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Modeling Mortality Rates for Leukemia Between Men and Women in the United States

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MODELING MORTALITY RATES FOR LEUKEMIA BETWEEN MEN AND WOMEN IN THE UNITED STATES

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ABSTRACT

Modeling Mortality Rates for Leukemia between Men and Women in the United States

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Leukemia related deaths increased dramatically over the last forty years. Leukemia is a malignant disease or cancer of the bone marrow and blood. It is characterized by the uncontrolled accumulation of blood cells. Leukemia is divided into two categories: myelogenous or lymphocytic, each of which can be acute or chronic. The terms, myelogenous or lymphocytic denote the cell type involved.

In this thesis, the proposed modeling techniques are applied to leukemia deaths data from the Surveillance Epidemiology and End Results (SEER). In particular, annual deaths data from 1969 to 2007 are used in the data analysis, which includes three major parts: 1) male and female death rate comparisons using the conditional test (Przyborowski and Wilenski, 1940); 2) development of the empirical recurrence rate (Ho, 2008) and the empirical recurrence rates ratio time series; and 3) the Autoregressive Integrated Moving Average (ARIMA) model: selection, validation, and forecasting for the leukemia death rates and ratio.

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CHAPTER 1

INTRODUCTION

Leukemia is cancer of the human blood cells. It starts in the bone marrow, the soft tissue inside most bones. Bone marrow is where blood cells are made. When you have leukemia, the bone marrow starts to make a lot of abnormal white blood cells, called leukemia cells. The leukemia leukocytes, do not work like the normal white blood cells (leukocytes), instead they grow faster and fail to stop growing than normal leukocytes. Over time, leukemia cells can crowd out the normal white blood cells. The abundance of leukemia leukocytes can lead to serious problems such as anemia, bleeding, and infections. Leukemia cells can also spread to other organs and cause swelling or pain. The four main types of leukemia are as follows:

- Acute lymphoblastic (ALL) is the most common leukemia in children.

  Adults can also get it.

- Acute myelogenous leukemia (AML) affects both children and adults.

- Chronic lymphocytic leukemia (CLL) is the most common leukemia in adults,

  Who are mostly older than 55years. Children almost never get it.

- Chronic myelogenous leukemia (CML) occurs mostly in adults.

Experts do not know the causes of leukemia, but some factors are known to increase the risk of some types of leukemia. One is more likely to develop leukemia if exposed to large amounts of radiation, certain chemicals at work such as benzene, chemotherapy to treat another cancer, Down syndrome or other genetic problems, and cigarette smoke. However few people who have these risk factors develop leukemia. Most people who acquire leukemia do not have any known risk factors (National Institute of Health, 2011).

The following report presents detailed data from 1969 to 2007 on death rates according to a number of social, demographic, and medical characteristics. This data provides information on mortality patterns among residents of the United States by variables such as age, sex, and marital status.

In 2007, a total of 2,423,712 resident deaths were registered in the United States. The five leading causes of death in 2007 were:

1. Heart disease
2. Malignant neoplasm (cancer)
3. Cerebrovascular disease
4. Chronic lower respiratory disease
5. Accidents (unintentional injuries)

With 77.9 being the current Life expectancy a continuing increasing is seen based on data from 2006 and 2007. Life expectancy increased for the total population, including both the black and white populations. Both black and white males and females experienced an increase in life expectancy in 2007 compared with 2006. Rates for the top three leading causes for death: heart disease, cancer, and stroke, continued a decreasing trend. The difference in mortality rates between men and women increased slightly in 2007 from 2006 (National Cancer for Health Statistics, 2010).

In this study, the proposed modeling techniques are applied to the leukemia deaths data from the SEER. First, the data of deaths will be divided into two, based on the gender, as follows: 1) Male deaths, and 2) Female deaths. In particular, annual data from 1969-2007 are used in the data analysis, which includes three major parts: 1) leukemia deaths rates comparisons using the conditional test (Przyborowski and Wilenski, 1940); 2) development of the empirical

recurrence rate (Ho, 2008) and the empirical recurrence rates ratio time series; and 3) the Autoregressive Integrated Moving Average (ARIMA) model selection: validation, and forecasting for the Leukemia death rates and ratio.

Death rate comparisons using the conditional test and the empirical recurrence rate time series will be presented in Chapter 2. The fundamental tools of ARIMA are introduced in chapter 3. Chapter 4 illustrates the ARIMA modeling techniques using the empirical recurrence rates ratio generated from annual leukemia deaths data. Chapter 5 concludes our work.

CHAPTER 2

THEORY AND METHOD FOR POINT PROCESSES

2.1 Leukemia Data

Statistics for deaths that occurred in the United States during the period 1969 to 2007 are obtained from Surveillance Epidemiology and End Results (SEER) Program (www.seer.cancer.gov). From 2003 to 2007 the median age of death for leukemia was 74 years of age. Approximately 3.0% died under age 20; 3.1% between 20 and 34; 3.3% between 35 and 44; 6.4% between 45 and 54; 12.6% between 55 and 64; 21.6% between 65 and 74; 31.6% between 75 and 84; and 18.4% 85+ years of age. (www.revolutionhealth.com)

In the data set, the year 1969 is the time origint_0, and 2007 is the present time 0. There were 709,534 leukemia related deaths during the past 39 years (Appendix Table 1).By using the raw data, we construct a line plot to observe any possible trends (Figure 2.1). It is clear from the line plots that the number of deaths due to leukemia is increasing for male and leveling off for female in the last five years.

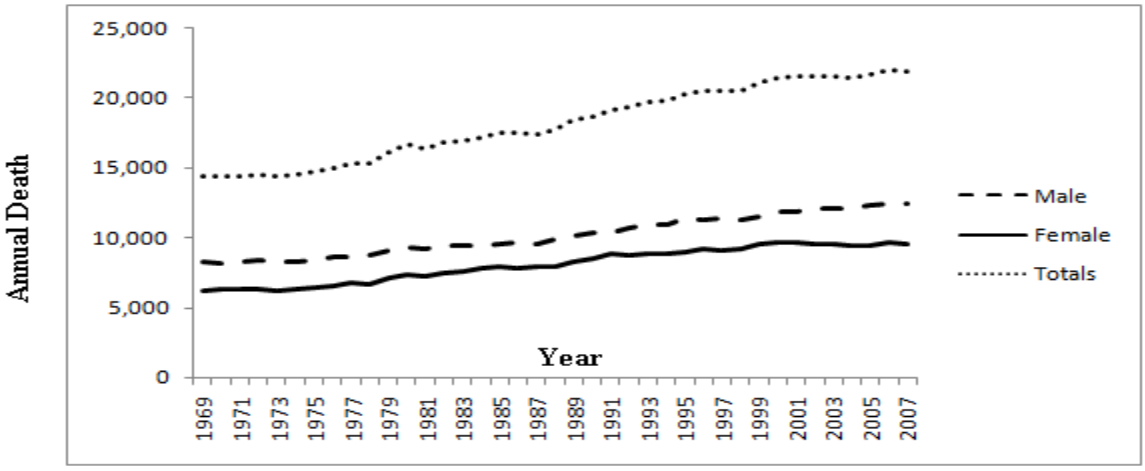


Figure 2.1 Annual leukemia related deaths data in the United States between 1969 and 2007.

2.2 Poisson Process

To reveal hidden characteristics of the leukemia data, we employ a point process to investigate the data and then conduct a conditional test to support our claim. A point process is a stochastic model that describes the occurrences of events. These occurrences are thought of as points on the time axis. Let N(t) be the random variable that denotes the number of events in the interval (0, t]. The intensity function of the process is defined as $\lambda(t) = \lim_{\Delta t \to 0} \frac{P(N(t,t+\Delta t]=1)}{\Delta t}$.A counting process N(t) is called a Poisson process, if and only if it satisfies the three conditions: (1) N(0) = 0; (2) the random variables N(a, b] and N(c, d] are independent, for any $a < b \leq c < d$; and (3) for any a < b, N(a, b] has the Poisson distribution with mean $\int_a^b \lambda(x)dx$. If $\lambda(t)$ is constant over t, the process is referred to as a homogeneous Poisson process (HPP). For an HPP, λ is treated as the rate of occurrences.

2.3 The Conditional Test.

The problem of hypothesis testing about two Poisson means is will be addressed. The usual conditional test (C-test) and a test based on estimated p-values (E-test) are considered. The exact properties of the tests are evaluated numerically. Numerical studies indicate that the E-test is almost exact because its size seldom exceeds the nominal level, and it is more powerful than the C-test. Power calculations for both tests are outlined below.

Let X and Y be respectively independent samples, from Poisson(λ_1) and Poisson(λ_2) processes, the joint distribution of X and Y:

$$f(x,y) = \left[\frac{\lambda_1{}^x e^{-\lambda_1}}{x!}\right]\left[\frac{\lambda_2{}^y e^{-\lambda_2}}{y!}\right] = \frac{\lambda_1{}^x \lambda_2{}^y}{x!y!} e^{-(\lambda_1+\lambda_2)}$$

Note that

$$X + Y = S \sim \text{Poisson}(\lambda_1 + \lambda_2),$$

X = 0, 1, 2, 3…

Y = 0, 1, 2, 3 …

The well- known method of testing the difference between two Poisson means is the conditional test (Przyborowski and Wilenski, 1940). The conditional distribution of X given X + Y = S follows a binomial distribution whose success probability is a function of the ratio $\frac{\lambda_1}{\lambda_2}$ = ρ. Considering the conditional distribution, X given S = s > 0, the probability function:

$$f(x \mid S = s) = \frac{P(X=x,\ X+Y=s)}{P(X+Y=s)}$$

$$= \frac{e^{-\lambda_1}\frac{{\lambda_1}^x}{x!}.e^{-\lambda_2}\frac{{\lambda_1}^{s-x}}{(s-x)!}}{e^{-(\lambda_1+\lambda_2)}\frac{(\lambda_1+\lambda_2)^s}{S!}}$$

$$= \binom{s}{x}\left(\frac{\lambda_1}{\lambda_1+\lambda_2}\right)^x\left(\frac{\lambda_2}{\lambda_1+\lambda_2}\right)^{s-x}$$

$$= \binom{s}{x}\left(\frac{1}{1+\rho}\right)^x\left(\frac{\rho}{1+\rho}\right)^{s-x} \sim \text{Binomial}\left(s, \frac{1}{1+\rho}\right)$$

Let $\frac{1}{1+\rho}$ = p, then to test the equality of two Poisson means is to test the following hypothesis:

$$H_0: p = \frac{1}{2} \text{ Vs } H_1: p \neq \frac{1}{2}$$

Which is equivalent to

$$H_o: \rho = 1 \quad \text{Vs} \quad H_1: \rho \neq 1.$$

It can be generalized as follows for comparison of leukemia deaths:

$$H_o: p \leq p_o \text{ Vs } H_1: p > p_o$$

where $0 < p_0 < 1$. And it is equivalent to

$$H_o: \rho \geq \rho_o \quad \text{Vs} \quad H_1: \rho < \rho_o$$

where $\rho_o = \frac{1-p_o}{p_0}$.

The conditional test rejects H_o, when X = k is observed, whenever

$$\text{P-value} = P(X \geq k \mid S = s) = \sum_{i=k}^{s}\binom{s}{i} {p_o}^i(1-p_o)^{s-i} \leq \alpha,$$

where α is the level of significance. Of course normal approximation can be implemented for the above binomial test for large number of s.

2.4 Conditional test for leukemia deaths.

In this thesis, I will divide the number of leukemia deaths into two main groups: female and male. For each death group, I will assume that the number of deaths follows a homogeneous Poisson process. Let λ_1 be the death rate of the male group, andλ_2 that of the female group. For the conditional test,

$$\rho_{12} = \frac{\lambda_2}{\lambda_1} \text{ and } p_{12} = \frac{1}{1+\rho_{12}} ,$$

Then the hypothesis for death rates between any two groups is equal to a reference value:

$$H_o : \rho_{12} \geq \rho_{12}^0 \quad \text{Vs} \quad H_1 : \rho_{12} < \rho_{12}^o$$

whereρ_{12}^o is a known reference ratio from female and male leukemia death rates and the corresponding Binomial (Conditional) test is

$$H_o: p_{12} \leq p_{12}^o \quad \text{Vs} \quad H_1 : p_{12} > p_{12}^o,$$

Where $0 < p_{12}^o < 1$ and $p_{12}^o = \frac{1}{1+\rho_{12}^0}$.

Define the average leukemia death rates ratio from the male and female groups as a reference ratio ρ_{12}^o, throughout the entire observation period. That is, we wish to test whether the rate ratio of the male leukemia deaths is significantly lower than the female group. In other words, if the death rate ratio (ρ_{12}), is significantly higher than that of the reference value ρ_{12}^o , male has a higher death rate. Let the reference value,ρ_{12}^o for the female death rate be 1, while p_{12}^0 = 0.5. The cumulated number of female death rate from 1969 to 2007 is 314,456 while that of men is 395,078. So the total number is 709,534. Based on the conditional test, p-value = $P(X \geq 395078 | S = 709{,}534)$

$$= \sum_{k=395078}^{709534} \binom{709534}{k} (0.5)^k (1-0.5)^{709534-k} \approx 0$$

The null hypothesis is rejected, that is, males are more likely to die from leukemia than female. A 95% one-sided confidence interval for p_{12} is [0.5562236078, 1].

2.5 Empirical Recurrence Rates.

A time series empirical recurrence rates are developed in order to monitor the deaths rates of the individual groups that is male and female.

Let $t_1,\ldots,t_n$ be the time of the n-ordered leukemia deaths during an observation period $(t_0,0)$, where t_0 is the time-origin and0 is the present time. If h is the time-step, then a discrete time series $\{z_\ell\}$ is generated sequentially at equidistant time intervals $t_o + h$, $t_0 + 2h$, …, $t_0 + \ell h$, …, $t_0 + Nh$ (= 0 = present time). z_ℓ is regarded as the observation at time t $(= t_0 + \ell h)$, for the leukemia deaths to be modeled. A key parameter desired by the modelers is the recurrence rate of the targeted leukemia deaths data. Therefore, a time series of the empirical recurrence rates (Ho, 2008) is generated as follows:

$$z_l = \frac{n_l}{lh} = \frac{total\ number\ of\ leukemia\ deaths\ in\ (t_o, t_o + lh)}{lh}$$

where ℓ =1, 2…*N*. Note that z_ℓ evolves over time and is simply the maximum likelihood estimator (MLE) of the mean, if the underlying process observed in $(t_0, t_0 + \ell h)$ is a homogeneous Poisson process. The time-plot of the empirical recurrence rate (ERR-plot), offers the possibility of further insights into the data. ERR plots for male and female leukemia deaths within the study period with time-step h = 1year.If we start at time T, the value z_{T+k}, $k \geq 1$ needs to be predicted based on the sample observation $(z_1,\ldots,z_T)$ of an ERR time series. In a regression modeling, let X denote the time index, z be the response values, and then use the fitted regression model to obtain z_{T+k}.ERR plots for male and female leukemia deaths within the study period with time-step h = 1year are shown in Figure 2.2.It is clear that the death rate for male and

female are rising approximately at the same rate. To enable us compare the leukemia death rates ratio between men and women we introduce empirical recurrence rates ratio chapter 3.

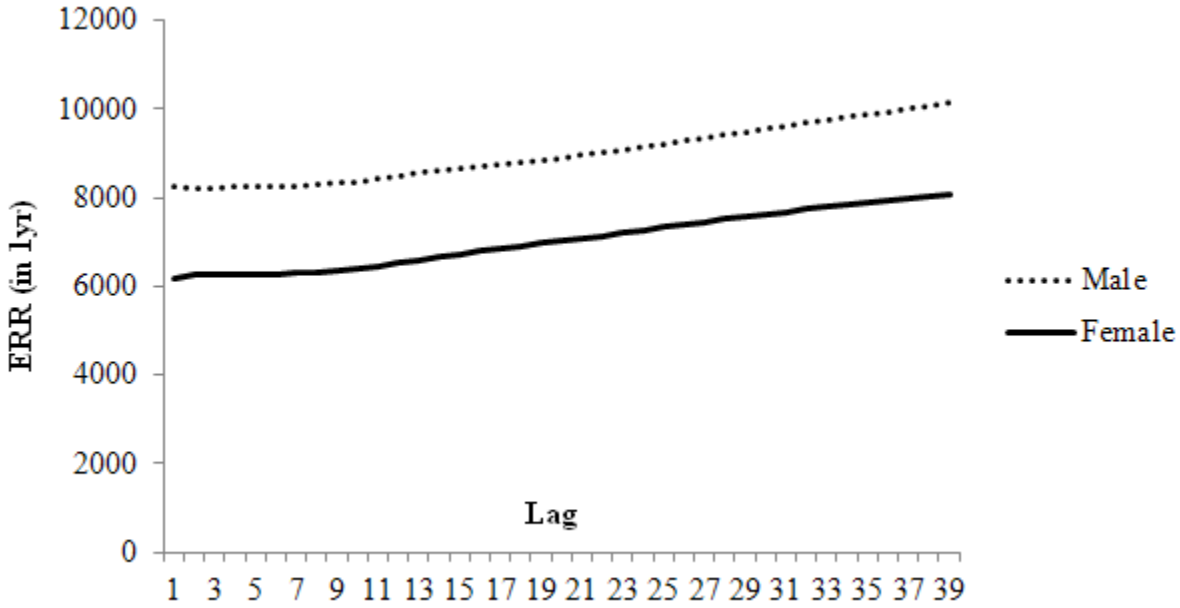


Figure 2.2 ERR plots for male and female leukemia deaths within the study period with time-step h = 1year.

