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Zheng Tan, Rituparna Sen and Kausik Chaudhuri

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TESTING CONTAGION IN FINANCIAL TIME SERIES

Zheng Tan[1], Rituparna Sen[†,2] and Kausik Chaudhuri[3]
[1]Adara Global, Mountain View, USA
[2] Indian Statistical Institute, Chennai, India
[3] Leeds University Business School, Leeds, UK

Abstract. Financial contagion indicates a process through which transmission of shock originating in the financial market of one economy spreads to others. Although the study of causes and prevention of contagion is popularized by economists, very few quantitative studies exist on detection of contagion. This paper provides a new idea of Residual and Recurrence Times (RRT) of high or low values for multivariate time series to detect contagion. In presence of financial contagion, the distributions of residual and recurrence times are not the same. We examine the equality of two distributions using the permutation test. In comparison to other methods in multivariate extreme value theory, our proposed method does not need the i.i.d. assumption. We derive asymptotic results under the GARCH model. Our method can handle the situation where the extremes for different components do not occur at the same time. We justify our methods in two ways: first using thorough simulation studies and then applying the proposed method to real data on weekly stock indices from seventeen markets.

Keywords: contagion; multivariate time series; permutation test; GARCH model; compound Poisson process.

1. Introduction

Contagion is primarily used to describe the spread of a disease by direct or indirect contact. In financial markets, contagion refers to the transmission of a financial shock in one market to other interdependent markets, in a manner similar to communication of medical disease. Financial contagion can be at both levels: at the domestic level, e.g., the crash of Lehman Brothers and subsequent depressed United States financial markets, and, at international level, e.g., the Mexican "Tequila crisis" in 1994 that spread to all countries in South America.

Despite the wide use of the term contagion there exists no universal mathematical definition for contagion. According to Forbes and Rigobon (2001), there have been four methods to test and measure contagion effects. The first and most straightforward one is based on cross-markets correlation coefficient in asset returns and examines whether inter-related financial markets exhibit anomalous patterns of correlation in returns during two different periods: stable period and the period following a shock. If the correlation coefficient increases significantly after the shock, this implies the presence of contagion. Details can be found in King and Wadhani (1990) and Lee and Kim (1993). In the second approach (as in Hamao et al. (1990)), the ARCH or GARCH models are used to test for the presence of significant volatility spillover from one market to another during or after the crisis. The third test, implemented by Longin and Solnik (1995), examines whether there is significant change in the co-integrating vector between markets. The fourth procedure applies probit model to ascertain the probability of a crisis occurring in one country conditional on a crisis that has already occurred in another country (Eichengreen et al (1996) and Kaminsky and Reinhart (1998)).

Contagion is observed when one or more entities are going through extreme high or low economic phases. Such phases are economically the most interesting and high-impact periods. Methods of multivariate time series are not suitable in this setting, since they concentrate on the joint behavior during stable and stationary periods. Another approach is through tail dependence in multivariate

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[†] *Corresponding author*, E-mail: `rsen@isichennai.res.in`.

extreme value theory, which is used to study the dependence between multiple variables at times of extreme high or low periods, see Sen and Tan (2012) and references therein. The main drawback of this approach is the assumption of independently and identically distributed (i.i.d.) observations. Thus, serial dependence in the time-series of extremes is ignored. Since, in general, it takes finite time for financial shocks to be transmitted from one market to another, the extremes do not necessarily occur in both series at the same point of time. Extreme value theory ignores this crucial fact. Our new method, Residual and Recurrence Times, focuses on the time lags of transmission of financial shocks and the assumption of i.i.d. observations is removed.

To illustrate our claim, we present two simulated series X and Y in Figure 1. The horizontal lines in the plot are 90th percentile of series X and Y, respectively. It is obvious that a large shock in series Y is followed by another large shock in series X in a few steps (less than two steps). Thus, contagion effect is present. We generate the non-extreme values (which accounts for 90% of the data) in the two series independently from standard normal distribution. The only dependent part comes from the extreme values, which accounts for 10% of the data. Our proposed method is apt at detecting the contagion effect despite presence of small cross-autocorrelation and where extreme dependence constitutes a small proportion of the data. We also observe that in Figure 1, the extreme events in X and Y do not necessarily occur at the same time point. Thus, bivariate extreme value theory may not be a good tool here. Furthermore, we find that extremogram, see Davis and Mikosch (2009), for this kind of series is very small and hence, extremogram may not be a good tool for detecting the extremal dependence largely due to an implicit assumption of fixed time lag between extreme events. Our proposed method does not suffer from fixed time lag problem.

The rest of the paper is organized as follows: Section 2 describes our proposed test and testing procedure. We detail the method validation for the RRT method under different scenarios in Section 3. Section 4 provides the simulation study. In Section 5, we apply our proposed test to real data from financial markets. Section 6 contains concluding comments.

2. Model Description

In this section, we describe the testing procedure for the Residual and Recurrence Times Test (RRT) Test. In Section 2.1, we introduce the used notations and definitions whereas Section 2.2 outlines the procedure for testing contagion.

2.1. **Some Notations and Definitions.**

Let X and Y be two time series, e.g., return on assets, volatility, volume, etc.

Definition 2.1 (Extreme Event).
An extreme event for series X (Y) is an event defined as being beyond a chosen threshold, say an upper or lower percentile of the empirical distribution of series X (Y).

Definition 2.2 (Recurrence Time).
Recurrence time, denoted by U_i (V_j), for series X (Y) is the time lag between two consecutive occurrences of extreme events in series X (Y).

Definition 2.3 (Raw Residual Time).
Raw Residual time, denoted by Z_k, for series X given series Y is the time lag from an extreme event in series Y to the following occurrence of an extreme event in series X. Mathematically,

$$Z_k = \sum_{i=1}^{N} U_i - \sum_{j=1}^{k} V_j + 1,$$

where

$$N = arg\ min_n \{\sum_{i=1}^{n} U_i - \sum_{j=1}^{k} V_j \geq 0\}.$$

Remark 2.1. *The Raw Residual Time is a measure of time needed for the transmission an extreme shock from one series to another. In the above definition for Raw Residual Times* $\{Z_k\}$*, it has "+1" on the right hand side of the equation. This is just a matter of convention. The "+1" means that if two extreme events occur at the same time, we consider the transmission time to be 1.*

Definition 2.4 (Residual Time)**.**
The sequence of residual times, denoted by $\{W_k\}$*, for series* X *given series* Y *is a subset of* $\{Z_k\}$ *by eliminating the overlapping raw residual times, and is equal to* $\{Z_k\}\backslash\{Z_{k'} : Z_{k'} + V_{k'} = Z_{k'-1}\}$.

In Figure 2, black dots represent extreme events; sequences of $\{U_i\}$ and $\{V_j\}$ denote the recurrence times for series X and Y, respectively; sequence of $\{Z_k\}$ is the raw residual times for series X given Y; sequence of $\{W_k\}$ is the residual times for series X given Y.

2.2. **Testing Procedure.** Given a bivariate time series (X, Y), we can choose a threshold (say 95th percentile or 5th percentile of the empirical series) and find the extreme events as the values beyond (above or below) the threshold. Then the recurrence times for X, $\{U_i\}$, and the residual times for X given Y, $\{W_k\}$ can also be obtained. The null hypothesis is that there is no contagion effect transmitted from Y to X, and the alternative hypothesis is that there exists contagion effect transmitted from Y to X. The testing rule is constructed as follows. If the distribution of recurrence times $\{U_i\}$ and the distribution of residual times $\{W_k\}$ are significantly different, one would reject the null hypothesis. There are well established non-parametric procedures for testing the equality of two distributions, such as Kolmogorov-Smirnov test (K-S test), Mann-Whitney-Wilcoxon test and Permutation test. We use the Permutation test for this purpose since this is appropriate for integer valued data with ties, while K-S test is for continuous distributions. Moreover, permutation test is an exact test which can deal with small sample size situations and we sometimes have small sample sizes (less than 30) for the sequences of residual times. As for Mann-Whitney-Wilcoxon test, although it is a choice, it uses rank-sum but our focus is not on ranks. Instead, we care about mean. More details about Permutation test can be found in Section 3.

Application of permutation test directly to residual times and recurrence times is problematic as it requires independence between two samples. But residual times and recurrence times are dependent. Simulation studies show that this problem leads to a very small size. To avoid this problem, we propose the following alternative. In order to obtain critical values, we permute the combined group $\{U_i\} \cup \{V_j\}$ since $\{U_i\}$ and $\{V_j\}$ are independent under null hypothesis. We use these critical values for the test statistic $\overline{U} - \overline{W}$. We summarize the testing procedure for existence of contagion effect from Y to X as follows:.

(a) Input two series X and Y, and find the time points of extreme events.
(b) Compute the corresponding recurrence times, $\{U_i\}$ and $\{V_j\}$; denote the the sample sizes as n_u and n_v for $\{U_i\}$ and $\{V_j\}$, respectively.
(c) Find residual times $\{W_k\}$ of X based on Y, and calculate $\overline{U} - \overline{W}$, denoted as Δ_0.
(d) Combine $\{U_i\}$ and $\{V_j\}$ as one group, then permute and divide it into two subgroups, denoted as $\{\widetilde{U}_i\}$ and $\{\widetilde{V}_j\}$, with one sample size equal to n_u, and the other sample size equal to n_v. Find the corresponding residual times $\{\widetilde{W}_k\}$ and calculate $\overline{\widetilde{U}} - \overline{\widetilde{W}}$, denoted as $\widetilde{\Delta}_i$.
(e) Repeat step (d) for all possible permutations (or permute the combined group randomly for many times), then we have a sequence of $\{\widetilde{\Delta}_i\}$, which will be considered to be critical value.
(f) Finally, the p-value is the proportion of the times when the absolute value of $\widetilde{\Delta}_i$ is larger than or equal to Δ_0.

