# Testing the Onset of Fertility Decline Accounting for Structural Variables

**Authors**
Renato M. Assunção, Joseph E. Potter

**Correspondence**
Joseph E. Potter, Population Research Center, University of Texas, 1 University Station G1800, Austin, Texas 78712-0544. E-mail: joe@prc.utexas.edu

**ABSTRACT**

Much of the debate in the fertility literature has concerned the presence and strength of spatial diffusion effects, as opposed to the role of development. Bocquet-Appel and Jakobi (1998) suggested the use of a space-time interaction test based on the Knox statistic to test for the evidence of spatial diffusion of contraception at the onset of fertility transition in Great Britain. This test has one major drawback: its failure to account for structural variables, which also change in space and time, induce biased results for the significance test increasing the real type I error level, even if the null hypothesis is true. We propose a Monte Carlo method for constructing unbiased space-time interaction tests. The procedure is illustrated with simulated data and with real fertility data from the last five Brazilian censuses.

## 1. INTRODUCTION

Just what factors lead to fertility decline has long been a subject of contentious debate. Some recent fertility studies have used spatial statistics methods to study the onset of fertility transition, and have attempted to demonstrate the existence and importance of diffusion effects, as compared to changes in social and economic conditions, as determinants of the timing of fertility decline in both historical and contemporary developing country populations.

Bocquet-Appell and Jakobi (1998) proposed an innovative way to test the hypothesis of spatial diffusion of fertility control. They used the test introduced by Knox (1964) to verify if the there is evidence of space-time interaction and applied the method to data from Great Britain. In general terms, to each locality they associated a time indicating its fertility decline onset. They verified if geographically close localities tend to have similar onset times as in a typical contagion process. Since they found a significant result, they conclude that there is evidence of diffusion processes underlying the fertility decline.

However, we argue that there is a major problem with this approach. Structural variables are changing at the same time as the demographic process, and they are generally spatially and temporally structured. In fact, we expect that development tends to be highly clustered in space and time since neighboring localities have similar natural resources and economic activities. If structural variables alone drive the fertility decline process, significant space-time clustering of fertility decline can be entirely due to this confounding variable. That is,

if the changes in the structural variables are not constant for all geographical areas, the null hypothesis distribution of the Knox test is biased towards large numbers and the real error type I level of the test will be much larger than the nominal value used. Therefore, space-time changing structural variables is a potential problem that must be adjusted for.

In this paper, we propose an unbiased version of the Knox test. The test adjusts for the space-time interaction inherent in the structural variables. The one drawback is that it assumes a parametric model for the structural variables effect on fertility. The new method is based on a Monte Carlo procedure.

In Section 2, we present the usual Knox test and its adaptation by Bocquet-Appel and Jakobi (1998) for testing for the spatial diffusion of fertility decline. Using simulated data, we show in Section 3 how it can be highly biased when structural variables have space-time interaction. In Section 4, we present our proposal, and we illustrate its use with simulated data and with real fertility data from Brazil in Section 5. We close in Section 6 discussing practical and theoretical issues.

## 2. THE KNOX TEST

Consider a map partitioned into $n$ small and contiguous geographical units indexed by $i$. We associate a random variable $y_i$ to the $i$-th area measuring its onset of fertility, recorded in terms of its timing. Typically, there will be substantial temporal variation in the values of $y_i$ affecting all areas and reflecting seasonal effects and other time trends. There could also be large spatial heterogeneity with small values of $y_i$ clustered in certain regions while other regions have larger values. Taking for granted the time clustering and the space clustering, the interest focus on the simultaneous space and time interaction effect. That is, after adjusting for purely spatial and purely temporal clustering, the interest is to test whether cases which are close in space are also relatively close in time, and vice versa. If so, we say that the data exhibit *space-time clustering* or *space-time interaction*.

Spatial statisticians and epidemiologists have been acquainted with this problem since Knox (1964) proposed his space-time clustering test. Many applications of his test have appeared in the literature. For example, Bhopal *et al.* (1992) used it and found strong evidence that apparently sporadic case of Legionnaire´s disease in Glasgow and Edinburgh exhibited space-time clustering. Samuelsson *et al.* (1994) supported the hypothesis that infectious agents are responsible to a portion of insulin-dependent diabetes mellitus after detecting space-time clustering of cases in South-East Sweden. The same conclusion concerning childhood leukaemia was reached by Birch *et al.* (2000). Lack of support for associations between environmental hazards and Down syndrome based on national registers data from England and Wales was the conclusion of Morris *et al.* (1998) who were motivated by anecdotal reports of occurrences of space-time clusters of Down syndrome. Veterinary epidemiologists are also using space-time clustering detection methods, as shown in the review papers by Ward and Carpenter (2000) and Carpenter (2001).

The most popular statistical technique for testing space-time interaction is still that proposed by Knox (1964) in the context of health events affecting risk populations. Specifying a spatial and a temporal critical distance, it is possible to indicate when a pair of

events is close in space or close in time (Is it clear that the EVENT is composed by the spatial coordinates and the timing $y_i$ ?). The test is based on the number of pairs of events which are simultaneously close in space and in time. A large number of such pairs would be an indication that cases which are close in space tend also to be close in time leading one to conclude that there is space-time interaction.

