

# Analyzing Short Time Series Data From Periodically Fluctuating Rodent Populations by Threshold Models: A Nearest Block Bootstrap Approach

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**SUMMARY.** The study of the rodent fluctuations of the North was initiated in its modern form with Elton's pioneering work. Many scientific studies have been designed to collect yearly rodent abundance data, but the resulting time series are generally subject to at least two "problems": being short and non-linear. We explore the use of the continuous threshold autoregressive (TAR) models for analyzing such data. In the simplest case, the continuous TAR models are additive autoregressive models, being piecewise linear in one lag, and linear in all other lags. The location of the slope change is called the threshold parameter. The continuous TAR models for rodent abundance data can be derived from a general prey-predator model under some simplifying assumptions; see also Stenseth and Chan (1998). The lag in which the threshold is located sheds important insights on the structure of the prey-predator system. We propose to assess the uncertainty on the location of the threshold via a new bootstrap called the nearest block bootstrap (NBB) which combines

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the methods of moving block bootstrap and the nearest neighbor bootstrap. The NBB assumes an underlying finite-order time-homogeneous Markov process. Essentially, the NBB bootstraps blocks of random block sizes, with each block being drawn from a non-parametric estimate of the future distribution given the realized past bootstrap series. We illustrate the methods on a particular rodent abundance time series from Kilpisjärvi, Northern Finland.

## 1. Introduction

The study of the rodent fluctuations of the North was initiated in its modern form with Elton's (1924) pioneering paper as well as with his book (Elton 1942). (See also Stenseth 1995.) Since then, many long-term scientific studies have been designed to collect rodent abundance data. For an overview, see, e.g., Finerty (1980), Stenseth and Ims (1993) and Stenseth (1999); most commonly these censuses are annual and biannual. While some of these studies have been ongoing for as long as thirty to fifty years, the resulting time series are still short in the context of time series analysis. Besides the problem of shortness, the analysis of such time series has been hampered by a general lack of appropriate methodologies for dealing with the underlying non-linear dynamics; see Sugihara (1994).

It is our view that the shortness of many ecological time series precludes complex models. On the other hand, non-linearity is prevalent. In this article, we consider an approach by linking the predator-prey model in ecological population theory (Hanski *et al.*, 1993; Stenseth, Bjørnstad and Falck, 1996a) with threshold autoregressive modeling in non-linear time series analysis (Tong, 1990). The aim is to seek a deeper understanding of real population time series by integrating empirical statistical modeling with substantive population dynamics. However, much of the insight gained here should be readily transportable to other areas of natural science (e.g., the incident rates of diseases such as measles across different cities) and social science (e.g., panel of economic and financial time series).

## 2. The Ecological Model

A general deterministic predator-prey interaction (often called “trophic interaction”) population dynamics may be modeled as (cf. May, 1981)

$$N_{t+1} = N_t F(N_t, P_t), \quad (1)$$

$$P_{t+1} = P_t G(N_t, P_t), \quad (2)$$

where  $N_t$  and  $P_t$  are the population abundances of the prey and a predator specializing on that prey at time  $t$ , and  $F$  and  $G$  are two functions describing both the intraspecific and interspecific interactions within this system. The functions  $F$  and  $G$  may assume fairly general forms so that  $\partial F/\partial N < 0, \partial G/\partial P < 0, \partial F/\partial P < 0, \partial G/\partial N > 0$  (cf. Stenseth *et al.*, 1996a). The preceding predator-prey model is commonly considered quite appropriate for the interpretation of small rodent cycles (cf. Hanski *et al.*, 1993; Stenseth *et al.*, 1996a).

In order to gain ecological insight, we may approximate (see Stenseth *et al.*, 1997) the above model to

$$N_{t+1} = N_t \exp[a_0(\theta_t) - a_1(\theta_t)X_t - a_2(\theta_t)Y_t],$$

$$P_{t+1} = P_t \exp[b_0(\theta_t) - b_1(\theta_t)Y_t + b_2(\theta_t)X_t],$$

where  $X_t = \ln N_t$  and  $Y_t = \ln P_t$  (cf. Gompertz, 1825; these log-transformed population abundances in the exponents appear to give a good fit for vertebrate populations; see, e.g., Saitoh *et al.*, 1997). The parameter  $\theta$  is an indicator representing the regime effects. Here,  $a_i(\theta_t)$  denote functions of  $(X_t, Y_t)$ . Assuming a predator-prey model as given above, biologically speaking,  $a_1(\theta_t)$  and  $b_1(\theta_t)$  represent the degree of intraspecific regulation in the prey and predator respectively,  $a_2(\theta_t)$  and  $b_2(\theta_t)$  represent the strengths of trophic interaction between the two species and  $a_0(\theta_t)$  and  $b_0(\theta_t)$  represent the ‘intrinsic growth rates’. Clearly the above equations, upon taking logs, describe a non-linear difference equation model for the two-dimensional vector time series,  $\{X_t, Y_t\}$ . This equation is said to be of order one in the sense that the vector at time  $t$  depends only on the vector at time  $t - 1$ . Quite often, we may have only data on either  $Y$  or  $X$ , but not both. In this case, we may wish to have a scalar

difference-equation model compatible with the above two-dimensional difference equation model.

In principle, we can eliminate, say,  $Y$  in order to obtain a model for  $X$  only. For the linear case (i.e., all  $a_i$ s and  $b_i$ s are constant), the scalar difference-equation model will be of order 2 (i.e.,  $X_t$  will be a linear function of  $X_{t-1}, X_{t-2}$  only). [More generally, within the class of linear difference equations,  $X_t$  will be of order  $k$  if the original vector time series is of dimension  $k$ .] On the other hand, for non-linear difference equations, eliminating  $Y$  generally yields an infinite-order scalar difference equation model for  $X$ , i.e.,  $X_t$  is a function of all past  $X$ 's. However, if the  $a_i$ s and  $b_i$ s are functions of  $X$  alone, or more specifically,  $\theta_t$  is a function of  $X_t$  only, then eliminating  $Y$  will lead to a scalar non-linear difference equation model of order 2. Specifically, consider  $X_t - \{a_2(\theta_{t-1})(1 - b_1(\theta_{t-2}))/a_2(\theta_{t-2})\}X_{t-1}$ ; after some algebra and assuming that all ratios in the following formula are well defined, it can be shown that (see the appendix)

$$\begin{aligned} X_t = & \{a_0(\theta_{t-1}) - a_2(\theta_{t-1})(1 - b_1(\theta_{t-2}))a_0(\theta_{t-2})/a_2(\theta_{t-2}) - a_2(\theta_{t-1})b_0(\theta_{t-2})\} \\ & + \{1 - a_1(\theta_{t-1}) + a_2(\theta_{t-1})(1 - b_1(\theta_{t-2}))/a_2(\theta_{t-2})\}X_{t-1} \\ & - \{a_2(\theta_{t-1})(1 - b_1(\theta_{t-2}))(1 - a_1(\theta_{t-2}))/a_2(\theta_{t-2}) + a_2(\theta_{t-1})b_2(\theta_{t-2})\}X_{t-2}. \end{aligned} \quad (3)$$