3. Method Validation

This section gives the detailed theoretical justification for the RRT method under different scenarios. The idea of RRT method comes from a simple scenario for i.i.d. series. Since the goal is to test the existence of contagion effect or extreme dependence among series, we would consider extreme events over or below a specified threshold. For two i.i.d. series, called X and Y, the recurrence times (denoted as $\{U_i\}$ for X, and $\{V_j\}$ for Y) over (below) a high (low) percentile follow Geometric distribution. If the two recurrence times are independent (or the two series X and Y are independent over high thresholds), by using"Memoryless" property for Geometric distribution, the residual times of X given on Y have the same distribution as the recurrence times of X. In such a way we can construct a hypothesis testing procedure to examine contagion effect from Y to X by testing the equality of distributions for $\{W_k\}$ and $\{U_i\}$.

Section 3.1 is devoted to the verification of the method under i.i.d. series setting. In section 3.2 the method is validated in the case of ARCH and GARCH model setting.

3.1. **Testing contagion in i.i.d. series.** As in section 2.1, an extreme event is defined as being beyond an extreme high or low threshold. Thus, threshold needs to be specified. There are two cases to deal with. One is when the threshold is a fixed number (i.e., the theoretical pth percentile of the distribution); the other one is when the threshold is the sample pth percentile of the empirical distribution. The RRT method is verified under the above two cases for i.i.d. setting.

The following theorem proves the feasibility of the RRT method under the i.i.d. series scenario when the threshold is a pth percentile of the population.

Theorem 3.1. *Let X and Y be two i.i.d. series with cumulative distribution function $F(x)$ and $G(y)$, respectively. Define $\{U_i\}$ ($\{V_j\}$) to be the recurrence times for series X (Y) above the $100p_1$th ($100p_2$th) percentile of the distribution $F(x)$ ($G(y)$), and $\{W_k\}$ be the residual times of X given Y. Then,*

(a) *$\{U_i\}$ is i.i.d. Geometrically distributed with success probability $(1-p_1)$, and $\{V_j\}$ is i.i.d. Geometrically distributed with success probability $(1-p_2)$.*

(b) *If X and Y are independent, $\{W_k\}$ is i.i.d. Geometrically distributed with success probability $(1-p_1)$, that is, $\{U_i\}$ and $\{W_k\}$ have the same distribution.*

Proof. : As shown in the Figure 3, U_i is distributed as Geometric$(1-p_1)$. Based on the assumption that X and Y are independent and the memoryless property for geometric distribution, one can obtain that Z_k is also distributed as Geometric$(1-p_1)$. □

The following theorem proves the feasibility of the method under the i.i.d. series scenario when the threshold is a pth sample percentile of the empirical distribution. Detailed proof can be found in Appendix 6.

Theorem 3.2. *Let $\{X_i\}_{i=1}^m$ and $\{Y_j\}_{j=1}^m$ be two i.i.d. series with length m. Their empirical distributions are $\hat{F}(x)$ and $\hat{G}(y)$, respectively. Define $\{U_i\}_{i=1}^M$ ($\{V_j\}_{i=1}^{M'}$) to be the recurrence times for series $\{X_i\}_{i=1}^m$ ($\{Y_j\}_{j=1}^m$) above the p_1th (p_2th) sample percentile, and $\{W_k\}_{k=1}^K$ be the residual times of $\{X_i\}_{i=1}^m$ given $\{Y_j\}_{j=1}^m$. Then,*

(a) *$(U_1,\dots,U_M) \overset{D}{=} (R_1, R_2, ..., R_M | R_1+\dots+R_M \le m, R_1+\dots+R_{M+1} > m)$, where $\{R_i\}_{i=1}^{M+1} \overset{i.i.d.}{\sim}$ Geometric$(1-p_1)$, and a similar result also holds for $(V_1,\dots,V_{M'})$.*

(b) *For any finite integer k, $\{U_i\}_{i=1}^k$ asymptotically $\overset{i.i.d.}{\sim}$ Geometric$(1-p_1)$ as $m\to\infty, \frac{M}{m}\to(1-p_1)$, and $\{V_j\}_{i=1}^k$ asymptotically $\overset{i.i.d.}{\sim}$ Geometric$(1-p_2)$ as $m\to\infty, \frac{M'}{m}\to(1-p_2)$.*

(c) *If $\{X_i\}_{i=1}^m$ and $\{Y_j\}_{j=1}^m$ are independent, for any finite integer k', $\{W_k\}_{k=1}^{k'}$ asymptotically $\overset{i.i.d.}{\sim}$ Geometric$(1-p_1)$ as $m\to\infty, \frac{M}{m}\to(1-p_1)$, that is, $\{U_i\}$ and $\{W_k\}$ have the same asymptotic distribution, as $m\to\infty, \frac{M}{m}\to(1-p_1)$.*

Remark 3.1. *According to above theorem part (c), an asymptotic hypothesis testing procedure for contagion*

$$H_0 : \textit{No contagion vs } H_1 : \textit{Exists Contagion}$$

can be constructed as

$$H_0 : \{U_i\} \textit{ and } \{W_k\} \textit{ follow the same distribution}$$

$$\text{vs} \quad H_1 : \{U_i\} \text{ and } \{W_k\} \text{ follow different distributions.}$$

3.2. **Testing contagion in ARCH and GARCH series.** The previous section verifies the RRT method under the i.i.d. series scenario, while this section gives the validation of the method under stationary ARCH and GARCH times series models. Section 3.2.1 briefly discusses the idea of addressing extremal events via point processes. Then, section 3.2.2 gives the theorems used in Point Processes for extremal events in ARCH and GARCH. Based on Point Processes, one can find the validation of the RRT method in the last section 3.2.3.

3.2.1. *Extremes via Point Processes.* The limit structure of the extremes of a stationary sequence $\{X_t\}$ is provided by weak convergence of the point processes N_n toward a point process N, e.g.,

$$N_n(\cdot) = \sum_{t=1}^{n} \epsilon_{X_t/a_n}(\cdot) \to N(\cdot),$$

where ϵ_x denotes *Dirac measure* at x and $\{a_n\}$ is a sequence of positive constants. The points of N can be expressed as the products of Poisson points with independent points from a clustered distribution. Convergence in distribution of a sequence of point processes $\{N_n\}$ toward a point process N, $N_n \xrightarrow{d} N$, is well explained in Kallenberg (1983), Daley and Vere-Jones (1988), Resnick (1987). Resnick (1987) describes the close relationship between the convergence of $\{N_n\}$ and extreme value theory. More specifically, choose a special set $B = [x, \infty)$ and let $X_{(1)} \leq ... \leq X_{(n)}$ be the order statistics of the sample $(X_1, ..., X_n)$, then $N_n \xrightarrow{d} N$ implies that

$$\begin{aligned} P(N_n(x,\infty) < k) &= P(a_n^{-1} X_{(n-k+1)} \leq x) \\ &\to P(N(x,\infty) < k) \\ &= \sum_{i=0}^{k-1} P(N(x,\infty) = i). \end{aligned}$$

For ARCH(1), GARCH(1, 1) and the general GARCH(p, q) processes $\{X_t\}$ and their absolute values $\{|X_t|\}$, the form of the limit point process N was determined in Davis and Mikosch (1998), Mikosch and Stărică(2000) and Basrak et al. (2002), respectively.

Before we go into details about the extreme exceedances for univariate ARCH (GARCH) models, we first introduce some basics in ARCH (GARCH). The following Section 3.2.2 follows Embrechts, Klüppelberg and Mikosch (1997), and Jacod and Shiryaev (2003).

3.2.2. *About ARCH(1) and GARCH(1,1) processes.* An ARCH(1) process is defined by the equation

$$X_t = \sqrt{\beta + \lambda X_{t-1}^2} Z_t, \quad t \in \mathbb{N},$$

for some initial random variable X_0 independent of $\{Z_t\}$, parameters $\beta > 0$ and $\lambda > 0$. If $\lambda \in (0, 2e^{\gamma})$, where γ is Euler's constant (i.e., $\gamma \simeq 0.577$), then $\{X_t\}$ is stationary.

Let $\kappa > 0$ be the unique positive solution of the equation

$$h(u) \equiv E(\lambda Z^2)^u = 1,$$

where Z is standard normal. Then, for stationary ARCH(1) process with parameters $\beta > 0$ and $\lambda \in (0, 2e^{\gamma})$, we have

$$P(X > x) \sim \frac{c}{2} x^{-2\kappa}, \quad x \to \infty,$$

where

$$c = \frac{E[((\beta + \lambda X^2)^{\kappa} - (\lambda X^2)^{\kappa})(Z^2)^{\kappa}]}{\kappa E[(\lambda Z^2)^{\kappa} \ln(\lambda Z^2)]} \in (0, \infty),$$

for a standard normal random variable Z, independent of $X = X_0$.

The following theorem is from de Hann et al. (1989).

Theorem 3.3 (The extremes of an ARCH(1) process)**.**
Let $\{X_t\}$ *be a stationary ARCH(1) process. For* $x > 0$, *let*

$$N_n(\cdot) = \sum_{i=1}^{n} \epsilon_{n^{-1}i}(\cdot) I_{\{X_i > xn^{1/(2\kappa)}\}}$$

be the point process of exceedances of the threshold $xn^{1/(2\kappa)}$ *by* $X_1, \dots, X_n$.
Then

$$N_n \xrightarrow{d} N, \quad n \to \infty,$$

in $M_p((0,1])$, *where* N *is a compound Poisson process with intensity* $c\theta^{-2\kappa}$ *and cluster probabilities*

$$\pi_k = (1 - \Pi^{(2)}(0.5))^{-1} \sum_{m=k}^{\infty} \binom{m}{k} \pi_m^{(2)} 2^{-m}, \quad k = 1, 2, \dots,$$

where $\theta = 2\theta^{(2)}(1 - \Pi^{(2)}(0.5))$, $\Pi^{(2)}(u) = \sum_{k=1}^{\infty} \pi_k^{(2)} u^k$, $\pi_k^{(2)} = \frac{\theta_k^{(2)} - \theta_{k+1}^{(2)}}{\theta^{(2)}}$, $\theta_k^{(2)} = k \int_1^{\infty} P(card\{n \in \mathbb{N} : \Pi_{t=1}^{n}(\lambda Z_t^2) > y^{-1}\} = k-1) y^{-\kappa-1} dy$, $\theta_1^{(2)} = \theta^{(2)}$.