CHAPTER 3

THEORY AND METHOD FOR ARIMA MODELS

3.1 Empirical Recurrence Rates Ratio

We produce an empirical recurrence rates ratio time series for the leukemia deaths rates ratio as follows: The C-test examines the relationship of two means of homogenous Poisson processes, which have constant expected values. Motivated by the ideas of the C-test and the empirical recurrence rate developed by Ho (2008), the empirical recurrence rates ratio time series for the leukemia deaths rates ratio is produced as follows:

Let $t_1, t_2, \ldots, t_n$ be the time of the n-ordered leukemia deaths during an observation period (t_0, t_0+Nh) from the past to the present. Then a discrete time series $\{d_l\}$ is generated sequentially as $t_0 + h,\ t_0 + 2h, \ldots, t_0 + lh, \ldots, t_0 + Nh$ (= the present time). h represents the time step. Let X_{ij} be the number of leukemia deaths in i^{th} group at j^{th} lag, where $i = 1, 2$ and $j = 1, 2, \ldots, \mathrm{N}$; and the Empirical Recurrence Rates Ratio (ERRR) is defined as follows:

$$d_l = \frac{\sum_{j=1}^{l} X_{1j}}{\sum_{j=1}^{l} (X_{1j} + X_{2j})},\ l = 1,2, \ldots, \mathrm{N}.$$

Both the ERR and ERRR offer the possibility of developing a model, monitoring and predicting leukemia death rate ratios. Moreover, if both of the targeted processes are homogeneous Poisson processes, then the ERRR is the maximum likelihood estimator (MLE) of p, and the MLE of ρ can be obtained by the invariance property of the MLE.

3.2 ARIMA Models

Since the 1970s, primarily due to the work of Box and Jenkins (1976), a class of mixed autoregressive (AR) and moving average (MA) models originally proposed by Yule (1927) and Slutsky (1937), have been useful in representing the serial dependent relationship of many time series encountered in practice. Autoregressive integrated moving average (ARIMA) models allow us not only to uncover the hidden patterns in the data, but also to generate forecasts and predict a variable's future values from its past values.

A branch of the ARIMA model known as the autoregression refers to a special kind of regression analysis aimed at analysis of time series. It rests on autoregressive models – that is, models where the dependent variable is the current value and the independent variable is previous p-values of the time series. The p is called "the order of the autoregression".

The moving average (MA) model is another form of ARIMA model in which the time series is described as a linear function of its prior errors plus a noise term.

Given a time series of datax_t the ARMA model is a tool for understanding and perhaps predicting future value in this series. The model consists of two parts, an autoregressive (AR) part and a moving average (MA) part. The model is usually referred to as the ARMA (p,q) model where p is the order of the autoregressive part and q is the order of the moving average part.

3.2.1 Autoregressive model of order p, AR(p)

An autoregressive model of order p is of the form $x_t = \phi_1 x_{t-1} + \phi_2 x_{t-2} + \cdots + \phi_p x_{t-p} + w_t$.

Where x_t is stationary, ϕ_1,ϕ_2, …,ϕ_p are constants ($\phi_p \neq 0$) and w_t is a Gaussian white noise series with mean zero and variance σ_w^2 . The mean of x_t is zero. If the mean, μ, of x_t is not zero, replace $x_t$by $x_t - \mu$; that is

$$x_t - \mu = \phi_1(x_{t-1} - \mu) + \phi_2(x_{t-2} - \mu) + \cdots + \phi_p(x_{t-p} - \mu) + w_t$$

The autoregressive operator is defined to be $\phi(B) = 1 - \phi_1 B - \phi_2 B^2 - \cdots - \phi_p B^p$.

3.2.2 Moving average model of order q, MA(q)

The moving average model of order q is defined to be

$$x_t = w_t + \theta_1 w_{t-1} + \theta_2 w_{t-2} + \cdots + \theta_q w_{t-q}.$$

Where there are q lags in the moving average and $\theta_1,\theta_2,\ldots,\theta_q$ $(\theta_q \neq 0)$ are parameters. The noise w_t is assumed to be Gaussian white noise. The moving average operator is

$$\theta(B) = 1 + \theta_1 B + \theta_2 B^2 + \cdots + \theta_q B^q.$$

3.2.3 Autoregressive Moving average model of order p, q. ARMA(p, q)

A sequence,$\{w_t\}$, of uncorrelated random variables, each with zero mean and variance σ^2, is referred to as white noise. This is indicated by the notation

$$\{w_t\} \sim \mathrm{WN}(0, \sigma^2).$$

The general ARMA models are a combination of the AR operators and MA operators.

A time series $\{x_t; t = 0, \pm 1, \pm 2, \ldots\}$ is ARMA if it is stationary and

$$x_t = \phi_1 x_{t-1} + \cdots + \phi_p x_{t-p} + w_t + \theta_1 w_{t-1} + \cdots + \theta_q w_{t-q}$$

where $\phi_p \neq 0, \theta_q \neq 0$. The parameter p and q are called the autoregressive and the moving average orders, respectively.

The following are the problems for ARMA(p, q):

(1) Parameter redundant models: A model is parameter redundant if it can be reparameterized in terms of a smaller number of parameters than the size of its defining parameter set, so that using classical inference it would not be possible to estimate all

the original parameters. One approach to removing parameter redundancy is to include covariates in a model, that set parameters to be appropriate functions of covariates.

(2) Stationary AR models that depend on the future: To overcome this problem of future-dependent model, we formally introduce the concept of causality. An ARMA (p,q) model is causal if and only if $\varphi(z) \neq 0$ for $|z| \leq 1$.

(3) MA models that are not unique: To address the problem of uniqueness we choose the model that allows an infinite autoregressive representation.

The introduction of correlation as a phenomenon that may be generated through lagged linear relations leads to proposing the autoregressive (AR) and autoregressive moving average (ARMA) models. Adding nonstationary models to the mix leads to the autoregressive integrated moving average (ARIMA) models popularized in the landmark work by Box and Jenkins (1970).

3.2.4 Stationary Time Series

A stationary process is a stochastic process whose joint probability distribution does not change when shifted in time or space. As a result, parameters such as the mean and variance, if they exist, also do not change over time or position. A weak stationary time series, x_t, is a finite variance process such that

(i) the mean value function, u_t is constant and does not depend on time t, and

(ii) the covariance function, $\gamma(s, t)$ depends on s and t only through their difference $|s - t|$.

Stationarity is used as a tool in time series analysis, where the raw data are often

transformed to become stationary; most data are often seasonal and/or dependent and are therefore nonstationary.

Although the theoretical autocorrelation functions are useful for describing the properties of the data, most of the analysis must be performed using sampled points $x_1, x_2, \ldots x_n$ that are available for estimating the mean, autocovariance, and autocorrelation functions. From the point of view of classical statistics, this poses a problem because we will typically not have iid copies ofx_t that are available for estimating the covariance and correlation functions. In the usual situation of only one realization, however, the assumption of stationarity becomes critical.

3.3 Data Transformation

In statistics, data transformation refers to the application of a deterministic mathematical function to each point in a data set that is, each data point $z_i$is replaced with the transformed value $y_i = f(z_i)$, where f is a function. Transformations are applied so that the data appear to more closely meet the assumptions of a statistical inference procedure that is to be applied or to improve the interpretability or appearance of graphs.

Nearly always, the function that is to be used to transform the data is invertible and generally is continuous. The transformation is usually applied to a collection of comparable measurements. We will introduce three common transformations that are called Box-Cox, differencing and subtracting the mean as follows.

3.3.1 Box-Cox Transformation

In statistics, the power transform is from a family of functions that are applied to create a rank-preserving transformation of data using power functions. This is a useful data processing technique used to stabilize variance, make the data more normal distribution-like, improve the

correlation between variables and other data stabilization procedures. The Box–Cox transformation, by statisticians George E.P. Box and David Cox, is one particular way of parameterising a power transform that has advantageous properties.

If the original observations are $Y_1, Y_2, Y_3, ...Y_n$, the Box-Cox transformation f_λ converts them to $f_\lambda(Y_1)$, $f_\lambda(Y_2), ... f_\lambda(Y_n)$, where:

$$f_\lambda(y) = \begin{cases} \dfrac{y^\lambda - 1}{\lambda}, & \lambda \neq 0 \\ \log(y), & \lambda = 0 \end{cases}$$

An extended form which could accommodate negative ys

$$\mathrm{y}(\lambda) = \begin{cases} \dfrac{(y+\lambda_2)^{\lambda_1 - 1}}{\lambda_1} & if \ \lambda_1 \neq 0; \\ \log(y+\lambda_2) \, if \ \lambda_1 = 0. \end{cases}$$

Here, $\lambda = (\lambda_1, \lambda_2)^1$. In practice we could choose λ_2 such that $y + \lambda_2 > 0$ for any y. So, researchers could only view λ_1 as the model parameter. This transformation is useful when the variability of the data increases or decreases with the level. By suitable choice of λ, the variability can be made nearly constant. For instance, positive data whose standard deviation increases linearly with level, the variability can be stabilized by choosing $\lambda = 0$ (Brockwell et al., 2002).

3.3.2 Differencing

In the case that the time series data at hand has a trend in it, we should first difference the data to remove the trend and then consider the autocorrelation function for the differenced data for signs of seasonality at the seasonal lags. Differencing is an important technique to transform data, to control autocorrelation, and to achieve stationary time series. The first difference is denoted as:

$$\nabla X_t = X_t - X_{t-1} = (1 - B) X_t$$

where B is the backshift operator. We may extend the notion further and define the differences of order d as:

$$\nabla^d X_t = (1-B)^d X_t$$

Usually, single differencing is used to remove linear trends and double differencing is used to remove quadratic trend. We can eliminate seasonality and trend of period d by introducing the lag d difference operator ∇_d:

$$\nabla_d X_t = X_t - X_{t-d} = (1-B^d)X_t.$$

This operator should not be confused with the operator $(1-B)^d$ (Ho, 2010a). Normally, the correct amount of differencing is the lowest order of differencing that yields a time series which fluctuates around a well-defined mean value and whose autocorrelation function (ACF) plot decays rapidly to zero, either from above or below. Thus, at every stage of differencing, we check the plots of sample autocorrelation function (ACF) and the sample partial autocorrelation function (PACF)to see where the ACF/PACF "cuts off" the bounds $\pm 1.96/\sqrt{n}$.

A time plot of the data will typically suggest whether any differencing is needed after the first differencing. However, over differencing may introduce dependence where none exist. In addition to the time plot, the sample ACF can help in indicating whether differencing is needed. The sample ACF will not decay to zero as fast as h increases. Thus a slow decay is an indication that differencing may be needed.

It is desirable to find a sample ACF that decays fairly rapidly. We say that a series is stationary if the sample ACF has very few significant spikes at very small lags and then cuts off drastically or dies down very quickly. If the samples ACF decay slowly, the series still has some trend. If the ACF has periodicity, the series has seasonality. If this occurs we should do some more differencing of the data before continuing. The Behavior of the ACF and PACF for ARMA models are summarized in table 3.1(Shumway and Stoffer, 2006).

Table 3.1 Behavior of the ACF and PACF for ARMA models.

	AR(p)	MA(q)	ARMA(p, q)
ACF	Tails off	Cuts off after lag q	Tails off
PACF	Cuts off after lag p	Tails off	Tails off

3.3.3 Subtracting the Mean

The term, ARMA model, is used in the programITSM2000 (Brockwell et al., 2002) to denote a zero-mean ARMA process. Therefore, the sample mean of the data should be small before modeling. Once the apparent deviations from stationary of the data have been removed, the sample mean of the transformed data should be subtracted from each observation. The search for a fitted ARMA model for a mean-corrected data set then follows.

3.4 Model Diagnostics

Model diagnostics is understood as a more or less formal check of properties that certain residuals should have under certain assumptions that the data were generated by the model which is under investigation. In this thesis we will check the residual ACF/PACF of the models that we develop. Also, the models need to pass the test for randomness of the residuals. After the model diagnostics process, further predictions and comparisons can be done.

3.4.1 The Sample ACF /PACF of the Residuals

The residuals autocorrelation function is the basic model checking tool in time series analysis, but it is useless when its distribution is incorrectly approximated because of parameter estimation or because an unnoticed higher serial dependence have not been taken into account.

The sample autocorrelations of an independent and identically distributed (iid)

sequence $y_1, y_2, \ldots, y_n$ are approximately iid with distribution N(0, $\frac{1}{n}$). We can therefore test whether or not the observed residuals are consistent with iid noise by examining the sample correlations of the residuals and rejecting the iid noise hypothesis if more than two or three out of 40 fall outside the bounds $\pm 1.96\sqrt{n}$ or if one falls far outside the bounds (Brockwell et al, 2002).

3.4.2 Tests for Randomness of the Residuals

A popular test, formulated by Ljung and Box (1978), called the Ljung-Box Test, is commonly used to check whether the residuals of a fitted model are observed values of independent and identically distributed random variables in ARIMA modeling. It is referred to as a portmanteau test, since it is based on the autocorrelation plot and tests the overall independence based on a few lags. Then, the definition of Ljung-Box test is as follows:

H_0 : The sequence data are iid

H_a : The sequence data are not iid

And use the test statistic as:

$$\hat{Q}(\hat{r}) = n(n+2)\sum_{k=1}^{m}(n-k)^{-1}\hat{r}_k^2,$$

where $\hat{r}_k = \sum_{l=k+1}^{n}\hat{a}_l\hat{a}_{l-k} \Big/ \sum_{l=1}^{n}\hat{a}_l^2$, the estimated autocorrelation at lag k ,

n = sample size,

m = number of lags being tested (As a rule of thumb, the sample ACF and PACF are good estimates of the ACF and PACF of a stationary process for lags up to about a third of the sample size (Brockwell and Davis, 2002) where $\hat{a}_1,...,\hat{a}_n$ are the residuals after a model has been fitted to a series $z_1,...,z_n$. If no model is being fitted, then $\hat{a}_1,...,\hat{a}_n$ are the "mean corrected" series of $z_1,...,z_n$.

If the sample size n is large, the distribution of $\hat{Q}(\hat{r})$ is roughly χ^2_{m-p-q} under the null hypothesis, where $m-p-q$ is the degree freedom of Chi-square distribution, and $p+q$ is the number of parameters of the fitted model. The null hypothesis will be rejected, if $\hat{Q} > \chi^2_{1-\alpha;m-p-q}$ at level α. Thus, the sequence data are not independent, or their autocorrelations are significantly different from zero.

3.4.3 AIC, BIC and AICC Statistics

We develop a small sample criterion (AICC) for the selection of the order of vector autoregressive model. AICC is an approximate unbiased estimator of the Kullback-Lieber information. Furthermore, AICC provides better model order choices than the Akaike information criterion (AIC) in small sample, but it should be used as a rough guide. The final decision is largely based on maximum likelihood estimation. Some other Model selection statistics, such as the BIC statistic, are available in ITSM 2000. The BIC statistic (Schwarz, 1978) is a Bayesian modification of the AIC statistic. The BIC statistics evaluated at the same time as the AICC, and it is used in the same way as the AICC. Each information statistic is defined as follows:

$$AIC_{p,q} = N \log \hat{\sigma}_{\varepsilon}^2 + 2r$$

$$AICC_{p,q} = N \log \hat{\sigma}_{\varepsilon}^2 + 2rN/(N-r-1)$$

$$BIC_{p,q} = N \log \hat{\sigma}_{\varepsilon}^2 + r \log N$$

Where $\hat{\sigma}_{\varepsilon}^2$ is the error variance, the error variance in this case is defined as

$$\hat{\sigma}_{\epsilon}{}^2 = \frac{1}{n}\sum_{i=1}^{n}(x_i - \overline{x})^2$$

One may point out from probability theory, that $\hat{\sigma}_{\epsilon}^{2}$ is a biased estimator for the true variance, σ^2, and $r = p + q + 1$ is the number of parameters estimated in the model, including a constant term. The second term in all three equations is a consequence for increasing *r*. Hence, if we want to minimize the values of these criteria, we should minimize the number of parameters. Therefore, the best model is the model that adequately describes data and has the fewest parameters.

