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**Non-Linearities in Monthly Measles
data for Italy**

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NON-LINEARITIES IN MONTHLY MEASLES DATA FOR ITALY

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1. INTRODUCTION

The study of infective diseases, such as measles, and their spread over time necessitates a combined effort on the part of a number of disciplines such as mathematical demography, epidemiology, zoology and statistics. Much attention has been dedicated to the understanding of dynamics of epidemic outbursts and a great part of the research has resulted in the definition of causal compartmental mathematical models (see Anderson and May (1991), Finkenstadt and Grenfell (2000), Bjornstad et al. (2002), Grenfell et al. (2002)) which incorporate interactions between the number of reported cases and variables such as births, age structures, residential populations and population densities. Pure time series modelling has generally been discarded as being inadequate for describing the phenomena. In this paper we take the view that time series analysis, through an understanding of how the phenomena has changed over time, can provide important information that could be taken into consideration by the model builder.

Particularly important to the model builder is the type of model that he should consider; i. e. should it be a linear or nonlinear model, and in case of the latter what type of nonlinearity should be modelled. Time series of the number of measles cases reported on a regional basis in Italy during a pre-vaccination period are characterised by changes that are not symmetric over the year; in fact, whereas a well defined minimum, in august, is rapidly reached, the maximum is often spread over two or three months between January and March. Such trajectories are often indicators of the presence of nonlinearities.

This paper attempts to investigate the presence of specific types of non-linearities in time series on the number of measles cases reported each month for each Region during the pre-vaccination period 1949 – 1976. A possible explanation for this non-linearity is advanced. The effect of compulsory vaccination is evaluated by carrying out the same analysis on a post-vaccine data set for the period 1977-1996.

The data analysed are published by the Istituto Nazionale di Statistica (ISTAT) of Italy. Each regional series was log transformed (a value of 1 was added to all the data before the transformation), detrended, using a function in time, and deseasonalised, using monthly dummies, before being further analysed. The residual pre-whitened series is very much dominated by a cycle due to the so-called inter-epidemic period (see Cleur (2004)) and hence the tests for linearity are, for the most part, evaluating the behaviour of this component.

The paper proceeds with testing for linearity against simple nonlinear alternatives which includes autoregressive models with ARCH (autoregressive conditional heteroschedastic) errors and bilinear models of orders one and two. When

the null hypothesis of linearity is rejected in favour of an alternative non-linear model, this non-linear model is estimated and the estimates are reported. Finally, on the basis of an observation made in Cleur(2004) regarding the possibility that the dynamics of the model may depend on the phase (ascending or descending) in which the observed phenomena is in, a self-exiting threshold autoregressive model (SETAR) is proposed. The results support this conjecture.

2. TESTING FOR LINEARITY

2.1 METHODS

A number of tests are available in the literature (see Priestley (1981), Barnett (1996)) useful for investigating the presence of non-linearities in the mean and second moment of univariate time series. The following tests are applied in this paper: Ramsey (1969) for testing against non-linearity in the mean, McLeod-Li (1983) for testing against second moment non-linearity, an LM (Lagrange multiplier) test for testing against ARCH alternatives, and a LM test for testing against bi-linear alternatives. With the LM tests, in case the null hypothesis of linearity is rejected the alternative ARCH or bi-linear model is estimated.

A brief description of the estimation procedures and tests applied follows.

Let Y_t , a column vector, indicate the series for a given Region, X_t a matrix of regressors the columns of which are given by a column of ones and by the vectors of lagged values Y_{t-j} , $j = 1, \dots, p$, and β the vector of autoregressive coefficients. The value of p was determined by applying the AIC statistic and is given in the first column of Tables 1 and 2.

The Ramsey Test

Let $\hat{Y}_t = X_t b$, where b is an estimate of β , and $e_t = \hat{Y}_t - X_t b$, the column vector of estimated residuals from an AR(p).

Regress Y_t on X_t , \hat{Y}_t^2 and \hat{Y}_t^3 . Let u_t be the estimated residuals from this regression.

Calculate the statistic

$$R = \frac{(e'e - uu)/2}{uu/(n-2)}$$

R has an $F(2, n-2)$ distribution. Higher powers up to k of \hat{Y}_t could have been used in which case the denominator 2 in the numerator would be $(k-1)$ and we would have an F distribution with $(k-1)$ and $(n-k)$ degrees of freedom.

The alternative in the Ramsey test is a departure from linearity in mean.

The McLeod-Li Test

Let r_j be the autocorrelation at lag j calculated from the squares of the estimated residuals e_t , i.e. e_t^2 . Then the statistic

$$M = n(n+2) \sum_{j=1}^m [r_j]^2 / (n-j)$$

has a $\chi^2(m)$ distribution.

