First of all the writer's deepest to Allah SWT, the lord of the universe and to our prophet Muhammad SAW, may peace and blessing be upon him, his family and his followers. We would also like to thank Fadrijani S, ST.M.Si for her guidance during the making of this abstract until we can finish it.

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# i - J a M C S I I X

## 2023

PUBLISHED BY:

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