3.5 Forecasting

This thesis outlines the practical steps which need to be undertaken to use autoregressive integrated moving average (ARIMA) time series models for forecasting death rates of male and female. The emphasis is on forecast performance which suggests more focus on minimizing death rates forecast errors than on maximizing in-sample "goodness of fit." Practical issues in ARIMA time series forecasting are illustrated. The candidate ARIMA models will be used to predict future values of the time series from the past values. The forecasting function $z_t = f(z_{t-1}, \dots, z_1) + a_t$ has the minimum mean square error. The first part of the above equation $f(z_{t-1}, \dots z_1)$ is a function of the past values of the series and it should be determined by the data. The second part a_t, called noise part, is a sequence of iid variables.

Predictions will be achieved by forecasting the residuals and then inverting the transformations adopted to arrive at forecasts of the original series. Also, we will observe which model is the best fitting model by comparing the prediction from the training set with the prediction set. Then, I will combine the training sample and the prediction set as a full data set to forecast death rates ratio for the predicted set, based on the same techniques as before.

CHAPTER 4

ANNUAL LEUKEMIA RELATED DEATHS DATA ANALYSIS

4.1 ERRR-plots

Since there are 709,534 Leukemia related deaths in the 39 years of study, which indicates there is approximately 18,194 Leukemia related deaths in every year. We choose h = 1year as the time-step and we will try to predict leukemia-related deaths with h = 1year. Figure 4.1 shows ERRR plots with time-step h=1year which show a continuous decline from lag 1 to lag 33 and then rises a little from lag 34 to lag 39.

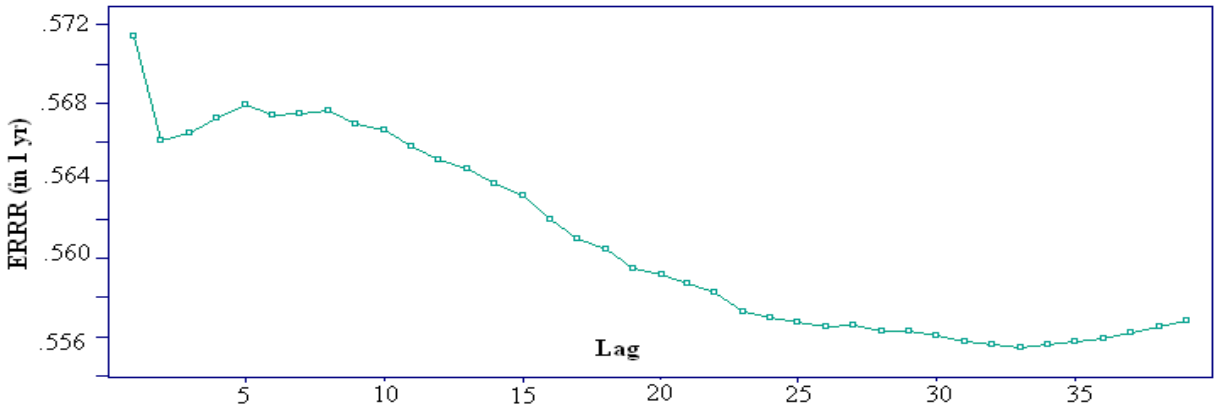


Figure 4.1ERRR plots with time-steps h=1year.

4.2 Data Splitting.

In some cases, researchers might want to separate several time series contained in one data set into different data sets: training sample and prediction set. Training sample is used to develop a model for prediction. Prediction set is used to evaluate the reasonableness and predictive ability of the selected model (one round of cross validation).

Cross–validation, sometimes called rotation estimation, is a technique for assessing how the results a statistical analysis will generalize to an independent data set. It is mainly used in

settings where the goal is prediction, and one wants to estimate how accurately a predictive model will perform in practice. Multiple rounds of cross-validation are performed using different partitions, and the validation results are averaged over the rounds. The application in this regard will be detailed in Section 4.3 and 4.4.

4.3 ARIMA Modeling with h = 1year.

We use the ITSM2000 software to model the ERRR data. The data set with time-step h = 1year has 39 lags in total. At first, we use the technique described in Section 4.2 to split the data into two sets: training sample and prediction set. In this case, our training sample is the original data set excluding the last 3 ERRRs, which is the prediction set (Figure 4.2).

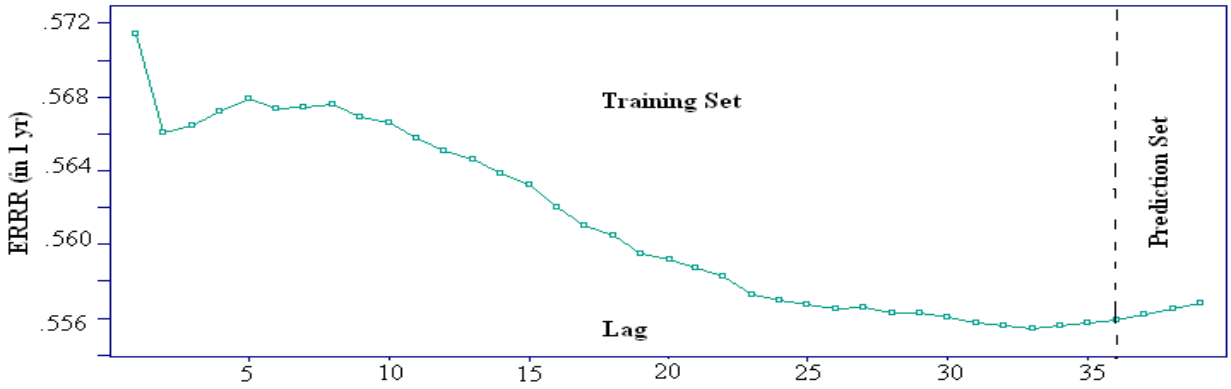


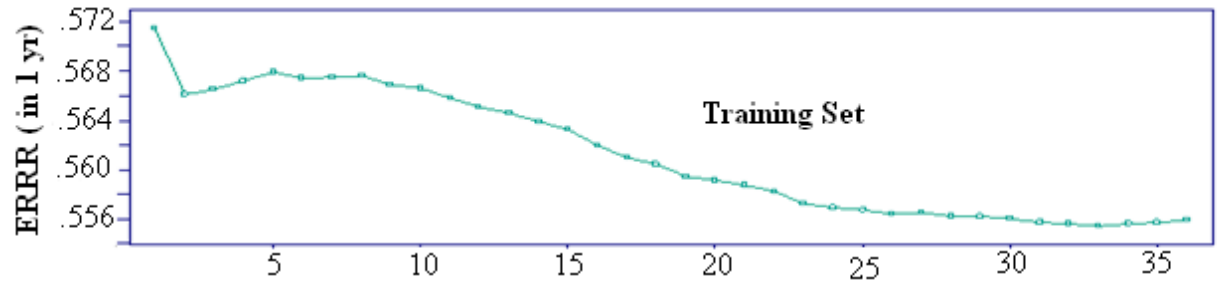
Figure 4.2 ERRR plots of the Training Sample and prediction set with h = 1year.

These three ERRR values in the prediction set, representing the number of leukemia-related deaths in three years, will be used to compare to those of the one to three-step predictions produced by a candidate model. Of course, the size of a prediction set is quite flexible as long as the prediction set fits a common goal of model selection. Then, we focus on the training sample set and plot the sample ACF and PACF to observe the data set (Figure 4.3). From the plot of sample ACF, we find that the spikes die slowly and have periodicity. This indicates non-

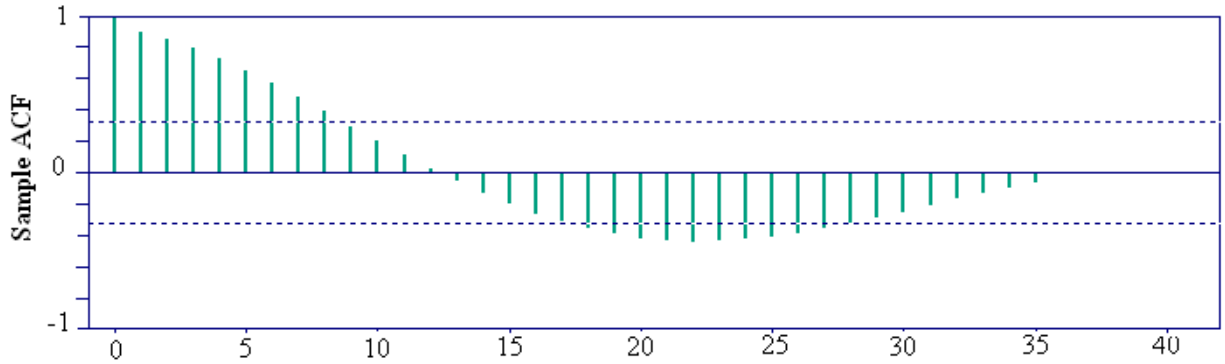
stationary behavior. As mentioned in Section 2.4, this data has trend and seasonality. Thus, differencing is considered.

4.3.1 Training Sample modeling

(a)



(b)



(c)

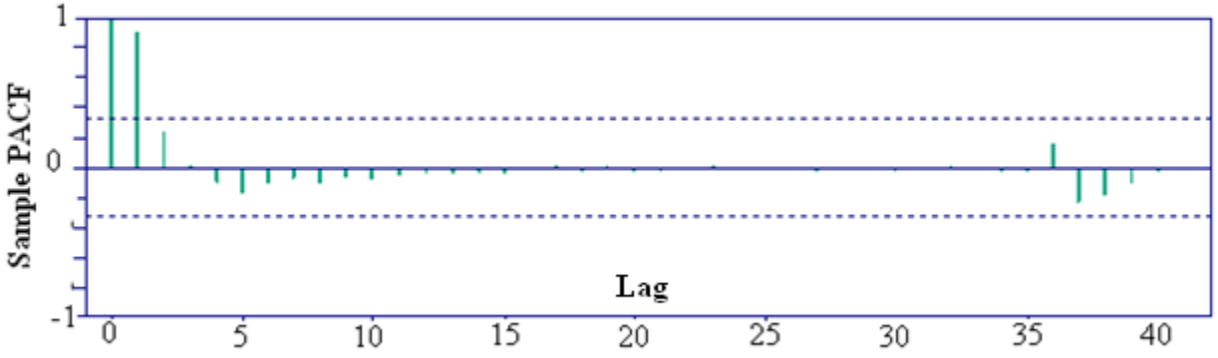
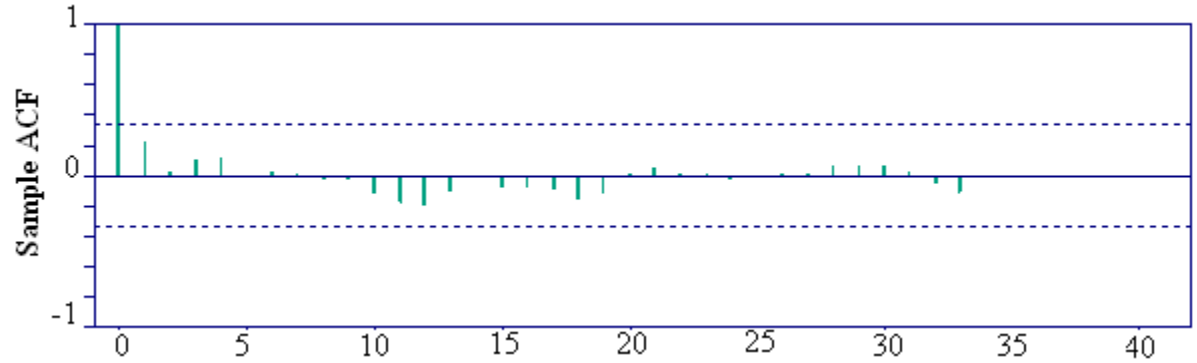


Figure 4.3**a**, Time-plot; **b**, Sample ACF; **c**, Sample PACF of the Training Sample with h = 1year.

Applying the differencing operator∇on the training sample, we take a difference at lag 2. Figure 4.4 tells us that the stationarity has almost been achieved. So we do further difference at lag1

(a)

(b)



(c)

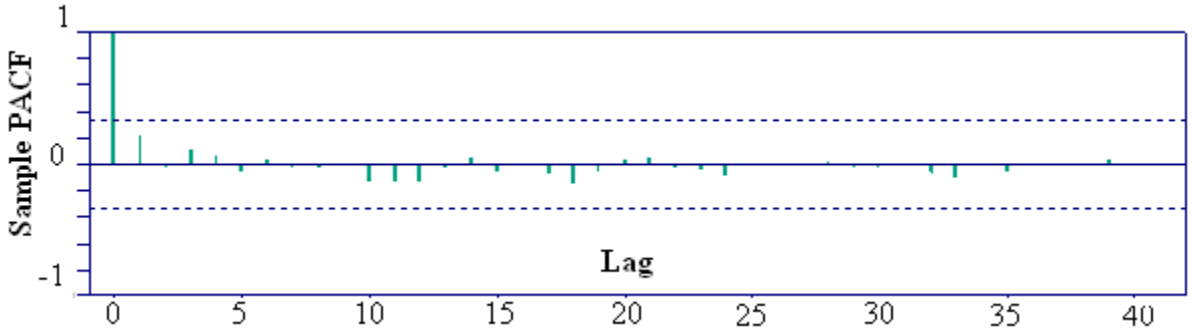
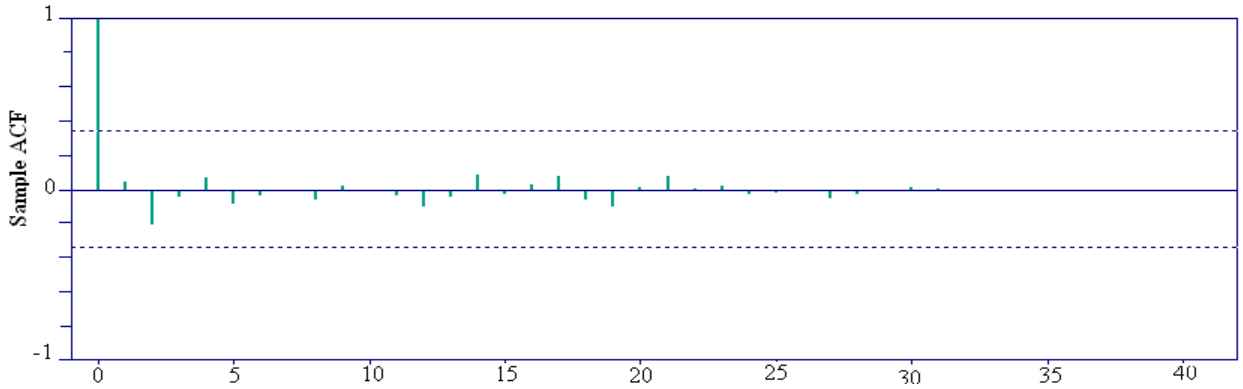


Figure 4.4 a, Time-plot; **b,** Sample ACF; **c**, Sample PACF of a lag-1 differenced Training Sample with h = 1 year.