The McLeod-Li test is based on the result that given an independent and identically distributed linear process, the squares of its autocorrelation function should be identical to the autocorrelation function of its squares. This test which tests against non-linearity in the second moment, may also be used as a test for ARCH residuals.

LM-ARCH Test

An autoregressive process Y_t , of order p , with conditional heteroschedasticity in the errors of order m is written $ARCH(m)$ and is defined as

$$Y_t = c + \sum_{j=1}^p \phi_j Y_{t-j} + \varepsilon_t, \text{ where } \varepsilon_t = \sqrt{h_t} v_t \text{ and } h_t = \xi + \sum_{j=1}^m \alpha_j \varepsilon_{t-j}^2$$

Estimate an $AR(m)$ model, with the constant, for the squares of the estimated residuals, i.e. for e_t^2 . Then the statistic nR^2 has a $\chi^2(m)$ distribution, where R^2 is the coefficient of determination for the $AR(m)$ model. We set $m = 1$. If the test is significant, an $ARCH(1)$ model is estimated.

LM-Bilinear Test

A Bilinear model may be written as

$$Y_t = c + \sum_{j=1}^p \phi_j Y_{t-j} + \sum_{i=1}^m \sum_{j=1}^k c_{ij} Y_{t-i} \varepsilon_{t-j} + \varepsilon_t$$

Let $SS0$ indicate the residual sum of squares from an $AR(p)$ model, with a constant, for the original series Y_t .

Regress e_t , the residuals from the $AR(p)$ model, on Y_{t-j} , $j = 1, \dots, p$, as well as on the cross-products $e_{t-j} Y_{t-i}$ for $i = 1, \dots, m$ and $j = 1, \dots, k$. Let $SS1$ indicate the residual sum of squares from this regression. Then the statistic

$$BL = n (SS0 - SS1) / SS0$$

has a $\chi^2(mk)$ distribution.

The orders p , r and s could be found using the AIC statistic. In this paper, two bi-linear alternatives with $r = 1$, $s = 1$ and with $r = 2$, $s = 2$ (indicated, respectively by $BL(p, 1, 1)$ and $BL(p, 2, 2)$) are imposed and in case the test is significant, the alternative bi-linear model is estimated.

For the estimation of an ARCH errors model see Hamilton (1994).

For the estimation of a Bilinear model see Priestley (1988) (Non-linear and non-stationary time series analysis, Academic Press, London) . In Tables 5 and 6 the least squares estimates are reported for which the repeated residuals estimates were used as starting values.

2.2 RESULTS

The agreement between the McLeod-Lee test and the LM-ARCH test suggest that in eight of the Regions there is non-linearity in the residual variance and hence an ARCH-type (GARCH models often provide better adaptations) model might be most suitable in these cases. The order, p , of the autoregressive part of the model does not exceed 2 so that the overall model with ARCH(1) errors remains very manageable.

In only two Regions, and both in the pre-vaccination period, was a bi-linear model chosen without an ARCH errors model being chosen as well. It is known that low order ARCH and Bilinear models are often confounded and this might be the case for the Regions of Abruzzo, Toscana and Trentino for which a Bilinear model of order 1 or 2 was chosen along with an ARCH(1) alternative.

The null hypothesis of linearity for the post-vaccination period is rejected in only 4 of the Regions, the alternative being an ARCH errors model.

Overall, these results suggest a tangible ARCH errors alternative to a linear model in the explanation of the univariate regional time series.

3. THRESHOLD AUTOREGRESSIVE MODELS

In Cleur (2004), it was observed that when the cycle due to the inter-epidemic period for measles reached a low, it took some time for this component to return to its usual pattern. In other words, a sort of conditional heteroschedasticity was observed which could be at the origin of the nonlinearities discovered above. The probable dependence of the heteroschedasticity from the level reached has led us to propose threshold models as a tool of analysis.

Threshold models (see Tong and Lim (1980), Priestley (1988) for an introduction) may be thought of as a desegregation of a nonlinear process into a number of piece-wise or local linear processes. In this Section we investigate the possibility of analysing the dynamics of the spread of measles in the 20 Italian Regions through threshold autoregressive time series models. Since the piece-wise models are autoregressive models, these can be easily transformed to the frequency domain where

the autoregressive (or gain) spectrum can be calculated (see Hamilton (1994), Priestley (1981)). Briefly, it is known that for the autoregressive model of order p

$$X_t = \mu + \sum_{j=1}^p \phi_j X_{t-j} + \varepsilon_t,$$

we can define the autoregressive spectrum (see Priestley (1981))

$$f(\lambda) = \frac{\sigma_\varepsilon^2}{2\pi} \frac{1}{|1 - \phi_1 \exp(i\lambda) - \dots - \phi_p \exp(ip\lambda)|^2}$$

Spectral analysis, as we know, is useful for identifying the predominant frequency components, often corresponding to cyclical behaviour, present in the series. In the present context, differences between the spectra will indicate differences in the properties of the series at different levels reached in a recent past.

