Contagion tests via copula threshold models

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Abstract

We develop threshold models that allow copula functions or their association parameters changing across time. The number and location of thresholds is assumed unknown. We use a Markov chain Monte Carlo strategy combined with Laplace estimates that evaluate the required marginal densities for a given model. We apply our methodology to financial time series emphasizing the ability to improve estimates of risk characteristics, as well as measuring financial contagion by inspecting changing dependence structures.

Keywords: Copulas, Kendall's τ, time-varying parameters, MCMC, reversible jump MCMC method.

1 Introduction

There is a considerable recent interest in modelling temporal dependence of financial returns by building copula functions. The key characteristic of this approach is the splitting of the joint distribution of returns into two components, the marginal densities and the dependence structure. The modelling process consists of first specifying the marginal distributions by exploiting well-known stylized facts based on one-dimensional studies of financial returns, and of second determining the appropriate copula function, that completely characterizes the returns dependence. There is a quite substantial empirical evidence that copulas allow for realistic description of the dependence behavior that goes beyond linear correlation; see, for example, Embrechts, McNeal and Straumann (2002), Mashal and Zeevi (2002). For an overview of the theory of copulas, see, for example, Joe (1997), Nelsen (1999), Bouye, Durrleman, Nikeghabali, Riboulet and Roncalli (2000), Embrechts, Lidskog and McNeal (2003).

A recent definition of contagion given by Forbes and Rigobon (2002) specifies contagion as an increase in cross-market linkages occurring if two markets (or group of markets) do not present high degree of comovement during both stability and crisis periods. Thus, a conditional correlation test can be carried out to investigate whether the correlation between two markets changes in contagion periods; see, for example, King and Wadhwani (1990), Forbes and Rigobon (2002), Caporale, Cipollini and Spagnolo (2005). If the correlation does not vary, the two markets are said to have interdependence. The advantages of this definition of contagion has been extensively discussed in Forbes and Rigobon (2002).

In this paper we propose a methodology for modelling dynamic dependence structure by allowing copula functions or copula parameters to change across time. Thus, we construct tests for contagion based on more general structures than correlation. We employ a threshold approach so these changes do not evolve in time but occur in distinct points. This strategy resembles the threshold or change-point models applied in time-series analysis, see for example Tong (1983). A key ingredient of our proposed methodology is that the number of thresholds is unknown. Moreover, our model determination strategy allows the choice of different copula functions and/or different parameter values between two time thresholds. This becomes feasible due to an adoption of a Markov chain Monte Carlo (MCMC) algorithm together with a Laplace approximation.

The rest of the paper is organized as follows: In section 2 we describe the set of models that capture time-varying dependency between financial returns. In Section 3 we develop an MCMC implementation algorithm that efficiently deals with the large space of models and provides estimates of posterior model probabilities. In Section 4 we test our strategy with simulated data and real data sets. In Section 5 we conclude with a brief summary.

2 Threshold models for copulas

Assume that we deal with two financial returns X_t and Y_t, $t = 1, \dots T$, which are considered to be realizations of the random variables X and Y. Although generalization of our method to multivariate settings is immediate, we only focus on the simple bivariate case throughout the paper. Moreover, emphasis is given to the dependence structure between X_t and Y_t, rather than the correct specification of their marginal densities. Thus, we follow Patton (2005) and we assume that the marginal distributions are characterized by the evolution of the conditional volatilities according to a GARCH(1,1) process. Conditional on this specification, our interest is to model via copulas the time-varying dependence structure of X_t and Y_t.

There have been some related efforts in the literature to deal with such modelling perspective. Patton (2005) proposes a constant functional form for a copula and a parametric model for the evolution of its parameters. Dias and Embrechts (2004) derive a hypothesis test for checking breaks in the association parameters. Rodriguez (2003) uses Markov switching parameters in the spirit of Hamilton and Susmel (1994). Our approach is based on Bayesian non-parametric modelling following ideas from Denison, Mallick and Smith (1998). In particular, we assume that a bivariate copula function C_θ:$[0,1]^2 \rightarrow [0,1]$, indexed by a parameter θ, is chosen to model the joint distribution function of the random variables X and Y, $H(X,Y) = P[X \leq x, Y \leq y]$ say, through

$$H(X,Y) = C_\theta(F(X), G(Y)), \tag{1}$$

with F and G denoting the distribution functions of X and Y respectively. For reasons that will be evident later θ lies in $(-\infty, \infty)$; if this is not the case, we just perform a simple transformation. We generalize the static relationship (1) by introducing disjoint sets I_j, $j = 1, \dots, J$, so that

$$H(X,Y) = \sum_{j=1}^{J} I_j(t) C_{\theta_j}(F(x_j), G(y_j)) \tag{2}$$

where $[0,T] = \bigcup_j I_j$, $I_j(t) = 1$ if $t \in I_j$, and in each interval I_j the parameter of the copula is θ_j and the corresponding samples x_j and y_j. To allow for full flexibility, the number of disjoined sets is unknown and estimated from the data. The model formulation (2) can be viewed as a change-point model in which the value of copula parameter jumps to a new value of some undetermined time.

A further realization of (2) is achieved by employing a collection of copula functions $\{C^i_\theta, i = 1, \ldots, \ell\}$ so that

$$H(X,Y) = \sum_{j=1}^{J} I_j(t) \sum_{i=1}^{\ell} w_{ij} C^i_{\theta_j}(F(x_j), G(y_j)) \tag{3}$$

where $C^i_{\theta_j}$ denotes the copula function C^i_θ with $\theta = \theta_j$ and w_{ij} denotes the probability of having the copula i in the interval I_j, so $\sum_{i=1}^{\ell} w_{ij} = 1$ for all j. Thus, our general model (3) allows both the functional form of the copula and the parameters to change within each interval I_j.