More formally, let $R = A$ x $[0, T_F]$ be a three-dimensional region where $A$ is a polygon and $[0, T_F]$ is a time interval. We observe $n$ events in $R$ with coordinates $(x_i, y_i, t_i)$ with $i=1,...,n$. Let $d_{ij}$ and $t_{ij}$ be the spatial and temporal distances between events $i$ and $j$, respectively, for $i \neq j$. Let $D$ and $T$ be the distance and temporal critical values. The thresholds $D$ and $T$ must be specified by the user.
The function $\delta_{ij}$ is a binary indicator that events $i$ and $j$ are neighbors in space:

$$\delta_{ij} = \begin{cases} 1, \text{if } d_{ij} < D \\ 0, \text{otherwise} \end{cases}$$

Likewise, define the binary indicator of closeness in time:

$$\tau_{ij} = \begin{cases} 1, \text{if } t_{ij} < T \\ 0, \text{otherwise} \end{cases}$$

A third function is the binary indicator that the events $i$ and $j$ are close in space and time:

$$\sigma_{ij} = \delta_{ij}\tau_{ij} = \begin{cases} 1, \text{if } t_{ij} < T \text{ and } d_{ij} < D \\ 0, \text{otherwise} \end{cases}$$

The Knox test statistic is given by $X = \sum_{i<j} \sigma_{ij}$ , the number of pairs of events which are simultaneously close in space and time. This statistic is compared to the reference distribution under the null hypothesis which is approximated by sampling $B$ permutations of the events' time indexes. $B$ pseudo datasets are generated and $X$ is evaluated in each one of them. The $p$-value is the proportion of datasets (including the original one) with $X$ equal or larger than the Knox statistic observed in the original dataset. A small $p$-value is evidence favoring of the presence of space-time interaction.

The Knox test has several advantages that make it a popular choice among epidemiologists and biostatisticians: it does not require population risk data; it is not affected by temporal variation of events' diagnosis, notification or population if this temporal variation is constant in space; and it is not affected by the spatially heterogeneous distribution of the risk population if this spatial variation is constant in time.

One cannot assume that population increase is spatially homogeneous and, in this case, the Knox test can be misleading (Mantel, 1967; Roberson and Fisher, 1983). Klauber and Mustachi (1970) proposed a partial solution by dividing the data into different time segments, calculating a test statistic in each one of them and then summing to obtain an overall test. Although this procedure reduces the bias it also decreases the power of the test. The effect of the bias caused by geographical population shifts was studied by Kulldorff

and Hjalmars (1999). They also proposed an unbiased test but it requires risk population information to adjust for the population shift bias.

Another problem with the Knox test is its dependence on the choice of the spatial and temporal critical thresholds, the usual solution being to repeat the analysis repetition for a number of distance and time ranges and their posterior combination or the use of Mantel´s extension of Knox proposal (Mantel, 1967). Baker (1996) and Kulldorff and Hjalmars (1999) solved this problem in a similar way by using the maximum over different scales as a test statistic. The null hypothesis reference distribution is found by Monte Carlo procedures.

Diggle *et al* (1995) showed how an approach based on point process second-order analysis could estimate the degree of space-time clustering as a surface function of the spatial and temporal critical thresholds and suggested to integrate the surface over the spatial and temporal ranges. Jacquez (1996) used a different procedure basing his method on a test statistic calculating the number of pair of events which are *k* nearest neighbors in both space and time.

Bocquet-Appel and Jakobi (1998) adapted this test for the case of fertility decline by first constructing a binary variable (transiting or non-transiting locality) determined by a threshold criterion for the change in marital fertility, and then testing for space-time interaction in this binary variable. Their data spanned four decades, and was based on 68 spatial units. Only after they had completed the test for diffusion, did they examine the level of other variables associated with the timing of the transition.

## 3. A NEW PROPOSAL

A large region is partitioned into *n* areas indexed by *I=1,…,n*. In each area, we have a *t*(generally short) time series of binary observations $y_{it}$ indicating if area *i* has entered the fertility decline by time *t*. Associated with these outcomes, we also have time dependent covariates in the form of a *k*-dimensional vector $\boldsymbol{x}_{it}$ .

Denote by $A_{it}$ the event that area *i* has not entered the fertility transition process past time *t*. Define the quantities

$$P_{it}(\boldsymbol{x}) = Prob(A_{it} \mid \boldsymbol{x}) = Prob(y_{it} = 0 \mid \boldsymbol{x}) ,$$

the conditional probability that area *i* has not undergone fertility decline by time *t* given the covariate values at that time. Define also the quantity

$$p_{it}(\boldsymbol{x}) = P_{it}(\boldsymbol{x}) / P_{i,t-1}(\boldsymbol{x}) = Prob(A_{it} \mid A_{i,t-1} , \boldsymbol{x})$$

We assume that $P_{i0}(\boldsymbol{x})=1$ for all $\boldsymbol{x}$.

This situation is well known in event history analysis where survival refers to the pre-transition status. A major complication in survival studies is the presence of censored

observations. However, in our case, censoring is very simple because only in the last period there could be areas that have not undergone the transition process and hence are possibly censored.

