RESEARCH REPORT

DISCUSSION OF 'AN ANALYSIS OF GLOBAL WARMING IN THE ALPINE REGION BASED ON NONLINEAR NONSTATIONARY TIME SERIES MODELS' BY BATTAGLIA AND PROTOPAPA

by

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Discussion of 'An analysis of global warming in the Alpine region based on nonlinear nonstationary time series models' by Battaglia and Protopapa

I would like to congratulate warmly Professors Battaglia and Protopapa on their most timely and stimulating paper.

Before I turn to the statistical aspects of the paper, please allow me to play the devil's advocate and pose some deliberately provocative scientific questions. As everybody knows, global warming is the hottest topic in town, attracting some of the best brains in the scientific world. It is universally accepted that there is undisputed evidence of large increase in the mean temperature globally over the past 200 years or so. However, is the claim that the increase is 'very likely due to human activities' really rock solid? Does it not require further evidence before non-human factors, e.g. natural variability of earth's climate, can be ruled out? Of course, if we had a time series of global temperature stretching back to the appearance of homo sapiens on earth or perhaps even earlier, as well as an equally long time series of CO_2 emission, then the claim could be tested more readily and the conclusion more definitive. In the absence of these (-I could be wrong about the absence), we can try and identify some suitable proxies. Now, can the authors tell us if proxies of the length mentioned above are available? I have tried to no avail.

Turning to the statistical aspects of the paper, I find many interesting ideas in the paper. However, due to limitation of space, I shall focus on just some of them as follows.

(1) *The Threshold Nonstationary-Nonlinear Time Series Model*:

We clearly have here a strong candidate for serious consideration of inclusion in the armory of nonstationary-nonlinear modelling. The idea of piecewise linearity is now well accepted since Tong and Lim (1980), although the widespread acceptance took much longer than I had anticipated. As for non-stationarity, the idea of sectional nonstationarity can be traced at least as far back as Ozaki and Tong (1975), which was further developed by Akaike and Kitagawa (1978). Sadly, the idea still seems to be under-exploited in the literature. Now, by a natural marriage of the two ideas, we have a new baby, namely the threshold nonstationary-nonlinear time series model. The baby was conceived at no later than Tong (1983), who reported, on page 273, the fitting of just one such model to the famous Nicholson's bi-daily counts of (living) blowflies kept inside a cage and subject to protein limitation. The model consists of a 2-regime self-excited threshold AR (or SETAR) model to

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the first 126 bi-daily observations and a linear AR model to the later 82 bi-daily observations. The threshold model admits a limit cycle, which accounts for the population cycles of the blowflies under protein limitation, while the switch to a linear AR model in the later period is consistent with the ento-mological theory of selection of autogenous fly after approximately one year of captivity so that less or no protein is required for egg production, thereby leading to the loss of cycle-generating mechanism with many eggs unhatched.

It gives me real pleasure to see that the baby is beginning to grow into a powerful man (-being Chinese, I ignore gender impedimenta) under the care of our authors, who have provided him with a genetic algorithm.

(2) *Nonstationarity vs Nonlinearity*:

I agree with the implicit premise of the authors that the real world is nonsta-tionary and nonlinear. However, to model these two features simultaneously, one of the first fundamental challenges is this: Can we always tell if a given single realization comes from a stationary nonlinear time series model or from a nonstationary linear time series model? A simple example will illuminate the situation. Let ε_t be iid $N(0, 1)$ random variables and t_0 a positive integer. First, consider Model (NL):

$$X_t = \varepsilon_t, \text{if } X_{t-1} \leq 3; 10 + \varepsilon_t, \text{if } X_{t-1} > 3.$$

Model (NL) is clearly nonlinear and stationary. Next, consider Model (NS):

$$X_t = \varepsilon_t, \text{if } t \leq t_0; 10 + \varepsilon_t, \text{if } t > t_0.$$

Model (NS) is clearly linear but nonstationary. In practice, given a single realization, it is almost impossible to tell from which of the above two models it comes. To illustrate the point, Professor Kung-Sik Chan has kindly simu-lated Model (NL) as shown in the figure. He has also provided R codes, which is appended below. For detail of the TSA library, see Cryer and Chan (2008).

R codes:

```
library(TSA)
set.seed(53975)
X=tar.sim(n=500, ntransient=0, Phi1=c(0,0), Phi2=c(10,0), thd=3,
d=1,p=1,sigma1=1,sigma2=1)
plot(ts(X$y),ylab='X',xlab='t')
abline(h=3,col='red')
```
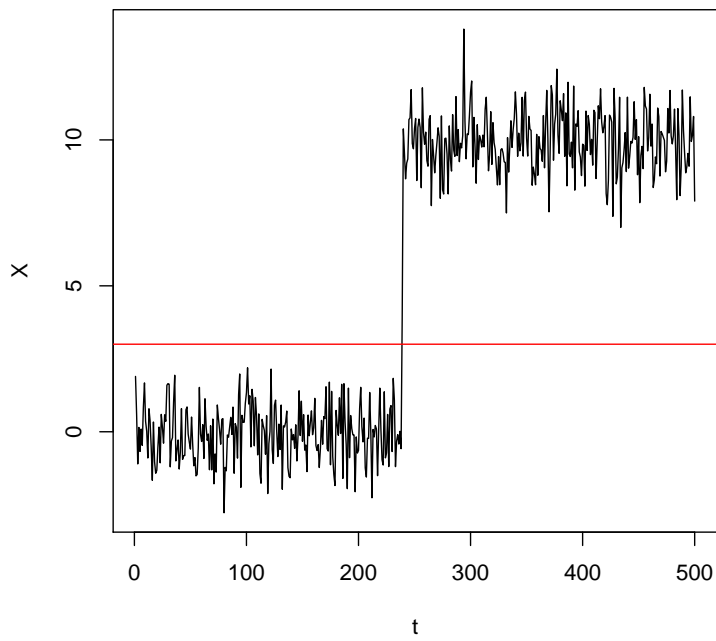
Figure 1: A realization from model (NL); the red horizontal line shows the threshold value.