By applying Theorem 3.3 and continuous mapping theorem, one can define a mapping $\widetilde{T} : M_p((0,1]) \to \mathcal{P}(\mathbb{D}((0,1]))$ by

$$\widetilde{T}(N_n) = N_n((0,\cdot]), \quad \widetilde{T}(N) = N((0,\cdot]).$$

Then, it follows

$$N_n((0,\cdot]) \to N((0,\cdot]) \text{ in } \mathcal{P}(\mathbb{D}((0,1])), \quad \text{as } n \to \infty.$$

Then, by using continuity property of Skorokhod topology (Billingsley (1999)), for any $0 < u < 1$, we have

$$T_i^n := T_i(N^n, u) \to T_i := T_i(N, u), \quad n \to \infty, \quad i = 0, 1, \dots \tag{3.1}$$

where T_i^n's and T_i's are occurrence times (or jumps of the point process).

An GARCH(1,1) process is defined as

$$X_t = \sigma_t Z_t, \quad t \in \mathbb{Z},$$

$$\sigma_t^2 = \alpha_0 + \beta_1 \sigma_{t-1}^2 + \alpha_1 X_{t-1}^2 = \alpha_0 + \sigma_{t-1}^2(\beta_1 + \alpha_1 Z_{t-1}^2),$$

The parameters α_0, α_1 and β_1 are nonnegative, $\{Z_t\}$ is a sequence of i.i.d. symmetric random variables with $EZ_1^2 = 1$. A sufficient condition for the existence of a stationary solution is as follows,

$$\alpha_0 > 0 \text{ and } E \ln(\alpha_1 Z^2 + \beta_1) < 0.$$

For convenience, let

$$A_t = \alpha_1 Z_{t-1}^2 + \beta_1, \quad t \in \mathbb{Z}.$$

Assume the law of $\ln A$ is non-arithmetic, $E\ln A < 0, P(A > 1) > 0$ and there exists $h_0 \le \infty$ such that $EA^h < \infty$ for all $h < h_0$ and $EA^{h_0} = \infty$. Then the equation

$$EA^{\kappa/2} = 1$$

has a unique positive solution.

Let $\{X_t\}$ be a strictly stationary GARCH(1,1) processes. For fixed $h \ge 0$, consider the strictly stationary sequence of random row vectors

$$\mathbf{X}_t = (X_t, \sigma_t, \dots, X_{t+h}, \sigma_{t+h}), \quad t \ge 1.$$

Under above conditions, there exists a sequence $\{a_n\}$ such that

$$nP(|\mathbf{X}| > a_n) \to 1, \quad n \to \infty,$$

and $a_n = n^{1/\kappa} l(n)$ for a slowly varying function l, i.e., $\lim_{t\to\infty} l(at)/l(t) = 1$, for any $a > 0$.

The following theorem is from Mikosch and Stărică (2000).

Theorem 3.4 (Point process for GARCH(1,1) process)**.**
Let $\{X_t\}$ be a GARCH(1,1) process satisfying the above conditions, then

$$N_n := \sum_{t=1}^{n} \epsilon_{\boldsymbol{X}_t/a_n} \xrightarrow{d} N := \sum_{i=1}^{\infty}\sum_{j=1}^{\infty} \epsilon_{P_i \boldsymbol{Q}_{ij}},$$

where $\sum_{i=1}^{\infty} \epsilon_{P_i}$ is a Poisson process on $\mathbb{R}^+$ with intensity measure $v(dy) = \theta_X \kappa y^{-\kappa-1} dy$ and θ_X is the extremal index of the sequence $\{|\boldsymbol{X}_t|\}$ which exists and positive. The process $\{P_i\}$ is independent of the sequence of i.i.d. point processes $\sum_{j=1}^{\infty} \epsilon_{\boldsymbol{Q}_{ij}}, i \geq 1$, and Q_{ij}=$((Q_{ij,X}^{(m)}, Q_{ij,\sigma}^{(m)}), m = 0, \ldots, h)$.

Note: more details can be found at Davis and Mikosch (1998), Mikosch and Stărică (2000).

Remark 3.2. *It is possible to extend the above results to point processes with points in time-space. Under the assumption of strong mixing (see Mori (1997)), the weak convergence of $\{N_n\}$ implies the convergence of $\hat{N}_n = \sum_{t=1}^{n} \epsilon_{(t/n, X_t/a_n)}$. For fixed $x > 0$, the point process of exceedances of the threshold xa_n by the sequence $\{X_t\}$ is*

$$\tilde{N}_n(\cdot) = \sum_{i=1}^{n} \epsilon_{i/n}(\cdot) I_{\{X_i > xa_n\}} = \hat{N}_n(\cdot \times (x, \infty)).$$

According to a result in Hsing (1998), the weak limit of $\{\tilde{N}_n\}$ is compound Poisson with compounding probabilities π_k and probability generating function $\Pi(u) = \sum_{k=1}^{\infty} \pi_k u^k$.

3.2.3. *Contagion Test for ARCH (GARCH) Series.*

Theorem 3.5 (Compound Poisson Processes for Residual Times)**.** *Assume that there are two compound poisson processes X and Y on $[0, 1]$ with intensity λ_1 and λ_2, respectively. Let U_i and V_j be the recurrence times for X and Y, respectively. Also, let $\{W_k\}$ be the residual times. Then,*

(a) $U_i \overset{i.i.d.}{\sim} \exp(\lambda_1)$ *and* $V_j \overset{i.i.d.}{\sim} \exp(\lambda_2)$.

(b) *If X and Y are independent,* $\{W_k\} \overset{i.i.d.}{\sim} \exp(\lambda_1)$.

proof. (a) This is obvious by using the "memoryless" property of exponential distribution.
(b) Define $\{Z_k\}$ to be raw residual times as in section 2.1 and as shown in Figure 2

$$\begin{aligned}
& P(Z_1 = z_1, \ldots, Z_n = z_n | V_j, j = 1, \ldots, n) \\
= & \left\{ \begin{array}{l}
\text{if } z_{n-1} < V_n : \\
\quad P(Z_1 = z_1, \ldots, Z_{n-1} = z_{n-1} | V_j, j = 1, \ldots, n-1) \times \\
\quad \quad \times P(Z_n = z_n | V_j, j = 1, \ldots, n), \\
\text{if } z_{n-1} \geq V_n : \\
\quad P(Z_1 = z_1, \ldots, Z_{n-1} = z_{n-1} | V_j, j = 1, \ldots, n-1) \ (note: z_{n-1} + V_n = z_n)
\end{array} \right. \\
= & P(Z_1 = z_1, \ldots, Z_{n-1} = z_{n-1} | V_j, j = 1, \ldots, n) \times \\
& \times P(Z_n = z_n | V_j, j = 1, \ldots, n)^{I_{\{z_{n-1} < V_n\}}} \\
= & \cdots\cdots \\
= & P(Z_1 = z_1 | V_1) \cdot P(Z_2 = z_2 | V_1, V_2)^{I_{\{z_1 < V_2\}}} \times \cdots \\
& \cdots \times P(Z_n = z_n | V_j, j = 1, \ldots, n)^{I_{\{z_{n-1} < V_n\}}}
\end{aligned}$$

By using "memoryless" property for exponential random variable, one would have

$$P(Z_k = z_k | V_j, j = 1, \ldots, k) = \lambda_1 e^{-\lambda_1 z_k}$$

Therefore,

$$\begin{aligned}
& P(Z_1 = z_1, \ldots, Z_n = z_n | V_j, j = 1, \ldots, n) \\
= & (\lambda_1 e^{-\lambda_1 z_1})(\lambda_1 e^{-\lambda_1 z_2})^{I_{\{z_1 < V_2\}}} \cdots (\lambda_1 e^{-\lambda_1 z_n})^{I_{\{z_{n-1} < V_n\}}}
\end{aligned}$$

Then, the distribution for residual times $\{W_k\}$ is

$$\{W_k\} \overset{i.i.d.}{\sim} \exp(\lambda_1).$$

□

Denote a metric space by S, and let $\mathcal{S}$ be the Borel σ-field, the one generated by the open sets. Let P be a probability measure on $\mathcal{S}$. If probability measures P_n and P satisfy $P_n f \to Pf$ for every bounded, continuous real function f on S, we say that P_n converges weakly to P and write $P_n \xrightarrow{w} P$.

Assume that the product $T = S' \times S''$ is separable, which implies that S' and S'' are separable and that the three Borel σ-fields are related by $\mathcal{T} = \mathcal{S}' \times \mathcal{S}''$. Denote the marginal distribution of a probability measure P on $\mathcal{T}$ by P' and P'': $P'(A') = P(A' \times S'')$ and $P''(A'') = P(S' \times A'')$. By continuous mapping theorem that $P_n \xrightarrow{w} P$ implies that $P'_n \xrightarrow{w} P'$ and $P''_n \xrightarrow{w} P''$.

Theorem 3.6.
If $T = S' \times S''$ is separable, then $P'_n \times P''_n \xrightarrow{w} P' \times P''$ if and only if $P'_n \xrightarrow{w} P'$ and $P''_n \xrightarrow{w} P''$

Based on the above Theorem 3.6 and extremal results about ARCH and GARCH in section 3.2.2, point processes P_X^n and P_Y^n for the extreme exceedances of two independent ARCH (GARCH) processes have convergence property as follows:

$$(P_X^n, P_Y^n) \xrightarrow{w} (P_X, P_Y) \tag{3.2}$$

where P_X and P_Y are two independent compound Poisson processes.

