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Tests for smooth-abrupt changes with applications

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In this paper, we study a smooth-abrupt change point model through two testing procedures based on likelihood ratio test and Schwarz information criterion under a normal distribution. Simulations are implemented to show the performance of these two procedures. The proposed testing procedures are applied to detect changes in gene expression patterns and in predator versus prey population patterns of the Isle Royale National Park.

Keywords: Smooth-abrupt change; Likelihood ratio test; Information approach; Normal distribution

1 Introduction

There has been a great interest in the statistical analysis of the change-point problem in the past years because of its wide use in applications, such as biology, economics, finance, geology, medicine, and so on. Many scholars have focused on parametric change point models, in particular, the change point in the parameters of normal variables. Chernoff and Zacks (1964) and Sen and Srivastava (1975) have discussed the change point in the mean from a Bayesian point of view. In addition, Moreno et al. (2005) generalize the Bayesian stopping rules and propose objective intrinsic prior distributions for the unknown model parameters. Likelihood ratio test (LRT), as the most traditional method, has been used to study change point problems under different parametric settings, such as Srivastava and Worsley (1986), Hawkins (1977), Worsley (1986) and Gombay and Horvath (1994) and

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Chen and Gupta (2011), to name a few. From the nonparametric aspect, detailed discussions and references on the nonparametric methods of detecting the change points are given by Horváth and Csorgo (1997).

In this article, we consider a change-point model which is called a smooth-abrupt change-point (SACP) model. That is, the mean of a sequence of independent normal random variables remains constant until encountering an unknown point of time, where a linear change in the mean occurs, and then the mean drops back abruptly to the original value when reaching another unknown point. The left graph in Figure 1 shows the expectation of the SACP model without random error. The right graph in Figure 1 displays the SACP model with the initial mean 5, two change locations $k_1 = 14$ and $k_2 = 29$ and the sample size $n = 40$ after standard normal random error is introduced.

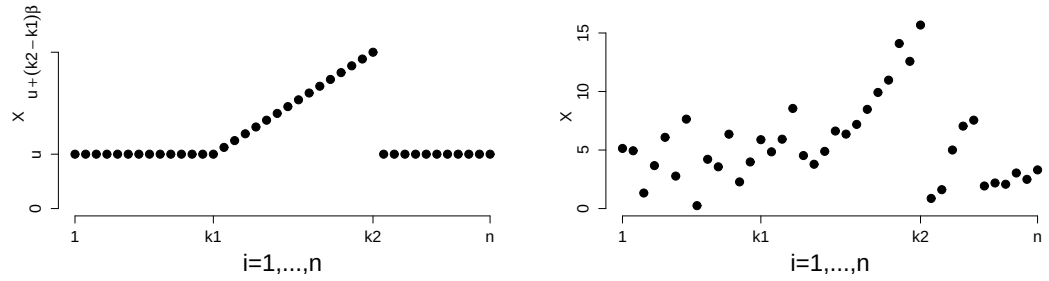

Figure 1: The left figure is the expected value of an SACP model; the right figure is an example of an SACP model after random error is introduced.

SACP model has broad applications in many fields such as medical research and genetic study. For example, monitoring and controlling the death rates during epidemics is often a challenge in epidemiology, public health, pathology, ecology, medicine, etc. The SACP model provides a basic option to study death rates of epidemics. For instance, death rates of a disease are often the same before an outbreak, and after the outbreak, the death rate increases until a cure is released to combat the disease. In addition to the change-point approximation, the estimated slope of the linear trend gives an insight of severity of the spread of the disease.

Previous research related to this type of change-point model has been done by Yao (1993), Levin and Kline (1985), Ramanayake and Gupta (2003) and
Ramanayake and Gupta (2004), to name a few. Unlike the SACP model, they studied epidemic changes instead of linear changes. Chen and Gupta (2007) studied a SACP model of independent normal random variables by using a Bayesian approach. Ning (2012) also proposed a nonparametric empirical likelihood ratio test for the same model, but his setting for the linear trend is different from ours. To the best of our knowledge, the procedures based on the likelihood ratio test (LRT) and the Schwarz information criterion (SIC) have not been studied for the SACP model. In this paper, we study the performance of these two procedures under different settings. This paper is organized as follows. The LRT procedure and the SIC-based procedure for this model are proposed in Section 2. Monte Carlo Simulations are conducted to demonstrate the performance of proposed methods in Section 3. We apply the proposed methods to gene expression

patterns in yeast, *Saccharomyces cerevisiae*, and the population trends of wolves and moose in Isle Royale National Park, USA in Section 4. Discussion and future work are stated in Section 5.