The intervals $\{I_j, j = 1, \ldots, J\}$, $J > 1$, are specified by $J - 1$ thresholds parameters $\gamma_1, \ldots, \gamma_{J-1}$. We set $\gamma_0 = 1$ and $\gamma_J = T$, so for $J = 1$, $I_1 = [1, T]$. Since our model assumes that the dependence between two consecutive thresholds is characterized by a copula function, we should allow some distance between thresholds, so that enough data points are used to estimate the parameter of the copula. Note that copula functions model dependence in the tails of the joint distribution, so small sample sizes are not adequate for gathering tail-behavior information. We denote this distance as d, so that we require $|\gamma_j - \gamma_{j-1}| \geq d$, $j = 1, \ldots, J - 2$, and we have used, in our empirical studies, $d = 100$.

It is evident that our models provide an immediate test for interdependence or contagion between two markets or group of markets since the model with zero thresholds corresponds to interdependence. Moreover, the increased flexibility offered by keeping the location and number of thresholds unknown allows full investigation of the time of the contagion.

3 Bayesian model formulation

3.1 Bayesian model determination

Suppose that we have data y that are considered to have been generated by a model m, one of the set M of the competing models. Each model specifies a joint distribution of Y, $f(y|m, \theta_m)$, conditional on the parameter vector θ_m. A Bayesian model determination approach requires the specification of the prior model probability of m, $f(m)$, and conditional prior densities

$f(\theta_m|m)$ for each $m \in M$. Then the posterior model probability is given by

$$f(m|y) = \frac{f(m)f(y|m)}{\sum_{m \in M} f(m)f(y|m)}, m \in M \tag{4}$$

where

$$f(y|m) = \int f(y|m, \theta_m) f(\theta_m|m) d\theta_m$$

is the marginal probability of model m.

If the number of possible models $|M|$ is large, and if analytical calculation of $f(y|m)$ is not possible, MCMC algorithms provide an efficient tool to explore the parameter-model product space for (m, θ_m); see for example Green (1995), Dellaportas, Forster and Ntzoufras (2002). Since the general model (3) involves a large number of models $|M|$, we describe in Section 3 how an MCMC algorithm together with Laplace approximation for $f(y|m)$ can be constructed to estimate (4). A key idea is that instead of obtaining samples form $f(m, \theta_m)$, we just approximate the posterior marginal density of $f(m)$ by integrating out θ_m for all m that lie in the high posterior probability region of $f(m)$.

3.2 Priors

We take the prior model probabilities to be $f(m) = |M|^{-1}$. Special care is needed in model choice problems for $f(\theta_m|m)$, since it is well known that very disperse priors cause the Bartlett's-Lindley paradox, see Kass and Raftery (1995). We follow Kass and Wassermann (1996) and we propose a unit information prior for $f(\theta_m|m)$. To specify this prior for a given interval $I_j = [\gamma_{j-1}, \gamma_j]$ and a copula function C, first calculate the corresponding maximum likelihood

$$\widehat{\theta} = \arg\max \prod_{t \in I_j} f(x_t) g(x_t) c_\theta(F(x_t), G(x_t)) \tag{5}$$

where f, g and c_θ are the corresponding density functions of F, G and C_θ, respectively. Then, we place a zero-mean Normal prior for θ with variance given by

$$(\gamma_j - \gamma_{j-1})|H(\widehat{\theta})|^{-1}$$

where $H(\widehat{\theta})$ is the Hessian matrix evaluated at $\widehat{\theta}$. As expected, this prior specification is also very non-informative within each model, obtaining standard deviations for the prior densities that are about 40 times larger than the corresponding posterior standard deviations.

4 MCMC Algorithm

4.1 Laplace approximation

Searching in both model and parameter space is possible via reversible jump algorithm of Green (1995). For an extensive list of applications in Bayesian non-linear modelling see Denison, Holmes, Mallick and Smith (2002). However, to facilitate our search, we integrate out the parameter uncertainty within each model by approximating the marginal likelihood by

$$\widehat{f}(y|m) = (2\pi)^{d/2}|\widehat{\Sigma}_m|^{1/2} f(y|\widehat{\theta}_m, m) f(\widehat{\theta}_m|m) \tag{6}$$

where $dim(\theta_m) = d$, $\widehat{\theta}_m$ is the maximum likelihood estimate calculated by (5) and Σ is the inverse of the Hessian matrix evaluated at $\widehat{\theta}_m$. For details see Kass and Raftery (1995), Raftery (1996). By performing this approximation for every model m, we are left with the task to sample in the space of (discrete) density function specified by (4) with $f(y|m)$ replaced by (6).

4.2 MCMC moves

We require an efficient Markovian scheme that mixes well in the model space. To achieve this, we employ a random walk Metropolis algorithm which is properly tuned with a proposal density that allows quick exploration of the state space; for details, see Dellaportas and Roberts (2003).

Assume that the maximum number of thresholds is K. This number is taken to be large enough so that it does not affect in any way the posterior density of the number of thresholds. The proposal density $q(m^{'}|m)$, which proposes a new model $m^{'}$, when the current model is m, is constructed as follows. Assume that model m has k thresholds. Then the possible proposal moves are formed as

- *'Birth'*: Propose adding a new threshold.
- *'Death'*: Propose removing one of the k current thresholds if the copula is the same in both sides of the threshold.
- *'Move'*: Propose a reallocation of one of the k current thresholds.

- *'Change'*: Propose a change of a functional form of a copula within two current thresholds.