Then we subtract the sample mean from each observation of the differenced series to generate a stationary zero-mean time series (Figure 4.5)

(a)

(b)



(c)

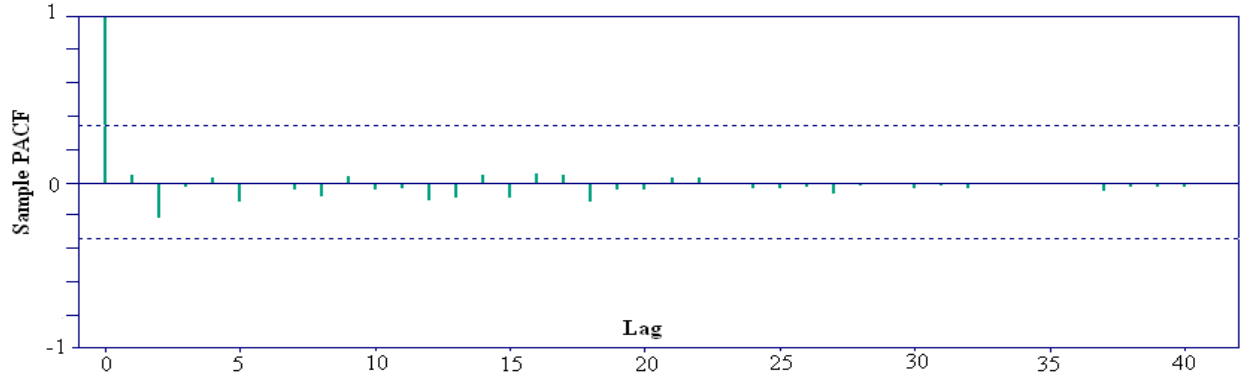


Figure 4.5 a, Time-plot; **b**, Sample ACF; **c**, Sample PACF of the twice-differenced training sample with h = 1 year.

We feel that the ACF and the PACF is tailing off. These suggest that an MA (2) should be considered. Indeed, our initial model selection process concludes that the estimated model is:

ARMA Model:

X(t) = Z(t) + .08686 Z(t-1) - .5965 Z(t-2)

WN Variance = .000001

MA Coefficients
.086863 -.596466

Standard Error of MA Coefficients
.139721 .139721

(Residual SS)/N = .00000107669

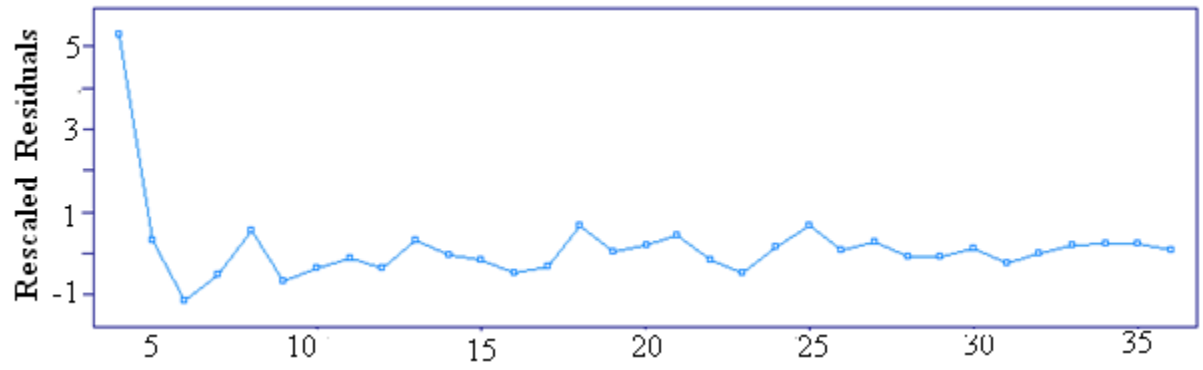
AICC = -.352068E+03
BIC = -.355605E+03

-2Log(Likelihood) = -.358896E+03

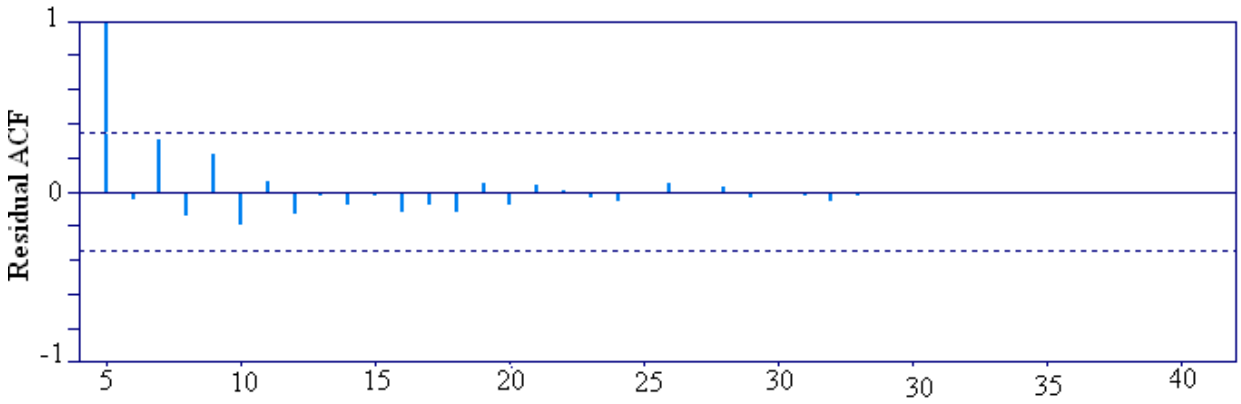
Note that X_t represents a twice-differenced stationary zero-mean time series and the error term Z_t represents a white noise process.

A set of diagnostic plots (Figure 4.6) is produced by the ITSM2000 package, consisting of the plot of the residuals, its ACF and its PACF for the MA (2) model in which all the spikes lies within the boundary line. The AICC statistic is.352068E+03 and the Ljung-Box test is not significant (p-value = .88320), indicating that the residuals are white noise. The numerical values of the actual ERRRs in the prediction set and the predicted ERRRs by the model MA (2) with their counterparts are shown in Table 4.1.

(a)



(b)



(c)

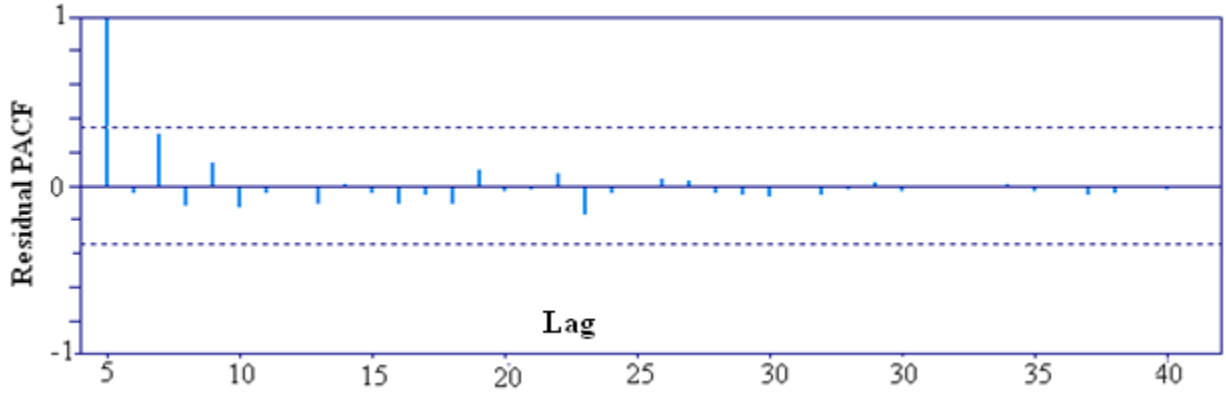


Figure 4.6 Diagnostics for the MA (2) fitted and twice-differenced Training Sample.

Residual **a**, Time-plot; **b**, Sample ACF; **c**, Sample PACF.

Table 4.1 The numerical values of the actual ERRRs in the prediction set and the predicted ERRRs and their confidence intervals using the MA (2) based on the training sample.

Year	Annual ERRR		Confidence interval	
	Actual	Prediction	Lower Bound	Upper bound
2005	0.55623	0.55624	0.55460	0.55789
2006	0.55649	0.55664	0.55421	0.55907
2007	0.55681	0.55712	0.55369	0.556057

We list the ratios of (estimated coefficients)/(1.96×standard error) for each coefficient, calculated from the output of an MA (2) model, shown in Section 3.2. The ratios are:

MA Coefficients

.086868 -.596464

Standard Error of MA Coefficients

.139722 .139722

Note that the ratio at lag1 of MA(2) in absolute value is less than 1, which indicates the corresponding coefficient is nonzero. We keep the corresponding coefficient.

Table 4.2 The numerical values of the predicted ERRRs and their confidence intervals using the MA (2) based on the full data set.

Year	Annual ERRR	Confidence interval	
	Prediction	Lower Bound	Upper bound
2008	0.55730	0.55567	0.55893
2009	0.55786	0.555546	0.56026
2010	0.55850	0.55511	0.56188

Table 4.2 shows numerical values of the predicted ERRRs and their confidence intervals using the MA (2) whilst Figure 4.7 depicts the confidence intervals for the predicted values based on the full data set.

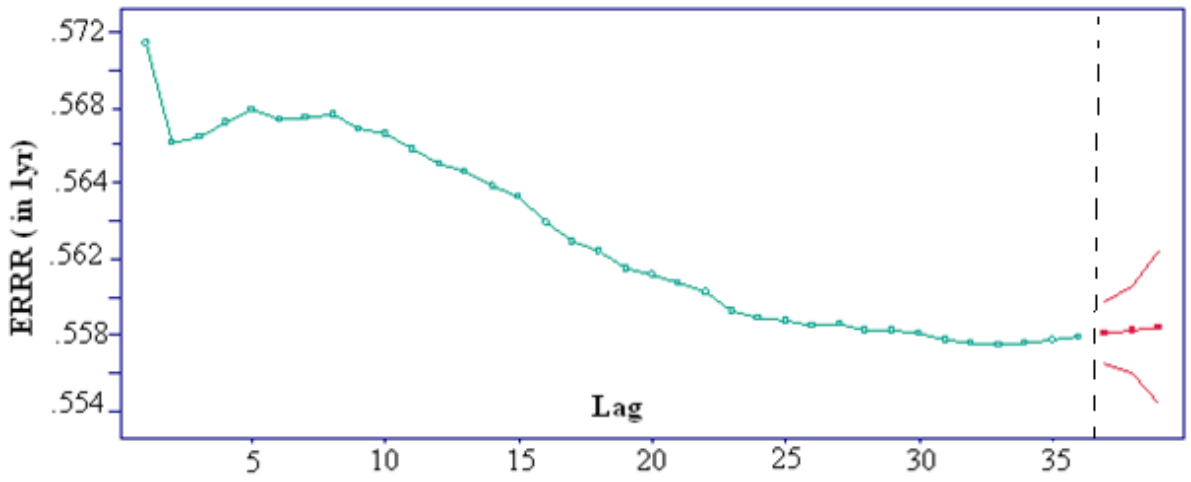


Figure 4.7 ERRR plot with Prediction intervals.

Comparisons of the results with the prediction set model are defined in Table 4.3. The predicted

values are very similar, indicating that this model is acceptable. Figure 4.8 shows a comparison of three forecasted ERRRs with the prediction set which appears to be moving in the same direction from lag 1 to lag 3 for both the predicted and the actual ERRR values.

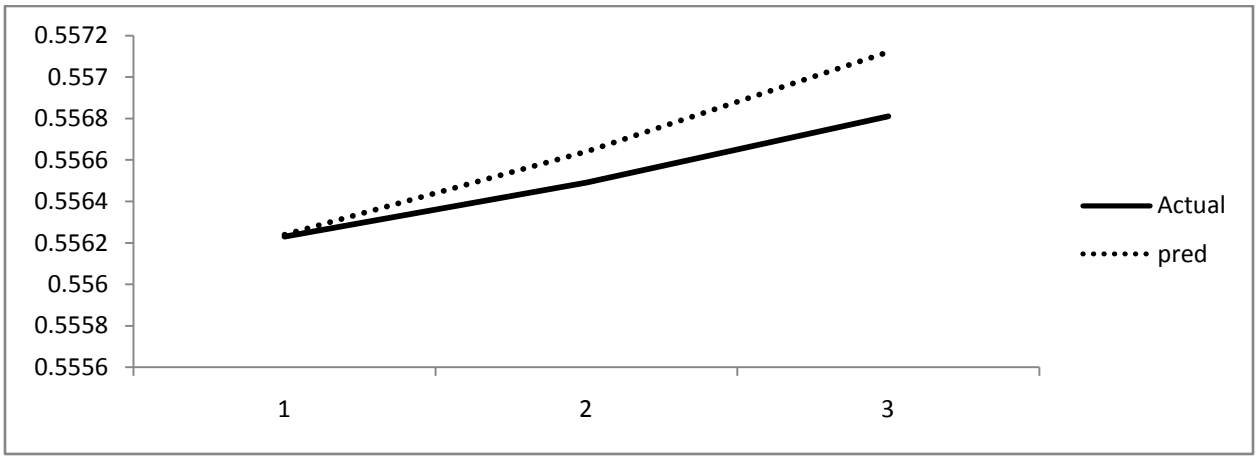


Figure 4.8 Comparison of three forecasted ERRRs with the prediction set.

Figure 4.9 depicts the complete Data (training sample and prediction set) with three predicted values appended to the training Sample for model validation; Inset: Comparison of three ERRRs with Prediction set

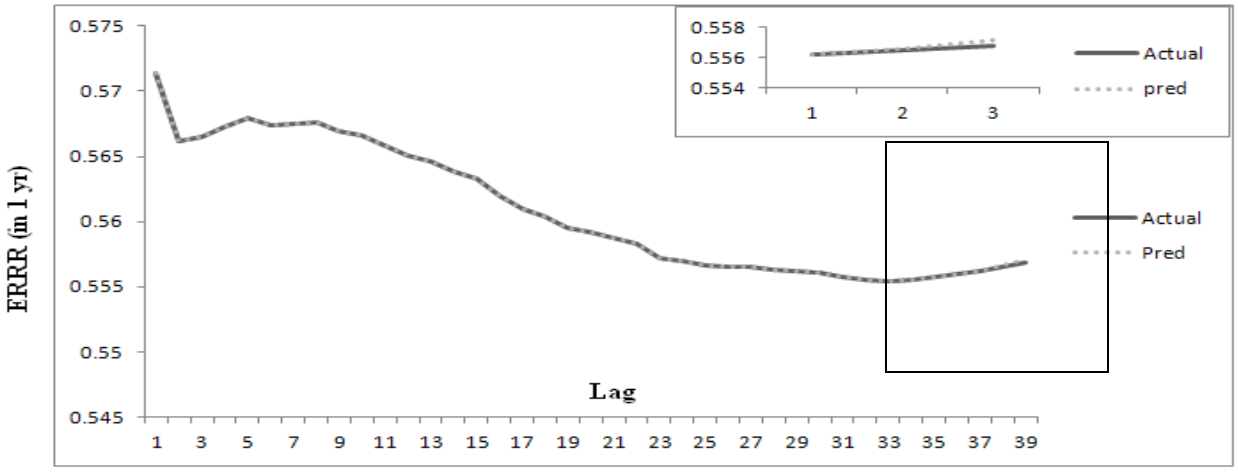


Figure 4.9 The complete Data (Training Sample and Prediction set) with three appended to training Sample for model validation; Inset: Comparison of three ERRRs with prediction set

4.3.2 Full-Data Forecasting

Finally, we use the full ERRR time series to forecast the probable number of leukemia related deaths in the future. This yields the best-fitted MA (2) model for the mean-corrected and twice-differenced value atlag1 (same as before).The estimated MLE:

ARMA Model:

X(t) = Z(t) + .08003 Z(t-1) - .6162 Z(t-2)

WN Variance = .982271E-06

MA Coefficients

.080027 -.616228

Standard Error of MA Coefficients

.209105 .143766

(Residual SS)/N = .982271E-06

The AICC statistic is -0.388089E+03, and the Ljung-Box test is significant (p-value = .80782). Then, we check the ratios as follows:

MA Coefficients

.080027 -.616228

Standard Error of MA Coefficients

.209105 .143766

4.3.2 ARIMA Models

The training samples with 36 lags are shown in Figure 4.2 above. The plots of sample ACF and PACF on the training sample (Figure 4.3) indicate non stationary behavior. No differencing is considered. This is also a suggestion of the AR(2) model. The estimated (MLE) model is: ARMA Model:

X(t) = .7194 X(t-1) + .2658 X(t-2)

+ Z(t)