2 Methodology

Let $X_1, X_2, ..., X_n$ be a sequence of independent normal random variables with means μ_i and constant, unknown common variance σ^2, for $i = 1, 2, \ldots, n$, $n \geq 3$. We are interested in testing the hypotheses

$$H_0 : \mu_i = \mu_0 \text{ for } i = 1, 2, \ldots, n \tag{2.1}$$

versus

$$H_1 : \mu_i = \begin{cases} \mu_1, & 1 \leq i \leq k_1 \\ \mu_1 + \beta(i - k_1), & k_1 + 1 \leq i \leq k_2 \\ \mu_1, & k_2 + 1 \leq i \leq n \end{cases} \tag{2.2}$$

for some positive integers k_1 and k_2 such that $1 < k_1 < k_2 < n - 1$.

Note that β is the slope of the linear trend starting at an unknown position k_1 and ending at an unknown position k_2. In the following section, we derive the maximum likelihood estimators (MLEs) of β, μ, and σ^2 under H_0 and H_1 in (2.1) and (2.2).

2.1 Maximum Likelihood Estimators of Parameters

Under H_0, the log-likelihood function is

$$\ln L_0 = \ln L_0(\mu_0, \sigma^2) = -\frac{n}{2} \ln(2\pi\sigma^2) - \frac{1}{2\sigma^2} \sum_{i=1}^{n} (x_i - \mu_0)^2.$$

Let $\hat{\mu}_0$ and $\hat{\sigma}_0^2$ be the MLEs of μ_0 and σ^2, respectively. Then

$$\hat{\mu}_0 = \bar{x} = \frac{1}{n} \sum_{i=1}^{n} x_i, \quad \hat{\sigma}_0^2 = \frac{1}{n} \sum_{i=1}^{n} (x_i - \hat{\mu}_0)^2,$$

and the maximum log-likelihood function is

$$\ln L_0(\hat{\mu}_0, \hat{\sigma}_0^2) = -\frac{n}{2} \ln(2\pi\hat{\sigma}_0^2) - \frac{n}{2}. \tag{2.3}$$

Under H_1, the log-likelihood function is

$$\ln L_1 = \ln L_1(\mu_1, \sigma^2, \beta, k_1, k_2) \tag{2.4}$$

$$= -\frac{n}{2} \ln(2\pi\sigma^2) - \frac{1}{2\sigma^2} \sum_{\{i|1,\ldots,k_1,k_2+1,\ldots,n\}} (x_i - \mu_1)^2 - \frac{1}{2\sigma^2} \sum_{j=k_1+1}^{k_2} (x_j - \mu_1 - \beta(j - k_1))^2. \tag{2.5}$$

Let $\hat{\beta}$, $\hat{\mu}_1$, and $\hat{\sigma}_1^2$ be the MLEs of β, μ_1, and σ^2 under H_1, respectively. Then

$$\hat{\beta} = \frac{\sum_{i=k_1+1}^{k_2}(i-k_1)x_i - \bar{x}\sum_{j=1}^{k_2-k_1} j}{\sum_{j=1}^{k_2-k_1} j^2 - \frac{1}{n}(\sum_{j=1}^{k_2-k_1} j)^2}, \tag{2.6}$$

$$\hat{\mu}_1 = \bar{x} - \frac{\hat{\beta}}{n}\sum_{j=1}^{k_2-k_1} j, \quad \hat{\sigma}_1^2 = \frac{1}{n}\left[\sum_{i=1}^{n}(x_i-\hat{\mu}_1)^2 - \hat{\beta}^2\sum_{j=1}^{k_2-k_1} j^2\right], \tag{2.7}$$

and the maximum log-likelihood function is

$$\ln L_1 = \ln L_1(\hat{\mu}_1, \hat{\sigma}_1^2, \hat{\beta}, k_1, k_2) = -\frac{n}{2}\ln(2\pi\hat{\sigma}_1^2) - \frac{n}{2}. \tag{2.8}$$

2.2 Approach Based on Likelihood Ratio Test

For a fixed pair of (k_1, k_2), the maximum log-likelihood ratio test statistic for testing (2.1) versus (2.2) is

$$Z_{k_1,k_2} = -2\ln\frac{L_0}{L_1} = -n\ln\frac{\hat{\sigma}_1^2}{\hat{\sigma}_0^2}.$$

Since k_1, k_2 are usually unknown, it is natural to use the maximally selected likelihood ratio and reject H_0 if

$$W_n = \max_{1<k_1<k_2<n-1} Z_{k_1,k_2}$$

is sufficiently large comparing to the critical value at a given significance level. $\hat{k}_1$ and $\hat{k}_2$ are estimates of k_1 and k_2 so that the maximum of Z_{k_1,k_2} is reached. Since the asymptotic null distribution of W_n is not available, therefore, critical values for this test procedure are obtained through simulations which are illustrated in section 2.4.