Denote by b_k,d_k,m_k and c_k the probabilities of 'Birth','Death','Move' and 'Change' moves respectively. Then the proposal densities, for the model m with k thresholds, are formed as:

$$q(m^{'}|m) = \begin{cases} \frac{b_k}{T-k}, & if \quad `Birth' \\ \frac{d_k}{k}, & if \quad `Death' \\ \frac{m_k}{k}, & if \quad `Move' \\ \frac{c_k}{k}, & if \quad `Change' \end{cases}$$

For example a sensible choice is b_k=d_k=m_k=c_k=$\frac{1}{4}$, $k = 1, \ldots, K-1$; b_K=d_0=$m_0 = 0$, b_0=c_0=$\frac{1}{2}$, b_K=m_K=c_K=$\frac{1}{3}$. For the 'Move' proposal density we chose a discrete uniform, which takes equidistant values around the current threshold, and we noticed that a length 21 time points, provides a reasonable density spread that achieves a good mixing behavior.

We have noticed that some combinations of the four basic moves offer great flexibility in our samplers (see Dellaportas, Forster and Ntzoufras (2002) for a discussion on 'local' and 'global' moves in model space), so the algorithm we suggest involves also the following moves:

- 'Birth-Change': Propose adding a new threshold and changing the copula function in one of the two resulting intervals.

- 'Death-Change': Propose removing one of the current k current thresholds when the copula functions are different in each side of the threshold and propose one of the two functions as a candidate for the new interval.

The way we incorporated these extra moves in our sampler is just split all b_k and d_k probabilities to half and thus allow equal proposal probabilities for the 'Birth-Change' and 'Death-Change' moves. Of course, all these choices only affect the mixing of the chain and might need to be tuned appropriately in other datasets. The acceptance probability for moving from model m to model $m^{'}$ is given by

$$\alpha = min\{1, \frac{\widehat{f}(y|m^{'})}{\widehat{f}(y|m)} \times R\}$$

where $\widehat{f}$ is the product of all estimated marginal likelihoods in each interval of $[0, T]$ calculated via (6), and R is given by

$$\tfrac{d_{k+1}}{b_k},\ \tfrac{b_{k-1}}{d_k},\ 1{,}1$$

for 'Birth', 'Death', 'Move' and 'Change' moves respectively.

We note here that the Metropolis-Hastings moves above resemble the usual reversible jump moves of Denison, Holmes, Mallick and Smith (2002), but our Laplace estimation (6) essentially removes all the parameter dimension difference between models resulting to a simple acceptance probability without the usual Jacobian terms.

5 Copulas

We describe in this section the mathematical derivations for our data analysis examples of the next section. We use the following copulas:

1. *Frank's copula*: $C^F_\theta(u,\nu) = -\frac{1}{\theta}\ln(1 + \frac{(e^{-\theta u}-1)(e^{-\theta\nu}-1)}{e^{-\theta}-1}), \quad \theta \neq 0$

2. *Clayton's copula*: $C^C_\alpha(u,\nu) = [u^{-\alpha} + \nu^{-\alpha} - 1]^{-1/\alpha}, \quad \alpha > 0$

3. *Gumbel's copula*: $C^G_\beta(u,\nu) = exp\{-[(-lnu)^\beta + (-ln\nu)^\beta]^{1/\beta}\}, \quad \beta \geq 1$

where the transformations $\theta = \log\alpha$ and $\theta = \log(\beta - 1)$ allow the parameters of the Clayton's and Gumbel's copulas to lie in the $(-\infty, \infty)$ interval. Frank's copula (Frank, 1979) was chosen for its nice symmetrical properties, whereas Clayton's (Clayton, 1978) and Hougaard - Gumbel's (Gumbel, 1960, Hougaard, 1986) copulas are somehow complementary, since they exhibit opposite upper and lower tail dependence properties. The marginal densities for all series we looked at, are specified by the usual GARCH(1,1) process (Bollerslev, 1986), so that the joint density functions are applied to the residuals of each series derived from the model fit in a generic interval I, say u_t and ν_t, $t \in I$. These joint density functions are:

- $c_\theta^F(U,V) = \prod_{t\in I}\theta(1-e^{-\theta})e^{-\theta(u_t+\nu_t)}[e^{-\theta}-1+(e^{-\theta u_t}-1)(e^{-\theta \nu_t}-1)]^{-2}$

- $c_\theta^C(U,V) = \prod_{t\in I}(e^\theta+1)(u_t+\nu_t)^{-e^\theta-1}(u_t^{-e^\theta}+\nu_t^{-e^\theta}-1)^{-e^{-\theta}-2}$

- $c_\theta^G(U,V) = \prod_{t\in I}(\log u_t \log \nu_t)^{e^\theta}(u_t\nu_t)^{-1}e^{-((-\log u_t)^{e^\theta+1}+(-\log \nu_t)^{e^\theta+1})^{\frac{1}{e^\theta+1}}}(e^\theta+((-\log u_t)^{e^\theta+1}+$
$$(-\log \nu_t)^{e^\theta+1})^{\frac{1}{\theta+1}}((-\log u_t)^{e^\theta+1}+(-\log \nu_t)^{e^\theta+1})^{-2+\frac{1}{\theta+1}}.$$

The resulting posterior densities are obtained by multiplying the likelihood functions in each interval with the non-informative prior densities of Section 3. When the maximizations or derivatives required for the Laplace approximations are analytically intractable, numerical techniques are used.