Consider the case that the  $a_i$ s and the  $b_i$ s are constant except that  $a_1$  is a piecewise constant (non-linear) function of  $X$  and  $b_1$  close to 1 (which might be considered approximately valid (cf. Stenseth *et al.*, 1996a). Then, eqn. (3) approximately becomes

$$X_t = (a_0b_1 - a_2b_0) + (1 - a_1(\theta_{t-1}))X_{t-1} - a_2b_2X_{t-2}, \quad (4)$$

a piecewise linear (non-linear) difference equation with the non-linearity in lag 1. On the other hand, if all the coefficients are constant except that  $b_2$  is a piecewise constant (non-linear) function of  $X$ , then we obtain

$$X_t = (a_0b_1 - a_2b_0) + (2 - a_1 - b_1)X_{t-1} + (a_1 + b_1 - a_1b_1 - a_2b_2(\theta_{t-2}) - 1)X_{t-2}, \quad (5)$$

again a piecewise linear (non-linear) difference equation but with the non-linearity in lag 2.

Piecewise linearity lies at the heart of threshold autoregressive modeling (Tong, 1990). [Following the terminology of Tong (1990), we effectively partition the state space of the vector time series into regimes, over each of which a linear autoregressive model applies and the above difference equations are called the skeletons of the corresponding stochastic models.] In eqn. (4),  $\theta_{t-1}$  indexes the different regimes and does often reflect what the ecologists call the *phase dependence*; see Framstad *et al.* (1997) and Stenseth *et al.* (1998) who interpreted the threshold as an indication of the phase of the cycle. In a similar vein, the coefficient of  $X_{t-1}$  reflects the so-called “density-dependence” and the coefficient of  $X_{t-2}$  the “delayed density-dependence” in ecology (see, e.g., Stenseth *et al.*, 1996b). [Note: the “densities” here refer to “biological population densities”; see Turchin (1995).] In this paper, we explore the phase-dependence in the following threshold form:

$$X_t = \begin{cases} \beta_{1,0} + \beta_{1,1}X_{t-1} + \beta_{1,2}X_{t-2} & \text{if } X_{t-d} \leq r, \\ \beta_{2,0} + \beta_{2,1}X_{t-1} + \beta_{2,2}X_{t-2} & \text{otherwise.} \end{cases}$$

Below, a stochastic noise-term will be added to the LHS of the preceding equation to account for other omitted factors such as weather. It is not essential to have a discontinuous function. In fact, in this article we will focus on the continuous threshold models typified by setting  $\beta_{1,0} = \beta_{2,0}$ ,  $\beta_{1,2} = \beta_{2,2}$  and  $d = 1$ ; see §4 for the general definition. By exploiting the relationship between the ecological parameters (i.e.  $a$ ’s and  $b$ ’s) with the statistical parameters (i.e.  $\beta$ s) we can estimate the latter and give ecological interpretation via the former.

The TAR model is a useful way of investigating non-linearities in the population fluctuations such as those of many northern rodent populations. It is particularly appealing because it facilitates ecological interpretation and inference with respect to the non-linearities. It has been applied in the ecological modeling of lynx and lemming (Tong, 1990; Framstad *et al.*, 1997; Stenseth *et al.*, 1998). Interpreting the threshold as an indication of the phase of the cycle has advanced our understanding of these fluctuating populations (Framstad *et al.*, 1997 and Stenseth *et al.*, 1998). However, it is pertinent to point out that the phase-dependence interpretation may not necessarily apply to other systems. We believe that the

phase dependency interpretation applies to the highly fluctuating populations because the population experiences dramatically different conditions during the low phase and the high phase (which subsequently result in, so to speak, different models for the various regimes). Indeed, much research on periodically fluctuating rodent populations has in effect emphasized such phase-shifts (Chitty 1960, 1967, Krebs 1978, 1993). The TAR modeling and the phase-dependency interpretation has been utilized in other fields far beyond fluctuating small rodents, for example economic time series (Tiao and Tsay, 1994).

Stenseth *et al.* (1996a) demonstrated that the periodically fluctuating small rodents of the North generally may be approximated as an order two process. If, for such a second order model, we find a threshold in either the first or the second lag, it may suggest a type of non-linearity which most appropriately may be seen as a phase dependency. Furthermore, whenever the threshold is located in the first lag, the phase dependency may be seen as due to the intrinsic processes of the kind hypothesized by Krebs (1978, 1993). Whenever the threshold non-linearity is in the second lag, the phase dependency is likely to be related to the predator-prey interaction (see, e.g., Stenseth, 1998). Hence, the location of the threshold is critical for ecological inference. The main purpose of this paper is to investigate the extent to which this may be elucidated statistically on the basis of the fairly short time series available. Further biological interpretations of these findings will be reported elsewhere.

### 3. The Rodent Abundance Data

In this paper we focus on a data series on abundances of the grey-sided vole (*Clethrionomys rufocanus*) from Kilpisjärvi, Northern Finland (Kalela 1957; Laine and Henttonen, 1983, 1987; Heikki Henttonen pers comm) covering almost 50 years. We will refer to this as the rodent series. Figure 1 shows the time series plot of the logarithmic transformed rodent series. The rodent data have been added with a constant 0.7 before taking the log-transformation. [To bring the noise terms of a statistical model, to be discussed below, closer to Gaussianity, it is sometimes convenient to add a constant to the data before taking the logarithm transformation. The above choice of 0.7 is based on the AIC (unpublished result).] Rodents have been regularly trapped with standardized techniques since the beginning of this time series

(Kalela 1957, Laine and Henttonen 1983, 1987, Heikki Henttonen, pers comm). It, hence, represents one of the longest and most standardized series on small rodent dynamics (see, e.g., Falck, Bjørnstad and Stenseth, 1995).

Following standard practice within the field of small rodent ecology (e.g., Henttonen *et al.*, 1985), we only use the fall samples: these are assumed to represent the underlying population dynamics the best; these samples are also those with the fewest zero-observations. The commonness of zero-samples is inherently a problem of the violent fluctuations of northern rodent populations since they are known to have extensive amplitudes (Krebs, 1993).