Let $R_t$ be the set of areas still under risk of entering transition at time *t-1*. This is called the *risk set*. Also, let $D_t$ be the set of areas entering transition in the period from *t-1* to *t*. The likelihood function is then

$$\prod_t \left( \prod_{i \in R_t} [1 - p_{it}(\boldsymbol{x}_{it})] \prod_{i \in R_t - D_t} p_{it}(\boldsymbol{x}_{it}) \right) \tag{1}$$

We assume a logistic function to describe the effect of the structural variables on the survival time of the pre-transition status:

$$\log \frac{p_{it}(\boldsymbol{x})}{1 - p_{it}(\boldsymbol{x})} = \boldsymbol{x}' \boldsymbol{\beta}_t \tag{2}$$

Note that we allow the structural variables to have different impacts depending on the time period considered. This makes sense because the impact of a certain small amount of development in the beginning of the period study, in 1950 say, is likely to decrease by the end of the period.

Equation (gato) does not envolve the spatial location of the areas but the resulting probabilities $p_{it}(\boldsymbol{x})$ will generally display a highly structured spatial pattern. This pattern is induced by the spatial pattern possessed by the structural variables. The interest is to know if the observed event times exhibit more space-time clustering than that induced by the structural variables alone.

A way to eliminate the structural variables bias and at the same time retain the space-time interaction test is by means of a bootstrap test. These tests are useful in situations like ours where the alternative hypothesis is not well specified. To carry out a bootstrap test, it is necessary to specify two quantities:

- A test statistic $T(\boldsymbol{y})$, a function of the data. In our case, this is naturally the Knox statistic *X* and its observed value with the sample data is denoted by $t_{obs}$.
- A null probability distribution $\hat{F}_0$ for the data under the null hypothesis.

This second quantity is more delicate to define. The objective of a hypothesis test (bootstrap or otherwise) is to calculate the p-value or achieved significance level

$$\Pr_{H_0} \left( T(\boldsymbol{y}^*) \geq t_{obs} \right)$$

where the quantity $t_{obs}$ is fixed at its observed value and the random vector $\boldsymbol{y}^*$ has a distribution $F_0$ specified by the null hypothesis $H_0$. The bootstrap test estimates $F_0$ by a

plug-in distribution $\hat{F}_0$ estimated from the observed data. Since we adopted a parametric model, we can let $\hat{F}_0$ be the distribution determined by fixing the unknown covariate parameters equal to their maximum likelihood estimates $\hat{\boldsymbol{\beta}}_t$.

Hence, the significance of $t_{obs}$ is assessed by the following algorithm:

(1) Fit model (2) by the maximum likelihood method obtaining the estimates $\hat{\boldsymbol{\beta}}_t$.

(2) Generate $B$ random datasets using the fitted values $\hat{\boldsymbol{\beta}}_t$, where each random replication changes only the dependent variable $\boldsymbol{y}^*$, the onset of the fertility transition of each area. Any spatial pattern exhibited by these simulated datasets is induced by the structural variables, spatial diffusion processes being absent from the data generating mechanism.

(3) For each simulated pattern, evaluate the Knox statistic $X$. The $B$ values $X_1,...,X_B$ of the Knox test statistic can be used to calculate a (parametric) bootstrap distribution of $X$ under model (1). This distribution will be almost always be different from the generally used null hypothesis distribution of $X$. If the structural variables have some degree of space-time clustering, we should observe the values $X_1,...,X_B$ shifted towards larger values than those expected under this commonly used distribution.

(4) Calculate the p-value for the space-time clustering hypothesis allowing for the structural variables effetcs. The reference distribution of the Knox test statistic $X$ under the null hypothesis and with structural variable effects is provided by the empirical distribution function of the values $X_1,...,X_B$. Hence, the p-value is easily computed as the number of values $X_1,...,X_B$ which are larger or equal to the observed value of $X$ based on the real dataset.

## 4. BEHAVIOR OF THE KNOX TEST AND OUR PROPOSAL WITH SIMULATED DATA

We study the behavior of the Knox test using simulated data to show how it can be strongly biased. More specifically, its p-value calculation is not correct since it does not calculate the probability under the true null distribution. We describe next the details of the simulation and its results.

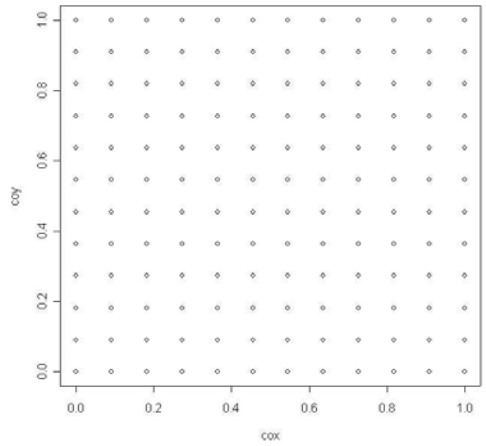


Figure 1: Regular Grid used in the simulation.

