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Time Series Analysis of Swiss Life Expectancy

Abstract

In this paper, we will analyze life expectancy at birth in Switzerland and fit a time series model to predict life expectancy in the upcoming years. The life expectancy data ranges from 1950 to 2021 and reveals that an ARIMA(1,1,0) model is best for modeling Swiss life expectancy. We use the maximum likelihood method to estimate the parameters in this model and use the minimum mean squared error forecast to predict future life expectancy from 2022 to 2029. COVID-19 caused the largest decrease in life expectancy in the entire data set, and this will be an interesting challenge for our models to forecast. We have provisional life expectancies from 2022 and 2023 to determine the accuracy of our model's predictions. These provisional life expectancies were well within the bounds of our prediction interval and only slightly off our predicted values, supporting our ARIMA(1,1,0) model.

Introduction

Over the past two centuries, we have seen significant growth in the average duration of a human life. Significant advances in food production, water access, modern medicine, sanitation, and significant economic growth have led to a steep decline in poverty.[6] Switzerland has one of the highest qualities of living in Europe, and as a result, has one of the highest life expectancies globally. Switzerland did not have any unusual periods of growth in life expectancy like some sub saharan countries with more people lifted out of poverty, from where life expectancy grew from 30 years to 60 years.[6] Switzerland has steadily adopted cutting-edge medical technologies and invested in public infrastructure, resulting in a relatively constant increase in life expectancy since 1950.

Life expectancy at birth is calculated using a life table which records the probability of dying for any person at each age. Using these probabilities, the life expectancy at birth is calculated by evaluating the age at which one is most likely to die. This means that life expectancy calculations assume the living standards in the year they are calculated persist for a newborn's entire life. The life expectancy at birth of the population of Switzerland data I used was collected by Our World in Data consisting of 72 observations spanning the years 1950 to 2021[1]. Before 1950, Switzerland did not have reliable and consistent census data due to small and infrequent population sampling. After 1950, data protocols were standardized globally to the point where all first-world countries reported life expectancy annually. This reporting came with the standardization of life expectancy data across UN nations in the 1950s. Switzerland further increased its life expectancy accuracy in 1962 when they were a founding nation of the Organisation for Economic Co-operation and Development (OECD), which organizes countries across the globe to share economic and developmental data.[3]

Recently, the COVID-19 pandemic caused the most significant drop in life expectancy since the 1960s, but Switzerland recovered remarkably quickly. This will be a significant challenge for a time series model to accurately account for the effects of COVID-19 and predict the future recovery of Switzerland. The first case of COVID-19 in Switzerland occurred on February 25th, 2020, and the Swiss Federal Council enforced social distancing and restriction of large gatherings from March to July 2020, reestablishing the restrictions in October after a significant second wave.[3] In late December 2020, the first COVID-19 vaccine was approved in Switzerland, achieving a vaccination rate of 51% by August 2021.[3] By early February, almost all lockdown restrictions were lifted. We will have to account for this in our predictions and the model which holds little weight in 2020 when prediction 2023 will probably perform well.[4]

Stationarity

We know life expectancy is not stationary and has increased significantly over the past 72 years. In the time series plot (Fig. 1), we can see that there is a clear positive trend. This trend seems linear but seems to slow slightly after the year 2000. Rather than use the detrending method and assume a linear trend that continues forever, we will use the differencing method to develop a stationary time series for the increase in life expectancy year over year. Differencing is part of the ARIMA(p,d,q) model for time series which implies the dth difference of our data is stationary with p AR coefficients and q MA coefficients. The general form of an ARIMA model is $\phi(B)(1-B)^d Y_t = \mu + \Theta(B)e_t$ where $\{Y_t\}$ is the time series data, $\{e_t\}$ is independent identically distributed white noise, B shifts time series objects back in time ($BX_t = X_{t-1}$), p represents the degree of our ϕ polynomial, μ is a constant, and q represents the degree of our Θ polynomial.

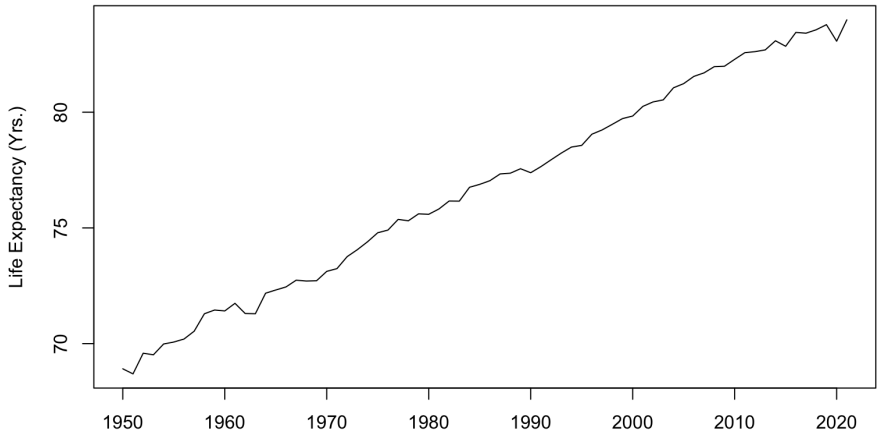


Fig. 1

Before we difference our data, we must determine if any transformations are needed; we see relatively constant variance, except for mildly increased variance in the first 20 values. By approximating a 95% confidence interval for lambda in a Box-Cox transformation, we can determine if a Box-Cox transformation would meaningfully reduce the heteroscedasticity present in our data. In the results (Appx. Fig. 2), we see that 1 is in our 95% confidence interval for lambda, implying that no Box-Cox transformation will meaningfully reduce the heteroscedasticity present in our data. This makes sense as the only variation we see in our data comes before the 1970s when both statistical sampling and population data analysis were being refined.

Without transforming our data, we difference the Swiss life expectancy time series data and the resulting time series seems stationary. When plotting the differences (Fig. 3), we see the difference in life expectancy year to year with the average increase in life expectancy coming out to 0.212 years.

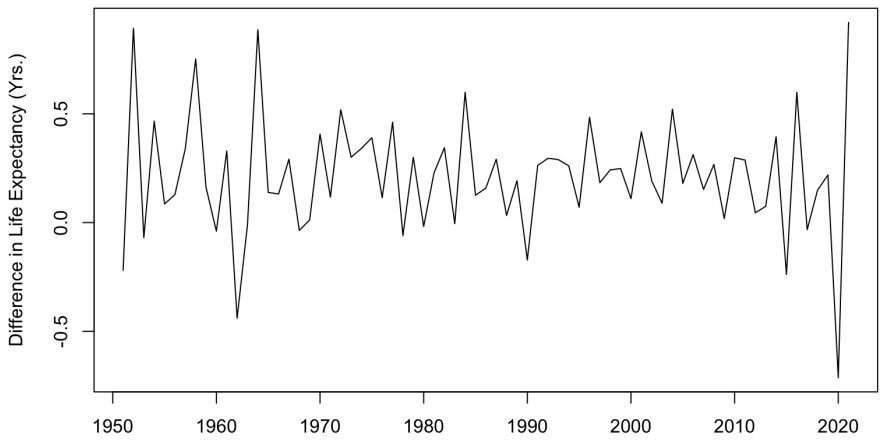


Fig. 3

We performed an Augmented Dickey-Fuller test to confirm the stationarity of the difference in life expectancy and found a p-value of less than 0.01, meaning we have significant evidence to say the difference in Swiss life expectancy is stationary.