Let U_i^n and V_j^n be the occurrence time for the point processes P_X^n and P_Y^n, and U_i^n and V_j^n be the recurrence times, and $\{W_k^n\}$ be the residual time, which are shown in Figure 2.

From Equation (3.1) and Theorem 3.5 part (a), we have

$$U_i^n \xrightarrow{w} U_i, \quad i = 1, 2, \ldots,$$

that is,

$$\{U_i^n\} \text{ asymptotically } \overset{i.i.d.}{\sim} \exp(\lambda_1). \tag{3.3}$$

From Equation (3.2) and Theorem 3.5, residual times $\{W_k^n\}$ have convergence property as

$$W_k^n \xrightarrow{w} W_k, \quad k = 1, 2, \ldots$$

that is,

$$\{W_k^n\} \text{ asymptotically } \overset{i.i.d.}{\sim} \exp(\lambda_1). \tag{3.4}$$

Therefore, based on the above Equations (3.4) and (3.3), one can construct a hypothesis for contagion as follows.

Remark 3.3 (Contagion Test for ARCH (GARCH))**.**
A hypothesis testing procedure for contagion

$$H_0 : \textit{No contagion vs } H_1 : \textit{Exists contagion}$$

can be constructed as

$$H_0 : \{U_i^n\} \textit{ and } \{W_k^n\} \textit{ follow the same distribution}$$

$$\textit{vs} \quad H_1 : \{U_i^n\} \textit{ and } \{W_k^n\} \textit{ follow different distributions}$$

4. Simulation Study

In this section, simulations under different scenarios are given. We compare the performance of our method with those of Censored Likelihood Method (CLM) of Ledford and Tawn (1996), Extremogram of Davis and Mikosch (2009) and some other methods in testing tail independence following Falk and Michael (2006). Section 4.1 shows an artificial time series where two independent series are superimposed with dependent extremes. In this case the correlation and extremogram cannot capture the extreme dependence, but Residual and Recurrence Times method can, as seen from the power. Section 4.2 to Section 4.3 obtain the power and size of Residual and Recurrence Times method by using simulated data under different models: the i.i.d. normal distribution model and the GARCH model (using indices time series to estimate parameters).

All results are reported with threshold 0.9 and significance level 0.05. Simulations for other values give similar results and are available from the authors on request.

4.1. Series with Dependent Extremes but Independent Non-extremes.

This section describes a procedure for generating a bivariate sequence with dependent extremes but independent non-extremes, where the dependent extremes account for a small proportion (say, 10%) and the independent non-extremes take up a large proportion (say, 90%). For such a bivariate sequence, the cross-correlation between the two components are very small. Thus, cross-correlation does not indicate extreme dependence.

The steps of series generating procedure is shown as below.

(a) First generate two independent i.i.d. standard normal series, called series x and series y (the cross-autocorrelation between x and y is close to zero, since they are independent).

(b) Find the time points (denoted as $\{t_j\}_{j=1}^{J}$) of series y, where extreme events occur (above 90th percentile of y), and make these values more extreme by adding 1 to each of them, then call the modified series, Y.

(c) Add 4 to the value in series x at each time point $t_j + k_j$, where k_j is an independent random variable taking value $\{0, 1, 2\}$ with probability $\{1/6, 1/3, 1/2\}$ and $1 \leq j \leq J$. Call the modified series, X. This step makes the modified series X and Y extreme dependent, since an extreme event in series Y will trigger another extreme event in series X in a few, say 0-2, time points later. Figure 1 shows one sample series X and Y.

By using the above procedure, one can generate 1000 bivariate series X and Y with length 1000, then apply the RRT method to test contagion effects and obtain the power of the test. Since the extreme events only account for 10% of the data and the independent part accounts for 90%, thus the cross-autocorrelation between X and Y are still close to zero (no cross-autocorrelation). Additionally, extreme events in the two series do not necessarily occur simultaneously and time lags between two extreme events in the two series are not fixed. We calculate the extremogram (with $A = B = (1, \infty) \times (1, \infty)$) for each generated series as above, with different thresholds (90%, 95%, 99%) and lags from 1 to 100. The values in the extremgram plot are all very small (nearly all are less than 0.05). Thus, using the extremogram cannot detect any extremal dependence in the simulated series. Using the same simulated series, we obtain the power for the other methods, namely, CLM, Neyman-Pearson (NP) test, Fishers κ (Fish) test, Kolmogorov-Smirnov (KS) test and Chi-square goodness-of-fit (ChiSq) test. The results in Table 1 show that the NP test outperforms the other three tests, but is still worse than RRT.

4.2. i.i.d. Normal Simulation.

In this section, we generate i.i.d. univariate and bivariate normal series to obtain the size and power of our Residual and Recurrence Times test. The simulation study is as follows.

(a) Size: simulate two independent series of i.i.d. normal samples with $\sigma_1 = 1, \sigma_2 = 10$, and length equal to 1000. Apply our algorithm to test independence of the two simulated series with significant level 0.05. Repeat the above procedure for 1000 times, then we can obtain the size of our algorithm.

(b) Power: simulate two kinds of i.i.d. bivariate normal random vector series, one with mean $\begin{pmatrix} 0 \\ 0 \end{pmatrix}$ and positive correlated covariance matrix $\begin{pmatrix} 10 & 2 \\ 2 & 3 \end{pmatrix}$; the other with mean $\begin{pmatrix} 0 \\ 0 \end{pmatrix}$ and negative correlated covariance matrix $\begin{pmatrix} 10 & -2 \\ -2 & 3 \end{pmatrix}$. The length for both is 1000. Apply our algorithm to test the independence of the two components in each of two series (with significant level 0.05). Repeat the above procedure for 1000 times, then we can obtain the powers of our algorithm.

4.2.1. *Size and Power for Residual and Recurrence Times Method.* This subsection describes the first column of table 2.

In the first row of Table 2, we have sizes of our test for the simulated series when extreme events for the two series are defined to be above the upper thresholds (Upper vs Upper). Using the same simulated series, one can also obtain similar size when extreme events are defined to be above a specified upper threshold for one series and below a specified lower threshold for another series (Upper vs Lower), and for the case of Lower vs Upper and Lower vs Lower.

In the second row of Table 2, we have powers of our test for the positively correlated and normally distributed simulated series when extreme events for the two series are defined to be above the upper thresholds (Upper vs Upper). Using the same simulated series, one can also obtain a similar table of rejection rates for the case of Lower vs Lower. The power for negatively correlated and normally distributed simulated series in the cases of Lower vs Upper and Upper vs Lower are also similar.

In the last row of Table 2, we have rejection rates of our test for the positively correlated and normally distributed simulated series when extreme events for series X is defined to be above the upper threshold and extreme events for series Y is defined to be below the lower threshold (Upper vs Lower). Using the same simulated series, one can also obtain a similar table of rejection rates for the case of Lower vs Upper. The rejection rates for negatively correlated and normally distributed simulated series in the cases of Upper vs Upper and Lower vs Lower are also similar.

Considering Table 2, one can find that as for the above positively corrected series, the power for the Upper vs Upper (and Lower vs Lower) case is much larger than the Upper vs Lower (and Lower vs Upper) case. It shows that the Residual and Recurrence Times test can not only detect contagion effect between the two components but also can tell in which quadrant contagion effect exists.

4.2.2. *Comparison with Other Methods.* By using the same simulated series, one can obtain the size and power for other methods.

(a) CLM

The size and power (positively correlated series and Upper vs Upper case) of CLM are shown in the second column of Table 2. It should be noted that the CLM test is based on maximum likelihood method and often encounters bad results, e.g., warning messages, errors and NaN. We present the percentage of such bad results in brackets in the tables. Since the simulated series are positively correlated, the rejection rates for the case of Upper vs Lower (or Lower vs Upper) should be small. However the last row of Table 2 portrays that only the very high thresholds for one components and very low thresholds for the other component lead to small rejection rates indicating problems with CLM. As for negatively correlated simulated series, the results are similar.

(b) Other Tail Independence Tests

The size and power (positively correlated series and Upper vs Upper case) of other tail independence testing methods are shown in the other columns of Table 2. The powers for the Fisher test, and the ChiSq test are not very good. Given that the simulated series are positively correlated, the rejection rates for the case of Upper vs Lower (or Lower vs Upper) should be small. But according to table 2, the KS test has a relatively large rejection rate. The NP test performs well in all these cases. As for negatively correlated simulated series, the results are similar.

4.3. **GARCH Simulation.** In this section, we use GARCH model to fit real indices series and use fitted model to simulate time series in order to find the size and power of our method. An introduction to DCC-GARCH model can be found in Nakatani and Teräsvirta (2008). The real data being used is weekly indices for Mexico and USA from May 2003 to May 2007 (about 4 years weekly data), since this time period data shows contagion effects from USA to Mexico with p-value very close to 0 (Lower vs Lower case, 0.10 vs 0.10 thresholds) and the p-value in the case of Upper vs Lower (0.90 vs 0.10 thresholds) is 0.685, which indicates no contagion transmission in Upper vs Lower quadrant.

(a) Size: use above data to fit two unitvariate GARCH models (GARCH(1,1)), then use the fitted models to simulate two series. Apply our algorithm to test independence of the simulated series. Repeat the above process for 1000 times, then we can obtain the size of our algorithm.
(b) Power: use the same data to fit a bivariate GARCH model (DCC-GARCH), then use the fitted model to simulate log returns. Apply our algorithm to test independence of the simulated series. Repeat the above process for 1000 times, then we can obtain the power of our algorithm:

4.3.1. *Size, Power and Rejection Rate for Residual and Recurrence Times Method.* The following simulation for bivariate GARCH series is using the DCC-GARCH model. Size, power and rejection rate of our proposed test for the simulated series are reported in the first column of Table 3.