#### 4. Threshold Autoregressive Models

Self-Exciting Threshold Autoregressive (SETAR) models, or simply the Threshold Autoregressive (TAR) models, introduced by Tong (1983, 1990), enjoy a diverse spectrum of dynamical behavior including chaos (Chan and Tong, in print), ease in computation and interpretation, and availability of computer programs (STAR, see Tong, 1990). Specifically, the SETAR(2;p,p) model takes the following form:

$$X_t = \begin{cases} \beta_{1,0} + \sum_{j=1}^p \beta_{1,j} X_{t-j} + \sigma_1 \varepsilon_t & \text{if } X_{t-d} \leq r \\ \beta_{2,0} + \sum_{j=1}^p \beta_{2,j} X_{t-j} + \sigma_2 \varepsilon_t & \text{otherwise,} \end{cases} \quad (6)$$

where the coefficients  $\beta, \sigma > 0$  and  $r$  are real numbers and  $d$  is a positive integer. The noise sequence  $\{\varepsilon_t\}$  is assumed to be iid, of zero mean and unit variance. The noise sequence is often further assumed to be Gaussian, although this assumption is not needed below. Here, the state space is decomposed into two regimes according to  $X_{t-d}$ , where  $d$  is called the delay parameter. The parameter  $r$  is called the threshold. Thus, if  $X_{t-d}$  is not greater than the threshold, the transition mechanism from  $\mathbf{X}_{t-1}$  to  $\mathbf{X}_t$  is governed by the AR(p) model whose coefficients are  $\beta_{1,i}, i = 0, \dots, p$ . On the other hand, if  $X_{t-d}$  exceeds the threshold, the transition mechanism is controlled by another AR(p) model with coefficients  $\beta_{2,i}, i = 0, \dots, p$ . Note that the noise variances may be different over the two regimes, and hence the SETAR model is also capable of modeling heteroscedasticity in the time series.

The conditional mean function of  $X_t$  given the past data  $X_{t-1}, X_{t-2}, \dots$  is known as the autoregressive function. The autoregressive function of the SETAR model is generally

discontinuous over the hyperplane defined by  $X_{t-d} = r$ . However, in some applications, substantive theory may strongly suggest that a continuous autoregressive function is more appropriate than a general TAR model. Population dynamics might indeed be such a field. This consideration motivates us to focus on a sub-class of TAR models which have continuous autoregressive functions. The so-called continuous TAR models take the following form:

$$X_t = \beta_0 + \sum_{1 \leq j \neq d \leq p} \beta_j X_{t-j} + \begin{cases} \beta_{d-}(X_{t-d} - r) + \sigma_1 \varepsilon_t & \text{if } X_{t-d} \leq r \\ \beta_{d+}(X_{t-d} - r) + \sigma_2 \varepsilon_t & \text{if } X_{t-d} > r, \end{cases} \quad (7)$$

where  $\beta, \beta_{d-}, \beta_{d+}, r$  and  $\sigma > 0$  are coefficients. With no loss of generality, it is assumed that the delay parameter  $d \leq p$ . Note that  $\beta_0$  equals the conditional mean of  $X_t$  given  $X_{t-j} = 0, 1 \leq j \neq d \leq p$  and  $X_{t-d} = r$ . The autoregressive function of a continuous TAR model is continuous everywhere but not differentiable on the hyperplane defined by  $X_{t-d} = r$  whenever  $\beta_{d-} \neq \beta_{d+}$ . We note a related approach by Chan and Tong (1986) who introduced the Smooth Threshold Autoregressive (STAR) model specified by a smooth transition between the two linear regimes.

As we shall make essential use of the method of conditional least squares (CLS) in estimating the unknown parameters, the relevant asymptotic results for the case of known  $p$  are briefly summarized below. Let  $\theta = (\beta_0, \beta_1, \dots, \beta_{d-}, \beta_{d+}, \dots, \beta_p, r)^T$  be the vector of all unknown parameters except the  $\sigma$ 's. The conditional least squares estimate  $(\hat{\theta}, \hat{d}) = (\hat{\theta}_N, \hat{d}_N)$  is obtained by minimizing the sum of squared 1-step ahead prediction errors, i.e.,  $\mathcal{L}(\theta, d) = \mathcal{L}_N(\theta, d) = \sum_{p+1 \leq t \leq N} \{X_t - E(X_t | \mathbf{X}_{t-1}; \theta, d)\}^2$ . For fixed  $r$  and  $d$ , the loss function  $\mathcal{L}(\theta)$  equals the residual sum of squares resulted from regressing  $X_t$  on  $X_{t-j}, 1 \leq j \neq d \leq p, (X_{t-d} - r)I(X_{t-d} \leq r), (X_{t-d} - r)I(X_{t-d} > r)$ , where  $I(\cdot)$  is the indicator function of the enclosed expression. The global minimization of the loss function can then be executed by a grid search over  $r$  and  $1 \leq d \leq p$ . Given  $\hat{\theta}, \sigma_i^2, i = 1, 2$  can be estimated as the normalized residual sum of squares of the two estimated regimes.

Under suitable regularity conditions including (1)  $\{X_t\}$  is stationary and ergodic, (2)  $E(|X_t|^{2+\delta}) < \infty$  for some  $\delta > 0$ , and (3)  $\beta_{d-} \neq \beta_{d+}$ , Chan and Tsay (1998) showed that the CLS estimator  $\hat{\theta}_N$ , as well as  $\hat{d}$  and  $\hat{\sigma}_i^2$  are consistent. Moreover,  $\hat{\theta}_N$  is asymptotically



unbiased and normal (see Chan and Tsay, 1998, for the formula of the asymptotic covariance matrix). Because  $d$  takes only finitely many values, the consistency of  $\hat{d}_N$  implies that  $\hat{d}_N$  eventually equals the true delay parameter. Hence, the delay parameter could and will be treated as known in the asymptotic distribution of  $\hat{\theta}_N$ .

## 5. Partial Residual Plots

The continuous TAR model is an additive model where for  $j \neq d$ ,  $f_j$ s are linear functions, and

$$f_d(x; \theta) = \begin{cases} \beta_{d-}(x - r) & x \leq r \\ \beta_{d+}(x - r) & \text{otherwise.} \end{cases}$$

See Hastie & Tibshirani (1990) for an account of additive models. Based on the analysis in the preceding section, the shift  $c$  is chosen to be 0.7. Moreover, the continuous TAR model with  $d = 1$  provides the best fit to the data. The estimated model for the log transformed data (with shift 0.7) is reported in Table 1. Before accepting this conclusion, it is important to check visually whether or not the data shed evidence of non-linearity in the form of a continuous TAR model with  $d = 1$ . In multiple linear regression, the partial residual plot provides a valuable tool for displaying graphically the relationship between the response variable and a particular explanatory variable after controlling for the other explanatory variables; see Weisberg (1985). The idea of partial residual plot can be readily extended to the setting of an additive model:  $X_t = f_1(Z_{t1}; \theta) + f_2(Z_{t2}; \theta) + \dots + f_k(Z_{tk}; \theta) + \varepsilon_t$  where  $\theta$  is a parameter vector;  $Z_{tj}$  is the  $t$ -th case value of the  $j$ -th explanatory variable;  $f_j$ s are possibly distinct scalar-valued functions.