Model Specification

To identify candidate models for our differenced life expectancy data, we will examine the sample autocorrelation function (ACF) correlogram, partial ACF (PACF) correlogram, extended ACF (EACF) table, and ARMA best subsets table which is evaluated using the Bayesian Information Criterion (BIC).` Using these criteria, we will select a p and q for an ARIMA(p,1,q) model for Swiss life expectancy.

For the sample ACF and PACF, we use the bounds ± 2/√Sample Size to determine significant ACF values, where we have a sample size of 71, meaning our bounds are roughly equal to ±0.24. In our ACF (Fig. 4.1), we see that only lags 1 and 4 have significant ACF values. We would not expect this for any ARMA model. If we assume that lag 4 is truly insignificant and it is due to pure chance that we observe significance, this would align with an AR(1) model. Otherwise, we could say that an AR(4) model may be sufficient with low values for our estimated ϕ*2 ϕ*3. We do not see any drop off so we can assume that an MA model would be inappropriate. We do see only insignificant values for any lag greater than 4.

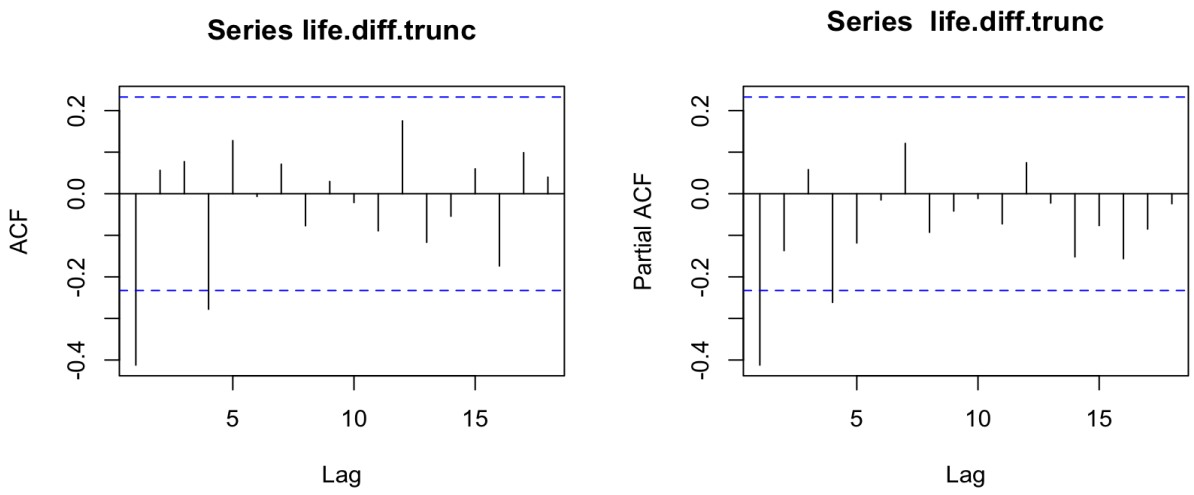


Fig. 4.1 , Fig. 4.2

Our PACF (Fig. 4.2) is confusing; I did not expect that only lags 1 and 4 would be significant for any ARMA model. Again, if we assume that lag 4 is truly insignificant, this would imply that an MA(1) model is appropriate, but that goes against our ACF plot. One could argue that if we treat the PACF(4) value as insignificant, there will be a decay present in PACF values, implying an AR model, although we have no statistical evidence to make that assumption.

In our EACF (Appx. Fig. 5), we see that an AR(4) model may be appropriate. An AR(1) model seems inappropriate due to a column of significance at lag 3. Any amount of MA component with the AR(4) model seems fine in the above EACF, but we opt for the parsimonious model, further supporting the AR(4) model.

Our ARMA subsets plot (Fig. 6) suggests an AR(5) model and an ARMA(5,1) model. For the AR(5) model, we see both (ϕ1,ϕ5) and (ϕ2,ϕ4,ϕ5) are recommended combinations of AR coefficients. Interestingly, we do not see the AR(4) model in the ARMA best subsets, we do not even see the ϕ4 coefficient perform best in the lowest BIC model (note: BIC imposes a heavy penalty to non-parsimonious models).

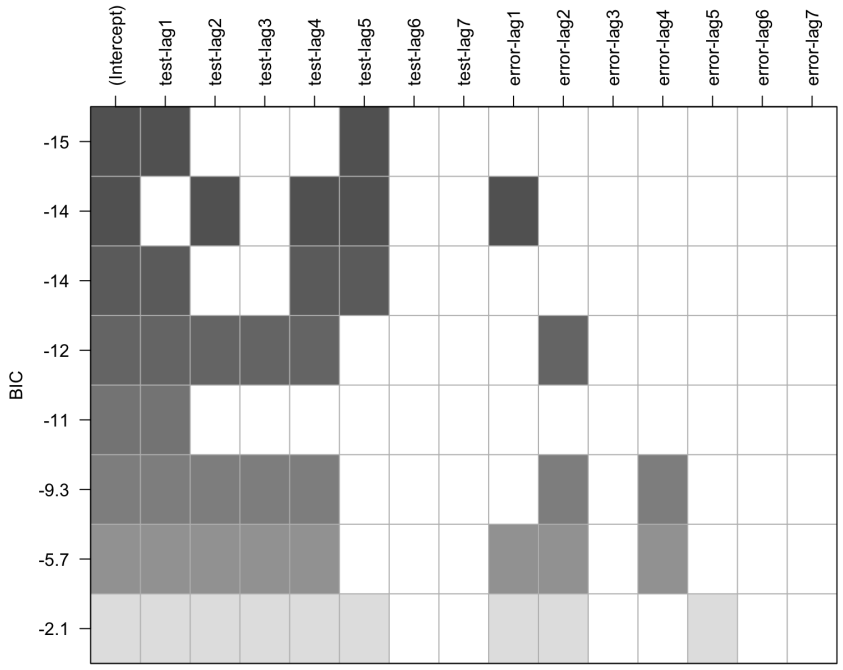


Fig. 6

Parameter Estimation

We see that the AR(4), AR(5), and ARMA(5,1) models all have some level of viability for modeling the year over year difference in Swiss life expectancy. We evaluate these models based on the Akaike Information Criterion (AIC), BIC, distribution of residuals, and the ACF of residuals. We use the Ljung-Box statistic to determine if any group of sample ACF values are significantly different from zero. This means we are evaluating the ARI(4,1), ARI(5,1), and ARIMA(5,1) models for Swiss life expectancy.