Consider a map with 144 areas located as a regular grid on the plane (see Figure 1). We considered 7 years of data and, in each area *i* and time *t*, we have a covariate $x_{it}$. All areas saw a temporal increase in their values of $x_{it}$. In each year, the set of values $x_{it}$ vary according to the ranges shown in Table 1. The spatial pattern is shown in Figure 2 with the more strong tone of red indicates a larger value. The pattern varies only along the horizontal direction, being constant in the vertical direction. It is clear that, as time passes, the whole region presents larger values of $x_{it}$. This mimics in our simulation a situation where, in each point in time, there is a spatial pattern for the covariate with neighboring areas having similar values. At the same time, economic development happens and all the areas increase their $x_{it}$ values.

| YEAR | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|---|---|---|---|---|---|---|---|
| Minimum | -3.0 | -2.5 | -2.0 | -1.5 | -1.0 | 0.0 | 1.0 |
| Maximum | 0.0 | 0.5 | 1.0 | 1.5 | 2.0 | 3.0 | 4.0 |

TABLE 1

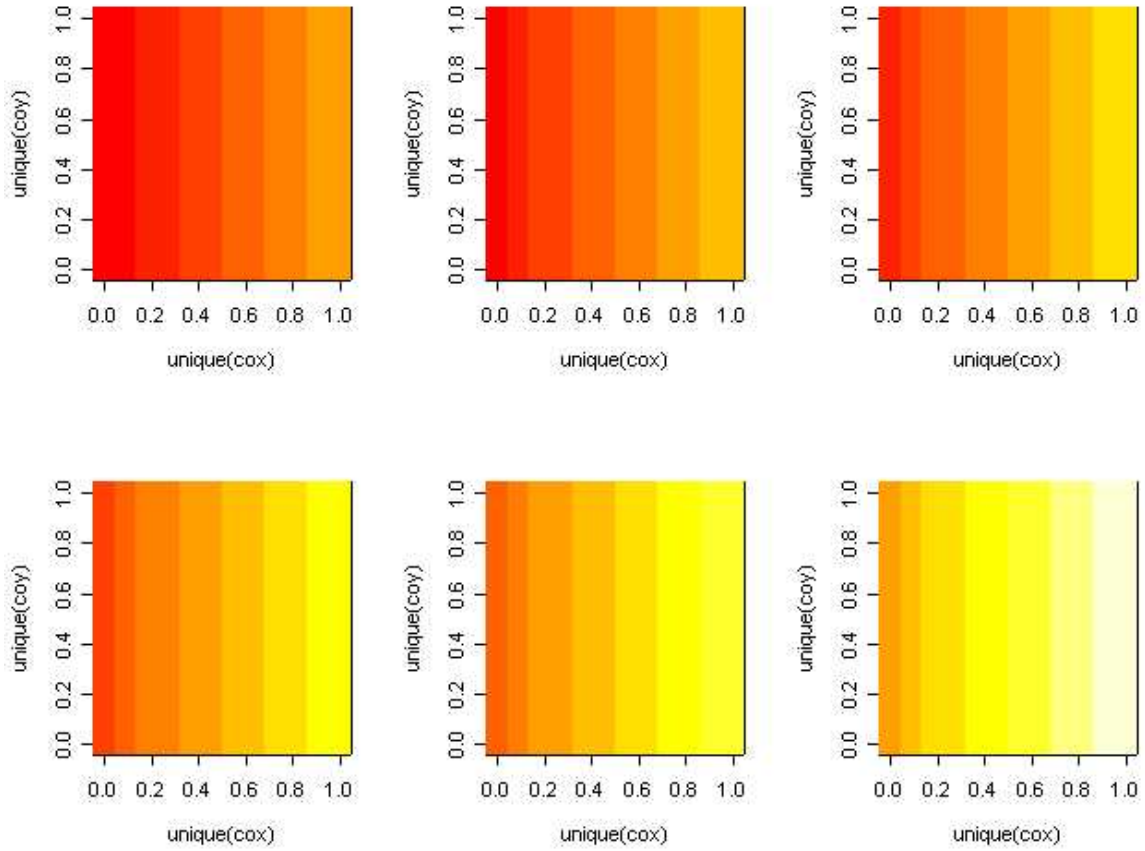


FIGURE 2: Spatial Pattern of Covariate Evolving in Time. The more white the color, the smaller the value.

The probabilities of fertility decline onset change with time due ONLY to the covariates change. This dependence is the same whatever the point in time (that is, the coefficient of the covariate does not change in time), it is always

$$\log \frac{p_{it}(x)}{1 - p_{it}(x)} = 4x$$

That is, $\beta_0$=0 and $\beta_1$=4. The covariate induces a spatial pattern in these probabilities and also makes them increase through time in each area considered individually. Figure 3 shows the space-time evolution of the probabilities of fertility decline onset. The probabilities for all areas in the last period are close 1 and so we do expect to see all areas entered decline fertility by the last year.

Based on these probabilities, we generated sequentially a history for each area, We kept flipping coins with the associated probability $p_{it}$ until we saw the first success, indicating the time the area entered fertility decline.

The onset variable is the year the area entered fertility decline and its pattern is shown in Figure 4. Note that the color pattern is the opposite of the previous plots. The

reason is that the areas with small values of covariates are those with the smaller probabilities of entering fertility decline and hence, they are the areas that will have the larger values of the onset variable. Likewise, the large covariate areas are those with the smaller values for onset.