5.1 Model averaging

Our MCMC sampler provides estimates for posterior model probabilities which are useful in picking the best model (under a zero-one loss function), which mostly represents the dependence between the two time series. However, it is rather common to exploit further this posterior density by adopting a predictive approach for inference, or averaging any posterior summary of interest by weighting it with the posterior probability of each model; see, for example, the discussion in Bernardo and Smith (1994). This model averaging approach can be used, for instance, when some dependence summary statistic, say $\phi(\theta)$, is estimated. Instead of deriving an estimate of $\phi(\theta)$ based on samples drawn from the model with the highest posterior probability, we can just use

$$\phi(\theta) = \sum_{m\in M} f(m|y)\phi_m(\theta)$$

where $f(m|y)$ is the posterior model probability of the model m and $\phi_m(\theta)$ is the estimate of $\phi(\theta)$ under model m. We will be using model averaging in Section 6 to illustrate how predictive inferences can be made for Kendall's τ, a common alternative to Pearson's correlation measure of association. For completeness we present below the Kendall's τ of the families of copulas that will be used in this paper:

1. *Frank's copula*: $\tau_F = \frac{1-4(1-D_1(\theta))}{\theta}, \quad \tau_F \in (-1,1)$, where $D_k(x)$ is the Debye function, $D_k(x) = \frac{k}{x^k}\int_0^x \frac{t^k}{e^t-1}dt$, $k \in \mathbb{N}$.

2. *Clayton's copula:* $\tau_C = \frac{\theta}{\theta+2}, \quad \tau_C \in [0,1)$

3. *Gumbel's copula:* $\tau_G = 1 - \frac{1}{\theta}, \quad \tau_G \in [0,1)$.

6 Examples

6.1 Artificial data

We report here one of many artificial data experiments we performed in order to illustrate the efficiency of our method. We simulate a bivariate series with standard normal marginals and the dependence structure specified by Frank's copula. Details of how to simulate from a copula can be found in Nelsen (1999). The parameter θ was set to $\theta = 3$, then at $t = 850$ it was set to $\theta = 5.5$, and at $t = 1700$ it was set back to $\theta = 3$. For Frank's copula this corresponds to Kendall's τ that jumps from about $\tau = 0.3$ to about $\tau = 0.5$; see Figure 1. We started the MCMC chain with zero breaks and after a burn-in period of 20,000 points we obtained our Markov chain output by collecting the next 20,000 points. An ergodic estimate of the posterior model probabilities, where each model represents a different number of thresholds, is given in Figure 2. The MCMC chain detected the correct model ($k = 2$) and the correct thresholds very early and a series of tests with many initial values showed that the mixing is very good.

6.2 Real data example 1

We apply our models to daily returns of Dow Jones average and Xetra DAX indices from 7/9/1998 up to 7/9/2004. This sample was selected to include the periods before and after the 9/11. We initiated our Markov chain with zero breaks and after a burn-in period of 20,000 points we obtained our Markov chain output by collecting the next of 20,000 points. An ergodic estimate of the posterior model probabilities, where each model represents a different number of thresholds, is given in Figure 3. The outcome supports model with 4 breaks. The posterior samples provide strong evidence of change-points in the dependence structure. Notice that there is a small increase in the estimates of Kendall's τ around 9/11. For comparison purposes, Figure 4 also depicts two rolling window-based sample estimates of Kendall's τ calculated as $\tau_r = (C_r - D_r)/(C_r + D_r)$ where C_r is the number of concordant pairs and D_r the number of discordant pairs obtained from the sample of interval $I_r = [r, r+\mathrm{W}]$, where W is the window width and $r = 1, \ldots, T - W$.

6.3 Real data example 2

We deal with daily returns from Mexico and Argentina stock indices during the period 7/4/1994 - 12/31/1996. These data have been analyzed in the past by Forbes and Rigobon (2002) and Rodriguez (2003) who studied quite extensively the changing structure of dependence in this period and its association with financial contagion. In this case we assumed that the dependence structure is modelled by either Clayton's or Gumbel's copula. An ergodic estimate of the posterior model probabilities, based on a burn-in period of 20,000 points and a collected sample of the next 20,000 points, is given in Figure 5. Figure 6 depicts Kendall's τ evaluated both with two sample-based estimators and based on our posterior sample based on model averaging. Our model search strategy clearly indicates that there is very strong evidence of two thresholds which result to an increase of Kendall's τ in the period $96/4 - 96/6$ from about 0.28 to about 0.37. According to our model, there is evidence of contagion between Mexico and Argentina during this period.

7 Conclusions

We studied the important question of modelling the dependence structure between economic series by allowing copula functions and parameters to change across time. Both simulated and real data examples provide evidence that this flexible threshold-based modelling is very promising and offers a good insight of the time-varying association between financial series. Contagion between markets or between groups of markets as defined by Forbes and Rigobon (2002) can be examined by testing whether the number of thresholds in our model is zero or not.