The following self exciting threshold autoregressive (SETAR) model is estimated.

$$X_t = c_1 + \sum_{j=1}^6 \alpha_j X_{t-j} + \varepsilon_{1t} \quad \text{if } 0 \leq X_{t-d} < T \quad (1a)$$

$$X_t = c_2 + \sum_{j=1}^6 \beta_j X_{t-j} + \varepsilon_{2t} \quad \text{if } X_{t-d} \geq T \quad (1b)$$

$$X_t = c_3 + \sum_{j=1}^6 \gamma_j X_{t-j} + \varepsilon_{3t} \quad \text{if } X_{t-d} < 0 \quad (1c)$$

The motivation for this model is as follows: Given that the series analysed are the residuals from a deterministic trend and seasonal component, negative residuals (differences) will correspond in general to low values of measles notification whilst positive and in particular large positive residuals (differences) will correspond in general to periods of epidemic outbursts, and hence it is natural that in studying the dynamics of the spread of the disease we will be mainly interested in the positive residuals. For these positive residuals we define a threshold T which, along with the value of d and the estimates of the parameters, are found using the AIC statistic as in Tong and Lim (1980), but with the following differences: instead of estimating the full autoregressive model with lag 6, the best sub-set autoregressive model with maximum lag 6 is estimated, and the optimum values of T and d are found simultaneously by minimising the AIC statistic, using a grid search method, over a two dimensional grid of values.

Results are presented here only for the Regions of Abruzzo and Toscana during the pre-vaccination period, i.e. the Regions for which the hypothesis of linearity was most often rejected. The results for the remaining Regions are omitted in order to avoid being repetitive. The estimates of the SETAR models are given in Tables 7a and 7b. In Figure 1 we have the autoregressive spectrum for the three models (1a) – (1c). The three spectra for each Region are inserted in the same graph with frequency along the

abscissa. Each spectrum is plotted only in a frequency range from zero to one since beyond this range it is very near zero.

The R-squares are not high although a number of parameters are significant including that at lag one. There are differences between the three subset models selected within each Region as well as differences between Regions. However, such differences are difficult to comment on.

If we take the Fourier transform of each piece-wise autoregressive model, thereby transforming it to the frequency domain, and calculate the autoregressive spectrum, we have very marked differences for the spectra within each Region as well as between Regions. Thus for Abruzzo we observe that if the series at a lag of three months, i. e. X_{t-3} , remained in the band of values (0.0, 0.6), the response at time t is characterized by a cyclical behaviour with periodicity of approximately 9 months (a sharp peak at frequency 0.68). If, on the other hand, the series at time $t-3$ crossed the threshold value of 0.6, the effect at time t was to prolong the ascending and descending phases thereby giving rise to a cycle with periodicity of just over 22 months (the minor peak in the spectrum at frequency 0.28). The three spectra for Abruzzo have different forms thereby suggesting different dynamic characteristics in the series in function of the level reached at a time lag of 3 months.

For Toscana instead, if at lag $d=3$ the series remained below the value of 0.4, low frequency components dominate the dynamic properties at time t , but if it had crossed the value of 0.4 at time $t-3$, the response at time t was cyclical with a periodicity of approximately 18 months (a peak at frequency 0.34). Even for this Region the three spectra are very different in form suggesting again distinct dynamic properties.

The above analysis was carried out on the data for the remaining 18 Regions and the results obtained are in line with those reported for the Regions of Abruzzo and Toscana. They are available on the web site : www.statmat.unipi.it/cleur.

4. CONCLUSIONS

This paper has examined the presence of nonlinearities in the monthly data of reported measles cases for the Italian Regions. Nonlinearities, for the great part autoregressive processes with ARCH errors was found in half of the pre vaccination data, but the number drastically decreased for the post vaccination period. SETAR models, which have occasionally been used for describing nonlinearities in variance, were found to provide a discrete fit to the data and their spectral properties indicate notable differences in the dynamic properties of the data at different levels reached in a recent past. It is thought that these differences might have been the reason for the nonlinearities present in the series analysed.