WN Variance = .000004

AR Coefficients

.719426 .265804

Standard Error of AR Coefficients

.366896 .367090

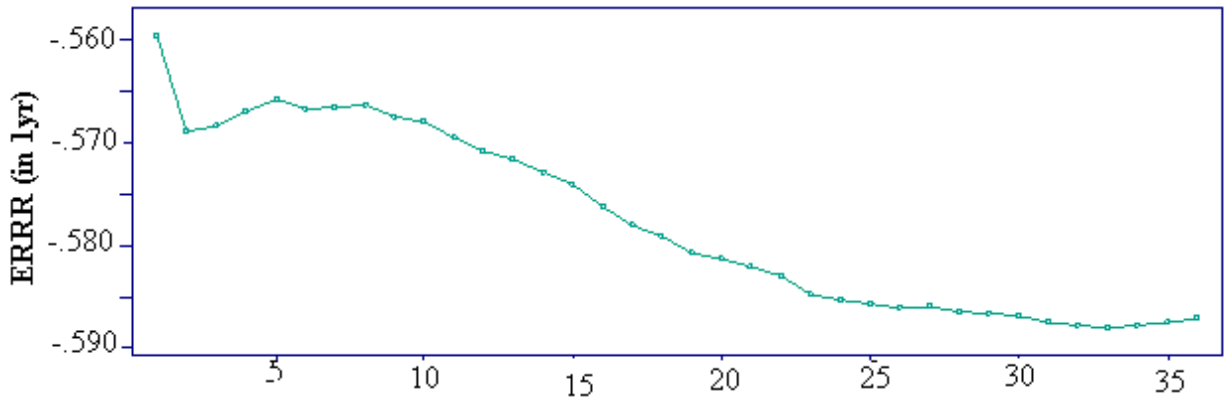
(Residual SS)/N = .00000377443

AICC = -.337258E+03

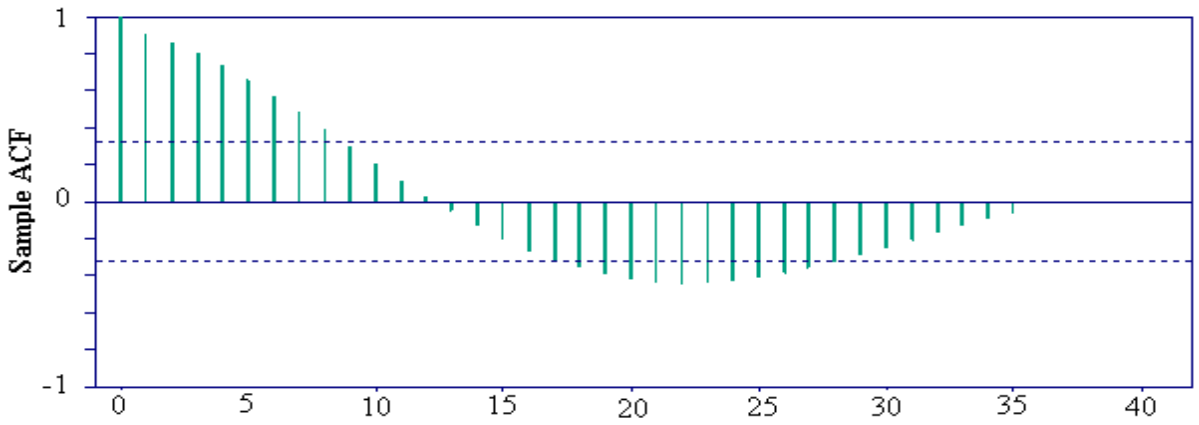
BIC = -.333769E+03

The AICC statistic is -0.337258E+03 The Ljung-Box statistic is 5.3557 and the p-value is .99934, which indicates that the residuals are approximately white noise.

(a)



(b)



(c)

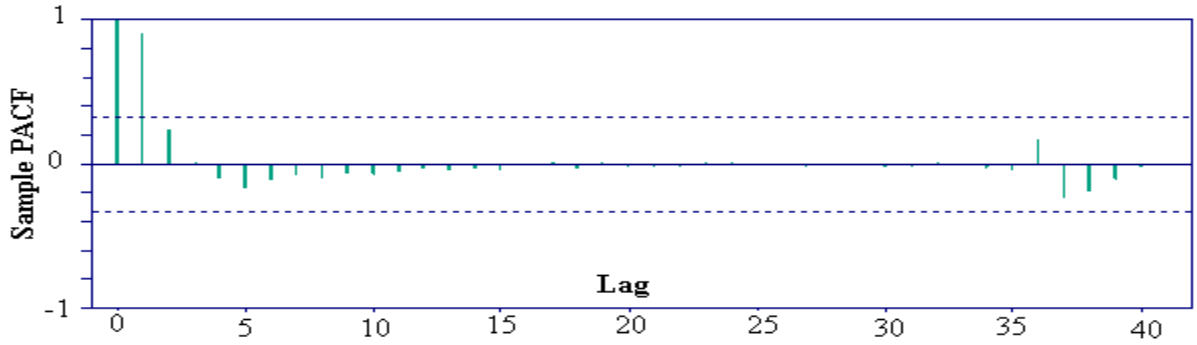


Figure 4.10a, ERRR plots after Box-Cox transformation at λ = 0; **b**, sample ACF; **c**, Sample PACF of the full data with h= 1year.

The plots of the training sample (including 36 lags) and its sample ACF and PACF in (Figure

4.10b, c) show nonstationarity and periodicity since some of the spikes extend beyond the required boundaries from lag 0 to lag7 and from lag 17 to lag 26 in the case of the ACF and at lag 0 in the case of the PACF. Therefore, the Box-Cox transformation will be employed to remove the trend and seasonality. Since the plot shows decreasing variability, we consider the Box-Cox transformation to stabilize the variability. After the λ=0 Box-Cox transformation. The actual and the predicted value based on the Training Sample using AR(2) are shown in Table 4.3.

Table 4.3 Numerical of the Actual and the Predicted based on the Training Sample using AR(2)

Actual	Prediction	Lower Bound	Upper Bound
0.55623	0.55595	0.55413	0.55778
0.55649	0.55602	0.55377	0.55828
0.55681	0.55608	0.55341	0.55878

A plot of the ERRR values and their prediction intervals are shown in Figure 4.11 in which the predicted values seems to be leveling off from lag 36 to lag 39.

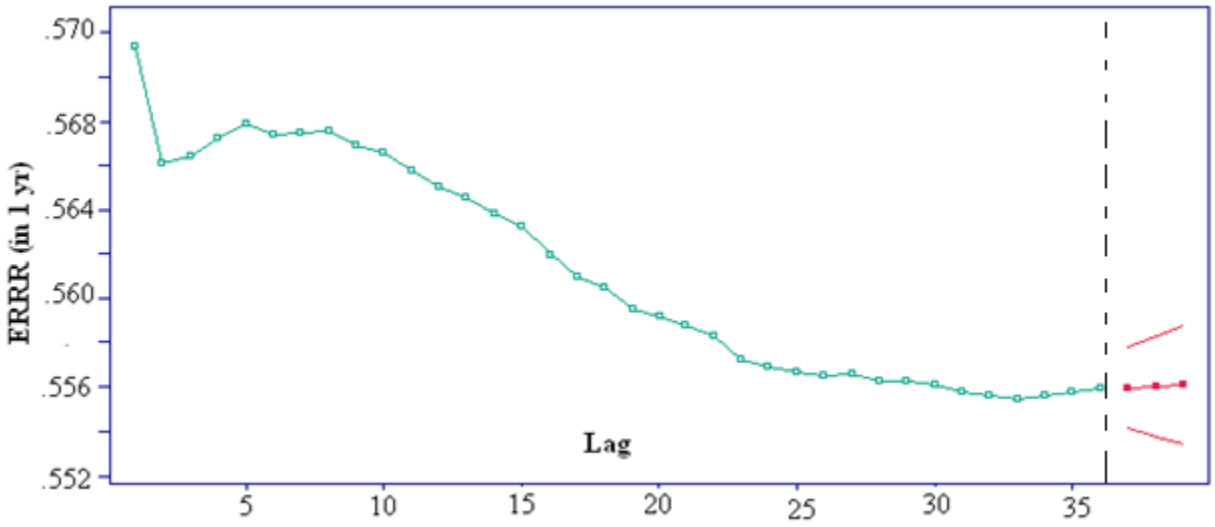
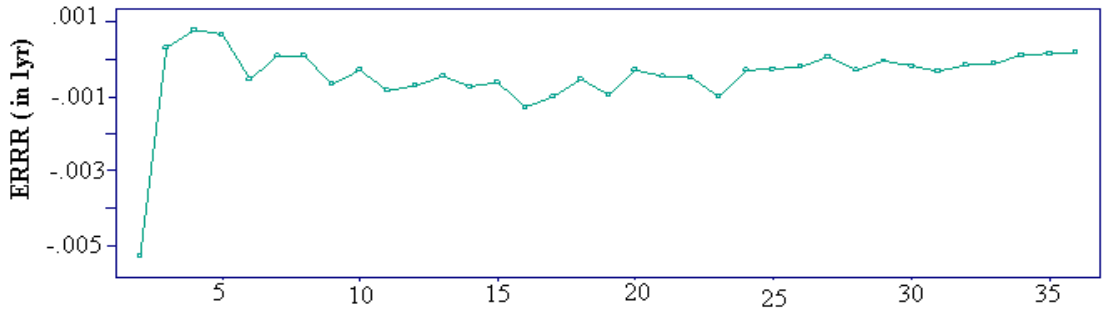


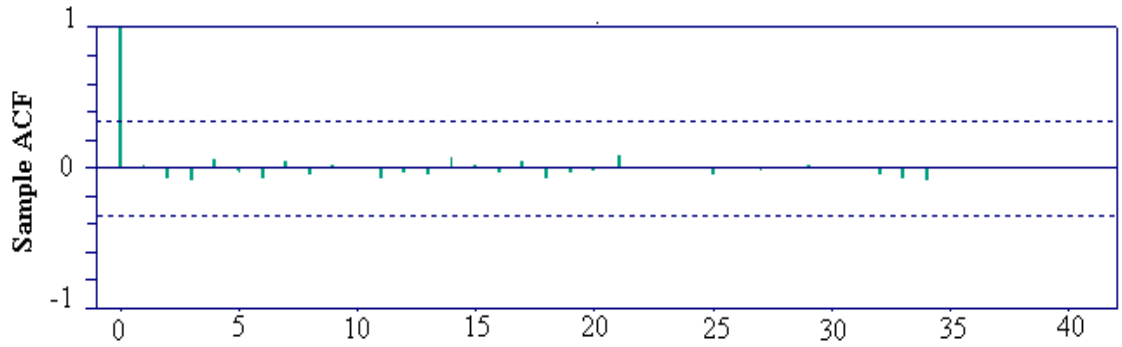
Figure 4.11 ERRR plot with prediction intervals using AR(2)

Another model to be considered based on the training sample is ARMA(1,1). Figure 4.12 shows a, an ERRR plot after first differencing at lag 1; b, sample ACF; c, Sample PACF based on the training sample with h = 1year, its ACF and PACF indicates a stationarity behavior.

(a)



(b)



(c)

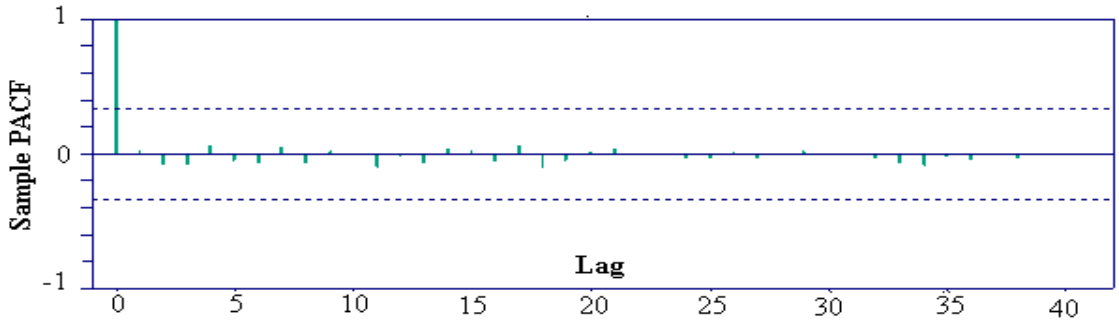


Figure 4.12a, ERRR plot after first differencing at lag 1; **b**, Sample ACF; **c**, Sample PACF based on the training Sample with h = 1year.

Figure 4.13 depicts a, ERRR plot after twice-differencing at lag 1; b, Sample ACF; b, Sample

PACF. The MLE is as shown below:

ARMA Model:

X(t) = - .9016 X(t-1)
+ Z(t) + .9999 Z(t-1)

WN Variance = .000001

AR Coefficients
-.901582

Standard Error of AR Coefficients
.074359

MA Coefficients
.999883

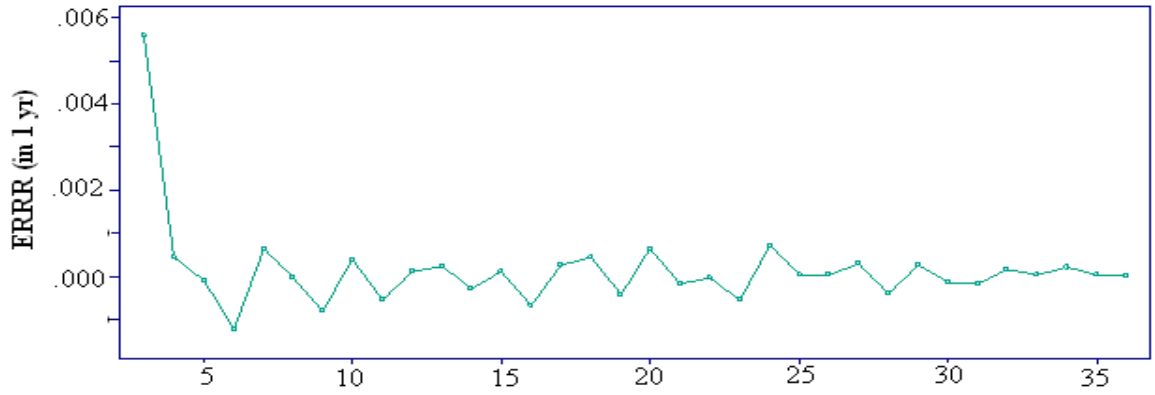
Standard Error of MA Coefficients
.002626

(Residual SS)/N = .00000103425

AICC = -.364283E+03
BIC = -.371031E+03

The AICC statistic is -0.36428E+03 The Ljung-Box statistic is 6.9634and the p-value = .99680, which indicates that the residuals are approximately white noise.

(a)



(b)

(c)

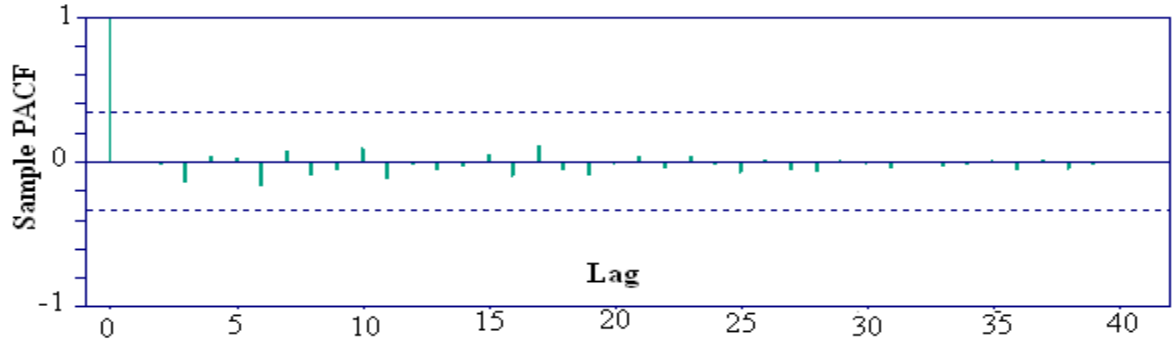


Figure 4.13 a, ERRR plot after twice-differencing at lag 1; b, Sample ACF; b, Sample PACF

The plots of the training sample and its sample ACF and PACF in (Figure 4.10) show nonstationarity and periodicity. Therefore, the Box-Cox transformation, and differencing will be

employed to remove the trend and seasonality. Since the plot shows decreasing variability, we consider the Box-Cox transformation to stabilize the variability. After the λ=1Box-Cox transformation, we see that the trend still exists. We then take the differencing twice at lag 1. Figures 4.12 and 4.13 tell us the series has reached stationarity. ARMA(1, 1) is then considered as a fitting model for the training sample. The Actual and the Predicted ERRRs with their confidence intervals based on the training sample using ARMA(1, 1) are shown in table 4.4.Figure 4.14 depicts ERRR plots with prediction intervals using ARMA(1, 1) with the predicted values rising from lag 36 to lag 39.Figure 4.15 shows a, Rescaled Residual-plots; b, Residual ACF; c, Residual PACF using ARMA(1, 1), this tells us that stationarity has been achieved.