4.3.2. *Comparison with Other Methods.* By using the same simulated series, one can obtain the size and power for other methods stated in section 4.2.2.
(a) CLM

Size and power are shown in Table 3. Although the size and power for this method are both good, the rejection rate for case of Upper vs Lower (say, 0.90 vs 0.10) is high as shown in Table 3.
(b) Other Tail Independence Tests

Size, power and rejection rate are shown in Table 3. The Fish test shows low power. Although the size and power for KS test and Chisq test are good, a high rejection rate for case of Upper vs Lower goes unfavorably against the these two tests.

5. Empirical Study for Stock Indices Data

In this section, we consider stock indices time series for 17 countries: Argentina, Brazil, Chile, Colombia, Mexico, Peru, China, India, Indonesia, Korea, Malaysia, Philippines, Taiwan, Thailand, Europe, USA and Japan. These are MSCI country indices obtained from Datastream and the data is weekly. Section 5.1 gives a table of pairwise p-values resulting from applying Residual and Recurrence Times test to the indices data where we have used the data from 2006 to the end of 2011. Section 5.2 focuses on two specific pairs: Europe given USA, and Mexico given USA using data from 1993 to 2011 using moving windows.

5.1. **Pairwise p-values.** By using Residual and Recurrence Times method to test contagion effect for the indices data set from 2006 to the end of 2011 , one can obtain a table of pairwise p-values. Pairwise p-values are shown in Table 6, using 0.1 vs 0.1 threshold, meaning that extreme events are defined to be below 10th percentile of the corresponding series data.

The evidence favoring the contagion is evident in those cases where the obtained p-value is less than 0.05. Many small-sized countries (defined in terms of their market capitalization) have contagion effects between each other. Country like USA, European countries and China cannot be easily effected.

5.2. **Moving Window Plots.** In this section, we examine contagion effects for two specific pair of countries. We concentrate on four specific pairs: Korea given Thailand (for the “Asian Flu” in 1997), Argentina given Brazil (for the crisis in Brazil in 1998/1999 and Argentina being the largest trading partner of Brazil), Europe given USA, and Mexico given USA (given the Tequila crisis and the Trade agreement between Mexico and USA). Scatter plots of p-value against initial time for a period are shown in Figure 4, Figure 5, Figure 6, and Figure 7, with a moving window of length of 3 years (about 156 data points) and 4 years (about 208 data points), and step of one month (about 4 data points).

The "Asian Flu" impact is clear from Figure 4. The crisis that has generated in 1997 following the devaluation of Thai Baht exerts its impact on Korea and the impact lasts until end 1999. The contagion effect is stronger until 2004. Figure 5 demonstrates that for Argentina and Brazil, the impact was strong during 1998-1999 and then again from late 2004. The contagion effect from USA to Europe after year 2000 becomes more significant when we consider thresholds 0.10 vs 0.10, and for 0.15 vs 0.15. This provides an evidence of continuous interaction between USA and European countries for the recent decade. For Mexico and USA, the contagion effects are stronger around year 2005 and it also shows large contagion effects around USA's sub-prime crisis.

6. Concluding Comments

Most of the development in recurrence time has been so far with univariate time series. This paper provides a new idea of Residual and Recurrence Times method of high or low values for bivariate time series to detect contagion. We document that our proposed method does not need the i.i.d. assumption and can handle the situation where the extremes for different components do not occur at the same time.

Although we apply the Residual and Recurrence Times to financial series, this method can be a valid tool in many areas, for example, analysis of spatial patterns of disease and spatial spread of epidemics, see Marshall (1991); analysis of spread of social influences, see Dodds and Watts (2005); transmission of neural signals on the onset of epilepsy with irregular behavior of one neuron triggering that of others and resulting in everything breaking down, see Nigram (2004).

Some interesting extensions can easily follow:

(a) Extend the bivariate method to multivariate scenario and detect if there are some series (say, indices series) that drive the other markets.
(b) How to choose good thresholds and how would thresholds affect the method.
(c) Establish a method of estimation of the time it takes for transmission of a shock from one market to another.
(d) How to deal with clusters of exceedances and strong serial dependence in the same series.

In all, we are looking forward to a deeper development of this method and more applications in the future.

Appendix

Proof of Theorem 3.2. *Proof.* (a) Using the definition of $\{U_i\}$, it follows

$$P(U_1 = u_1, U_2 = u_2, ..., U_M = u_M) = \frac{1}{\binom{m}{M}}.$$

Let $R := (R_1, R_2, ..., R_{M+1})$ be $(M + 1)$ i.i.d. Geometric(q) random variables, where $q = 1 - p_1$. Then,

$$\begin{aligned} & P(R_1 = r_1, R_2 = r_2, ..., R_M = r_M | R_1 + \cdots + R_M \le m, R_1 + \cdots + R_{M+1} > m) \\ = & \frac{P(R_1 = r_1, R_2 = r_2, ..., R_M = r_M, R_1 + \cdots + R_M \le m, R_1 + \cdots + R_{M+1} > m)}{P(R_1 + \cdots + R_M \le m, R_1 + \cdots + R_{M+1} > m)} \\ = & \frac{q^M p_1^{m-M}}{q^M p^{m-M} \binom{m}{M}} \\ = & \frac{1}{\binom{m}{M}}. \end{aligned}$$

As a result,

$$(U_1, \ldots, U_M) \overset{D}{=} (R_1, R_2, ..., R_M | R_1 + \cdots + R_M \le m, R_1 + \cdots + R_{M+1} > m).$$

(b) For any integer $k \leq M$,

$$\begin{aligned} & P(U_i = u_i, i = 1, \dots, k) \\ = \quad & \frac{\binom{m-u_1}{M-1}/\binom{m}{M}}{1} \times \frac{\binom{m-u_1-u_2}{M-2}/\binom{m}{M}}{\binom{m-u_1}{M-1}/\binom{m}{M}} \times \\ & \frac{\binom{m-u_1-u_2-u_3}{M-3}/\binom{m}{M}}{\binom{m-u_1-u_2}{M-2}/\binom{m}{M}} \times \cdots \times \frac{\binom{m-u_1-\dots-u_k}{M-k}/\binom{m}{M}}{\binom{m-u_1-\dots-u_{M-1}}{M-(k-1)}/\binom{m}{M}} \\ \xrightarrow{M \approx (1-p_1)m} \quad & (1-p_1)p_1^{u_1-1} \times (1-p_1)p_1^{u_2-1} \times \cdots \times (1-p_1)p_1^{u_k-1}. \end{aligned}$$

As a result, for any finite k,

$$\{U_i\}_{i=1}^k \text{ is asymptotically } \overset{\text{i.i.d.}}{\sim} \text{ Geometric}(1-p_1) \text{ as } m \to \infty, \frac{M}{m} \to (1-p_1).$$

In the same way, we have

$$\{V_j\}_{j=1}^k \text{ is asymptotically } \overset{\text{i.i.d.}}{\sim} \text{ Geometric}(1-p_2) \text{ as } m \to \infty, \frac{M'}{m} \to (1-p_2).$$

(c) In order to find the asymptotic joint distribution for the residual times $\{W_k\}$, one would first find the asymptotic joint distribution for raw residual times $\{Z_k\}$. Let $\nu := (V_1, \dots, V_M)$. Note that

$$P(U_n = s - t | S_{n-1} = t) = \frac{\binom{m-s}{M-n}}{\binom{m-t}{M-n+1}}$$

$$\text{and} \qquad P(U_n \geq \nu - t | S_{n-1} = t) = \frac{\binom{m-\nu+1}{M-n+1}}{\binom{m-t}{M-n+1}}.$$

Thus, for any $t < \nu$,

$$\begin{aligned} & P(S_n = s | S_{n-1} = t, S_n \geq \nu) \\ = \quad & \frac{P(S_n = s, S_n \geq \nu | S_{n-1} = t)}{P(S_n \geq \nu | S_{n-1} = t)} \\ = \quad & \frac{P(U_n = s - t, U_n \geq \nu - t | S_{n-1} = t)}{P(U_n \geq \nu - t | S_{n-1} = t)} \\ = \quad & \frac{P(U_n = s - t | S_{n-1} = t)}{P(U_n \geq \nu - t | S_{n-1} = t)} \\ = \quad & \frac{\binom{m-s}{M-n}}{\binom{m-\nu+1}{M-n+1}}, \quad \text{which is not depending on } t. \end{aligned}$$

Then,

$$\begin{aligned} & P(S_n = s | S_{n-1} < \nu, S_n \geq \nu) \\ = \quad & \frac{P(S_n = s, S_{n-1} < \nu | S_n \geq \nu)}{P(S_{n-1} < \nu | S_n \geq \nu)} \\ = \quad & \frac{\sum_{t=0}^{\nu-1} P(S_{n-1} = t | S_n \geq \nu) P(S_n = s | S_{n-1} = t, S_n \geq \nu)}{\sum_{t=0}^{\nu-1} P(S_{n-1} = t | S_n \geq \nu)} \\ = \quad & \frac{\binom{m-s}{M-n}}{\binom{m-\nu+1}{M-n+1}}. \end{aligned}$$

Since N satisfies

$$\begin{cases} \sum_{i=1}^N U_i \geq \nu, \\ \sum_{i=1}^{N-1} U_i < \nu, \end{cases}$$

then,

$$P(N = n|\nu) = \frac{\binom{\nu-1}{n-1}\binom{m-\nu+1}{M-n+1}}{\binom{m}{M}}.$$

Thus,

$$\begin{aligned}
& P(S_N = s|\nu) \\
= & \sum_{n=1}^{\nu} P(S_N = s, N = n|\nu) \\
= & \sum_{n=1}^{\nu} P(S_n = s|\nu, N = n)P(N = n|\nu) \\
= & \sum_{n=1}^{\nu} P(S_n = s|S_n \geq \nu, S_{n-1} < \nu)P(N = n|\nu) \\
= & \sum_{n=1}^{\nu} \left[\frac{\binom{m-s}{M-n}}{\binom{m-\nu+1}{M-n+1}} \times \frac{\binom{\nu-1}{n-1}\binom{m-\nu+1}{M-n+1}}{\binom{m}{M}} \right] \\
= & \sum_{n=1}^{\nu} \frac{\binom{m-s}{M-n}\binom{\nu-1}{n-1}}{\binom{m}{M}} \\
= & \frac{\binom{m-s+v-1}{M-1}}{\binom{m}{M}}.
\end{aligned}$$