2.3 Approach Based on Schwarz Information Criterion

Alternatively, a change-point problem can also be treated as a model selection problem. Detecting changes in a dataset parallels to selecting the best model to fit the data. In model selection, Schwarz information criterion (SIC) proposed by Schwarz et al. (1978) is one of the popular methods. In this section, we propose a testing procedure based on SIC.

The null and alternative hypotheses are described previously in (2.1) and (2.2), respectively. The SIC calculation will be used repetitively over the fixed choices of k_1 and k_2. Recall that the SIC quantifies a model's appropriateness by considering the fit of the model to the data and its simplicity. Generally, $SIC = -2\ln L(\boldsymbol{x}, \hat{\boldsymbol{\theta}}) + k\ln n$ where $L(\boldsymbol{x}, \hat{\boldsymbol{\theta}})$ is the likelihood function based on the model assumption and evaluated at the observations $\boldsymbol{x} = (x_1, x_2, \ldots, x_n)$ and the estimators $\hat{\boldsymbol{\theta}} = (\hat{\mu}_0, \hat{\sigma}_0^2)$ with the number of parameters, k, and sample size, n. A model with the smallest SIC value will be considered the best one to fit the data. For the model under H_0, the SIC is:

$$SIC(n) = -2\ln L_0(\hat{\mu}_0, \hat{\sigma}_0^2) + 2\ln n.$$

And for the model under H_1 with a fixed pair (k_1, k_2), the SIC is:

$$SIC(k_1, k_2) = -2 \ln L_1(\hat{\mu}_1, \hat{\sigma}_1^2, \hat{\beta}, k_1, k_2) + 3 \ln n.$$

Since k_1 and k_2 are unknown, $SIC(k_1, k_2)$ is calculated for all k_1 and k_2 such that $1 < k_1 < k_2 < n - 1$. Let $K = \{k_1, k_2 | 1 < k_1 < k_2 < n - 1\}$. Then, $\min\limits_{k_1, k_2 \in K} SIC(k_1, k_2)$ is the SIC value associated with the best model under H_1. The decision to reject H_0 occurs when $\min_{k_1, k_2 \in K} SIC(k_1, k_2) < SIC(n)$, that is, the best model under H_1 is more appropriate to describe the data than the best model under H_0 which concludes there are changes in the data. $\hat{k}_1$ and $\hat{k}_2$ are estimates of k_1 and k_2 so that the minimum of $SIC(k_1, k_2)$ is reached. The corresponding estimates for μ_1, β, and σ^2 are denoted $\hat{\mu}_1$, $\hat{\beta}$, and $\hat{\sigma}_1^2$ and are calculated from (2.6) and (2.7). Otherwise, we fail to reject H_0 which leads to the conclusion of no change in the data.

Table 1: Powers and Type I error of LRT Approach with $k_1 = 14$, $k_2 = 24$, $\alpha = 0.05$.

β	Power	MSE of β	MSE of μ_1	MSE of σ
-0.5	0.791	1.0729777	0.1667815	0.06420553
-0.4	0.553	0.9931794	0.2221598	0.08253751
-0.3	0.257	2.3848345	0.2843259	0.10275381
-0.2	0.127	6.3443056	0.3150671	0.12713209
-0.1	0.064	9.6517017	0.3068496	0.15032457
0.1	0.067	5.9536738	0.4841837	0.18823868
0.2	0.129	6.3586059	0.3762464	0.11617703
0.3	0.271	1.5878656	0.2864857	0.11183417
0.4	0.580	1.6871640	0.2209664	0.07448546
0.5	0.826	0.5726376	0.1823276	0.06160162

β	Type I error	MSE of μ_0	MSE of σ
0.0	0.045	0.1047409	0.05106262

2.4 Simulation Study

In this section, we conduct simulations to investigate the performance of LRT and SIC-based procedures under different settings.

The data satisfying H_1 were generated with change locations $(k_1, k_2) = (14, 24)$ or $(14, 29)$, $\mu_1 = 4$, $\sigma = 2$, $n = 40$ and β varies from -0.5 to 0.5 with the increment 0.1. The data satisfying H_0 were generated with $\mu_0 = 4$, $\sigma = 2$, and $n = 40$.