Table 4.4 Numerical values of the Actual and the Predicted ERRRs with their confidence intervals based on the Training Sample using ARMA(1, 1)

Actual	Prediction	Lower Bound	Upper Bound
0.55623	0.55623	0.55495	0.55788
0.55649	0.55673	0.55291	0.55055
0.55681	0.55763	0.55098	0.56375

Figure 4.14 depicts the ERRR values, the predicted values and their confidence intervals using ARMA(1, 1) based on the training sample.

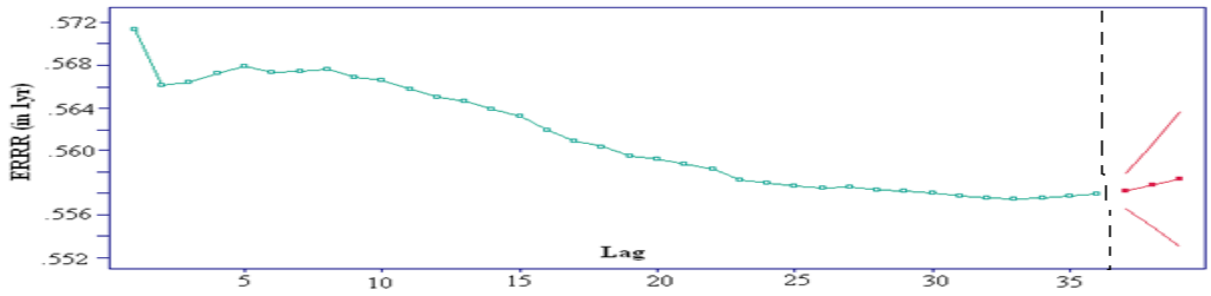
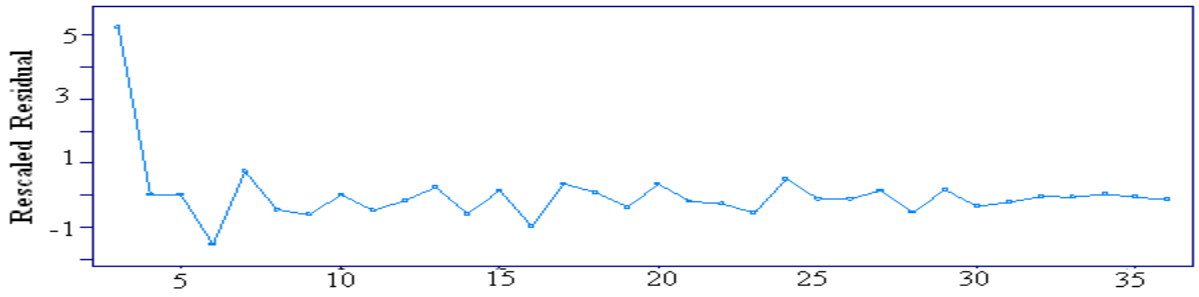
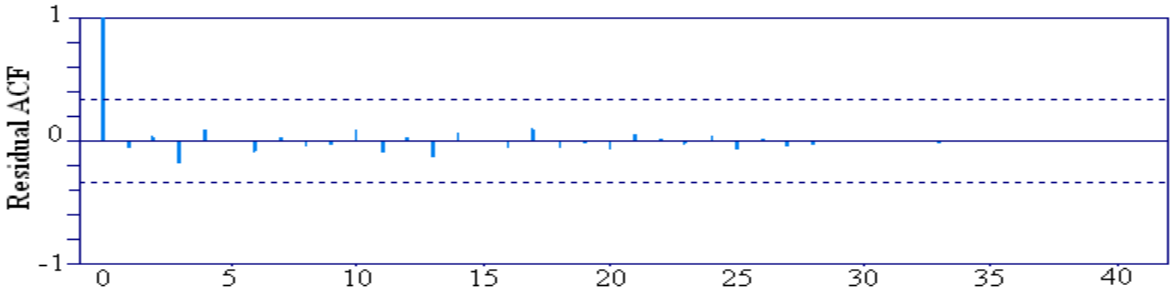


Figure 4.14 ERRR plots with prediction intervals using ARMA(1, 1).

(a)



(b)



(c)

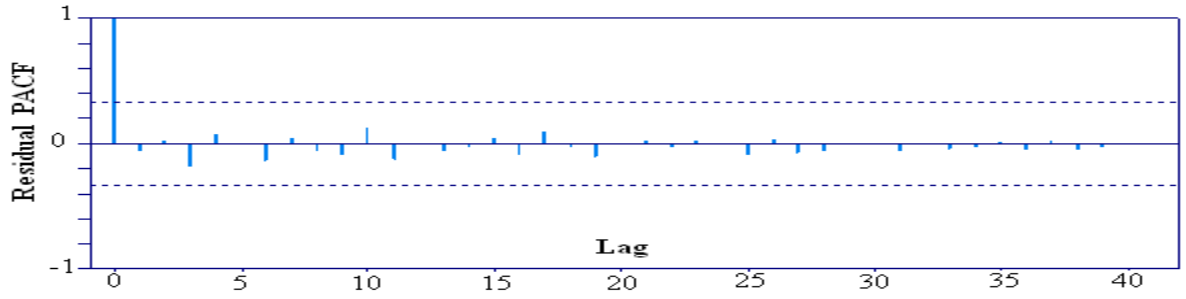


Figure 4.15a, Rescaled Residual-plots; b, Residual ACF; c, Residual PACF with using ARMA(1, 1).

The Actual ERRR values and the three models predictions, that is MA(2), ARMA(1,1), and AR(2) are then plotted and compared to find which of the three predictions is closer to the actual ERRR values. Table 4.5 shows the actual values and the models predicted values and figure 4.16 displays the actual ERRR values and the predicted values by the three models. There is an upward trend from lag 1 to lag 3 with the MA(2) prediction much closer to the actual

ERRRs

Table 4.5 Actualand Model predicted values for MA (2), ARMA (1, 1) and AR (2)

Actual	MA(2)	ARMA(1,1)	AR(2)
0.55623	0.55624	0.55623	0.55595
0.55649	0.55664	0.55673	0.55602
0.55681	0.55712	0.55763	0.55608

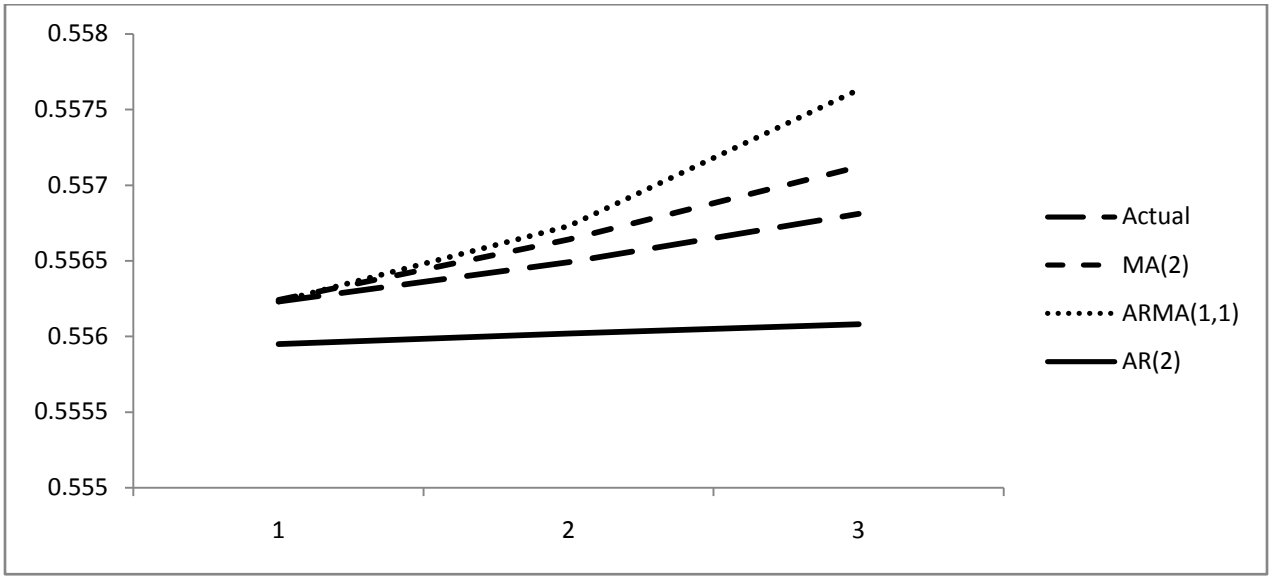


Figure 4.16 Comparison of the models with the actual values based on the training sample.

4.3.3 More ARIMA Models

We extend the same techniques from the training sample to the full data to confirm our results. The data set with the time-step h = 1years has39 lags. The training sample with 36 lags and the prediction set with 3 lags are shown in Figure 4.2 above. The plots of sample ACF and PACF on the training sample (Figure 4.3) indicate nonstationary behavior. Thus no differencing is considered. This is also a suggestion of the AR (2) model. The estimated (MLE) model is:

ARMA Model

X(t) = .7056 X(t-1) + .2817 X(t-2)
+ Z(t)

WN Variance = .000004

AR Coefficients
.705584 .281745

Standard Error of AR Coefficients
.357722 .357757

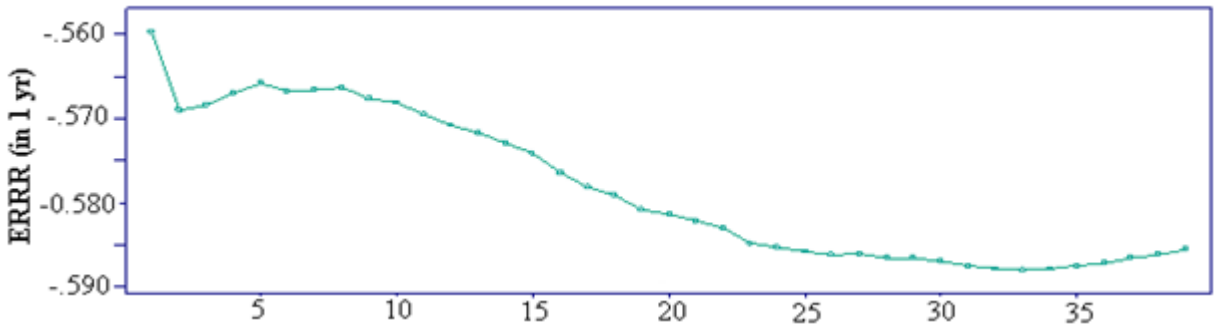
(Residual SS)/N = .00000351228

AICC = -.368929E+03

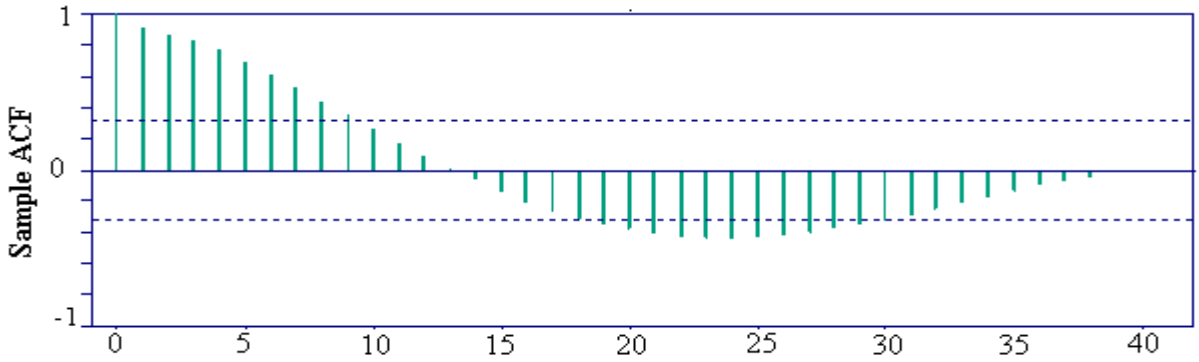
BIC = -.365232E+03

The AICC statistic is -0.368929E+03. The Ljung-Box statistic is 5.3557 and the p-value is 0.9953, which indicates that the residuals are approximately white noise. Figure 4.17 shows a, ERRR plots after Box-Cox transformation at $\lambda = 0$; **b,** sample ACF; **c,** sample PACF of the full data with h= 1year. This indicates nonstationary in its ACF and PACF as some of the spikes falls outside its boundaries. Figure 4.18 shows ERRR plot with prediction intervals using AR(2), the prediction values is leveling off from lag 36 to lag 39.Table 4.6 displays the numerical values of the predicted ERRRs with their confidence intervals using AR(2). Figure4.19is a, residual-plot; b, residual ACF; c, residual PACF of the full data with h = 1year. This figure indicates stationarity.

(a)



(b)



(c)

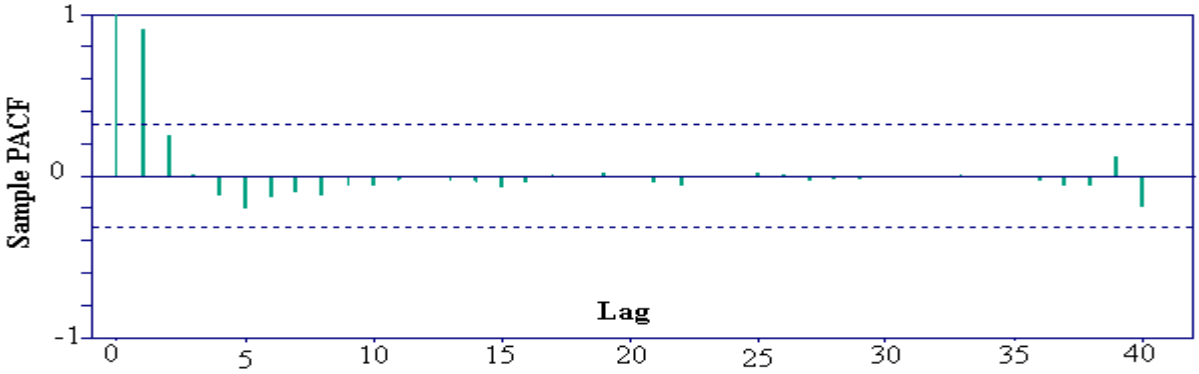


Figure 4.17 a, ERRR plots after Box-Cox transformation at λ = 0; **b,** Sample ACF; **c,** Sample PACF of the full data with h= 1year.

Table 4.6 The numerical values of the Predicted ERRRs with their confidence intervals using AR(2).