Let  $\hat{\theta}$  be an estimate of  $\theta$ . The partial residuals equal  $f_j(Z_{tj}; \hat{\theta}) + \hat{e}_t = X_t - \sum_{1 \leq i \neq j \leq k} f_i(Z_{ti}; \hat{\theta})$ , so that the effects of the other explanatory variables have been eliminated. The partial residual plots are primarily useful for displaying the pattern and the strength of the relationships between the response and the explanatory variables.

The partial residual plots of the rodent series is shown in figure 2. In the top panel of figure 2 are the lag 1 and lag 2 plots for the fitted continuous TAR model with  $d = 1$ ; those in the bottom panel are for the case that  $d = 2$ . These plots suggest that the

relationship between  $X_t$  and  $X_{t-2}$  after adjusting for  $X_{t-1}$  is approximately linear, but the relationship between  $X_t$  and  $X_{t-1}$  is approximately piecewise linear, after adjusting for lag 2. Furthermore, it seems that there are some outliers in the data. For example, the partial residual in the upper right corner of the upper right plot seems an outlier. This residual corresponds to the data of 1983; figure 1 reveals that the series attains its maximum in 1983.

## 6. Nearest Block Bootstrap

Using the AIC, a continuous TAR model with  $d = 1$  is chosen over its counterpart with  $d = 2$  as well as the AR models. A pertinent question is how strong is the evidence in favor of this model. Put differently, we need to assess the uncertainty in this conclusion. A classical approach to this problem consists of the following two steps: (1) test whether or not the data are consistent with the AR models against the alternative of the continuous TAR models, and (2) in the case that TAR non-linearity seems supported by the data, test whether  $d = 1$  or  $d = 2$ . As argued in §2, the two different lags imply different biological explanations. Unfortunately, each of the above two steps has its intrinsic difficulty. In step (1), the threshold parameter and the delay parameter are absent under the null hypothesis. Consequently, the asymptotic null distribution of the likelihood ratio test is non-standard; see Chan and Tong (1990) and Chan (1990). Moreover, given the small sample size here, it does not seem justifiable to rely on asymptotics to calibrate such a test for non-linearity. As to step (2), the two hypotheses  $d = 1$  and  $d = 2$  are non-nested, thereby leading to a non-standard test situation. See Cox (1961).

Here, we take a different approach. We shall abuse the notation by saying that  $d = 0$  in the case that the true model is an AR model. Thus, the three competing hypotheses become:  $d = 0$ ,  $d = 1$  and  $d = 2$ . The ‘true’ value of  $d$  is estimated by  $\hat{d} = \hat{d}_N$  according to the AIC. The uncertainty in  $\hat{d}$  is summarized by its sampling distribution. The true sampling distribution of  $\hat{d}$  is unknown, but we propose to estimate it via the bootstrap; Efron (1979). For an introduction to bootstrap, see Efron and Tibshirani (1993) and Young (1994). For dependent data, the usual bootstrap of drawing from the empirical distribution of the data is inappropriate as it ignores the dependence in the data. Two broad approaches

for bootstrapping dependent data are described below.

### **(A) Moving Block Bootstrap (MBB)**

Blocks of consecutive  $l$  data are randomly sampled and then pasted together to form the bootstrap series. The idea is to preserve the dependence structure through blocking. The block size should be longer than the characteristic time of the data. That is, data  $l$  units apart in their time indices should be almost independent. See Künsch (1989) and Liu and Singh (1992) for further discussions of MBB. Politis and Romano (1994) proposed the method of stationary bootstrap for which the sequence of block sizes is iid geometric, and the time indices are defined modulus the sample size. In the case that a random block extends beyond the last observation, it will continue from the other end of the observed time series. One drawback of the MBB and the stationary bootstrap is that artificial discontinuity may be introduced when gluing together two random blocks. Smoothing procedure may be applied to alleviate this problem. We shall return to this problem later.

### **(B) Nearest Neighbor Bootstrap (NNB)**

This recent approach, introduced by Lall and Sharma (1996), assumes that the underlying model is some time-homogeneous  $p$ -th order Markov process, that is,  $\{\mathbf{X}_n = (X_n, \dots, X_{n-p+1})^T\}$  is a time-homogeneous Markov process. Hence, the transition probability distribution is  $F(x|\mathbf{x}) = P(X_{n+1} \leq x | \mathbf{X}_n = \mathbf{x})$ , being independent of  $n$ . This transition probability distribution is the conditional cdf of the next observation given the current and past observations. A non-parametric estimate of the measure induced by the distribution function  $F(\cdot|\mathbf{x})$  may be constructed as follows: Suppose that  $\mathbf{X}_u = \mathbf{x}$ . Let  $\mathbf{X}_{n(i)}, i = 1, 2, \dots, m$  be  $m$  nearest (observed)  $\mathbf{X}$ 's closest to  $\mathbf{x}$  in Euclidean norm. Let  $K$  be a  $p$ -dimensional probability density function. Then estimate the preceding conditional probability measure by the discrete probability measure which, for  $i = 1, 2, \dots, m$ , assigns to  $X_{n(i)+1}$  (the chronological descendant of  $\mathbf{X}_{n(i)}$ ) the probability mass proportional to  $K(\mathbf{X}_{n(i)} - \mathbf{x})$ . In other words, the support of this non-parametric estimate consists of the future observations immediately following the nearest neighbors of  $\mathbf{x}$ . If it is known a priori

that the conditional probability distributions are continuous, then a smoothed version of the preceding estimate can be obtained by modifying the preceding discrete probability estimate with each probability point mass smeared into some continuous distribution, say a Gaussian distribution, with a suitable spread. There are many variations of these estimation schemes. See Lall and Sharma (1996).

The basic idea of the NNB is to bootstrap a series by repeatedly drawing from some non-parametric versions of the conditional distributions of the next observation given the past and current bootstrap series. Specifically, the NNB is defined recursively as follows:

- (1) Suppose that the partial bootstrap series so far consists of  $X_1^*, X_2^*, \dots, X_s^*$ . If  $s \geq N$ , the sample size, then  $\{X_1^*, \dots, X_N^*\}$  is the desired bootstrap series.
- (2) If  $s < N$ , form  $\mathbf{X}_s^* = (X_s^*, X_{s-1}^*, \dots, X_{s-p+1}^*)^T$ . Draw  $X_{s+1}^*$  from some non-parametric estimate of the conditional distribution  $F(x|\mathbf{X}_s^*)$ .
- (3) Repeat (1) and (2), if necessary.