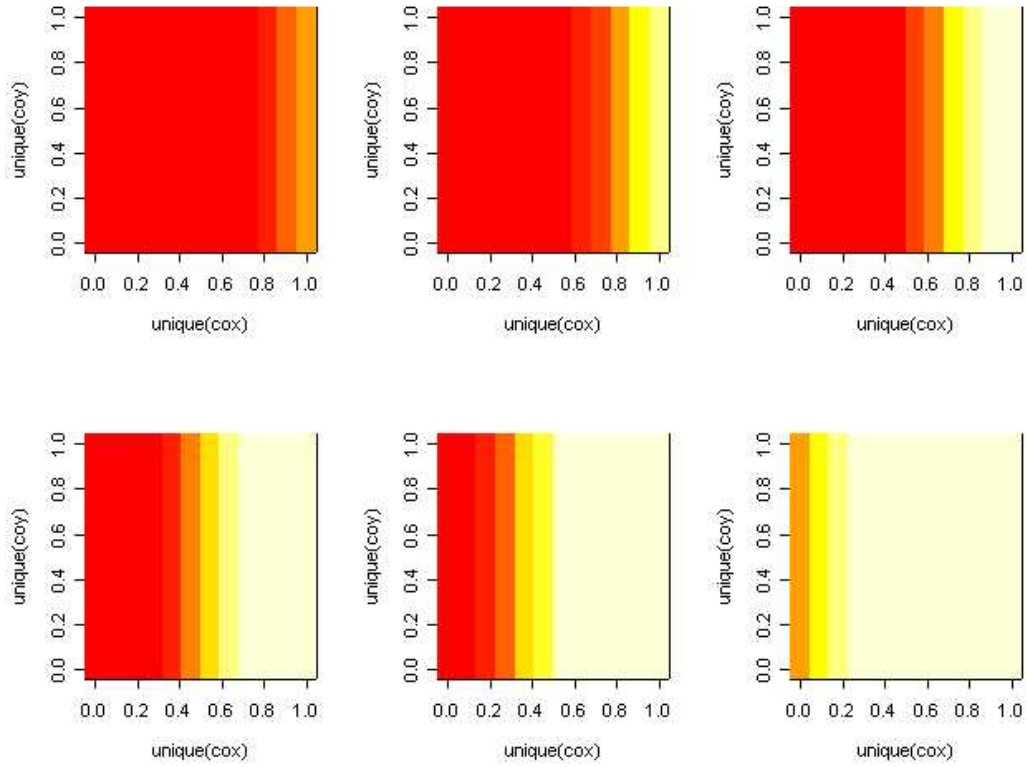


FIGURE 3: Spatial Pattern of Probability of entering decline. The larger the covariate value, the larger the probability of entering fertility decline.

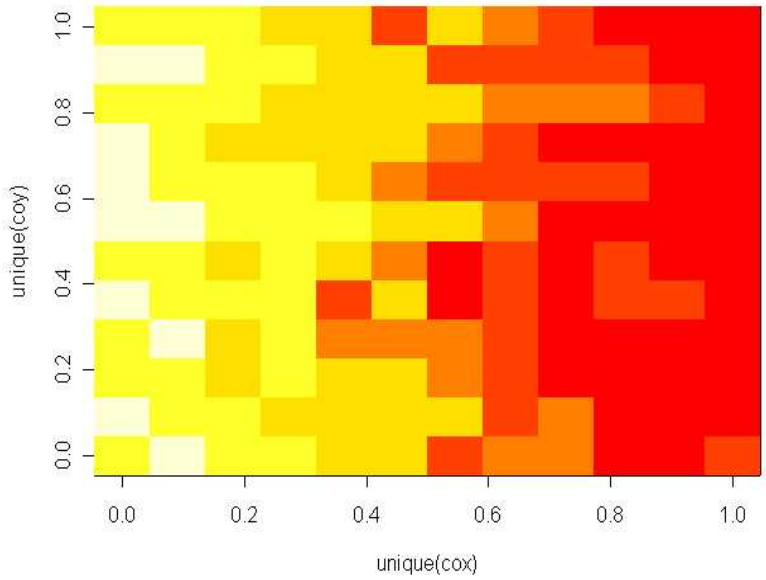


FIGURE 4: Spatial Pattern of Onset Variable.

We considered as neighbor in space if two areas were separated by, at most, $\sqrt{2}$ times the unit distance in the regular grid of Figure 1. As with time, events were close if were separated by 1 or 0 years. The Knox statistic with this dataset was equal to 344, a highly significant value according to the usual permutation distribution for the Knox statistic (See Figure 5. The vertical line is the observed Knox statistic and the histogram shows the permutation-based distribution of the Knox statistic.