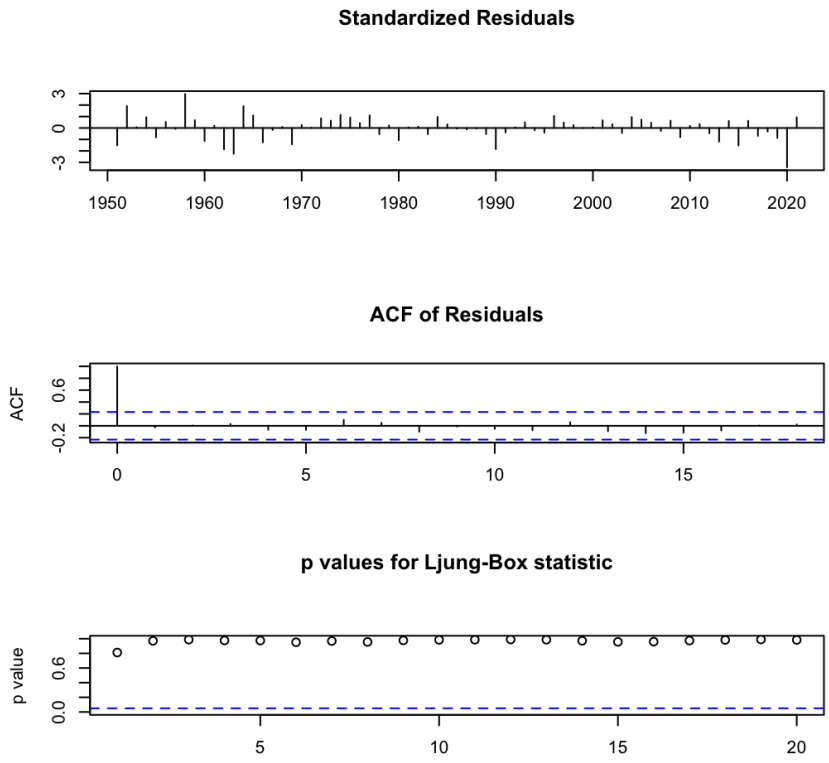
When fitting our ARIMA(4,1,0) model, we use the maximum likelihood method to estimate the parameters in our AR(4) model of the difference in Swiss life expectancy:

$$(1+0.4413B+0.0778B^2-0.0035B^3+0.3520B^4)(1-B)(Y_t-0.2115) = e_t$$

We observe that -0.0778 and 0.0035 are within 2 standard deviations of zero, meaning they are not statistically significant, unlike ϕ*1, ϕ*4, and μ*. This model has an AIC=5.65 and BIC=19.23.

When observing our residuals (Fig. 8.1), we see that there seems to be no issue with independence. We can confirm this by performing a runs test, where we observe 38 runs and expect 35.92 runs, to get a p-value of 0.704, meaning we do not have significant evidence to reject our assumption of independence. In the QQplot of standardized residuals (Appx. Fig. 7.2), we see an approximately normal distribution of residuals, except for some fat-tailedness. We can perform a Shapiro-Wilk test on our standardized residuals to determine if they are approximately normal. We return a p-value of 0.047, which is significant evidence to say our residuals are not normally distributed.

In our sample ACF (Fig. 8.2), We see that there are no significant ACF values for our residuals. This implies that this ARMA(4,0) model accurately represents the increase in Swiss life expectancy. We can statistically test this implication with the Ljung-Box test statistic, which has a null hypothesis that our ARMA(4,0) model is appropriate. The p-values of our Ljung-Box statistic (Fig. 8.3) are all above 0.05, meaning that an ARIMA(4,0) appropriately represents the increase in Swiss life expectancy each year.



(Top to Bottom) Fig. 8.1 , Fig. 8.2 , Fig. 8.3

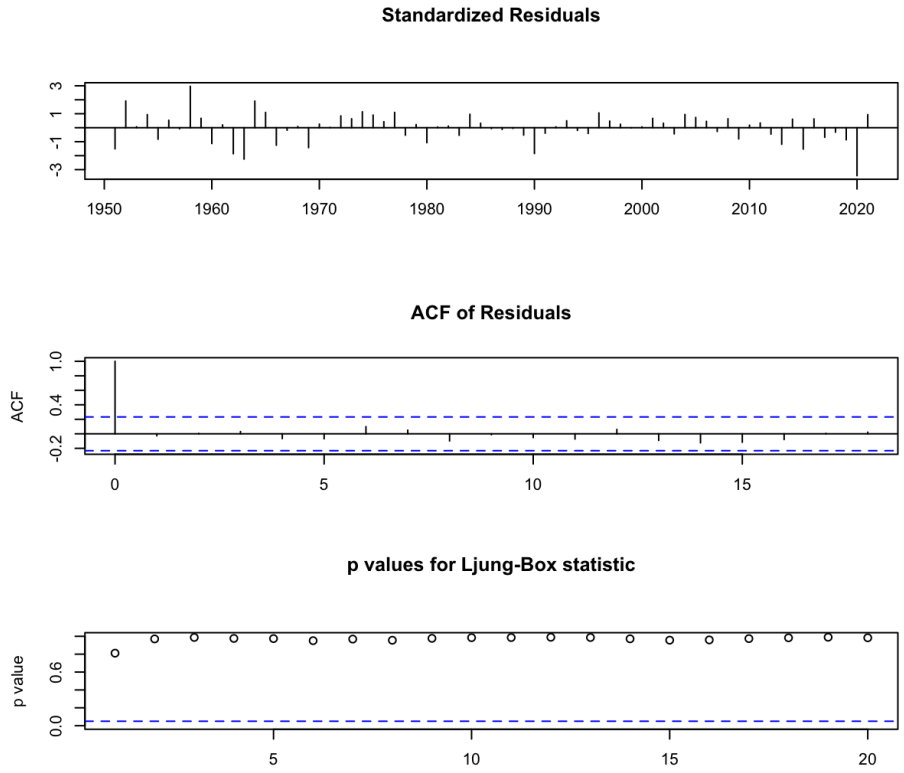
Seeing these results for the ARIMA(4,1,0) model suggests that our ARIMA(5,1,0) will be overfit. By fitting an ARMA(5,0) model on our difference in Swiss life expectancy data, we see that our ϕ*2, ϕ*3, and ϕ*5 coefficients are all not significantly different from zero. This is sufficient evidence that an AR(5) model should not be considered for our residuals.

As a result, rather than consider an ARIMA(5,1,1) model, I will consider the following ARIMA(4,1,1) model estimated using the maximum likelihood method:

$$(1+0.2486B-0.0157B^2-0.0113B^3+0.3804B^4)(1-B)(Y_t-0.2118) = (1+0.2149B)e_t$$

With this model, none of the parameters except for the intercept and ϕ*4 are significantly different from zero, with an AIC=5.2 and BIC=19.23. We see independence in the residuals (Fig. 10.1) and observe 38 runs while expecting 35.9, resulting in the runs test being

unable to reject our assumption of independence. Similar to the AR(4) model, we see a fat-tailed QQplot (appx. Fig 9.2) and reject normality when performing a Shapiro-Wilk (SW) test.