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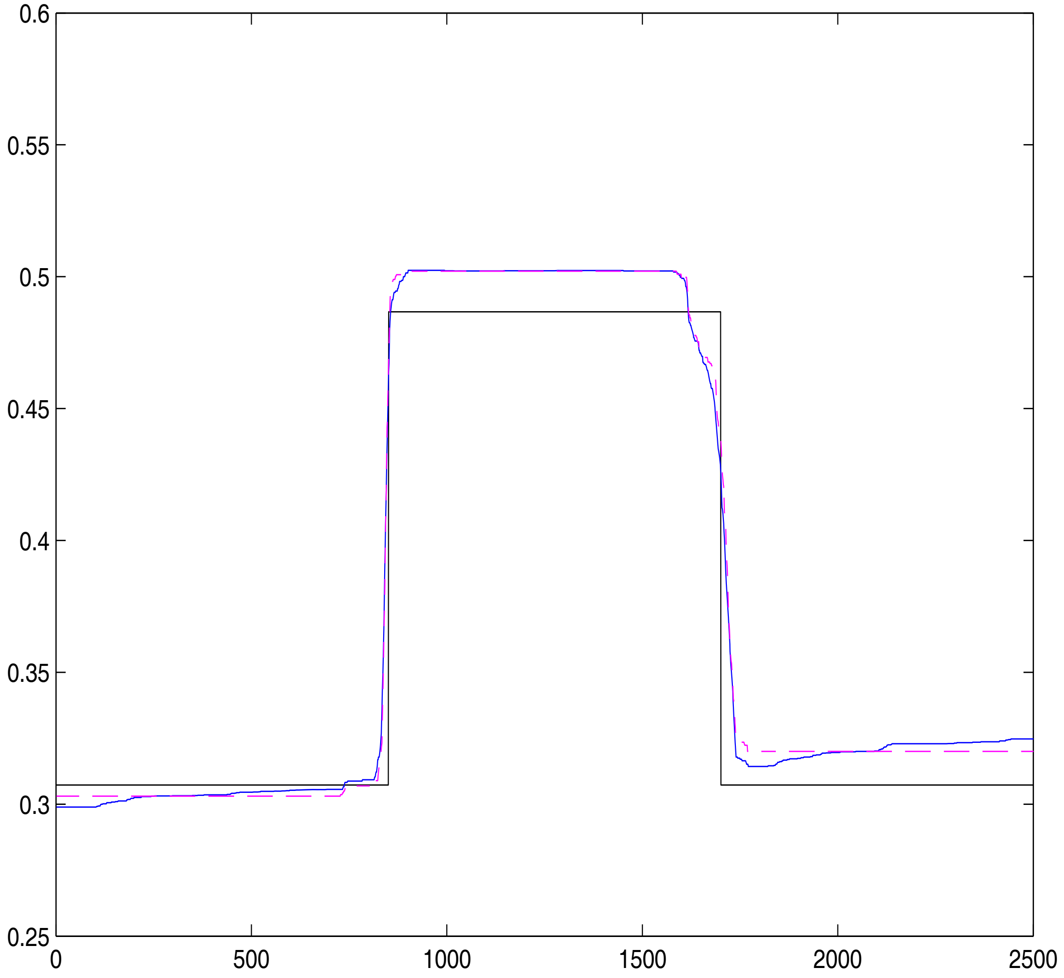

Figure 1: Kendall's τ for simulated data. Solid line: real τ; dotted line: estimated τ based on the model with two thresholds; dashed line: estimated τ based on model averaging.

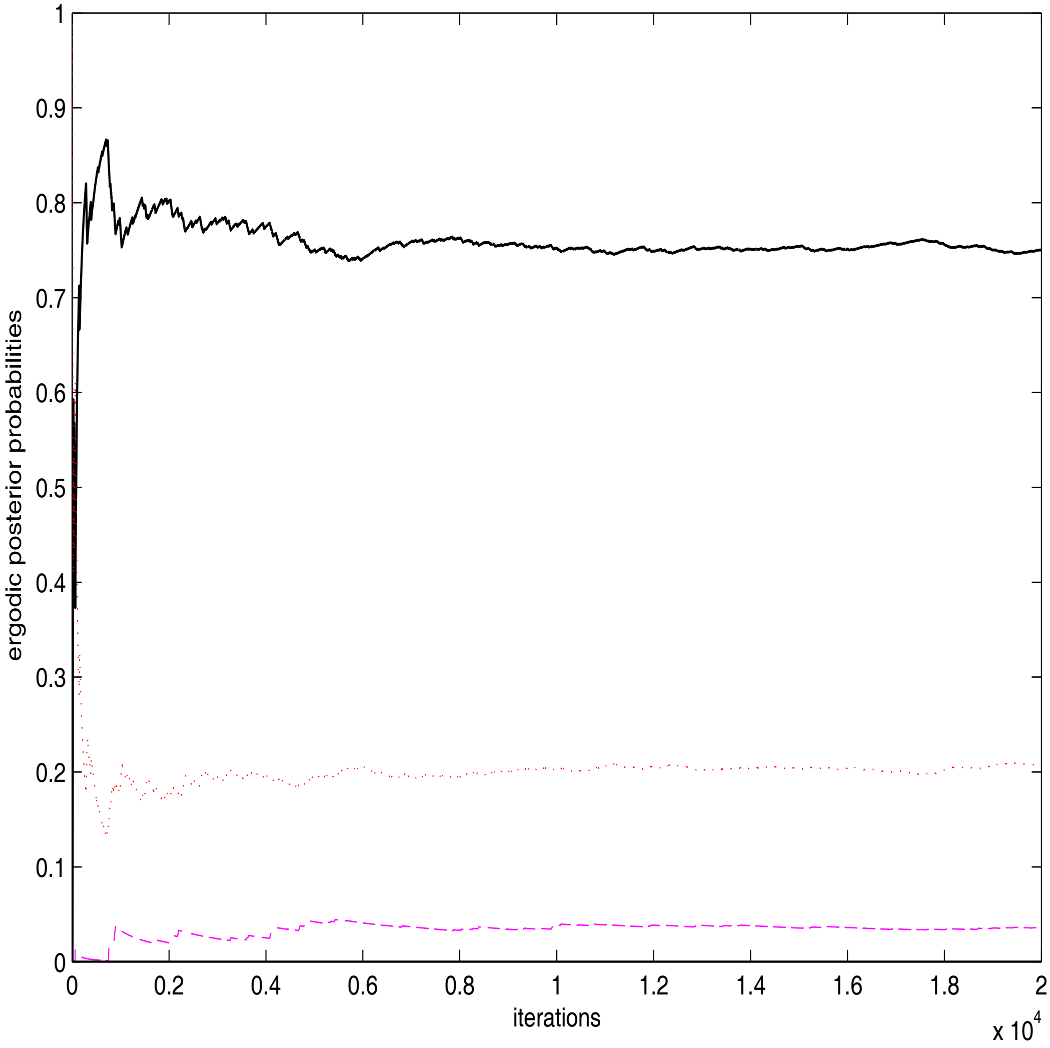

Figure 2: Posterior probabilities for different models. k represents the number of thresholds in the model. Solid line: $k = 2$; dotted line: $k = 3$; dashed line: $k = 4$.