Since $Z_k = S_N - \sum_{j=1}^{k} V_j + 1$,

$$\begin{aligned}
P(Z_k = z_k|\nu) \quad & = \quad P(S_N = z_k + \nu - 1|\nu) \\
& = \quad \frac{\binom{m-z_k-\nu+1+\nu-1}{M-1}}{\binom{m}{M}} \\
& = \quad \frac{\binom{m-z_k}{M-1}}{\binom{m}{M}} \\
& \xrightarrow{M\approx(1-p_1)m} \quad (1-p_1)p_1^{z_k-1} \text{as} \qquad m \to \infty.
\end{aligned}$$

Thus,

$$(Z_k|V_1, \ldots, V_M) \overset{\text{appr.}}{\sim} \text{Geometric}(1-p_1), \quad \text{which does not depend on } k.$$

To find the asymptotic joint distribution for $(Z_1, \ldots, Z_k * |V_1, \ldots, V_M)$, where

$$\tilde{k} = \text{ the number of non-overlaps } = M - \sum_{j=1}^{M-1} \mathbb{I}_{\{z_i = z_{i+1}+v_{i+1}\}}.$$

Step 1:

$$P(Z_1 = z_1|V) = \frac{\binom{m-z_1}{M-1}}{\binom{m}{M}} \to (1-p_1)p_1^{z_1-1} \text{ as } m \to \infty.$$

Step 2: In order to find $P(Z_1 = z_1, Z_2 = z_2|V) = P(Z_2 = z_2|Z_1 = z_1, V)P(Z_1 = z_1|V)$, one needs to find is $P(Z_2|Z_1 = z_1, V)$.

$$P(Z_2 = z_2|Z_1 = z_1, V) = \begin{cases} \text{if } z_1 \leq V_2 : \\ \quad \frac{P(Z_1,Z_2|V)}{P(Z_1|V)} = \frac{\binom{m-z_1-z_2}{M-2}/\binom{m}{M}}{\binom{m-z_1}{M-1}/\binom{m}{M}} \to (1-p_1)p_1^{z_2-1}; \\ \text{if } z_1 > V_2 : \\ \quad \mathbb{I}_{\{z_1 = z_2 + V_2\}}. \end{cases}$$

Therefore,

$$\begin{aligned} P(Z_1=z_1,Z_2=z_2|V) &= P(Z_2=z_2|Z_1=z_1,V)P(Z_1=z_1|V) \\ &= \frac{\binom{m-z_1}{M-1}}{\binom{m}{M}} \cdot \left(\frac{\binom{m-z_1-z_2}{M-2}/\binom{m}{M}}{\binom{m-z_1}{M-1}/\binom{m}{M}}\right)^{\mathbb{I}\{z_1=z_2+V_2\}} \\ &\to (1-p_1)p_1^{z_1-1}\cdot((1-p_1)p_1^{z_2-1})^{\mathbb{I}\{z_1=z_2+V_2\}}. \end{aligned}$$

Step 3: By applying the same technique

$$\begin{aligned} & P(Z_k=z_k|Z_1=z_1,\cdots,Z_{k-1}=z_{k-1},V) \\ = & \left(\frac{\binom{m-w-z_k}{M-\tilde{k}-1}}{\binom{m-w}{M-\tilde{k}}}\right)^{\mathbb{I}\{z_{k-1}\le V_k\}} \\ \to & \left((1-p_1)p_1^{z_k-1}\right)^{\mathbb{I}\{z_{k-1}\le V_k\}} \end{aligned}$$

where $w=$ the length of the coverage of all the intervals $\{z_1,\cdots,z_{k-1}\}$.

In conclusion,

$$\begin{aligned} & P(Z_1=z_1,\cdots,Z_k=z_k|V) \\ = & \left(\frac{\binom{m-z_1}{M-1}}{\binom{m}{M}}\right)\cdot\left(\frac{\binom{m-z_1-z_2}{M-2}}{\binom{m-z_1}{M-1}}\right)^{\mathbb{I}\{z_1\le V_2\}}\cdots\left(\frac{\binom{m-w-z_k}{M-\tilde{k}-1}}{\binom{m-w}{M-\tilde{k}}}\right)^{\mathbb{I}\{z_{k-1}\le V_k\}} \\ \to & ((1-p_1)p_1^{z_1-1})\cdot((1-p_1)p_1^{z_2-1})^{\mathbb{I}\{z_1\le V_2\}}\cdots((1-p_1)p_1^{z_k-1})^{\mathbb{I}\{z_{k-1}\le V_k\}}. \end{aligned}$$

As defined in the section 2.1, $\{W_k\}$ is a subset of $\{Z_k\}$ with constraint that $Z_k\le V_{k+1}$. Thus,

$$\{W_k\}\text{ i.i.d. }\overset{appr.}{\sim}\text{ Geometric}(1-p_1).$$

$\square$

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Method	RRT	CLM	NP	Fish	KS	ChiSq
Power	1	0.358	0.223	0.092	0.130	0.082

Table 1. Power, Dependent extremes with Independent non-extremes

Method	RRT	CLM	NP	Fish	KS	ChiSq
Size	0.042	0.051(0.176)	0.068	0.048	0.035	0.032
Power	0.954	1.000(0.185)	0.870	0.144	0.467	0.329
Rej. Rate	0.161	1.000(0.165)	0.000	0.379	0.667	0.474

Table 2. Size, Power and Rejection Rate. Normal Positively correlated.

Method	RRT	CLM	NP	Fish	KS	ChiSq
Size	0.038	0.066(0.119)	0.067	0.050	0.060	0.055
Power	0.911	1.000(0.153)	1.000	0.169	0.876	0.785
Rejection Rate	0.195	0.823(0.156)	0.924	0.111	0.533	0.419

Table 3. Size, Power and Rejection Rate. GARCH Mex | USA

Table 4. Pairwise p-values with 0.1 vs 0.1 threshold

	Arg	Bra	Chile	Colombia	Mexico	Peru	China	India	Indonesia	Korea	Malaysia	Phili	Taiwan	Thailand	Europe	USA	Japan
Arg	NA	0.055	0.320	**0.040**	0.095	**0.005**	0.300	0.180	0.105	0.250	0.595	0.050	0.130	0.105	0.180	0.985	0.310
Bra	0.060	NA	0.380	**0.020**	**0.030**	**0.000**	0.220	0.100	0.140	0.135	0.335	**0.045**	0.060	**0.010**	0.225	0.500	0.255
Chile	0.070	0.125	NA	0.130	0.150	**0.005**	0.435	0.215	0.320	0.520	0.650	0.100	0.110	0.070	0.180	0.840	0.220
Colombia	0.175	**0.010**	0.840	NA	0.080	**0.000**	0.415	0.360	0.185	0.530	0.630	0.100	0.150	**0.025**	0.345	0.910	0.990
Mexico	0.085	0.065	0.655	0.075	NA	**0.000**	0.930	0.335	0.365	0.550	0.975	0.385	0.345	0.100	0.055	0.275	0.240
Peru	**0.015**	**0.000**	0.230	**0.020**	0.015	NA	0.390	0.165	0.145	0.080	0.915	0.020	0.180	0.010	0.285	0.835	0.245
China	0.125	0.030	0.415	0.235	0.225	**0.010**	NA	0.240	0.130	0.185	0.385	**0.015**	0.070	0.025	0.555	0.795	0.295
India	0.175	0.055	0.710	0.050	0.240	**0.035**	0.295	NA	0.210	0.380	0.390	0.170	0.270	0.120	0.385	0.560	0.615
Indonesia	0.300	**0.045**	0.695	0.115	0.200	**0.030**	0.095	0.170	NA	0.510	0.410	0.060	0.060	**0.010**	0.405	0.895	0.415
Korea	0.170	0.210	0.240	0.380	0.200	**0.045**	0.430	0.445	0.365	NA	0.430	0.095	0.070	0.155	0.240	0.685	0.220
Malaysia	0.130	0.290	0.390	0.230	0.225	0.060	0.165	0.245	0.300	0.350	NA	0.090	0.115	0.100	0.415	0.930	0.200
Phili	0.195	**0.045**	0.375	**0.025**	0.125	**0.005**	0.330	0.240	0.070	0.285	0.800	NA	0.050	**0.030**	0.430	0.915	0.305
Taiwan	0.185	0.065	0.460	0.125	0.210	**0.025**	0.170	0.220	0.120	0.210	0.425	**0.045**	NA	**0.015**	0.230	0.780	0.090
Thailand	0.395	**0.005**	0.980	**0.015**	**0.035**	**0.000**	0.690	0.405	0.215	0.200	0.870	0.415	0.175	NA	0.370	0.910	0.190
Europe	0.145	0.240	0.355	0.165	0.160	**0.040**	0.615	0.240	0.170	0.690	0.475	0.300	0.160	0.135	NA	0.390	0.170
USA	0.115	0.295	0.660	0.285	0.340	0.130	0.525	0.540	0.470	0.610	0.705	0.280	0.545	0.545	0.185	NA	0.550
Japan	0.170	0.170	0.695	0.145	0.250	0.075	0.825	0.430	0.280	0.990	0.625	0.730	0.190	0.100	0.240	0.795	NA