A problem with the NNB bootstrap is that for small sample size the non-parametric estimates of the conditional distribution of the immediate future observation may be imprecise, and hence affecting the quality of the bootstrap. See Falck *et al.* (1995) for an application of using NNB to assess the uncertainty of the Lyapunov exponent estimates for rodent data, including the rodent series studied here.

In this paper, we use a combination of the MBB and the NNB, which may be more suitable for short to moderately long time series. In particular, we assume that the underlying true model is a time-homogeneous  $p$ -th order Markov process. The basic idea is to construct the bootstrap series by repeatedly drawing (random-size) blocks from the conditional distribution of the future series given the current and past realized bootstrap series. The conditional distribution of the future  $l$  observations given the current state equals

$$P(X_{t+1} \leq c_1, \dots, X_{t+l} \leq c_l | \mathbf{X}_t = \mathbf{x}) = P(X_{p+1} \leq c_1, \dots, X_{p+l} \leq c_l | \mathbf{X}_p = \mathbf{x}),$$

by the homogeneity assumption. Using the notation in the description of the NNB, the measure induced by the preceding conditional distributions can be estimated by the dis-

crete probability measure which assigns probability mass  $\propto K(\mathbf{X}_{n(i)} - \mathbf{x})$  to the sequence  $(X_{n(i)+1}, \dots, X_{n(i)+l})^T$ ,  $i = 1, 2, \dots, m$ . In other words, the preceding conditional probability measure may be approximately simulated by randomly drawing a nearest neighbor of  $\mathbf{x}$  (according to the probability specified above) and the  $l$  observations immediately following the chosen nearest neighbor are taken as a realization of the conditional distribution of the next  $l$  observations given the current state  $\mathbf{x}$ .

In the analysis in the next section,  $K$  is taken as the pdf of the multivariate normal distribution  $N(0, \sigma^2 I)$  where  $\sigma^2$  is the variance of the data and  $I$  the identity matrix. The block size is randomized to avoid entraining the bootstrap series into some artificial pattern. In our examples, the block sizes are determined (independently of the preceding values of the bootstrap series) from a truncated Poisson random variable (zero is truncated). Notice that other distributions such as the negative binomial distribution may be used instead of the Poisson distribution. We conjecture that once the mean and the standard deviation of the block size are fixed, the exact shape of the distribution may not be very important. The new bootstrap method will be called the Nearest Block Bootstrap (NBB), which is recursively defined as follows:

- (1) Suppose that the partial bootstrap series so far consists of  $X_1^*, X_2^*, \dots, X_s^*$ . If  $s \geq N$ , the sample size, then  $\{X_1^*, \dots, X_N^*\}$  is the desired bootstrap series.
- (2) If  $s < N$ , form  $\mathbf{X}_s^* = (X_s^*, X_{s-1}^*, \dots, X_{s-p+1}^*)^T$ . Determine the next block size  $l$  independently of the past bootstrap values,  $X_1^*, X_2^*, \dots, X_s^*$ , for example from a truncated Poisson distribution. Draw  $X_{s+1}^*, \dots, X_{s+l}^*$  from some non-parametric estimate of the conditional distribution of the future  $l$  observations given the current state  $\mathbf{X}_s^*$ . (The block size  $l$  may have to be truncated if there are less than  $l$  future data associated with the realized nearest neighbor.)
- (3) Repeat (1) and (2), if necessary.

Note that for fixed block size  $l \leq p$ , the NBB is equivalent to applying the NNB to the vector process  $\{(X_{n-i}, i = 0, 1, 2, \dots, l-1)^T\}$ ; hence the NBB and the NNB share similar

theoretical properties, under suitable regularity conditions. The NBB method improves on the MBB method in that consecutive selected blocks match in their end conditions through the requirement that the next block is drawn approximately from the conditional distribution of the future given the current state. The sample size requirement should be less a problem with the NBB method than the NNB. Moreover, NBB may be more robust to slight departure from the assumption that the underlying model is a  $p$ -th order time-homogeneous Markov process if the mean block size is long compared to the characteristic time of the data. Note that in step (2), there are at most  $\binom{N}{p}$  distinct  $\mathbf{X}_s^*$ , and hence at most the same number of conditional future distributions. These distributions could be stored beforehand so as to speed up the bootstrap procedure. If  $l \geq p$  a.s., then  $\mathbf{X}_s^*$  equals some observed  $\mathbf{X}_k$ , and hence there are at most  $N - p$  distinct conditional future distributions, which greatly simplifies the automation of the NBB. In practice, if  $E(l) \geq p$ , then it is very likely that if  $X_s^* = X_k$ , then  $\mathbf{X}_s^* = \mathbf{X}_k$  either because  $l$  turns out to be actually greater than or equal to  $p$ , or because this is a good approximation owing to the nearest neighbor procedure. In the analysis in the next section, the preceding assumption is taken to simplify the programming task. A numerical experiment reported below suggests that this assumption seems justified for our examples.

To implement the NBB, we need to specify the number of nearest neighbors (or equivalently the local kernel size), and the distribution of the block size. Below, we report some preliminary experience in the context of the rodent data, with the simple approach of trying a few values of the neighbor size and the mean block size to gain a feel for their appropriate values. More experience will surely be needed for a systematic recommendation on the choice of these parameters, which we shall not attempt here.

## 7. Assessing the Uncertainty in the Location of the Threshold

Reported in table 2 are the NBB estimates of the sampling distribution of  $\hat{d}$  for some experiments with the (log-transformed with shift 0.7) rodent series. Here, all bootstraps are replicated 1,000 times. The block sizes are iid Poisson, with zero being truncated. All boot-

strap series are conditional on the first two observations. This conditioning is to ensure that the bootstrap series resemble the original data in their initial conditions. As argued in §2, the order is two for the rodent data. The NBB sampling distribution estimate for  $\hat{d}$  is obtained as follows: For each bootstrap series  $X_1^*, \dots, X_N^*$ ,  $\hat{d}^*$  is the estimate of  $d$  using the AIC. The preceding procedure is then replicated 1,000 times, and the frequency distribution of  $\hat{d}^*$  is the bootstrap estimate of the sampling distribution of  $\hat{d}$ . In the first experiment (experiment a), The data is a stationary series with Gaussian errors and of size 44 that was generated from the fitted model to the rodents series with  $d = 1$  as reported in §6. The NBB sampling distribution estimate for  $\hat{d}$  is sharply peaked at  $d = 1$ , suggesting that the NBB works nicely in this case.