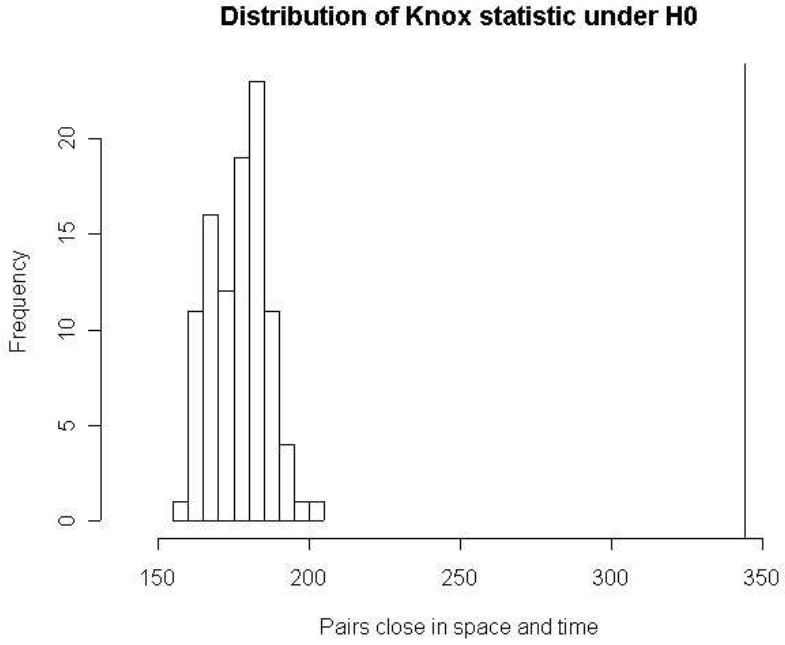

Figure 5: Permutation distribution of the Knox statistic.
Vertical line is the observed value.

Hence, we generated data that had all the space-time interaction driven by covariates and hence no spatial diffusion was going on. However, the Knox statistic is highly significant. This shows that the permutation distribution is not the right way to look at the diffusion evidence when confounding covariates are present.

We turn now to the analysis of this dataset with our bootstrap method. We applied the bootstrap simulation algorithm described in Section ??? with $B$=999. The result is in Figure 6. The $p$-value is now 0.51.

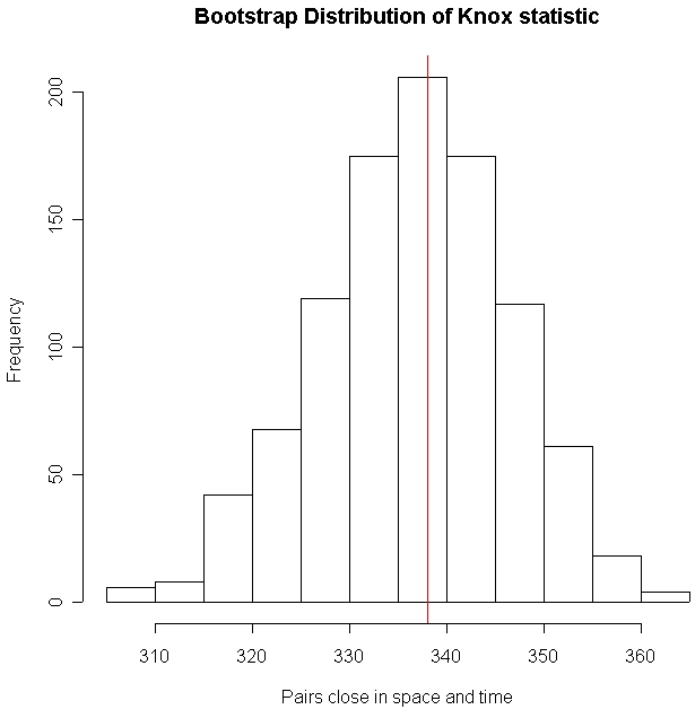


Figure 6: Permutation distribution of the Knox statistic for the model with covariate effects. Vertical line is the observed value.

### 4.1 The power study

Does the bootstrap test work if there is interaction on top of covariates effects? We want to know if the bootstrap test is able to detect true dispersion effects if they are present in addition to the effects of temporal change and spatially structured covariates. To answer that, we carry out a small simulation study using the framework presented before.

We will generate datasets where there is a certain amount of fertility behavior diffusion among spatially neighboring areas. That is, if an area experiences fertility decline onset at a

certain moment, this stimulates neighboring areas to also enter fertility decline. This influence can be felt at the same Census year data or in a next Census year data. Our model allows for synchronous influence within the same Census year data.

The map and the single covariate are the same as previously. The dependent data are generated in two steps at each year. Starting from the first Census year data, we generate $y_{i1}$ initially as independent Bernoulli random variables with probabilities given by the covariate link function:

$$\log \frac{p_{i1}(\mathrm{x})}{1-p_{i1}(\mathrm{x})} = \beta x$$

Considering the majority of areas that have not entered fertility decline, we allow them to still undergo fertility decline in this first Census year by means of influence of their neighbors who have entered fertility decline. More specifically, each *i*-th area still under the risk of entering fertility decline flips a loaded coin where "head" means onset. The loaded coin "head" probability is given by $\theta\gamma$ where $\theta$ is a number between 0 and 1 and $\gamma$ is a score for the presence of fertility decline onset in the spatial neighborhood score. There are several possible choices. For example, for $\gamma$, one can choose the proportion of neighboring areas that have entered fertility decline. Another option, which we used, is to set $\gamma$ equal to 1 if there is at least one neighbor out of the fertility decline risk, and 0 otherwise. The parameter $\theta$ measures the degree of shrinkage of $\mu$ towards zero. Note that, if $\theta\gamma = 1$, the area will enter fertility decline with certainty in this second step as a result of an extreme diffusion effect. The smaller $\theta\gamma$ is, the less influence has the diffusion process. If $\theta\gamma = 0$, there is no chance that area *i* will enter fertility decline by influence of its neighbors. We selected some different values for $\theta$.