The level shift models can easily be extended to cover changing trends by simply noting that a linear trend becomes a level upon first differencing. The above discussion suggests that some caution is needed when drawing conclusions such as '...the genetic algorithm never selected a nonlinear structure.....'

(3) *Model Complexity*

The discussion in (2) has another ramification. Specifically, it raises the question of how to count the dimension of the parameter space. Note that in most order determination criteria (e.g. AIC, BIC, etc.), the P of equation (8) is the number of *independently adjusted* unknown parameters. The key words are 'independently adjusted'. The discussion in (2) shows that the counting is not as straightforward as it might appear at first sight. Another difficulty in counting P arises from a non-standard situation, namely the absence of nuisance parameters under the restricted model. To explain, let us follow the notation of Tong and Lim (1980) and consider a 2-regime SETAR(2;1,1) model with threshold r and zero intercepts. Let the parameters be $\theta_i; i = 1, 2$, one for each regime. We have a total of 3 parameters. Consider the reduced model with $\theta_1 = \theta_2$, i.e. a linear AR(1) model. Now, in the reduced model, the threshold parameter r is a nuisance parameter that is redundant (i.e. absent). So, what is P here? The answer to this question is clearly related to the choice of the value for c in equation (8). First, note that the difference of the AICs of two nested models is the corresponding likelihood ratio test statistic minus twice the degrees of freedom (Tong, 1975). Now, *if r is known*, then under normality assumption of the white noise process, the likelihood ratio statistic of the test of the hypothesis of $\theta_1 = \theta_2$ has asymptotically a χ_1^2. In this case, the standard AIC (i.e. $c = 2$) applies. However, when r is unknown, as is usually the case in practice, the above asymptotic argument breaks down and the standard AIC does not apply. In fact, we have here a stochastic process indexed by r of mutually dependent χ_1^2 random variables. Following the arguments of Chan and Tong (1990), it can be shown that the 5% point of the likelihood ratio test statistic is approximately that of a χ_3^2 under suitable conditions. For higher order AR models, see Chan and Tong (1990).

(4) *Miscellanies*

(i) I am very grateful to the authors for their kindness in referring to Tong and Lim (1980) in respect of hidden thresholding. In fact, in the early 1980s, Tong and his colleagues already started to exploit TAR models driven by hidden thresholds. For example, Tong (1983, p. 63) first revealed the connection between the exponential autoregressive model of Lawrance and Lewis

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(1980) and a TAR model with a *hidden* threshold variable. Chan (1986, Ch. 4; 1988) developed the link more systematically. See Tong (2011, esp. p.110 and p.111) for further discussion of thresholding, observable, hidden or partially hidden.

(ii) Rissanen's quote in 2007 can be compared with the famous quote among statisticians: "All models are wrong but some are useful." (George Box, 1979.) It is a curious fact that, despite this almost universal recognition, standard frequentist as well as standard Bayesian methods of statistical estimation of unknown parameters of a time series model are typically predicated on the model being true. Even George Box has not deviated from this practice. Of course, he and the late Professor G. Jenkins started the specification-estimation-diagnostics strategy as their way of addressing the issue. However, a frontal attack of the issue remains challenging. For a recent attempt to remove this assumption at the estimation stage, see Xia and Tong (2011), who proposed a 'catch-all' approach to estimation by considering an objective function based on n-step-ahead predication errors for $n \geq 1$ rather than for $n = 1$ only as in conventional methods. In fact, the celebrated Whittle likelihood is a forerunner in this endeavour.

(iii) It seems to me that the notion of fitness in genetic algorithm is related to Akaike's likelihood of a time series model. (Akaike, 1978.)

(iv) I am very grateful that the authors have referred to Chan and Tong (1986) in connection with STAR models. These models were first developed by Chan and Tong (1986), who christened them *smooth threshold autoregressive* (hence the acronym STAR) models. Chan and Tong (1986) gave a comprehensive probability theory and statistical inference of the STAR models. Essentially, they replaced the indicator function in TAR models by a 'sufficiently smooth function with a rapidly decaying tail' (Chan and Tong, 1986, p.187). They did this in two steps. First they gave a comprehensive treatment of the case of a distribution-type extension of the indicator function; then they pointed out on p.187 that the same arguments could be repeated for the more general case under virtually identical conditions. Thus, it is a historical fact that the smooth transition autoregressive models (including his LSTAR models and ESTAR models) that Teräsvirta proposed, bearing the same acronym as STAR, in 1994 are special cases of Chan and Tong's STAR models of 1986. It is curious that this fact is not more widely known in the literature. Of course, our priority does not detract from the many worthwhile contributions made by Professor Teräsvirta to STAR modelling in econometrics. On hindsight, it might be better to adopt the engineers' ter-

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minology and call our model a 'soft threshold autoregressive model', which carries the same acronym.

In conclusion, I must thank the authors once again for a most enjoyable paper and the Editor for giving me the opportunity to discuss it. The paper represents an important step into the vast territory of nonstationary-nonlinear modelling and beyond. I say beyond, because I can almost envisage the possibility of a delightful nonlinear-nonstationary spatial-temporal model. After all, like knowledge, climates travel in time and space.

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