Henceforth in all experiments, the rodent series is taken as the data. In experiments b–j, we have a 3 by 3 factorial design with the Poisson parameter taking values 4, 6, 8 (and hence  $E(l) \approx 4.07, 6.01, 8.00$ ) and the number of nearest neighbors  $m$  varying over 4, 6 and 8. For each combination of  $m$  and  $E(l)$ , the frequency distribution of  $\hat{d}^*$  is reported. It is expected that the larger is the mean block size, the closer the bootstrap series resemble the original data. Consequently, the NBB distribution of  $\hat{d}$  should be more concentrated with larger mean block size, which seems to be somewhat confirmed by these results. The situation with the effect of the number of nearest neighbors is more delicate. For smaller  $m$ , the estimates of the conditional future distributions will have smaller bias but they will be more variable. Thus, the choice of  $m$  hinges on an appropriate trade-off between bias and variability. From table 2, it can be seen that for each fixed mean block size, the bootstrap estimate is most concentrated when  $m = 6$ . This suggests that when  $m = 6$ , the bootstrap series distribution appears to resemble the original data most closely, and may signify that  $m = 6$  strikes an optimal trade-off between the bias and the variability in the non-parametric conditional future distribution estimates. For the choice of the mean block size, it is important to bear in mind that the mean block size should not be too large in order that the bootstrap series can embody “sufficient” diversity from the original data. Based on this criterion, one may choose either a mean block size of 4.07 or 6.01.

The sampling distribution of  $\hat{\theta}$  can also be estimated via the NBB. Asymptotically,  $\hat{d}$

is independent of  $\hat{\theta}$ ; see §4. Consequently, the asymptotic distribution of  $\hat{\theta}$  is the same whether or not it is conditioned on  $\hat{d}$ . However, such a conditioning seems desirable when we assess the parameter uncertainty for the fitted continuous TAR model with  $\hat{d} = 1$ . The conditional distribution of  $\hat{\theta}$  given  $\hat{d}$  can be readily estimated via the NBB by sub-sampling those bootstrap series for which  $\hat{d}^* = \hat{d}$ , 1 here. Figure 3 displays the histograms of the marginal bootstrap conditional distributions of  $\hat{\theta}^*$  given that  $\hat{d}^* = 1$ . (Here,  $m = 6$  and the mean block size is 4.07.) Superimposed on these histograms are their smooth kernel density estimates produced by the density function of Splus with the width parameters set as the interquartile ranges. It can be seen from these plots that  $\hat{\beta}_{1-}^*$ ,  $\hat{\beta}_{1+}^*$  and  $\hat{r}^*$  have very skewed distributions. The distribution of  $\hat{\beta}_{1+}^*$  has very thick tails. Individual 95% confidence intervals for  $\hat{\theta}$  can be estimated by the intervals with the lower (upper) endpoints being the 2.5% (97.5%) percentiles of the bootstrap distributions; see chapter 13 of Efron and Tibshirani (1993) for further discussion of the percentile method. These are reported in table 3. For purpose of comparison, also reported in table 3 are the confidence intervals based on the unconditional bootstrap and the asymptotic normality approximations summarized in §4. The conditional bootstrap intervals are generally shorter than their unconditional counterparts, as irrelevant samples have been included in calibrating the unconditional bootstrap intervals. It is interesting to note that when the bootstrap sampling distributions are approximately symmetric, all three methods yield similar confidence intervals. However, for estimates with skewed distributions, there is a big disparity between the bootstrap intervals with those from the asymptotics, which is expected as the asymptotically normal distributions would be hard pressed to mimic asymmetric distributions. Based on the conditional bootstrap confidence intervals, there is some evidence that  $\beta_{1+}$  is positive,  $\beta_2$  is negative, but with marginal evidence that  $\beta_{1-}$  might be zero. Moreover, there are substantial uncertainty in all estimates, owing to the noisiness and shortness of the data.

## 8. Conclusion

Taking these results together, we obtain a consistent picture that the sampling distribution peaks at  $d = 1$ . There seems some evidence that the underlying biological mechanism



is non-linear, and the "odds" in favor of  $d = 1$  to  $d = 2$  ranges from about 2:1 to 3:1. This result has important ecological significance in two respects: (1) the specification of the non-linear nature of the observed rodent dynamics is of general relevance to the current discussion on non-linear ecological dynamics; (2) the particular location of the threshold (i.e., the location of the non-linearity) in this particular ecological system is of great significance in the ecologists' effort in identifying the underlying population dynamics process.

It is significant to observe that the threshold falls in lag one as opposed to lag two. Referring to the model formulation given in §2, we may then conclude that the non-linearities may be expected to be located in the self-regulatory component of the ecological model (i.e., either  $a_1$  or  $b_1$ ); for a general discussion of this aspect, see Stenseth (1999). On the other hand, Stenseth *et al.* (1998) showed that for Canadian lynx, the threshold is concluded to fall in lag two, suggesting that the non-linearity in the lynx cycle owes to an entirely different process. We believe that it is this type of discussion of the underlying biological processes which might help us better understand non-linearities in ecological systems. In particular, modeling the non-linearity in a short time series in terms of the continuous TAR model facilitates biological interpretation. Another point is that Framstad *et al.* (1997) and Stenseth *et al.* (1998) have suggested that the threshold in fact separates different phases of the population cycles into the increase and decrease phases. This further suggests that different biological processes operate during the increase and decrease phases of the cycle, and in effect that the non-linearity primarily may be seen as a phase-dependency in the density-dependent structure. Such a discussion we believe is of great help in the interpretation of the observed ecological dynamics.

Regarding the method of the nearest block bootstrap, further research is needed on (1) developing the theoretical aspects of the method, (2) "optimal" implementation of the NBB, and (3) comparing the pros and cons between the moving block bootstrap, the nearest neighbor bootstrap and the nearest block bootstrap. It should be noted that for iid data, the (usual) bootstrap may yield misleading results in some non-regular cases of non-smooth and/or non-Gaussian statistics; see section 3.6 in Shao and Tu (1995) for details and remedies. This problem may carry over to the case of dependent data. Further study is needed to

elucidate when the NBB or other bootstrap method is (asymptotically) valid for dependent data. With the availability of these bootstrap methods appropriate for dependent data, we could expect a substantial increase in the exploitation of bootstrap in time series analysis.