The generation process goes on similarly. In the first step if year 2, for those areas which has not entered fertility decline on year 1, we generate $y_{i2}$ as independent Bernoulli random variables with probabilities given by the same covariate link function as before:

$$\log \frac{p_{i2}(\mathrm{x})}{1-p_{i2}(\mathrm{x})} = \beta x$$

Note that we do not change the covariate parameter $\beta$ although this is also possible. In the second step, the areas that have not entered fertility decline interact with their neighbors and, as result of flipping the loaded coin with the parameter $\theta\gamma$ described previously, they can also experience starting the decline. The simulation process goes on like that for 7 time periods. At the end, it is practically certain that all the areas have entered fertility decline. This generates a dataset where we have diffusion effects additionally to the effect of covariates. The observed value of the Knox statistic for this dataset is equal to 362. According to the wrong null distribution (the permutation distribution), this is a highly significant value, with *p*-value equal to 0.001 (see Figure left hand side plot of Figure 7).

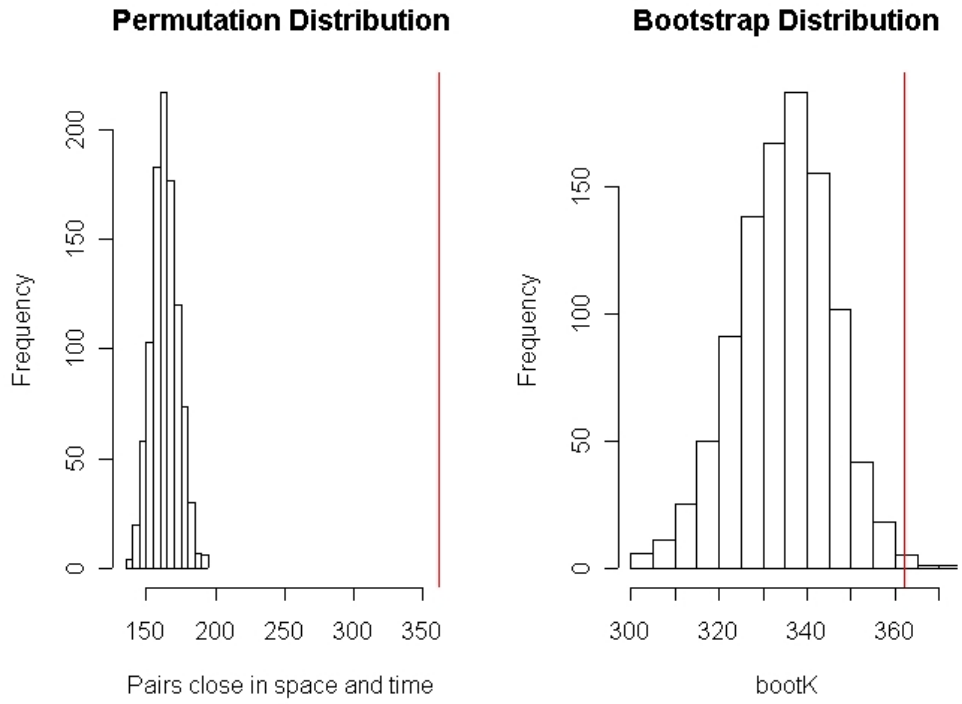


Figure 7: Permutation distribution of the Knox statistic for the model with covariate effects. Vertical line is the observed value.

We proceed with our bootstrap test. Now, since there is diffusion effect we expect the test will reject the null hypothesis, even after taking into account the presence of covariates. We fitted the logistic models. Incidentally, we could not get the covariate parameters estimates for the last two years because all areas have undergone fertility decline by then. To run the procedure, we just fixed the estimated parameters for the last two years equal to the last available parameter, that corresponding to year 5. We simulated 999 bootstrap samples for the onset dependent variable using the estimated coefficients and then we calculated the Knox statistic in each one of these datasets. The empirical distribution is that of the right hand side of Figure 7. The p-value is equal to 0.006, a highly significant value. This shows that our bootstrap testing procedure is sensitive to the presence of interaction on top of the covariate effects.

## 5. ILLUSTRATION WITH BRAZILIAN DATA AND SIMULATED DATA

To illustrate our methods, we use the Brazilian Demographic Census microdata from 1960, 1970, 1980, and to calculate fertility rates along with the average levels of a number of key indicators of development for 518 micro-regions at each census date. The data are based on a long-form questionnaire in which information on births is collected. The sampling fraction is 10% and 20% for municipalities with an estimated population larger and smaller than 15,000 inhabitants, respectively. We used the data from women from 15 to 49 years old grouped in five year age groups. These women provided information on the number of births they had in the year previous to the Census date. Generally, this information is more reliable to fertility studies than the birth registration system information due to severe under reporting in poor areas.

We used three independent covariates as proxies for structural development, as well one ideational variable, religion. The three structural variables were the average educational attainment of women of reproductive age, their labor force participation rate, and the proportion of households with electricity.