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APPENDIX

TABLE 1

Tests for Non-Linearity

Pre Vaccination period 1949-76. Significant Tests, at 1% level, are indicated with a black dot (•)

	Order AR(p)	Ramsey	McLeod-Li	ARCH(1)	BL(1,1)	BL(2,2)
Abruzzo	1		•	•	•	
Basilicata	1					
Calabria	1					
Campania	4					
Emil-Rom.	1				•	
Friuli	4					
Lazio	1			•		
Liguria	2					
Lombardia	3					
Marche	1		•	•		
Molise	1					
Piemonte	2					
Puglia	2		•	•		
Sardegna	2		•	•		
Sicilia	1					•
Toscana	1	•	•	•	•	•
Trentino	1		•	•		•
Umbria	1					
Val d'Aosta	1					
Veneto	1		•	•		

TABLE 2. Tests for Non-Linearity

Post Vaccination period 1977-96. Significant Tests, at 1% level, are indicated with a black dot (•)

	Order AR(p)	Ramsey	McLeod-Li	ARCH	BL(1,1)	BL(2,2)
Abruzzo	3	•	•	•		•
Basilicata	4					
Calabria	2					
Campania	3					
Emil-Rom.	1					
Friuli	1		•	•		
Lazio	2			•		
Liguria	1					
Lombardia	1					
Marche	1					
Molise	2					
Piemonte	1					
Puglia	1					
Sardegna	1					
Sicilia	6		•	•		
Toscana	1					
Trentino	1					
Umbria	1					
Val d'Aosta	1					
Veneto	1					

TABLE 3. Estimates of ARCH(1) models passing the LM-ARCH test
Pre-vaccination period 1949-76

Region	c	ϕ_1	ϕ_2	ξ	α_1
Abruzzo	0.0094	0.8485	-	0.2397	0.2528
Lazio	-0.0144	0.8335	-	0.0867	0.4196
Marche	-0.0106	0.8498	-	0.2597	0.1145
Puglia	-0.0094	0.6538	0.0805	0.1402	0.1927
Sardegna	-0.0343	0.7492	0.1680	0.3038	0.3549
Toscana	0.0173	0.8244	-	0.1216	0.2133
Trentino	0.0100	0.7696	-	0.2437	0.1343
Veneto	0.0000	0.8269	-	0.0936	0.1155

TABLE 4. Estimates of ARCH(1) models passing the LM-ARCH test
Post-vaccination period 1977-96

Region	c	ϕ_1	ϕ_2	ϕ_3	ϕ_4	ϕ_5	ϕ_6	ξ	α_1
Abruzzo	-0.0104	0.7568	-0.1474	-	-	-	-	0.4506	0.1727
Friuli	0.0132	0.8277	-	-	-	-	-	0.2745	0.2360
Lazio	0.0222	0.6753	0.1760	-	-	-	-	0.1944	0.2181
Sicilia	0.0059	0.8410	0.0313	0.0240	0.1315	0.0178	-0.1851	0.3078	0.2722

TABLE 5. Estimates of Bilinear model $Y_t = c + \sum_{j=1}^p \phi_j Y_{t-j} + \sum_{i=1}^m \sum_{j=1}^k c_{ij} Y_{t-i} \varepsilon_{t-j} + \varepsilon_t$

Pre-vaccination period 1949 - 76

Region	c	ϕ_1	c_{11}	c_{12}	c_{21}	c_{22}
Abruzzo	-0.0294	0.8435	0.1103	-	-	-
Emilia-Rom	0.0161	0.8486	-0.1674	-	-	-
Sicilia	-0.0100	0.8229	-0.1220	0.0649	0.4201	-0.3424
Toscana	0.0306	0.7878	0.1322	0.3251	-0.4375	0.1985
Trentino	0.0325	0.7638	0.1730	0.2180	0.0278	-0.1561

TABLE 6. Estimates of Bilinear model $Y_t = c + \sum_{j=1}^p \phi_j Y_{t-j} + \sum_{i=1}^m \sum_{j=1}^k c_{ij} Y_{t-i} \varepsilon_{t-j} + \varepsilon_t$

Post-vaccination period 1977 - 96

Region	c	ϕ_1	ϕ_2	ϕ_3	c_{11}	c_{12}
Abruzzo	-0.0266	0.6872	0.2069	-0.1466	0.1009	0.0232
	c_{21}	c_{22}				
	0.1391	-0.0905				

Table 7a. Abruzzo : Estimates of SETAR model (1a)-(1c)