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#### APPENDIX

##### *Derivation of (3).*

Suppose that

$$X_t = c_{0,t-1} + c_{1,t-1}X_{t-1} + c_{2,t-1}Y_{t-1}, \quad (\text{A.1})$$

$$Y_t = d_{0,t-1} + d_{1,t-1}Y_{t-1} + d_{2,t-1}X_{t-1}, \quad (\text{A.2})$$

holds for all  $t \geq 1$  and  $c_{i,t}$  ( $d_{i,t}$ ) are functions of  $X_t$  and  $Y_t$ . Consider

$$\begin{aligned} & X_t - \{c_{2,t-1}d_{1,t-2}/c_{2,t-2}\}X_{t-1} \\ &= c_{0,t-1} + c_{1,t-1}X_{t-1} + c_{2,t-1}Y_{t-1} - (c_{2,t-1}d_{1,t-2}/c_{2,t-2})(c_{0,t-2} + c_{1,t-2}X_{t-2} + c_{2,t-2}Y_{t-2}) \\ &= c_{0,t-1} + c_{1,t-1}X_{t-1} - c_{2,t-1}d_{1,t-2}c_{0,t-2}/c_{2,t-2} - (c_{2,t-1}d_{1,t-2}c_{1,t-2}/c_{2,t-2})X_{t-2} \\ &\quad + c_{2,t-1}(Y_{t-1} - d_{1,t-2}Y_{t-2}) \\ &= c_{0,t-1} - c_{2,t-1}d_{1,t-2}c_{0,t-2}/c_{2,t-2} + c_{1,t-1}X_{t-1} - (c_{2,t-1}d_{1,t-2}c_{1,t-2}/c_{2,t-2})X_{t-2} \\ &\quad + c_{2,t-1}(d_{0,t-2} + d_{2,t-2}X_{t-2}). \end{aligned}$$

The first equality in the above formulas follows from (A.1). Similarly, the last equality follows from (A.2) with  $t = t - 1$ . Therefore,  $X_t = \{c_{0,t-1} - c_{2,t-1}d_{1,t-2}c_{0,t-2}/c_{2,t-2} + c_{2,t-1}d_{0,t-2}\} + \{c_{1,t-1} + c_{2,t-1}d_{1,t-2}/c_{2,t-2}\}X_{t-1} + \{c_{2,t-1}d_{2,t-2} - c_{2,t-1}d_{1,t-2}c_{1,t-2}/c_{2,t-2}\}X_{t-2}$ . Equation (3) follows upon setting  $c_{0,t} = a_0(\theta_t)$ ,  $c_{1,t} = 1 - a_1(\theta_t)$ ,  $c_{2,t} = -a_2(\theta_t)$ ,  $d_{0,t} = b_0(\theta_t)$ ,  $d_{1,t} = 1 - b_1(\theta_t)$ , and  $d_{2,t} = b_2(\theta_t)$ .

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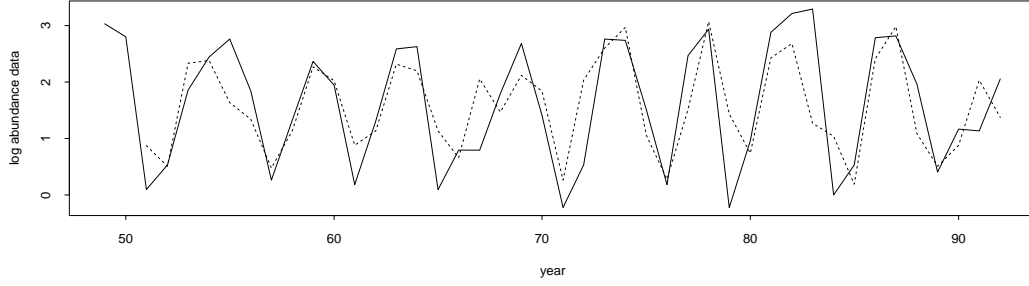
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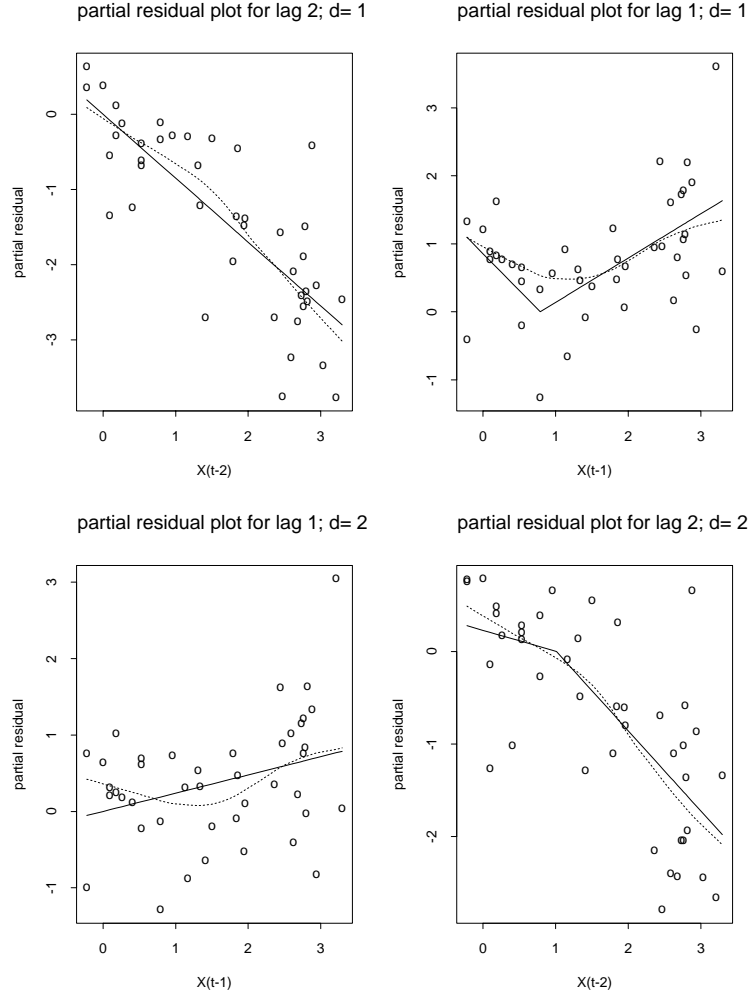


**Figure 1.** The solid line is the time series plot of the log transformed rodent series from northern Finland (Kalela, 1957, Laine and Henttonen, 1983, 1987, Heikki Henttonen, pers comm), with a pre-shift of 0.7. The dotted line is the time series plot of the 1-step ahead predicted values from the continuous TAR model with  $d = 1$ ; see §6.