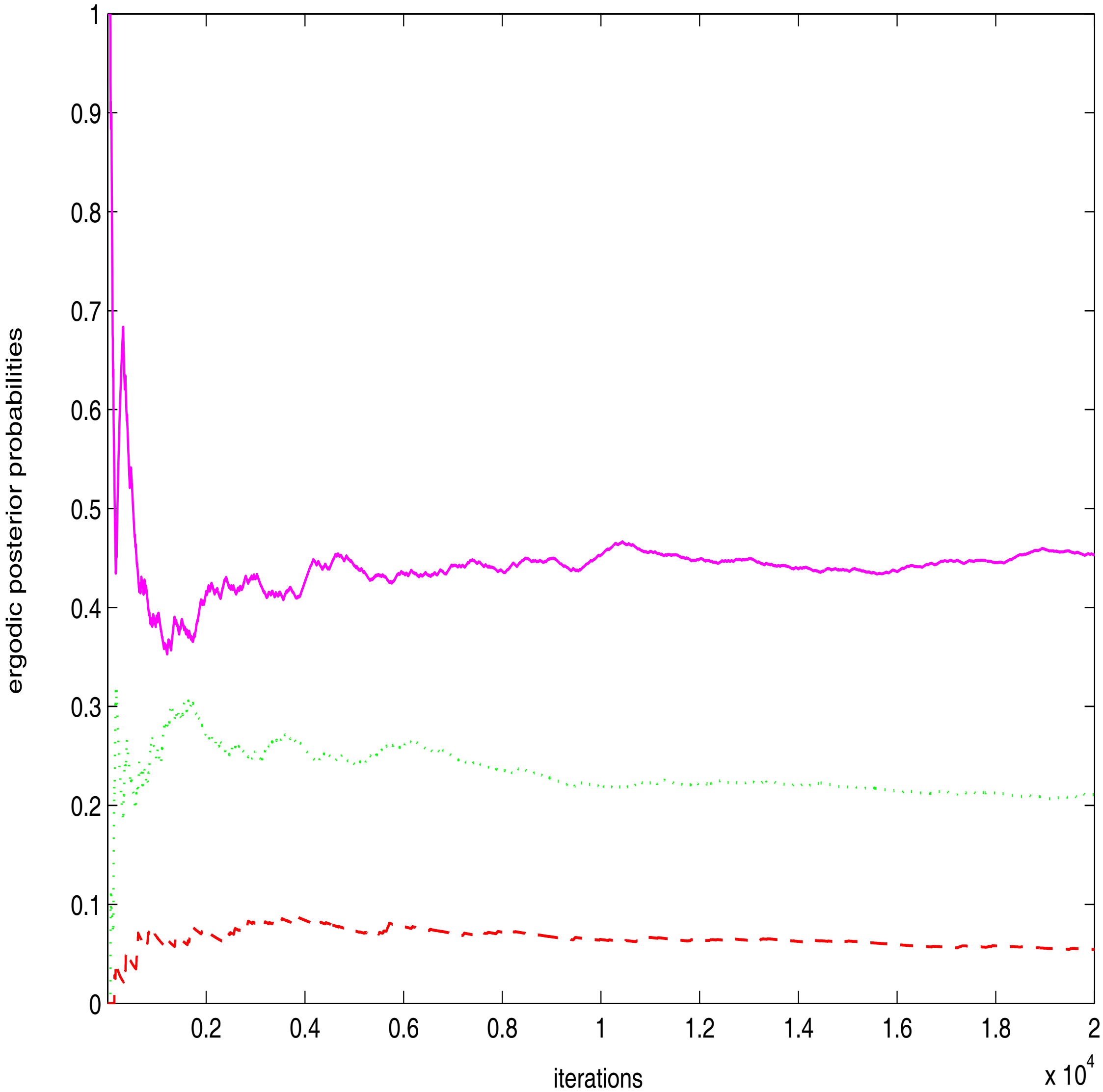

Figure 3: Ergodic posterior probabilities for different models. k represents the number of thresholds in the model. Solid line: $k = 4$; dotted line: $k = 5$; dashed line: $k = 3$.