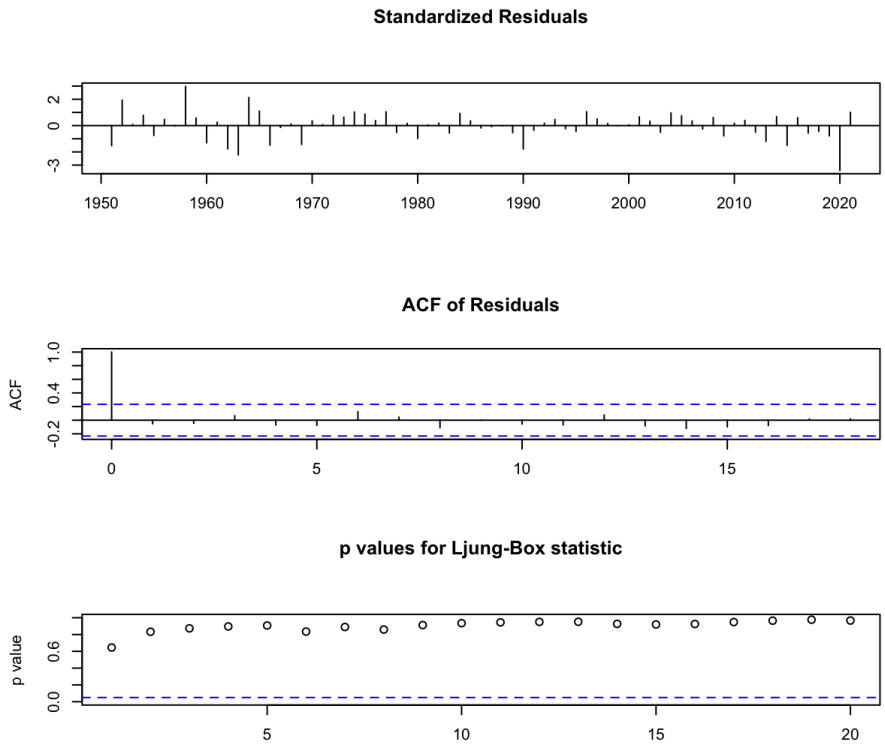
(Top to Bottom) Fig. 10.1 , Fig. 10.2 , Fig. 10.3

We do not have any significant ACF values of our residuals and see that we fail to reject the appropriateness of this model using the Ljung-Box statistic (Fig. 10.3). Based on the insignificance of the MA component, we can say that ARIMA(4,1,1) does not outperform ARIMA(4,1,0) here.

We have significant evidence to say the ARIMA(4,1,0) model is best to model Swiss life expectancy, but we know that $\phi 2$ and $\phi 3$ are not significant. Using this insight, I used the maximum likelihood method to fit a reduced model where $\phi 2$ and $\phi 3$ were not included:

$$(1+0.4205B+0.3567B^4)(1-B)(Y_t-0.2115) = e_t$$

All of the parameters in this model are significantly different from zero. The reduced AR(4) model outperformed the original AR(4) model with an AIC=0.01 and BIC=11.06169. We see that our residuals seem independent of each other (Fig. 12.1). Using the runs test, we observe 38 runs and expect 35.9 runs, returning a p-value of 0.704, meaning we do not have significant evidence to reject our assumption of independence. Similar to the full AR(4) model, we see some fat-tailedness in our QQ-plot (Appx. Fig. 11.2), and when performing a SW test we return a p-value of 0.02988, providing significant evidence to reject our assumption of normality in the residuals.



(Top to Bottom) Fig. 12.1 , Fig. 12.2 , Fig. 12.3

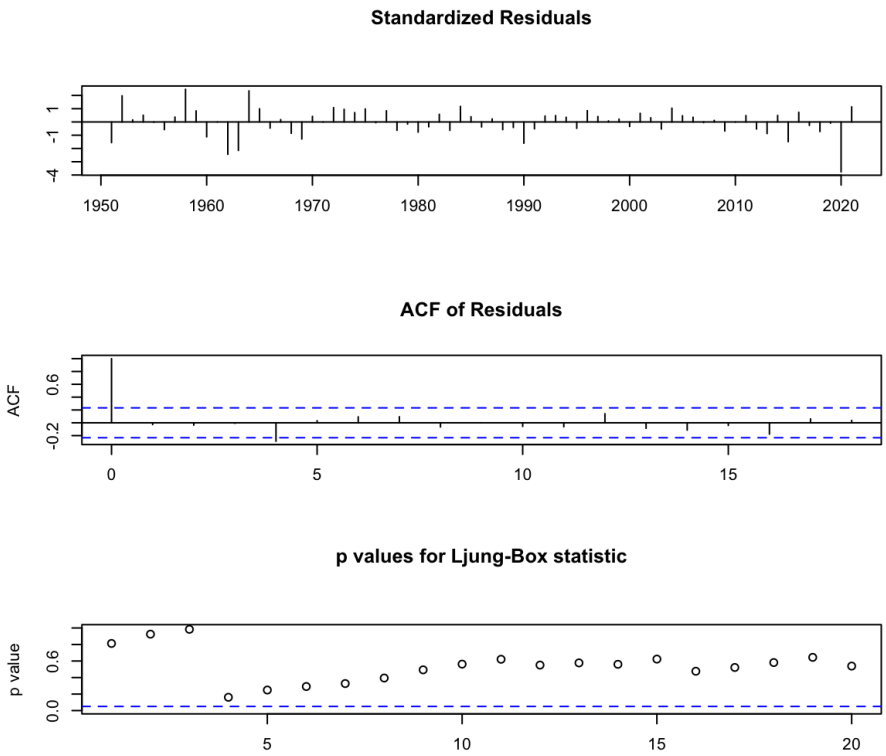
In our sample ACF (Fig. 12.2), we see no ACF values outside the bounds of white noise. When performing a Ljung-Box test (Fig. 12.3), we do not have any p-values less than 0.05 up to lag 20, providing significant evidence that our reduced AR(4) model is appropriate.

There is a possible overfitting issue where the ϕ4 component is the result of random error and we are not correct in assuming there is some correlation at lag 4. In this case, I fit an ARIMA(1,1,0) model on the yearly increase in Swiss life expectancy using the maximum likelihood method to estimate the following model:

$$(1+0.4663B)(1-B))(Y_t-0.2111) = e_t$$

Both parameters are statistically significant and this model has an AIC=5.66 and BIC=14.45. We see a similar plot of residuals as the ARIMA(4,1,0) model (Fig. 14.1) with 40 runs when we would expect 36.4 runs for independent data, resulting in the runs test failing to reject the independence of residuals. We see a QQplot (Appx. Fig. 13.2) with much fatter tails in the residuals and when we perform a SW test, we overwhelmingly reject the normality of residuals with a p-value of 0.0082.

We see that there is one ACF value at lag 4 for our residuals. We can say that this is the correlation that is being explained by the AR(4) reduced model. It is not impossible for one ACF value out of our 20 plotted residual ACF in a white noise process, so we will use the Ljung-Box test to determine the appropriateness of this model. Because no p-value resulting from the Ljung-Box test is greater than 0.05 (Fig. 14.3), we do not have significant evidence to say that the AR(1) process is inappropriate for the differences in Swiss life expectancy. We do not have a good explanation for a ϕ4 coefficient, supporting a parsimonious argument for this model.