Prediction	Lower Bound	Upper Bound
0.55677	0.55494	0.55861
0.55683	0.55460	0.55908
0.55687	0.55422	0.55953

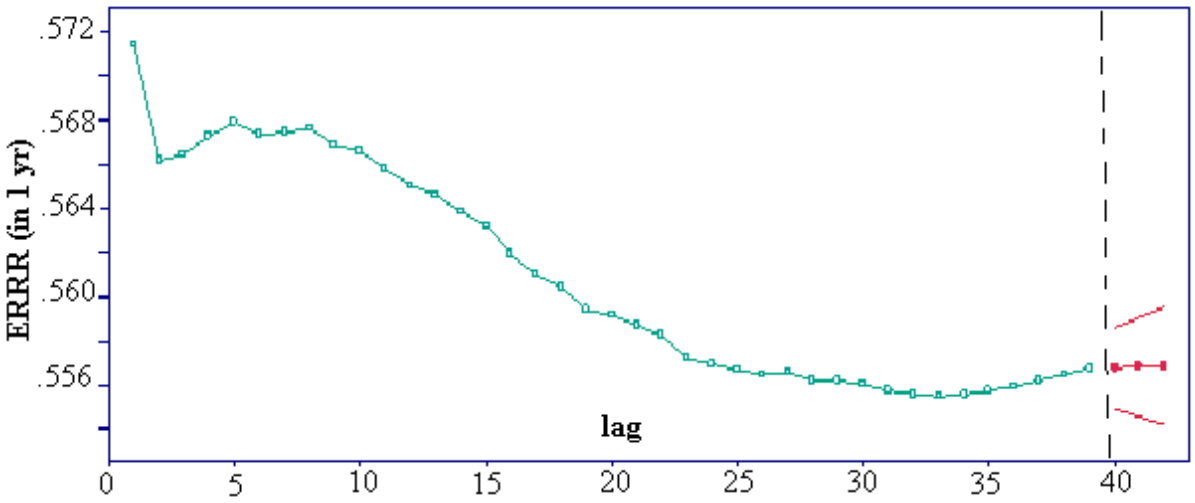
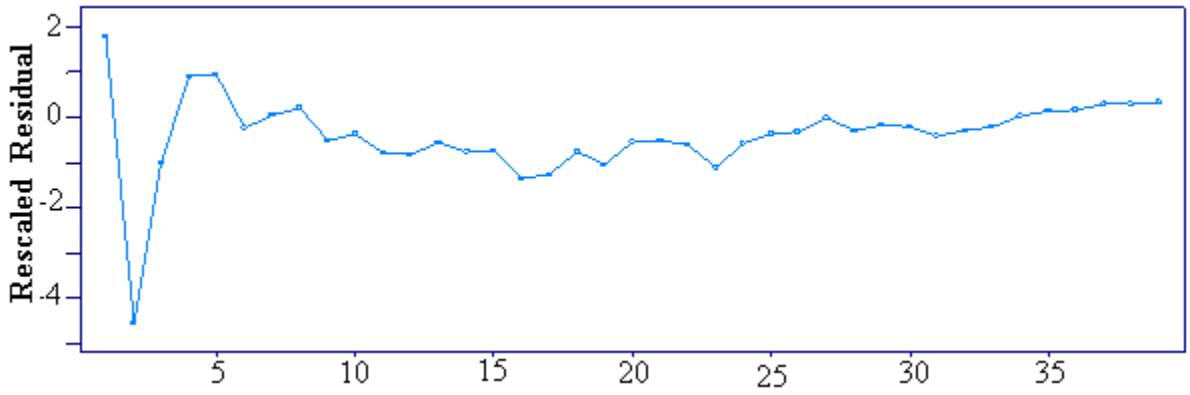
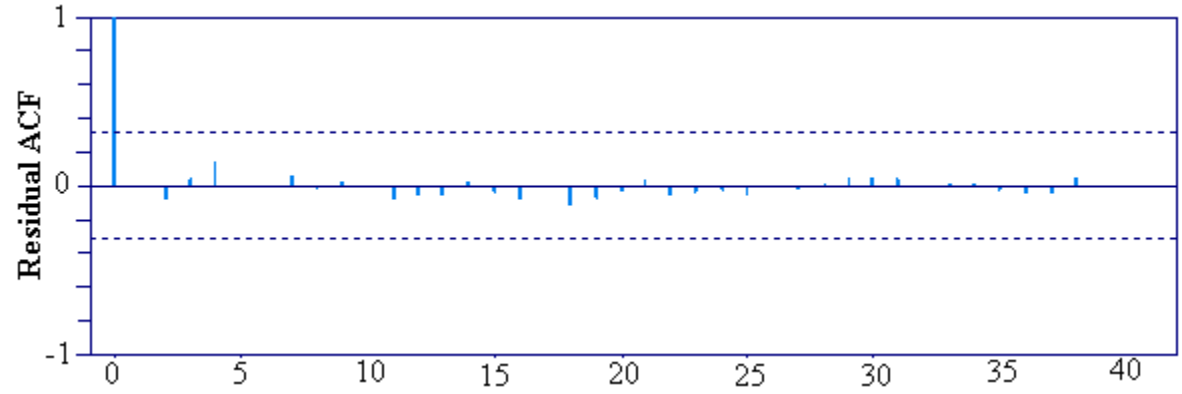


Figure 4.18 ERRR plot with Prediction intervals using AR(2)

(a)



(b)



(c)

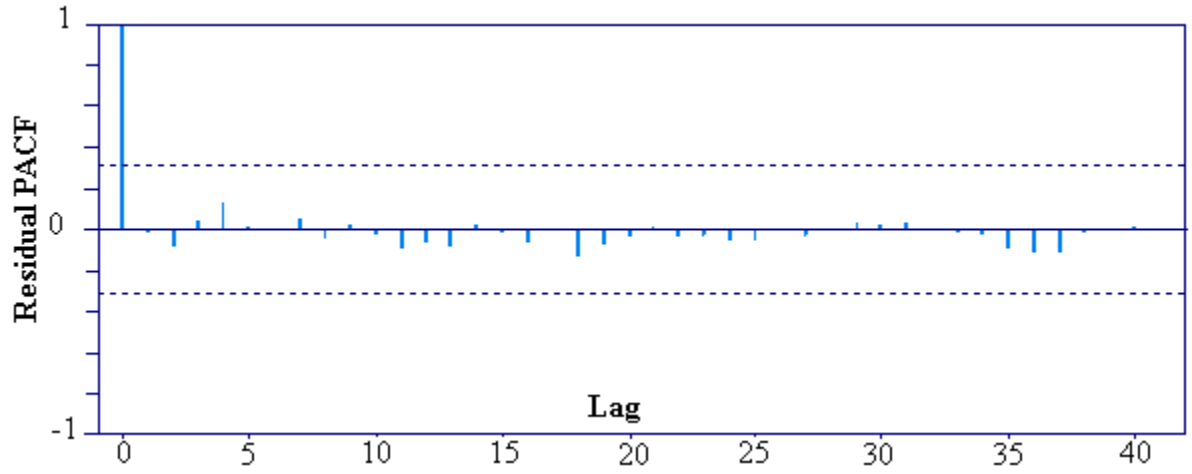


Figure4.19 a, Residual-plot; **b**, Residual ACF; **c**, Residual PACF of the full data with h = 1year.

Twice-differencing the full data set at lag1, the AICC statistic is -.399986E+03, the Ljung - Box statistic is 6.9192 and the p-value is 0.99694, which indicates that the residuals are approximately white noise. This is also a suggestion of the ARMA (1, 1) model. Figure 4.20 shows a, ERRR plots after differencing at lag 1; b, sample ACF; **c**, sample PACF of the full data with h = 1year, while Figure 4.21is**a**, ERRR plots after twice-differencing at lag 1; b, Sample ACF; **c**, sample PACF of the full data with h = 1year. Figure 4.22 is an ERRR plot with prediction intervals Using ARMA(1, 1). There is an upward trend from lag 36 to lag 39.Table 7 shows the numerical values of the predicted ERRR with their confidence intervals using ARMA(1,1). Figure 4.23 depicts a, residual-plot; b, residual ACF; c, residual PACF of the full data with h = 1year. The estimated (MLE) model is:

ARMA Model

X(t) = - .6858 X(t-1)
+ Z(t) + .6121 Z(t-1)

WN Variance = .985063E-06

AR Coefficients
-.685763

Standard Error of AR Coefficients
.745346

MA Coefficients
.612102

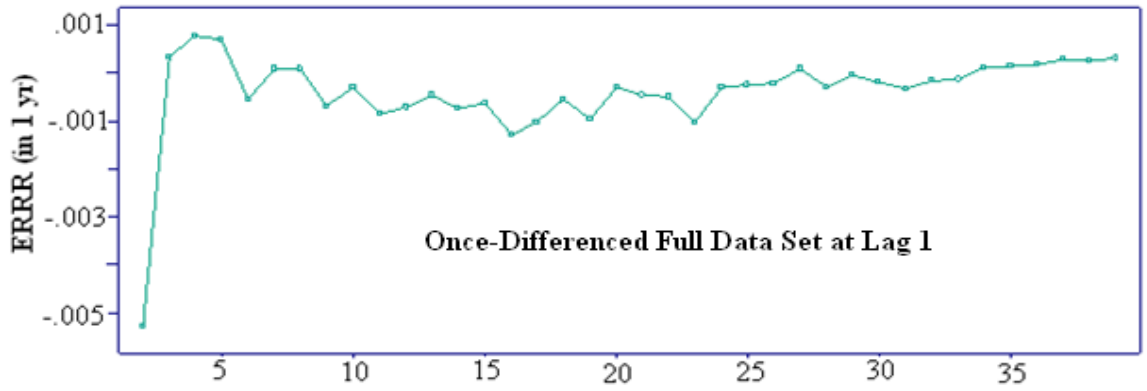
Standard Error of MA Coefficients
.749744

(Residual SS)/N = .985063E-06

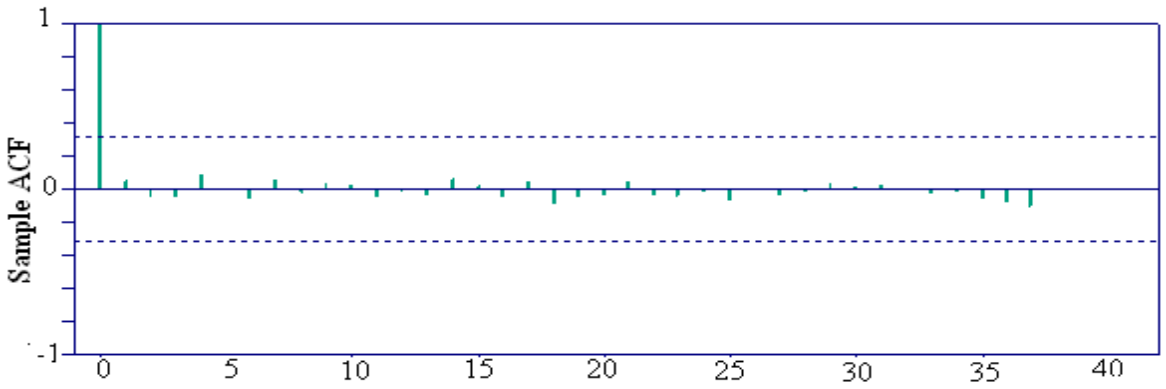
AICC = -.399986E+03

BIC = -.410756E+03

(a)



(b)



(c)

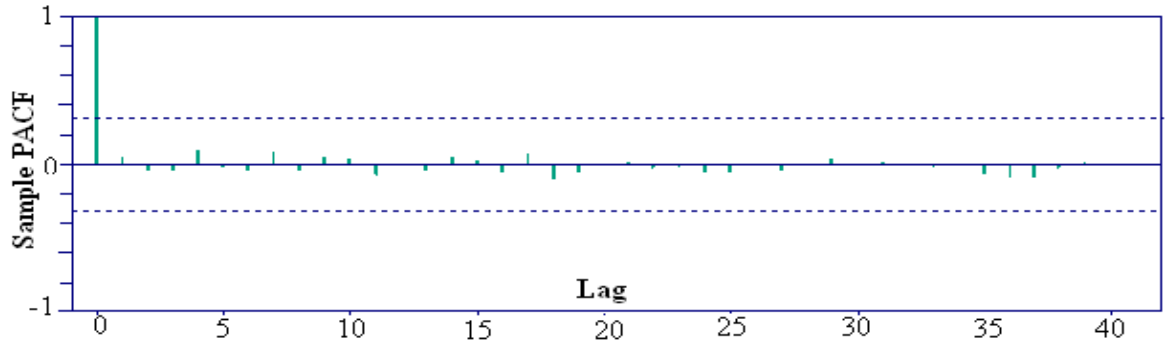
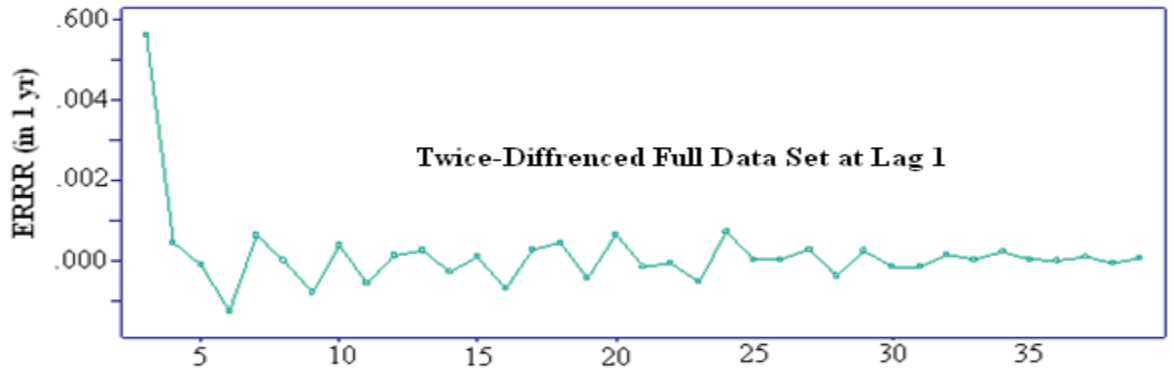
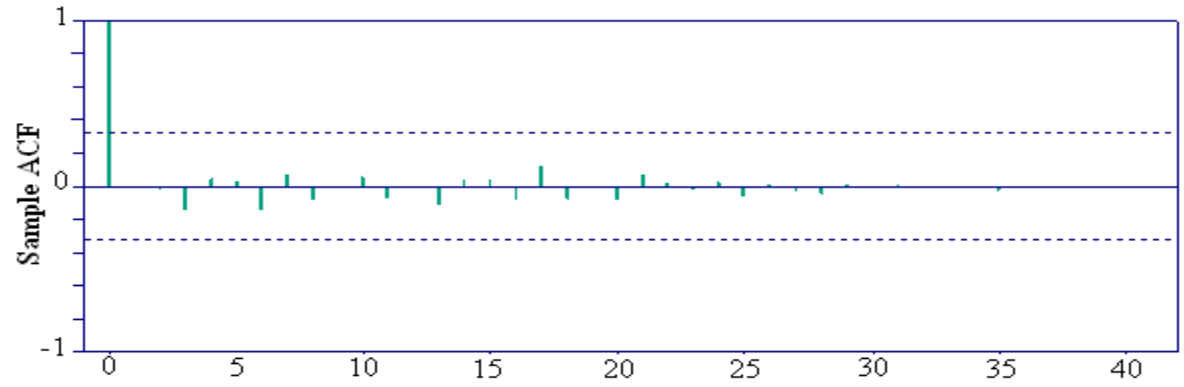


Figure 4.20 a, ERRR plots after differencing at lag 1; **b**, Sample ACF; **c**, Sample PACF of the full data with h= 1year.

(a)



(b)



(c)

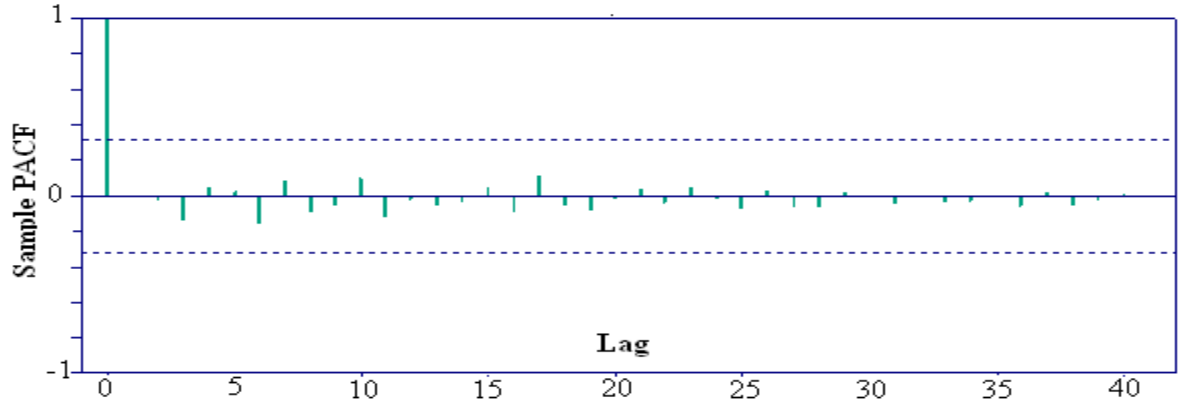


Figure 4.21 a, ERRR plots after twice-differencing at lag 1; **b**, Sample ACF; **c**, Sample PACF of the full data with h = 1year.

Table 4.7 The numerical values of the predicted ERRRs with their confidence intervals using ARMA(1, 1).