Due to the large variance of the micro-regions areas, the choice of a neighborhood structure for the Brazilian map is not simple. The map in Figure 8 (to be added) shows that it is not appropriate to use a neighborhood definition based on a threshold distance $D$ between the areas' centroids. In the North, the areas' centroids are separated by large distances while, in the South, these distances tend to be very short. An adequate threshold to create neighborhoods for the North region will be too large for the South part of the country. Hence, we defined a neighborhood structure based on adjacency between the polygons defining the micro-regions. That is, two micro-regions are neighbors if they share boundaries. With this definition, the neighborhood sizes varied from 1 to 22 neighbors, with quartiles equal to 5, 7, and 8.

With a temporal threshold of one Census year of separation, we found an observed Knox statistic equal to 1285. Applying the usual permutation based distribution as the null distribution, we find an expected value equal to 1007.4 and a 999 randomly selected permutations histogram shown in the left hand side plot of Figure 9. The red vertical line is the observed value of the Knox statistic and it is highly significant sinde none of the permuted values was larger than it.

We fitted the parametric survival model (1) and (2) and we found the coefficients in Table 1. We should emphasize that we are not interested in a high quality fit of the model to the data but rather only on controlling for the effects of space-time varying covariates.

With the coefficients fixed at the estimated values, we generated 999 bootstrap samples based on our survival model (cao) and (gato). Afterwards, we calculated the Knox statistic in each one of the bootstrap datasets and the histogram is in the right hand side plot of Figure 9, with the observed value of the Knox statistic as the red vertical line. We still find

the Knox statistic highly significant. This provides some evidence that diffusion of fertility behavior is a possible mechanism explaining the decline on fertility in Brazil.

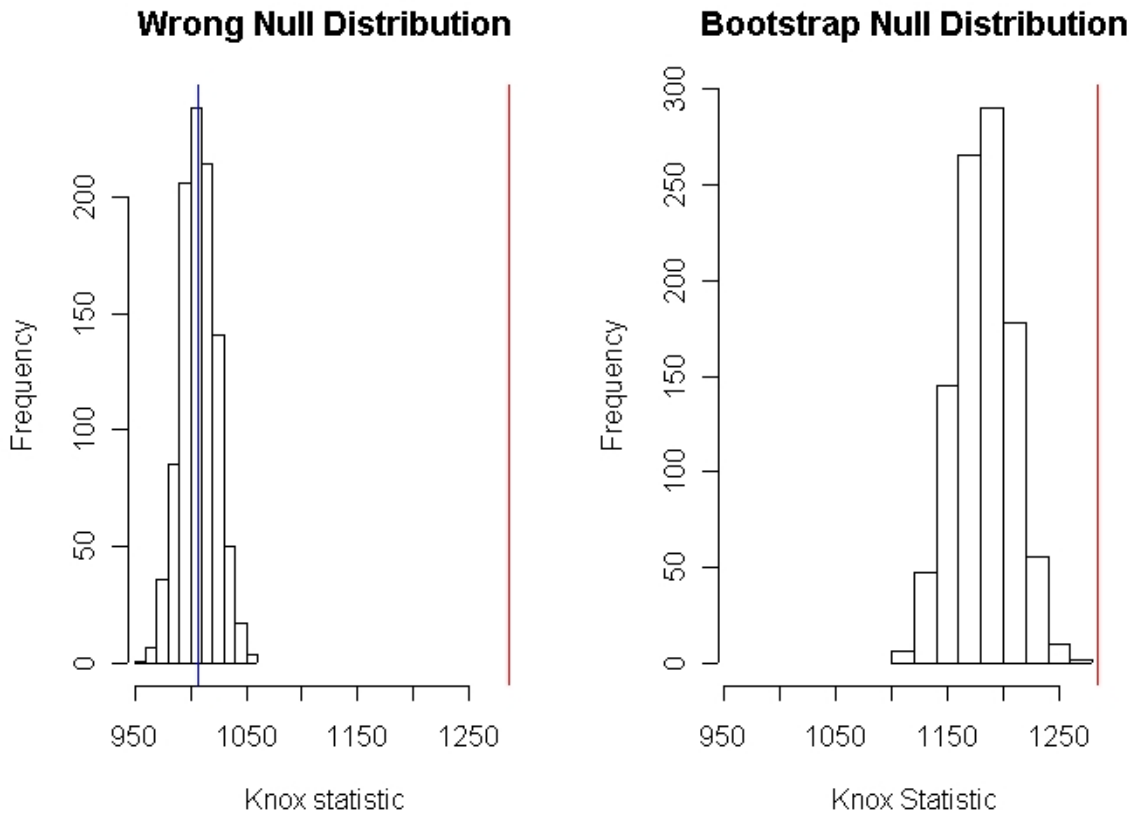


Figure 9: Permutation distribution (on the left) and bootstrap distribution (on the right) of the Knox statistic for the Brazilian fertility data. The parametric bootstrap testing used a model with covariate effects to simulate samples from the null distribution. The red vertical line is the observed value of the test statistic.

## 6. DISCUSSION AND CONCLUSION

Our modification of the Knox test described here can increase the evidence weight of fertility diffusion studies. The uncertainty of whether a significant result is due to space-time clustering of structural variables would no longer be present. Bocquet-Appel and Jakobi (1998) approach to testing for spatial diffusion using the Knox test was a major innovation. By resolving its major weakness with our proposed test, however, it can be turned into a more useful tool.

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