(Top to Bottom) Fig. 14.1 , Fig. 14.2 , Fig. 14.3

Model Diagnostics

Table 1	**ARIMA(4,1,0)**	**ARIMA(4,1,0)***	**ARIMA(4,1,1)**	**ARIMA(1,1,0)**
Significant Parameters	ϕ*1,ϕ*4,μ*	ϕ*1,ϕ*4,μ*	ϕ*4,μ*	ϕ*1,μ*
(AIC, BIC)	(3.65,19.23)	(0.01,11.06)	(5.20,19.23)	(5.66,14.45)
Estimated σ_e^2	0.0529	0.0532	0.0525	0.0597
Runs p-value	0.704	0.704	0.704	0.464
SW p-value	0.047	0.030	0.047	0.008
Ljung-Box	Fail to Reject	Fail to Reject	Fail to Reject	Fail to Reject

* Reduced

In Table 1, we see all models have extremely similar estimates of σ_e^2, have independent residuals, do not have normally distributed residuals at alpha=.05, and fail to be statistically deemed inadequate. The two models that outperform are the reduced ARIMA(4,1,0) model and the ARIMA(1,1,0) model. The reduced ARIMA(4,1,0) model has the lowest AIC and BIC, and it performs much better on the SW test. Because both models' SW p-values are insignificant at an alpha = .05, we cannot put much weight on the difference in p-values, and this difference could even be explained by the lag 4 ACF value being the result of random error. Despite the increased AIC and BIC values in the ARIMA(4,1,0) model, the ARIMA(1,1,0) is more parsimonious and theoretically sound. We see that both models provide very similar predictions and prediction intervals (Fig. 15 & Appx. Fig. 16) with the ARIMA(4,1,0) model containing more noise in the prediction interval bounds. We will focus on the ARIMA(1,1,0) model in the next section because it is parsimonious without a significant decrease in performance from our reduced model while avoiding the issue of overfitting.

Forecasting

We have provisional data from 2022 and 2023 from OECD stating the life expectancy in Switzerland for 2022 is 83.5 years and for 2023 is 83.9 years[2]. We can compare these values with the predictions from our ARIMA(1,1,0) model. To calculate the predicted values, we use the minimum mean squared error (MMSE) forecast with standard errors for each prediction. Because we fit our models onto the difference in life expectancy data, we have to sum our forecasted values from our first forecasted change to the year we are forecasting to get our forecast for a given year. To calculate the prediction interval, we similarly have to sum the standard errors across all predictions that we sum. This can be succinctly written as follows {with the optional prediction interval term in curly brackets}:

$$Y^*(l) = Y_T + \sum_{i=1}^{l} \nabla Y_i^* \ \{ \pm 1.96 \sum_{i=1}^{l} SE(\nabla Y_i^*) \}$$

$$\nabla Y_t^* = 0.2111 - 0.4663(\nabla Y_{t-1} - 0.2111)$$

$Y^*(l)$ predicts the value of Y_{T+l} where T=the index of the last observation in $\{Y_t\}$ and ∇Y_i^* is the predicted value of our difference using the MMSE forecast. It is worth noting that we are assuming independence and additivity of standard error of residuals. If we fit an ARIMA(1,1,0) on our non-differenced data, we see narrower confidence intervals on our projections (Appx. Fig. 17), meaning I am not very confident in the prediction limits. Notably, we see this ARIMA(1,1,0) model fitted on the non-differenced data has no increasing trend and worse performance of predictions compared with our actual values versus our ARIMA(1,1,0) model fitted on the differences. This new ARIMA(1,1,0) model also has an insignificant AR coefficient, further supporting our ARIMA(1,1,0) model's fit. In Table 2, we see that the ARIMA(1,1,0) model provides an accurate prediction of Swiss life expectancy in 2022 and 2023 with our observed values well within the 95% prediction interval. This further supports the appropriateness of the ARIMA(1,1,0) model. We see extremely similar results from our reduced ARIMA(4,1,0) model (Appx. Fig. 16), further supporting the hypothesis that our $\phi 4$ term is the result of overfitting.

Table 2	**Actual**	**Lower CI**	**ARIMA(1,1,0) Pred**	**Upper CI**
2022	83.5	83.39	83.87	84.35
2023	83.9	83.23	84.23	85.24

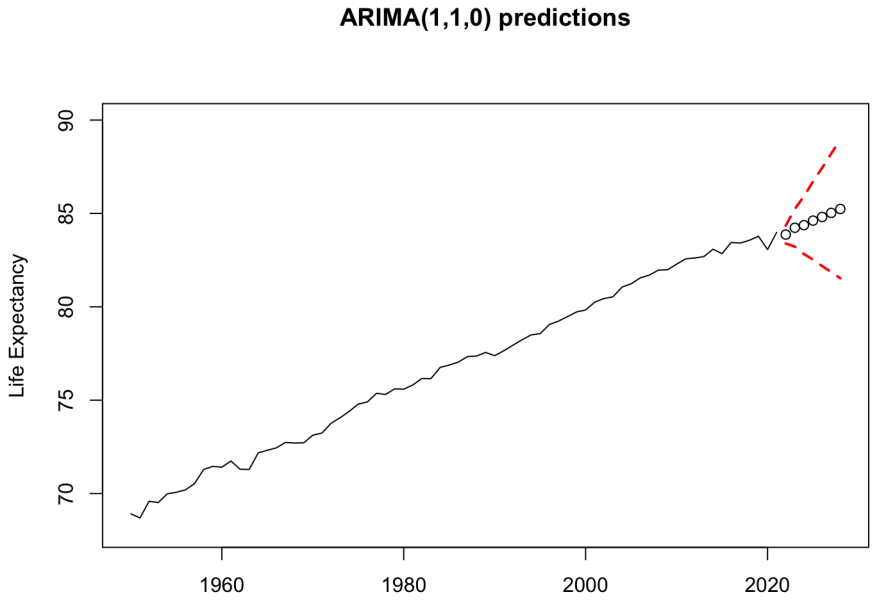


Fig. 15

We see our prediction interval plotted (Fig. 15) and see that we do not have confidence that life expectancy will increase in the next 7 years. We predict that the increase will continue, but are not confident that this increase is sustainable.

Discussion

Overall, the ARIMA(1,1,0) model is the most appropriate model for the life expectancy at birth in Switzerland. We have a significant issue with the normality of our residuals, which was slightly, but not significantly, improved when including an AR(4) coefficient. I assume this is the result of random error and including this AR(4) coefficient would be overfitting the model. The ARIMA(1,1,0) model provided the most accurate prediction of life expectancy in 2022 and 2023, but we are limited by the small sample size of validation data. We can explain the ARIMA(1,1,0) model as an average increase of 0.211 in life expectancy annually, where the difference between the previous year's increase in life expectancy and 0.211 is mildly inversely correlated with the next year's life increase in life expectancy. This makes sense because if we

have a medical breakthrough that significantly increases life expectancy in one year, it is less likely that we will have another significant increase in life expectancy the next year, therefore expecting a smaller growth in life expectancy the next year. This also accounts for the COVID-19 pandemic, where after the significant drop in life expectancy in 2020, we expect a greater-than-average increase in life expectancy next year, which is what we observed in 2021. Interestingly, with an ARIMA(1,1,0) model, the 2020 pandemic does not affect our life expectancy predictions for 2023 and beyond, which follows our experience in the world of COVID-19 becoming a smaller and smaller cause of death each year after 2021.