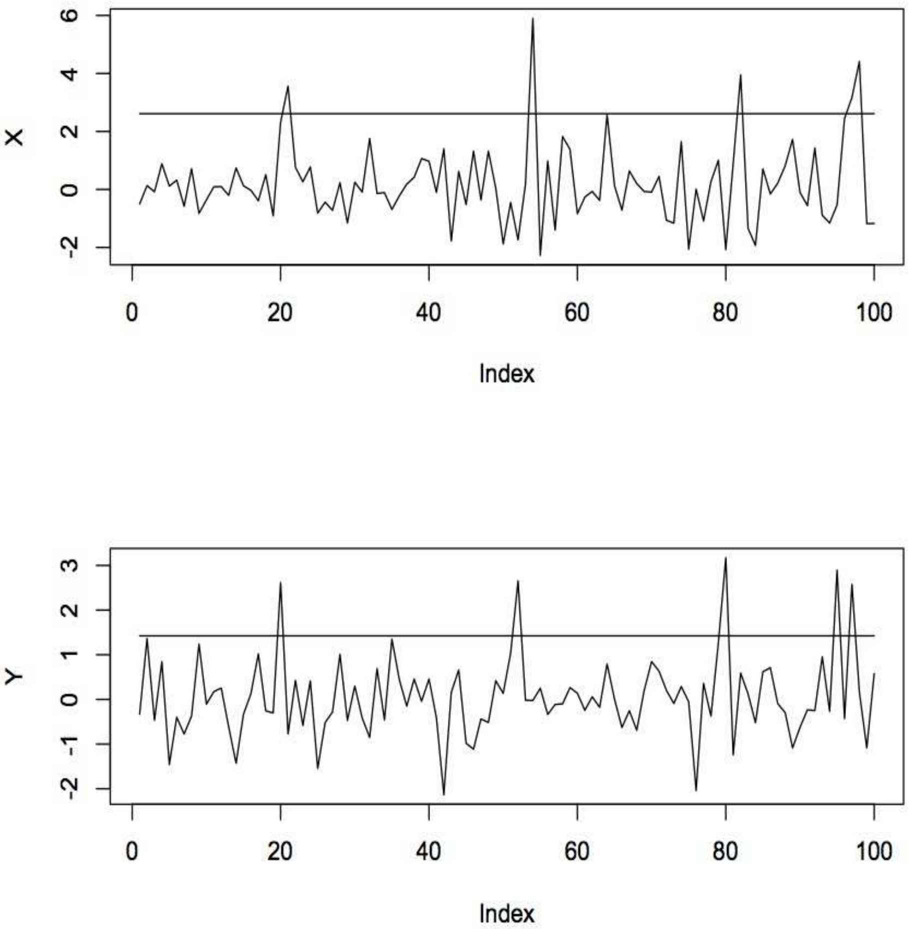

FIGURE 1. Series X and Y with horizontal line as threshold

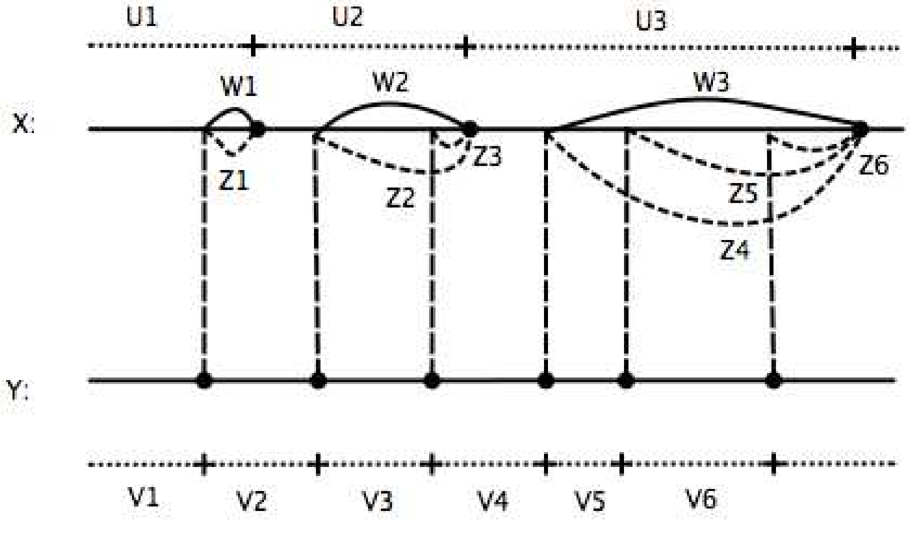

FIGURE 2. Recurrence, Raw Residual and Residual Times

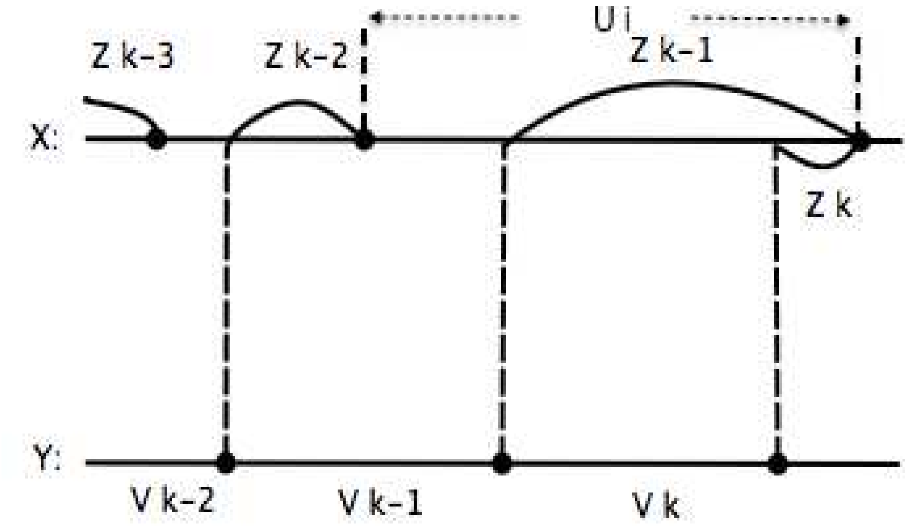

FIGURE 3. Memoryless Property

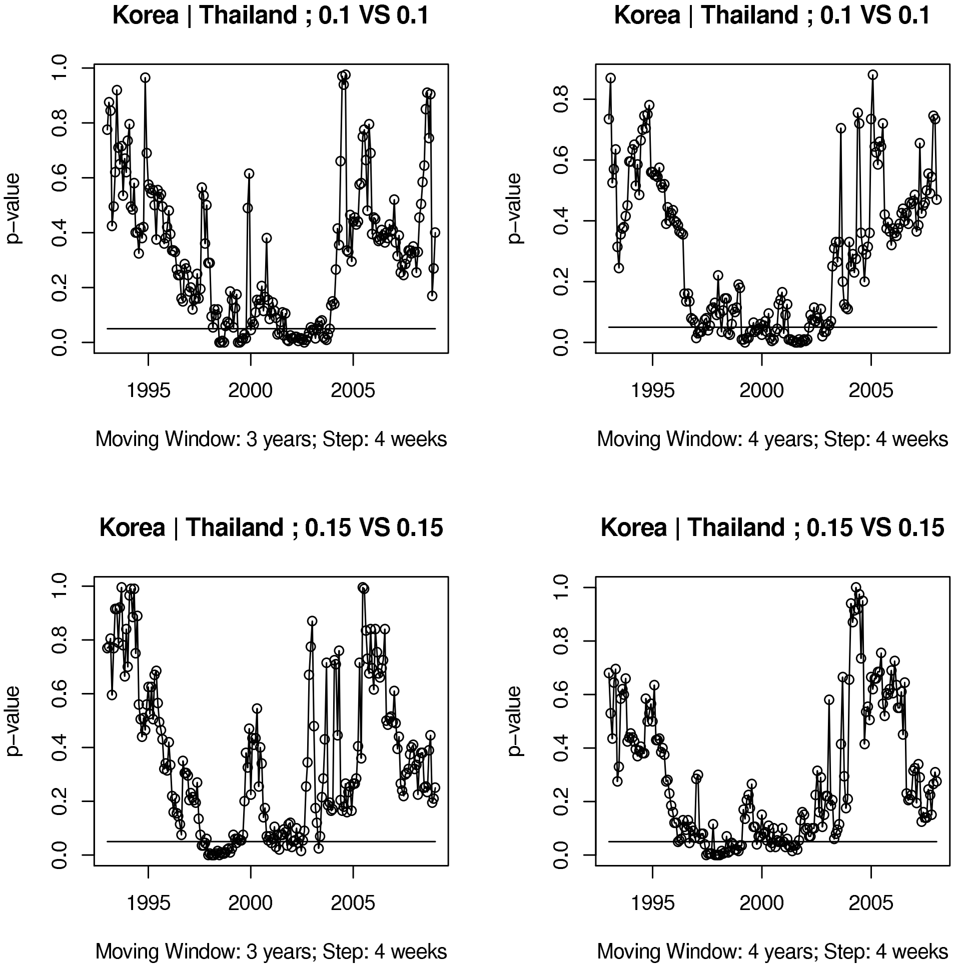