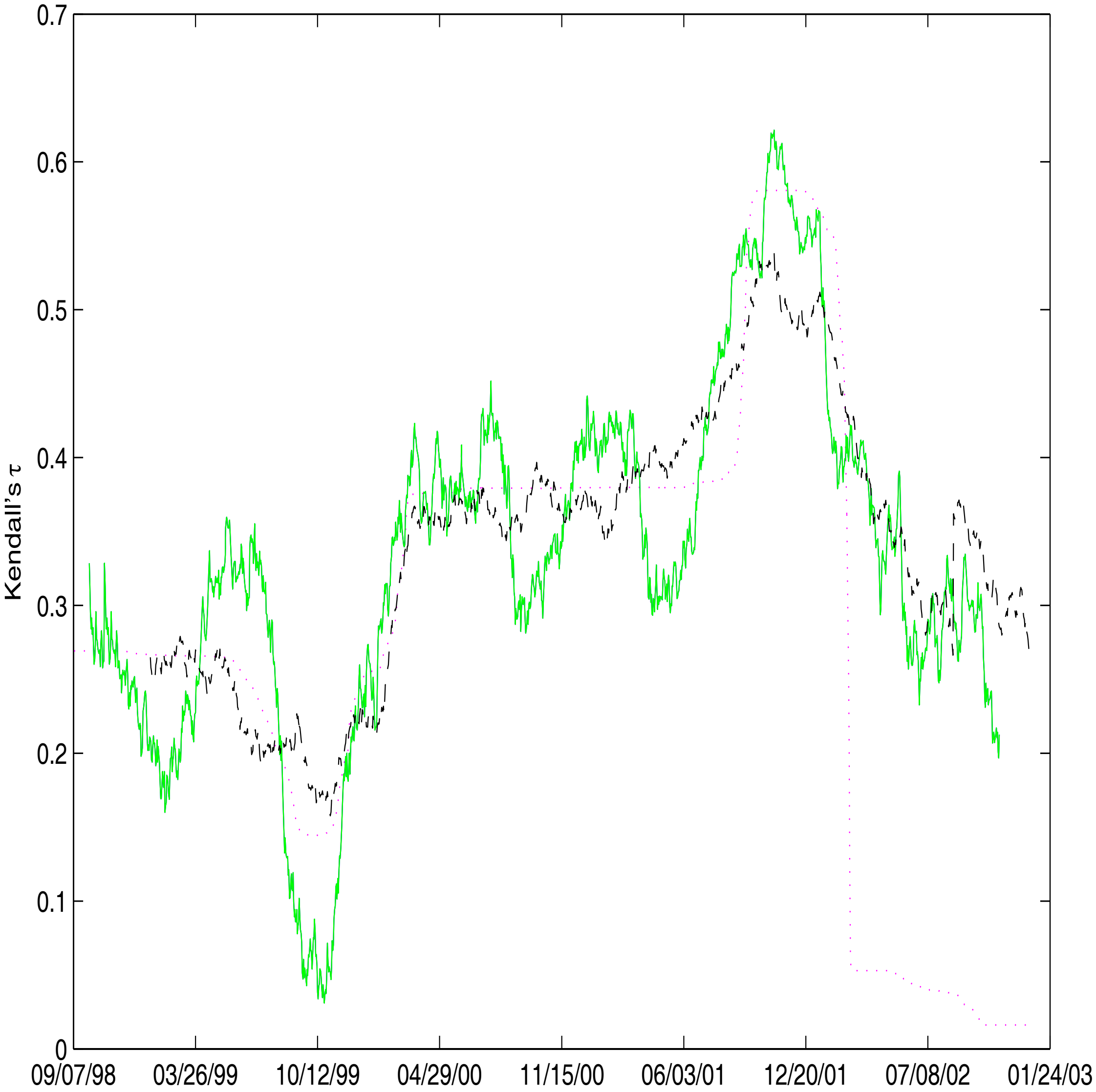

Figure 4: Kendall's τ for Dow Jones-Xetra Dax. Solid line: sample τ for window size 100; dashed line: sample τ for window size 250; dotted line: estimated τ based on model averaging.