Plot Appendix

Fig. 1: `>plot ( life.ts,ylab = 'Life Expectancy (Yrs.)')`

Fig. 2: `>BoxCox.ar(life.ts)`

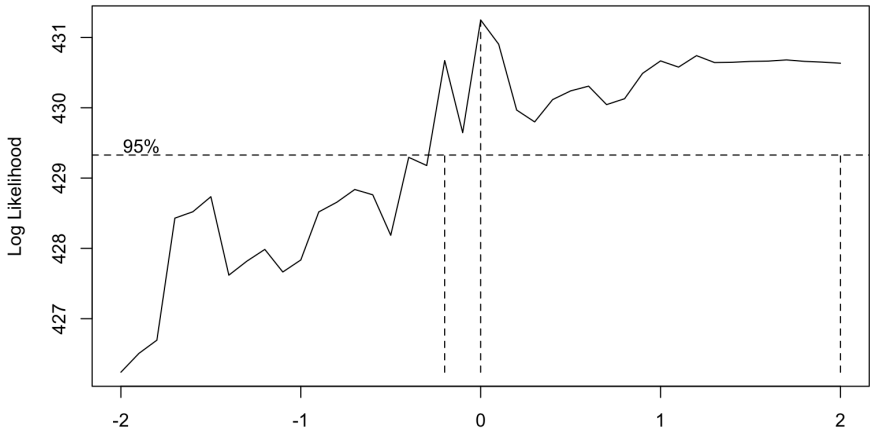


Fig. 2

Fig. 3: `>plot(life.diff,ylab='Difference in Life Expectancy (Yrs.)')`

Fig. 4: `>acf(life.diff) >pacf(life.diff)`

Fig. 5: `>eacf(life.diff)`

```
AR/MA
  0 1 2 3 4 5 6 7 8 9 10 11 12 13
0 x o o x o o o o o o o  o  o  o
1 o o o x o o o o o o o  o  o  o
2 x o o x o o o o o o o  o  o  o
3 x o x x o o o o o o o  o  o  o
4 x o x o o o o o o o o  o  o  o
5 o o x x o o o o o o o  o  o  o
6 o x o o o o o o o o o  o  o  o
7 x x o o x o o o o o o  o  o  o
```

Fig. 5

Fig. 6: `>res=armasubsets(y=life.diff,nar=7,nma=7,y.name='test', ar.method='ols') >plot(res)`

Fig. 7: `>plot(ar4.diff$residuals,ylab='AR(4) Residuals')`
`>qqnorm(rstandard(ar4.diff))`
`>qqline(rstandard(ar4.diff))`

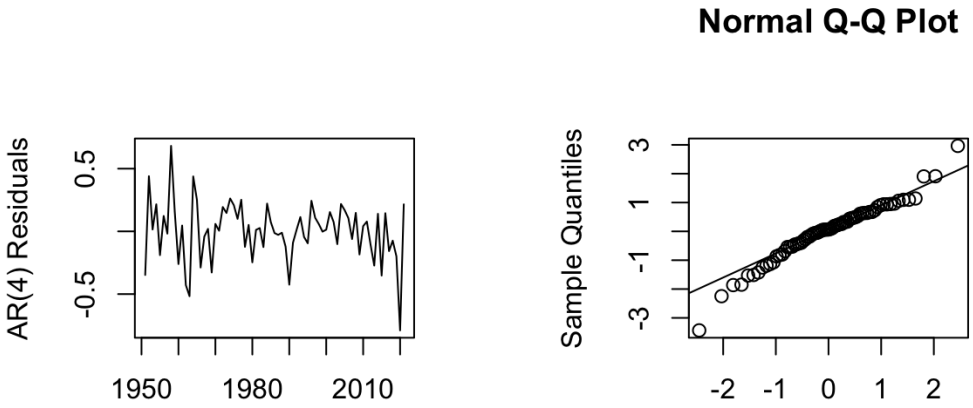


Fig. 7.1 , Fig 7.2

Fig. 8: `>tsdiag(ar4.diff,gof=20,omit.initial=F)`

Fig. 9: `>plot(arma41.diff$residuals,ylab='AR(4) Residuals')`

```
>qqnorm(rstandard(arma41.diff))
>qqline(rstandard(arma41.diff))
```

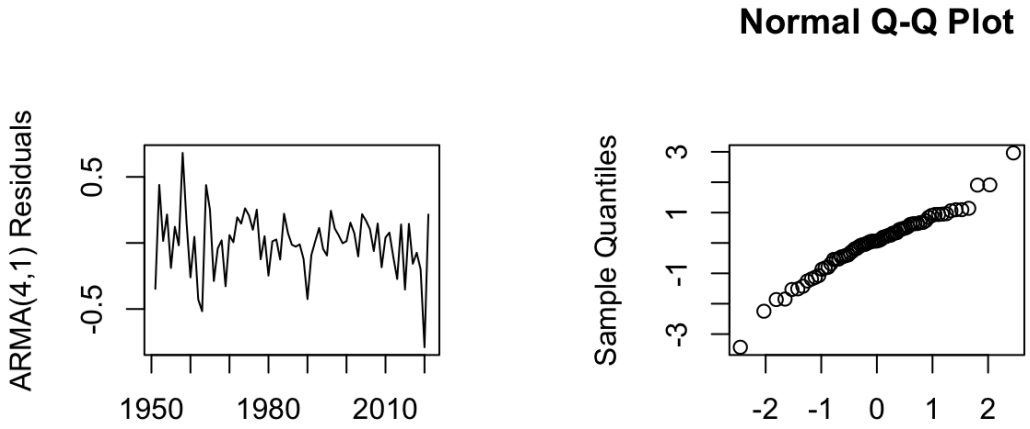


Fig. 9.1 , Fig. 9.2

Fig. 10: `>tsdiag(ar4.diff,gof=20,omit.initial=F)`

Fig. 11: `>plot(ar4.reduced$residuals,ylab='Reduced AR(4) Residuals')`

```
>qqnorm(rstandard(ar4.reduced))
>qqline(rstandard(ar4.reduced))
```

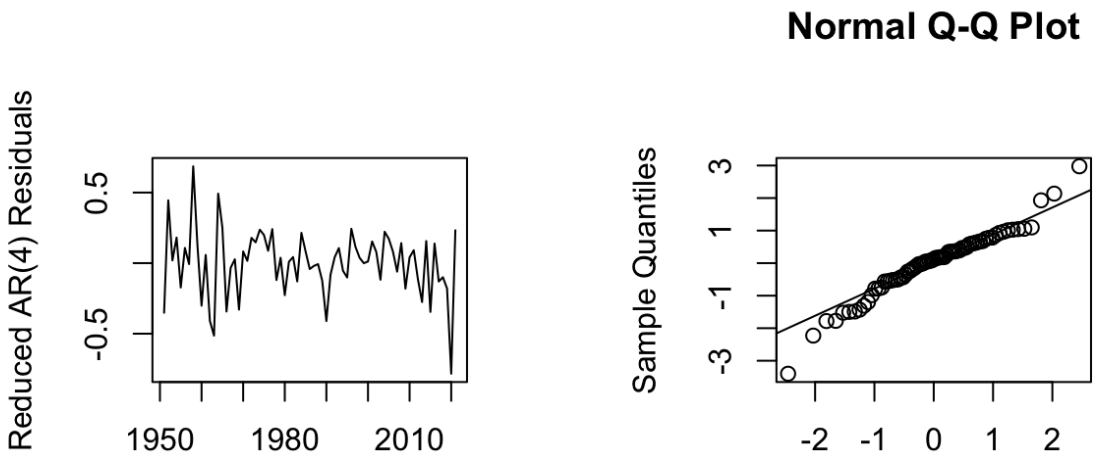


Fig. 11.1 , Fig. 11.2

Fig. 12: `>tsdiag(ar4.reduced,gof=20,omit.initial=F)`

Fig. 13: `>plot(ar1.diff$residuals,ylab='AR(1) Residuals')`

```
>qqnorm(rstandard(ar1.diff))
>qqline(rstandard(ar1.diff))
```