	$\hat{\beta}_0$	$\hat{\beta}_2$	$\hat{\beta}_{1-}$	$\hat{\beta}_{1+}$	$\hat{r}$	$\hat{\sigma}_1^2$	$\hat{\sigma}_2^2$
coef	2.1310	-0.8494	-1.087	0.6514	0.7869	0.3242	0.5748
std. err.	0.2326	0.1054	1.101	0.2063	0.3221		

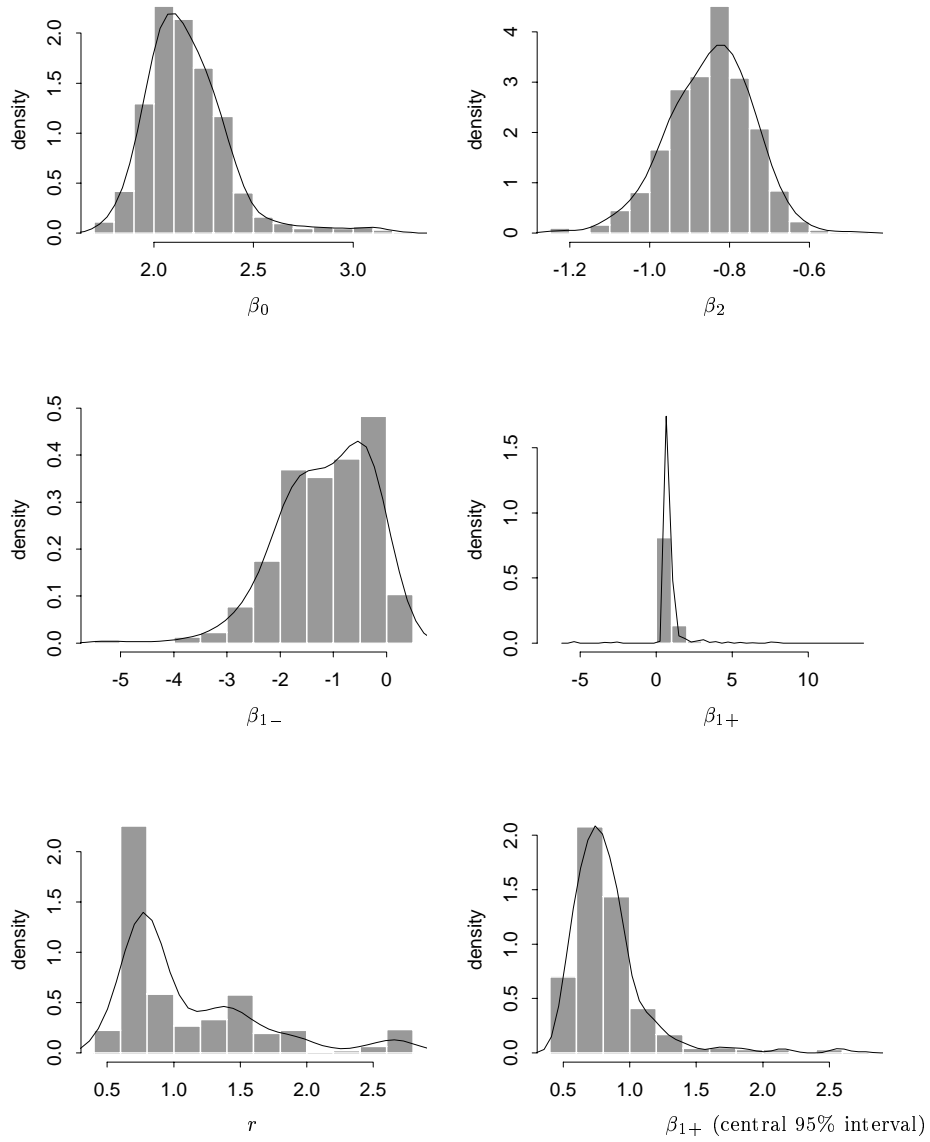
**Table 1**

*Fitted continuous TAR model to the log rodent series with  $p = 2, d = 1$ . Threshold searched from the 18.2 percentile to the 77.3 percentile using a grid search of 101 points evenly distributed over the range (0.2624, 2.76). Number of observations in the first and the second regime respectively are 12 and 30; corresponding noise variance estimates respectively are 0.3242 and 0.5748. The percent of variance explained by the fitted continuous TAR model is 56.2% as compared to 49.7% for the AR(2) model. The AIC, in the log scale, are -16.97 and -20.13 respectively for the AR(2) model and the continuous TAR model.*



**Figure 2.** The top two figures are the lag-2 and lag-1 partial residual plots for the fitted continuous TAR model with  $d = 1$ . The bottom two figures are the lag-1 and lag-2 partial residual plots for  $d = 2$ . The solid lines are the autoregressive functions of the estimated models after controlling for the other lag. The dashed lines are non-parametric regression functions of the partial residuals on the corresponding lag, as estimated by the loess function in Splus.





**Figure 3.** Nearest block bootstrap sampling distributions of the parameters,  $\hat{d}^* = 1$ . Superimposed on the histograms are the smooth kernel pdf estimates produced by the density function from Splus with the width parameters set as the interquartile ranges. The lowest left histogram is that of the central 95% bootstrap estimates of  $\beta_{1+}$ .

experiment	$m$	mean	bootstrap freq.		
		block size	$\hat{d}^* = 0$	$\hat{d}^* = 1$	$\hat{d}^* = 2$
a	4	4.07	4	985	11
b	4	4.07	164	609	227
c	4	6.01	194	620	186
d	4	8.00	184	646	170
e	6	4.07	174	618	208
f	6	6.01	187	641	172
g	6	8.00	182	646	172
h	8	4.07	207	563	230
i	8	6.07	197	612	191
j	8	8.00	181	648	171

**Table 2**

*Nearest block bootstrap estimate of the sampling distribution of  $\hat{d}$ . All replication sizes are 1,000. For experiment a, the data is a stationary series simulated from the continuous TAR model fitted to the log transformed rodent series (shift=0.7). The latter series is the data for experiments b–j. In experiments b–j, we have a 3 by 3 factorial design with the Poisson parameter taking values 4, 6, 8 (and hence  $E(l) \approx 4.07, 6.01, 8.00$ ) and the number of nearest neighbors  $m$  varying over 4, 6 and 8. For each combination of  $m$  and  $E(l)$ , the frequency distribution of  $\hat{d}^*$  is reported here.*

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	conditional	unconditional	asymptotics
constant	( 1.852 , 2.751 )	( 1.855 , 2.951 )	( 1.675 , 2.587 )
$\beta_{1-}$	(-2.945 , 0.1734)	(-2.790 , 0.2518)	(-3.245 , 1.071 )
$\beta_{1+}$	( 0.4280, 2.784 )	(-1.945 , 2.574 )	( 0.2471, 1.056 )
$\beta_2$	(-1.071 , -0.6673)	(-1.040 , -0.6269)	(-1.056 , -0.6428)
$r$	( 0.5416, 2.658 )	( 0.5867, 2.734 )	(0.1556, 1.418 )

**Table 3**

*95% confidence intervals of the parameters of the continuous TAR model for the log-transformed rodent data, based on conditional bootstrap, unconditional bootstrap, and asymptotics as summarized in §4.*

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