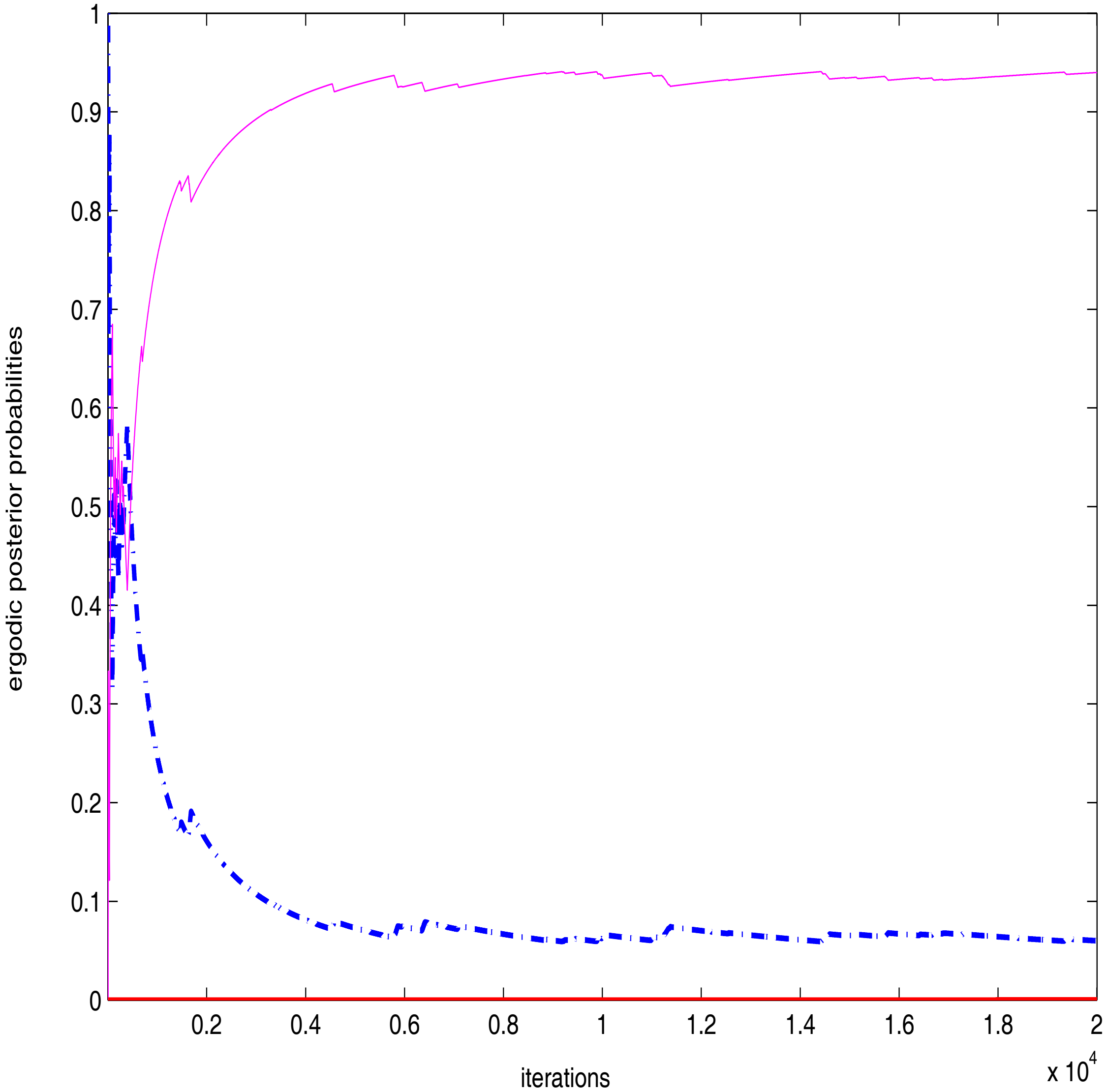

Figure 5: Mexico-Argentina: Ergodic posterior probabilities for different models. k represents the number of thresholds in the model. Solid line: $k = 1$; dashed-dotted line: $k = 0$; dotted line: $k = 2$.

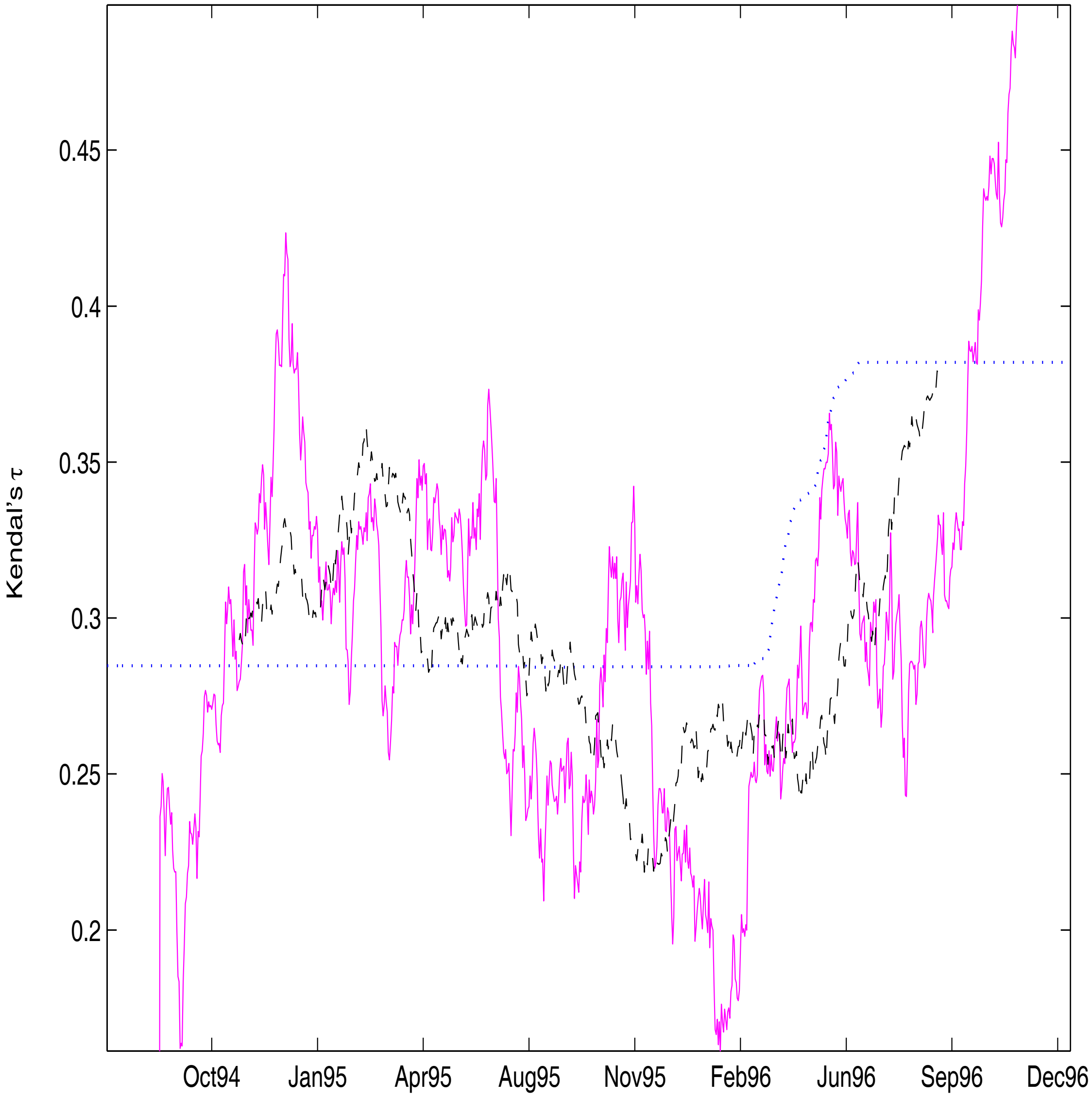

Figure 6: Kendall's τ for Mexico-Argentine. Solid line: sample τ for window size 100; dashed line: sample τ for window size 250; dotted line: estimated τ based on model averaging.