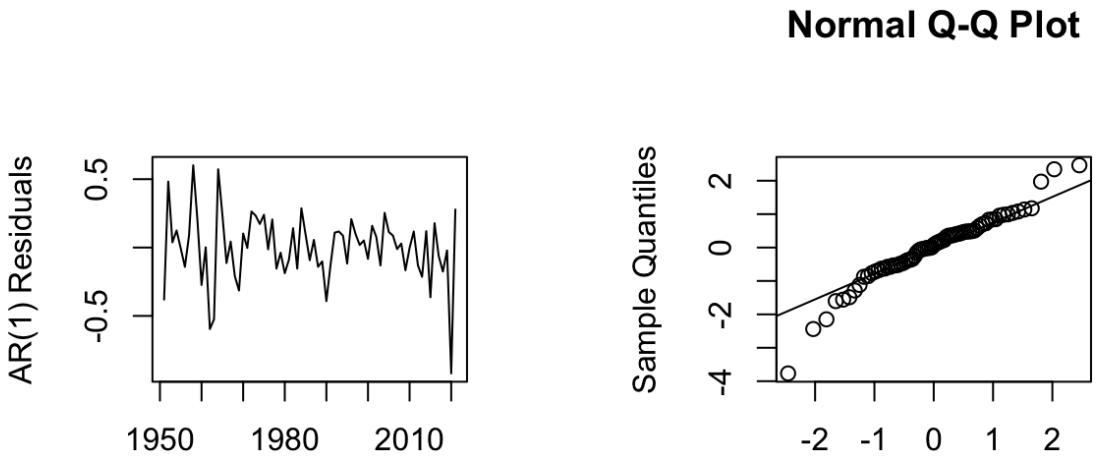


Fig 13.1 , Fig. 13.2

Fig. 14: `>tsdiag(ar1.diff,gof=20,omit.initial=F)`

Fig. 15: `>ar1.pred = predict(ar1.diff,n.ahead = 8)`

```
>plot(ts(c(life.ts[1:72]),start=1950,end=2021),ylab="Life
Expectancy",xlim=c(1950,2028),ylim=c(68,90),main="ARIMA(1,1,0)
predictions")
>ar1.real.pred = cumsum(c(life.ts[72],ar1.pred$pred[1:7]))
>points(c(2022:2028),ar1.real.pred[2:8],pch=1)
```

```
>lines(y=ar1.real.pred[2:8]+1.96*cumsum(ar1.pred$se[1:7]),x=c(20
22:2028),lwd=2,col="red",lty="dashed")
>lines(y=ar1.real.pred[2:8]-1.96*cumsum(ar1.pred$se[1:7]),x=c(20
22:2028),lwd=2,col="red",lty="dashed")
```

Fig. 16:

```
>ar4.pred = predict(ar4.reduced,n.ahead = 8)
>plot(ts(c(life.ts[1:72]),start=1950,end=2021),ylab="Life
Expectancy",xlim=c(1950,2028),ylim=c(68,90),main="ARIMA(4,1,0)
predictions")
>ar4.real.pred = cumsum(c(life.ts[72],ar4.pred$pred[1:7]))
>points(c(2022:2028),ar4.real.pred[2:8],pch=1)
>lines(y=ar4.real.pred[2:8]+1.96*cumsum(ar4.pred$se[1:7]),x=c(20
22:2028),lwd=2,col="red",lty="dashed")
>lines(y=ar4.real.pred[2:8]-1.96*cumsum(ar4.pred$se[1:7]),x=c(20
22:2028),lwd=2,col="red",lty="dashed")
```

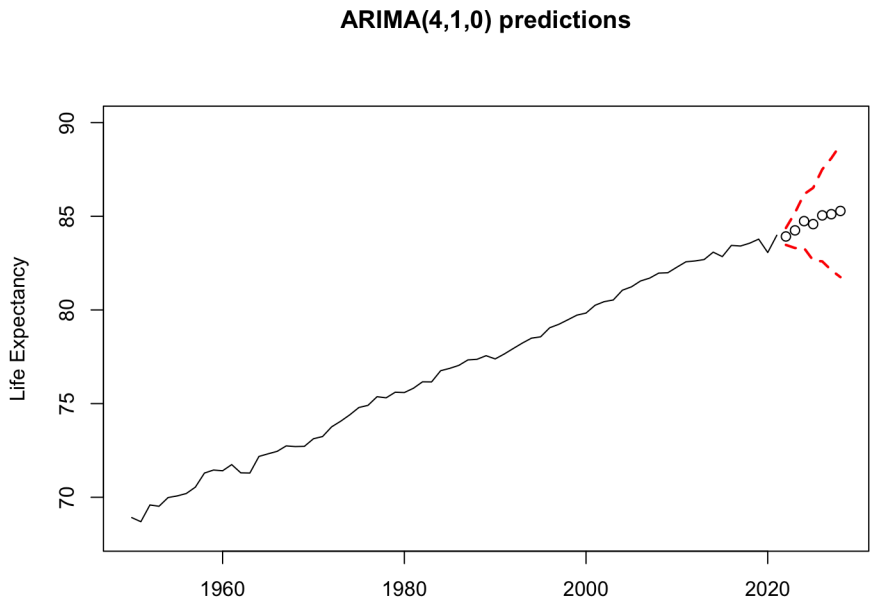


Fig. 16

Fig. 17:

```
>arima11.model = arima(life.ts,order=c(1,1,0))
>plot(arima11.model,main="ARIMA(1,1,0) Fitted On Non-Differenced
Data")
```