FIGURE 4. Moving Window Plot for Korea | Thailand

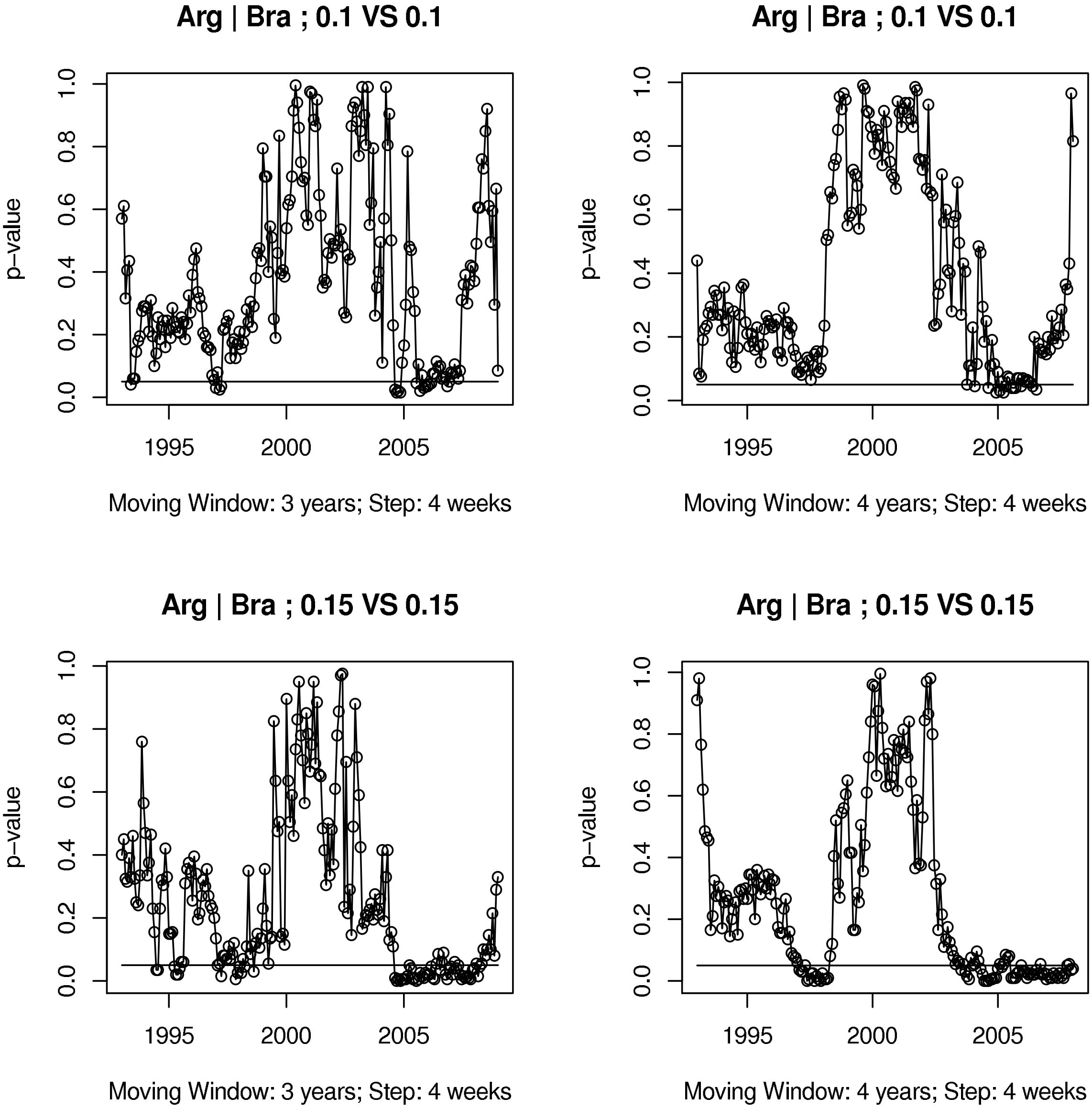

Figure 5. Moving Window Plot for Argentina | Brazil

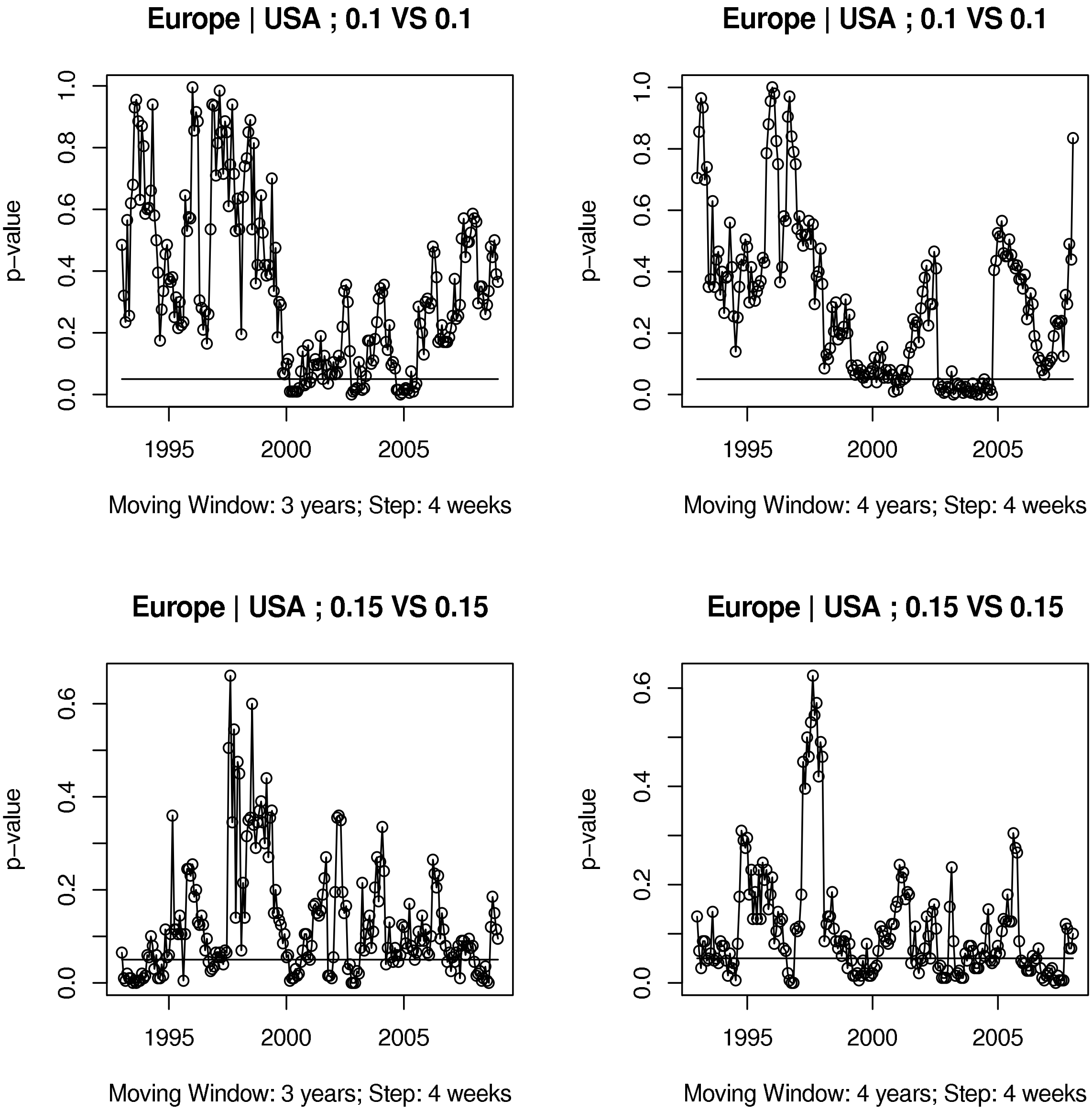

FIGURE 6. Moving Window Plot for Europe | USA.

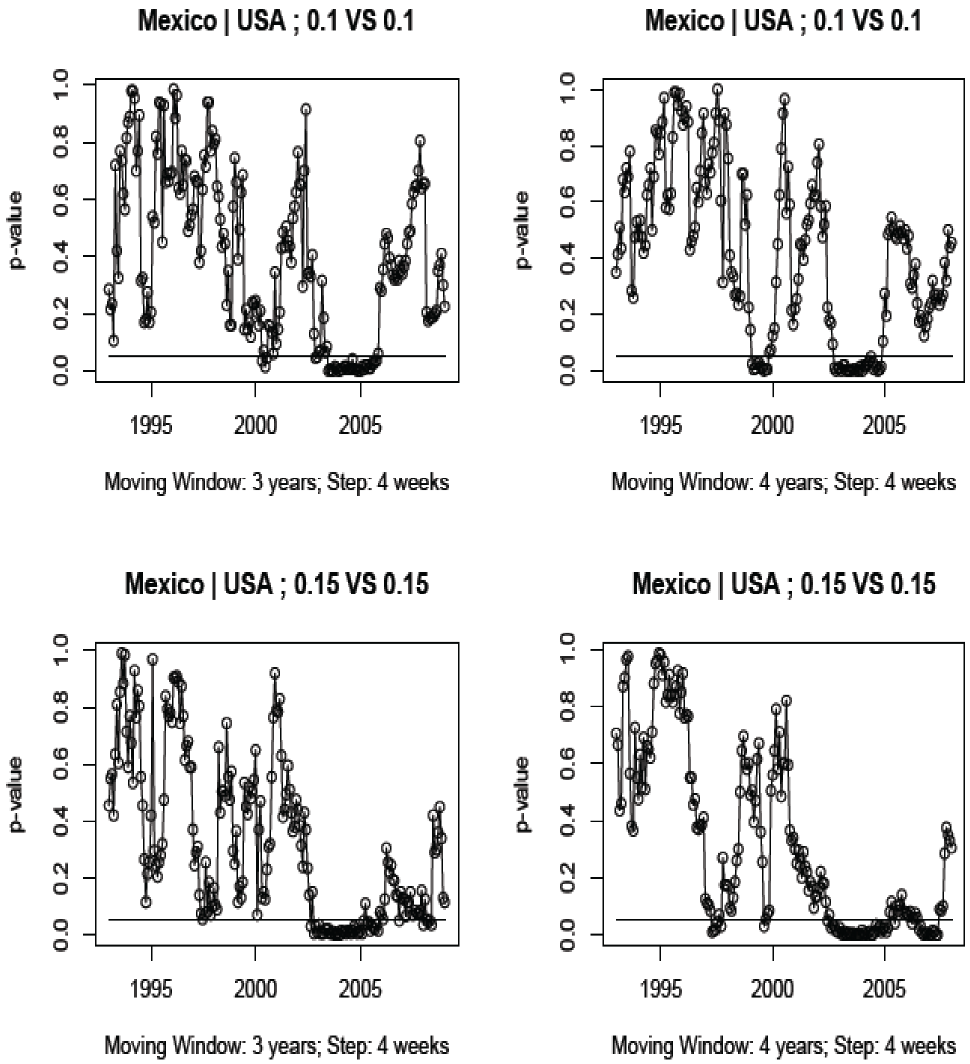

FIGURE 7. Moving Window Plot for Mexico | USA.