(1a) $0 < X_{t-d} < T$ (1b) $X_{t-d} > T$ (1c) $X_{t-d} < 0$. $T = 0.6$, $d = 3$

N = number of data points used in estimation of the model in column 1

	N	μ	ϕ_1	ϕ_2	ϕ_3	ϕ_4	ϕ_5	ϕ_6	R^2
(1a)	79	0.1315	0.7975	0.1927	-0.6958	-	-	0.0456	0.4793
(1b)	89	0.0152	0.8873	-	-	-	0.1326	-0.2912	0.6577
(1c)	153	0.0016	0.7005	-	-	-	0.0070	-	0.6168

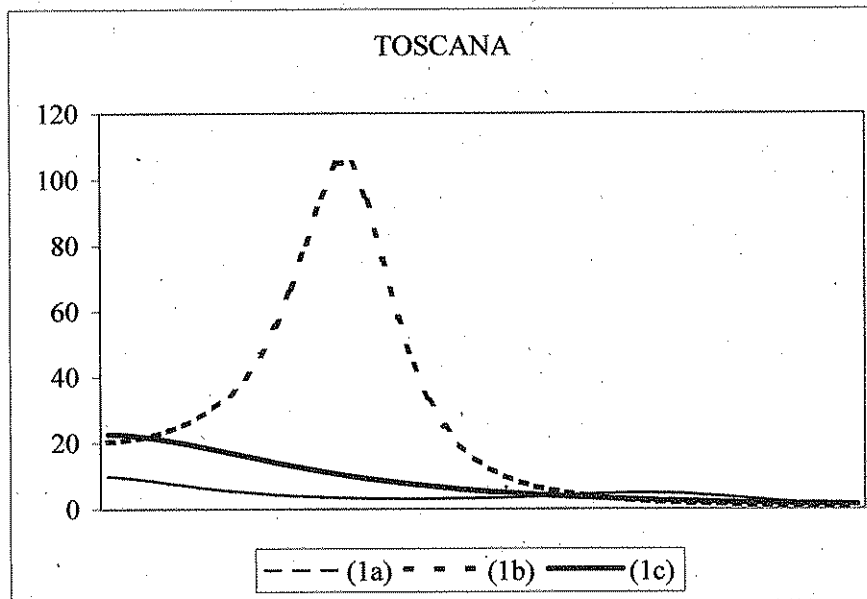
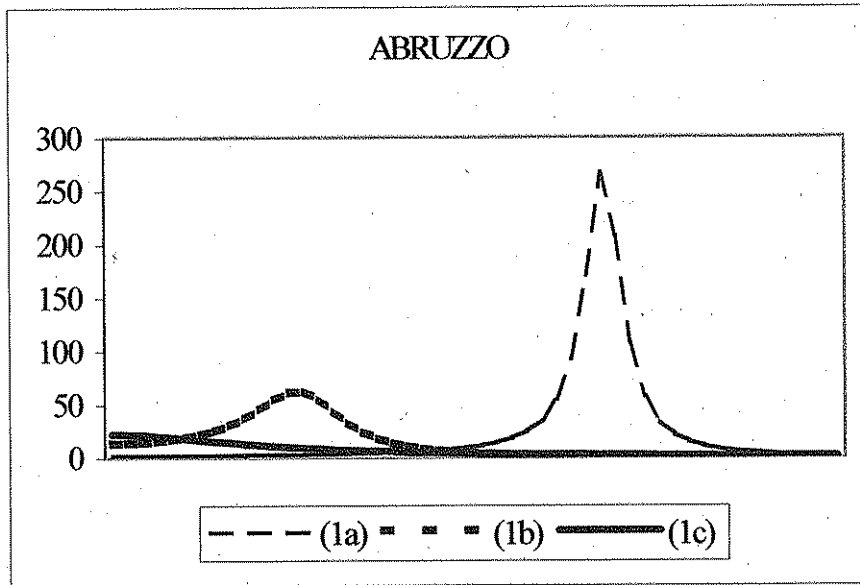
Table 7b. Toscana : Estimates of SETAR model (1a)-(1c)

(1a) $0 < X_{t-d} < T$ (1b) $X_{t-d} > T$ (1c) $X_{t-d} < 0$. $T = 0.4$, $d = 3$

N = number of data points used in estimation of model in column 1

	N	μ	ϕ_1	ϕ_2	ϕ_3	ϕ_4	ϕ_5	ϕ_6	R^2
(1a)	81	0.0948	0.3595	0.7640	-0.6361	-	-	0.1977	0.5040
(1b)	92	0.0219	1.0599	-	-	-0.2827	-	-	0.7011
(1c)	148	0.0105	0.8653	-	-0.0744	-	-	-	0.6760

FIGURE 1. Autoregressive spectra for threshold model (1a) – (1c) calculated for the Regions of Abruzzo and Toscana.



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