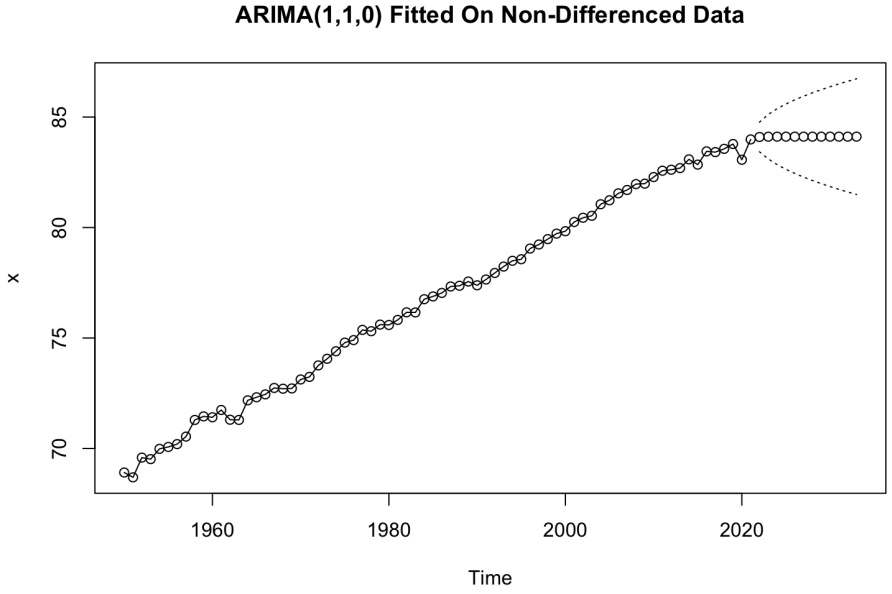


Fig. 17

Supplementary R-Output

```
> adf.test(life.ts)

     Augmented Dickey-Fuller Test

data:  life.ts
Dickey-Fuller = -1.9043, Lag order = 4, p-value = 0.6143
alternative hypothesis: stationary

> adf.test(life.diff)

     Augmented Dickey-Fuller Test

data:  life.diff
Dickey-Fuller = -4.9932, Lag order = 4, p-value = 0.01
alternative hypothesis: stationary
> ar4.diff

Call:
arima(x = life.diff, order = c(4, 0, 0), method = "ML")
```

```
Coefficients:
          ar1      ar2     ar3      ar4  intercept
      -0.4413  -0.0778  0.0035  -0.3520     0.2115
s.e.   0.1133   0.1408  0.1389   0.1311     0.0148

sigma^2 estimated as 0.05286:  log likelihood = 3.17,  aic = 3.65
> BIC(ar4.diff)
[1] 19.23074
> runs(rstandard(ar4.diff))
$pvalue
[1] 0.704

$observed.runs
[1] 38

$expected.runs
[1] 35.92958

$n1
[1] 31

$n2
[1] 40

$k
[1] 0

> shapiro.test(rstandard(ar4.diff))

     Shapiro-Wilk normality test

data:  rstandard(ar4.diff)
W = 0.96539, p-value = 0.04739
> ar5.diff

Call:
arima(x = life.diff, order = c(5, 0, 0), method = "ML")
```

```
Coefficients:
          ar1      ar2      ar3      ar4      ar5  intercept
      -0.4706  -0.0777  -0.0066  -0.3850  -0.1038     0.2118
s.e.   0.1194   0.1402   0.1391   0.1379   0.1389     0.0136

sigma^2 estimated as 0.05246:  log likelihood = 3.45,  aic = 5.1
> arma41.diff

Call:
arima(x = life.diff, order = c(4, 0, 1), method = "ML")

Coefficients:
          ar1     ar2     ar3      ar4      ma1  intercept
      -0.2486  0.0157  0.0113  -0.3804  -0.2149     0.2118
s.e.   0.2843  0.1865  0.1334   0.1305   0.2942     0.0136

sigma^2 estimated as 0.05252:  log likelihood = 3.4,  aic = 5.2
> BIC(ar4.diff)
[1] 19.23074
> runs(rstandard(ar4.diff))
$pvalue
[1] 0.704

$observed.runs
[1] 38

$expected.runs
[1] 35.92958

$n1
[1] 31

$n2
[1] 40

$k
[1] 0
```

```
> shapiro.test(rstandard(ar4.diff))

     Shapiro-Wilk normality test

data:  rstandard(ar4.diff)
W = 0.96539, p-value = 0.04739
> ar4.reduced

Call:
arima(x = life.diff, order = c(4, 0, 0), include.mean = TRUE, fixed =
c(NA,
    0, 0, NA, NA), method = "ML")

Coefficients:
          ar1  ar2  ar3      ar4  intercept
      -0.4205    0    0  -0.3567     0.2115
s.e.   0.1078    0    0   0.1231     0.0156

sigma^2 estimated as 0.05315:  log likelihood = 2.99,  aic = 0.01
> BIC(ar4.reduced)
[1] 11.06169
> runs(rstandard(ar4.reduced))
$pvalue
[1] 0.704

$observed.runs
[1] 38

$expected.runs
[1] 35.92958

$n1
[1] 31

$n2
[1] 40
```

```
$k
[1] 0

> shapiro.test(rstandard(ar4.reduced))

     Shapiro-Wilk normality test

data:  rstandard(ar4.reduced)
W = 0.96186, p-value = 0.02988
> ar1.diff

Call:
arima(x = life.diff, order = c(1, 0, 0), method = "ML")

Coefficients:
          ar1  intercept
      -0.4663     0.2111
s.e.   0.1128     0.0199

sigma^2 estimated as 0.05973:  log likelihood = -0.83,  aic = 5.66
> BIC(ar1.diff)
[1] 14.44561
> runs(rstandard(ar1.diff))
$pvalue
[1] 0.464

$observed.runs
[1] 40

$expected.runs
[1] 36.43662

$n1
[1] 34

$n2
[1] 37
```

```
$k
[1] 0

> shapiro.test(rstandard(ar1.diff))

     Shapiro-Wilk normality test

data:  rstandard(ar1.diff)
W = 0.95164, p-value = 0.008216
> ar4.reduced.pred.interval
     lower    upper predicted actual
1 83.47117 84.37488  83.92302   83.5
2 83.30586 85.18992  84.24789   83.9
3 83.30290 86.18024  84.74157     NA
4 82.64522 86.51812  84.58167     NA
5 82.59219 87.50317  85.04768     NA
6 82.12129 88.10222  85.11175     NA
7 81.75278 88.81646  85.28462     NA
> ar1.pred.interval
     lower    upper predicted actual
1 83.38855 84.34656  83.86756   83.5
2 83.22531 85.24037  84.23284   83.9
3 82.82575 85.91821  84.37198     NA
4 82.52946 86.70369  84.61658     NA
5 82.18352 87.44047  84.81200     NA
6 81.86042 88.20028  85.03035     NA
7 81.52659 88.94943  85.23801     NA

> arima11.pred = predict(arima11.model,n.ahead=7)
>newar1.pred.interval=data.frame("lower"=c(arima11.pred$pred-1.96*cums
um(arima11.pred$se)),"upper"=c(arima11.pred$pred+1.96*cumsum(arima11.p
red$se[1:7])))
> newar1.pred.interval <-
cbind(newar1.pred.interval,data.frame('predicted'=arima11.pred$pred))
> newar1.pred.interval <-
cbind(newar1.pred.interval,data.frame('actual'=c(83.5,83.9,NA,NA,NA,NA
,NA)))
> newar1.pred.interval
     lower    upper predicted actual
```

```
1 83.42528 84.77021  84.09774   83.5
2 82.42881 85.79324  84.11102   83.9
3 81.16482 87.06041  84.11262     NA
4 79.68665 88.53897  84.11281     NA
5 78.02244 90.20322  84.11283     NA
6 76.19111 92.03456  84.11284     NA
7 74.20670 94.01897  84.11284     NA
```

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