Prediction	Lower Bound	Upper Bound
0.55729	0.55566	0.55892
0.55792	0.55437	0.56146
0.55870	0.55278	0.56461

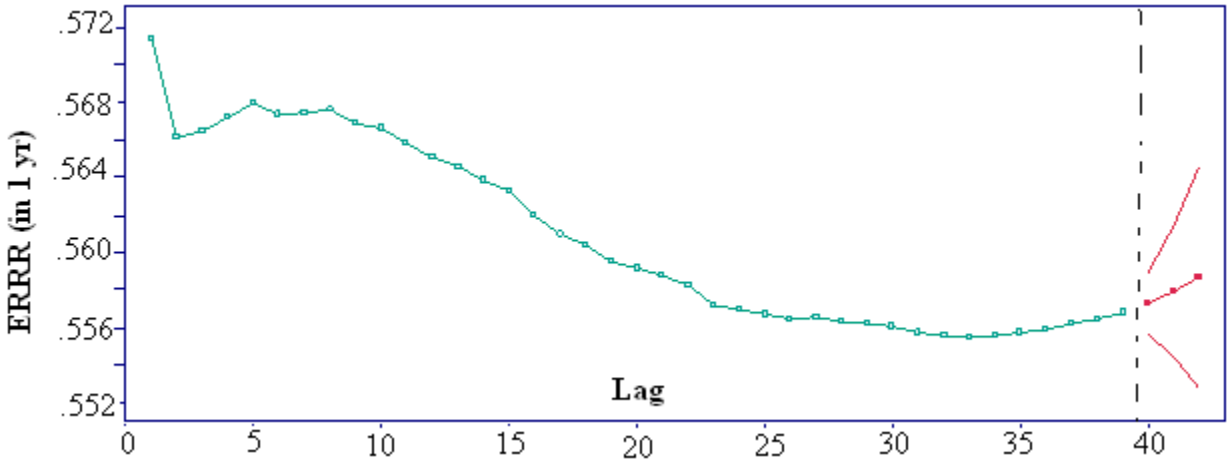
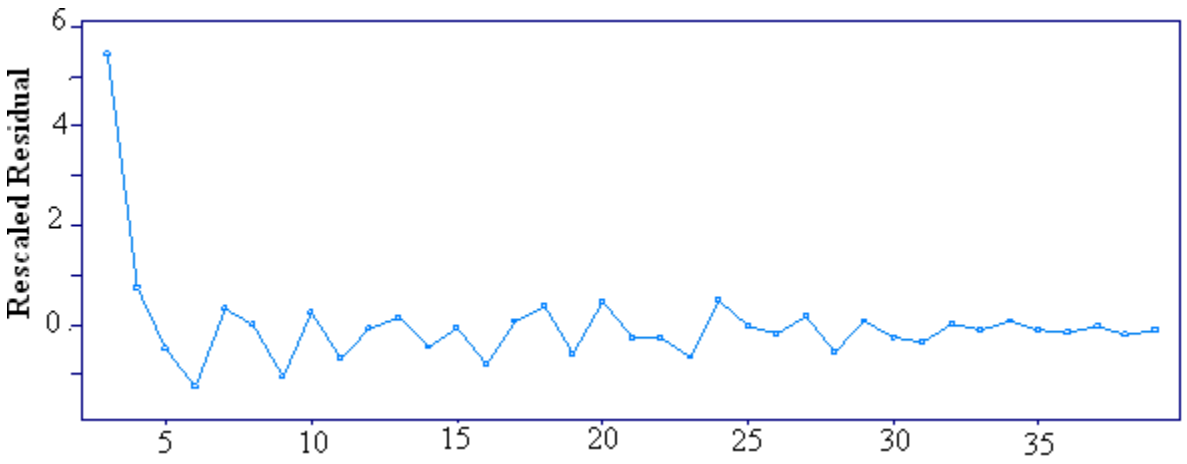
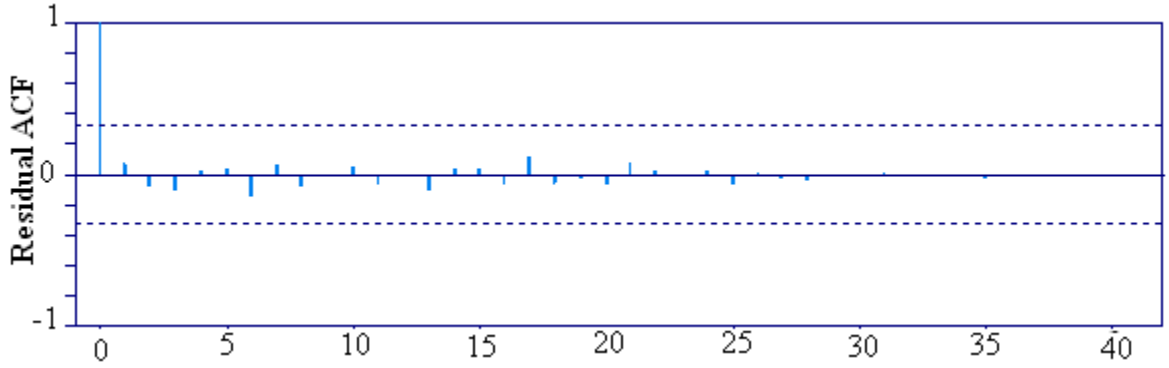


Figure 4.22 ERRR plot with prediction intervals Using ARMA(1, 1)

(a)



(b)



(c)

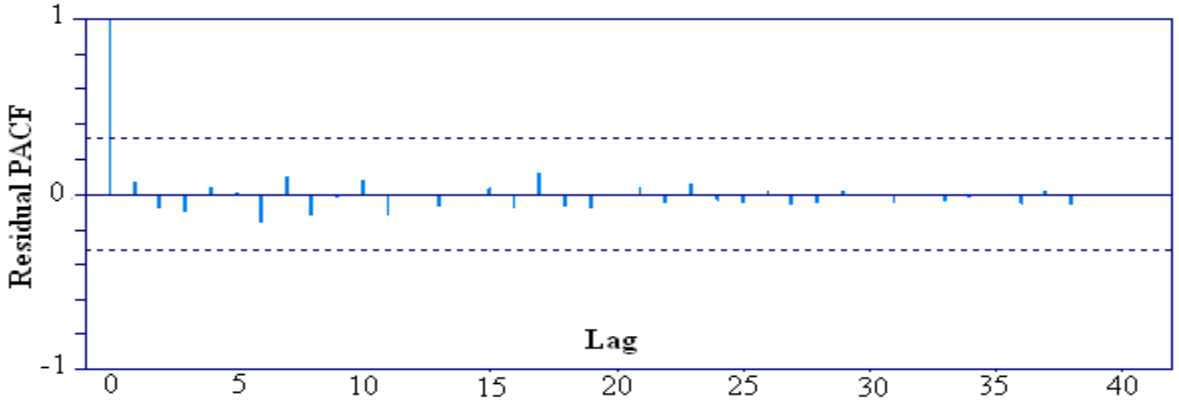


Figure 4.23a, Residual-plot; **b**, Residual ACF; **c**, Residual PACF of the full data with h = 1year.

Figure 4.24 depicts the temporal trends. All the results point to the same directions: male are more likely to die from leukemia than their female counterparts confirming the results of our finding based on the training sample as before. Table 4.8 shows predicted values of the three models based on the full data.

Table 4.8 Predicted value of the three models based on the full data

Year	MA(2)	ARMA(1,1)	AR(2)
2008	0.55730	0.55729	0.55677
2009	0.55786	0.55792	0.55683
2010	0.55850	0.55870	0.55687

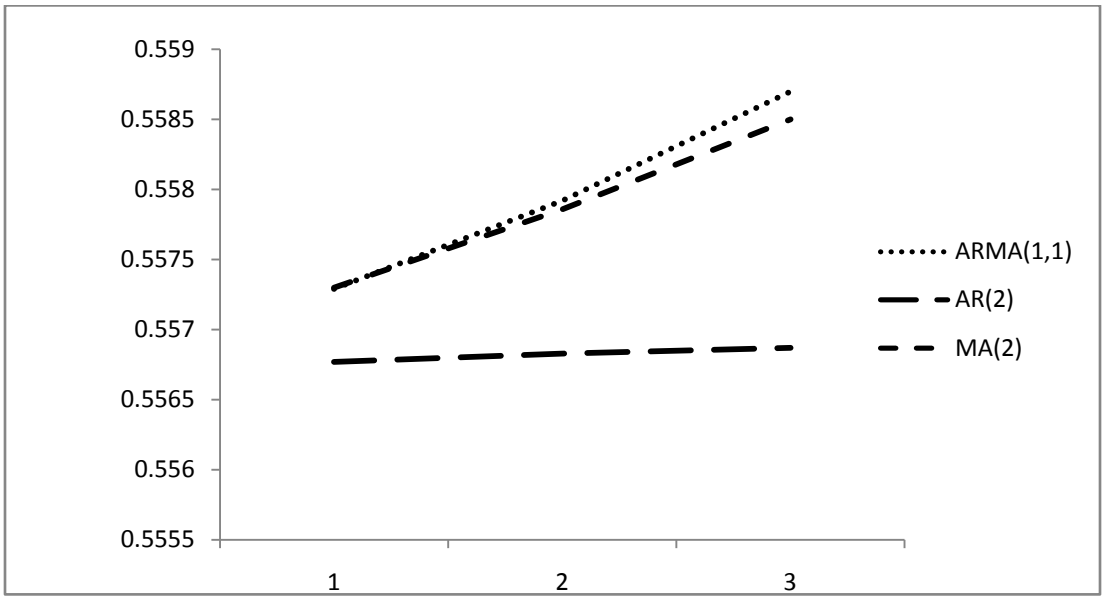


Figure4.24 Comparison of the three models based on the full model

CHAPTER 5

CONCLUSIONS

Coupled with the conditional test (Przyborowski and Wilenski, 1940), the empirical recurrence rates ratio extended from the empirical recurrence rate (Ho, 2008), which allows us to apply the well-known ARIMA modeling techniques to compare and forecast leukemia related death rates ratio in the United States of America based on the 39 years mortality data. The ERR and ERRR not only smooth and explain deaths rates modeled by a stochastic process, but also operate as a link between a classical time series and a point process.

We split the leukemia ERRR time series into a training sample and a prediction set. The training sample is used to develop the candidate models. For time-step h = 1year, we used the last three ERRRs as a prediction set to make model comparisons by checking the predictive ability of the candidate models developed from the training sample. Before modeling, we must make sure the ARMA process is stationary. After taking twice difference at lag 1, an MA (2) model yields predictions that are the closest to the actual values, therefore we conclude that MA(2) is the best of the three resulting models .

The limitation to this paper is the fact that the data used in the write up has a present value of 2007, instead of a more current value of 2011. In addition we could not use the empirical recursive rates (ERR) values to predict future counts of the leukemia deaths for the male and female.

The application of ARIMA models for long-term leukemia prediction will further facilitate the research in the areas monitoring the occurrence of death rates of other disease, such as pneumonia and influenza, diabetes, accidents and their adverts effects, teen pregnancy, suicide, as well as other disease of interest. Therefore this research will be beneficial to other researchers in this vital field of study.

APPENDIX

Table 1A: Leukemia Deaths in the United States. (www.seer.cancer.gov)

Years	Counts		
	Male	Female	Total
1969	8,256	6,193	14,449
1970	8,128	6,364	14,492
1971	8,205	6,263	14,468
1972	8,325	6,292	14,617
1973	8,262	6,215	14,477
1974	8,230	6,344	14,574
1975	8,382	6,372	14,754
1976	8,556	6,500	15,056
1977	8,609	6,717	15,326
1978	8,682	6,708	15,390
1979	9,019	7,140	16,159
1980	9,325	7,383	16,708
1981	9,201	7,241	16,442
1982	9,376	7,509	16,885
1983	9,447	7,561	17,008
1984	9,392	7,849	17,241
1985	9,563	7,927	17,490
1986	9,685	7,851	17,536
1987	9,487	7,953	17,440
1988	9,831	7,910	17,741
1989	10,142	8,264	18,406
1990	10,290	8,435	18,725
1991	10,286	8,817	19,103
1992	10,705	8,712	19,417
1993	10,872	8,834	19,706
1994	10,948	8,885	19,833
1995	11,347	8,976	20,323
1996	11,265	9,229	20,494
1997	11,379	9,105	20,484
1998	11,297	9,172	20,469
1999	11,543	9,528	21,071
2000	11,803	9,594	21,397
2001	11,894	9,638	21,532
2002	12,058	9,523	21,581
2003	12,104	9,504	21,608
2004	12,051	9,421	21,472
2005	12,273	9,443	21,716
2006	12,426	9,590	22,016
2007	12,434	9,494	21,928

January 1969-December 2007

Table 2A: ERRR with Time step h= 1year

	Count		
Time-step	Total	Male	ERRR
1969	14449	8256	0.571389
1970	14492	8128	0.566117
1971	14468	8205	0.566449
1972	14617	8325	0.567228
1973	14477	8262	0.567921
1974	14574	8230	0.567383
1975	14754	8382	0.567489
1976	15056	8556	0.567591
1977	15326	8609	0.566911
1978	15390	8682	0.566621
1979	16159	9019	0.565784
1980	16708	9325	0.565075
1981	16442	9201	0.564618
1982	16885	9376	0.563881
1983	17008	9447	0.563259
1984	17241	9392	0.561972
1985	17490	9563	0.560971
1986	17536	9685	0.560433
1987	17440	9487	0.559478
1988	17741	9831	0.559181
1989	18406	10142	0.558735
1990	18725	10290	0.558250
1991	19103	10286	0.557240
1992	19417	10705	0.556948
1993	19706	10872	0.556698
1994	19833	10948	0.556484
1995	20323	11347	0.556567
1996	20494	11265	0.556269
1997	20484	11379	0.556237
1998	20469	11297	0.556065
1999	21071	11543	0.555741
2000	21397	11803	0.555583
2001	21532	11894	0.555464
2002	21581	12058	0.555581
2003	21608	12104	0.555741
2004	21472	12051	0.555924
2005	21716	12273	0.556225
2006	22016	12426	0.556487
2007	21928	12434	0.556813

January 1969- December 2007

Table 3A. ERR with a Time-step h = 1year.

Count	Number of male	ERR (in 1 yr.)	Number of Female	ERR (in 1 yr.)
1	8,256	8256	6,193	6193
2	8,128	8192	6,364	6278.5
3	8,205	8196.333333	6,263	6273.333333
4	8,325	8228.5	6,292	6278
5	8,262	8235.2	6,215	6265.4
6	8,230	8234.333333	6,344	6278.5
7	8,382	8255.428571	6,372	6291.857143
8	8,556	8293	6,500	6317.875
9	8,609	8328.111111	6,717	6362.222222
10	8,682	8363.5	6,708	6396.8
11	9,019	8423.090909	7,140	6464.363636
12	9,325	8498.25	7,383	6540.916667
13	9,201	8552.307692	7,241	6594.769231
14	9,376	8611.142857	7,509	6660.071429
15	9,447	8666.866667	7,561	6720.133333
16	9,392	8712.1875	7,849	6790.6875
17	9,563	8762.235294	7,927	6857.529412
18	9,685	8813.5	7,851	6912.722222
19	9,487	8848.947368	7,953	6967.473684
20	9,831	8898.05	7,910	7014.6
21	10,142	8957.285714	8,264	7074.095238
22	10,290	9017.863636	8,435	7135.954545
23	10,286	9073	8,817	7209.043478
24	10,705	9141	8,712	7271.666667
25	10,872	9210.24	8,834	7334.16
26	10,948	9277.076923	8,885	7393.807692
27	11,347	9353.740741	8,976	7452.407407
28	11,265	9422	9,229	7515.857143
29	11,379	9489.482759	9,105	7570.655172
30	11,297	9549.733333	9,172	7624.033333
31	11,543	9614.032258	9,528	7685.451613
32	11,803	9682.4375	9,594	7745.09375
33	11,894	9749.454545	9,638	7802.454545
34	12,058	9817.352941	9,523	7853.058824
35	12,104	9882.685714	9,504	7900.228571
36	12,051	9942.916667	9,421	7942.472222
37	12,273	10005.89189	9,443	7983.027027
38	12,426	10069.57895	9,590	8025.315789
39	12,434	10130.20513	9,494	8062.974359

January 1969-December 2007

Notation and acronyms

NHPP	Non homogeneous Poisson process
HPP	Homogeneous Poisson process
M(t)	Mean function of an NHPP
$\lambda(t)$	Intensity function of an NHPP
ARIMA	Autoregressive integrated moving Average
ARMA	Autoregressive moving average
MLE	Maximum likelihood estimator
ERRR	Empirical recursive rates ratio
AR	Autoregressive
MA	Moving Average
$\{z_l\}$	A discrete time series
B	Backshift Operator
Lag	Time separation or time step
SAFC	Sample autocorelated function
SPACF	Sample partial autocorelated
ITSM	Time series computing package
AIC	Akaike mode information formation criterion
BIC	Schwartz model selection information Criterion
AICC	Estimated corrected version of AIC

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