We conduct $1,000$ repetitions for each setting. For each repetition, the Schwarz information approach and the likelihood ratio test approach are applied. For the likelihood ratio test, we adopt the bootstrapping sampling procedure to obtain an empirical critical value corresponding to the level of significance. Under the null hypothesis, we assume there is no change. We generate a sample of size $n = 40$ from the normal distribution with $\mu = 4$ and $\sigma = 2$. Then, we calculate W_n. We repeat this $10,000$ times and get

$10,000$ W_n's. These $10,000$ values of W_n compose an estimated sampling distribution of W_n. The critical values at different significant levels are corresponding to the percentiles of the estimated sampling distribution of W_n. For instance, the critical value at $\alpha = 0.05$ is the 95^{th} percentile of the estimated sampling distribution of W_n. In this simulation study, the significance level $\alpha = 0.05$ is used to generate the empirical critical value of 13.38868.

Table 2: Powers and Type I error of LRT Approach with $k_1 = 14$, $k_2 = 29$, $\alpha = 0.05$.

β	Power	MSE of β	MSE of μ_1	MSE of σ
-0.5	1.000	0.03060304	0.2042551	0.05558257
-0.4	0.992	0.07697240	0.2064190	0.06090523
-0.3	0.830	0.53180229	0.2445720	0.06731005
-0.2	0.402	1.99511634	0.3051697	0.08835839
-0.1	0.133	7.55239857	0.5820727	0.12935431
0.1	0.107	4.58134718	0.4186879	0.13032007
0.2	0.380	2.50618344	0.2931828	0.08700124
0.3	0.838	0.54217285	0.2496442	0.06090420
0.4	0.989	0.06926793	0.1915168	0.05761837
0.5	1.000	0.02605817	0.1793414	0.05589740

β	Type I error	MSE of μ_0	MSE of σ
0.0	0.046	0.1020306	0.05069541

The power and Type I error of LRT approach are calculated under H_1 and H_0 respectively. The simulation results are listed in Table 1 and Table 2. For the SIC approach, the success rate of detecting an SACP change under H_1 and success rate of concluding no SACP change under H_0 are also calculated. The simulation results are listed in Table 3 and Table 4. From all the tables, we observe that the power and success rate of LRT and SIC respectively increase as the increase of $|\beta|$. That is, the shaper the linear change is, the higher of the capability these two tests have. For example, in Table 2, the power of LRT approach increases from 0.380 to 0.989 as the slope β increases from 0.2 to 0.4. Similarly, in Table 4, the success rate of SIC approach increases from 0.610 to 0.962 as the same increase of β. We also observe that more observations between two change locations, that is, the more observations on the linear trend change, the higher detection ability for both LRT and SIC approaches. For example, the power of LRT approach is 0.271 when $k_1 = 14, k_2 = 24$ and $\beta = 0.3$ in Table 1 while the power increases to 0.838 when the change locations $k_1 = 14$ and $k_2 = 29$ in Table 2. Similar performance of SIC approach can be observed in Table 3 and Table 4. From Table 1 and Table 2, we also can observe that the LRT method can control the Type I error well. For the SIC method, we report the probability that such a method can choose a correct model when $H_0 : \beta = 0$ is true. In Table 3 and Table 4, those probabilities are reasonable high with values 0.839 and 0.836 respectively. Such a probability is similar to the value of (1-Type I error) in LRT method and we denote it by "success rate". The reason is that the Type I error is always associated with a significance level α and the model selection process with the information

criterion does not involve any significance level α. Therefore, we calculate the "success rate" which is the probability to reflect its performance under H_0. Moreover, we notice that the SIC approach performs more sensitive to the change between small slopes with the same sign than the LRT approach does. For example, in Table 3, the power of the LRT approach increases from 0.107 to 0.380 as the increase of β from 0.1 to 0.2. For the SIC approach, the power increases from 0.279 to 0.610 under the same scenario in Table 4 as the increase of β from 0.1 to 0.2.

Table 3: Success Rate of SIC Approach with $k_1 = 14$ and $k_2 = 24$

β	Success Rate	MSE of β	MSE of μ_1	MSE of σ
-0.5	0.655	0.03350302	0.1913452	0.05971379
-0.4	0.547	0.04028336	0.2578228	0.06802841
-0.3	0.417	0.03561660	0.3034518	0.06801632
-0.2	0.288	0.05022339	0.3772295	0.08813410
-0.1	0.169	0.04877874	0.5127114	0.09814135
0.1	0.187	0.05524288	0.5277621	0.07997807
0.2	0.283	0.04746516	0.3853301	0.07751565
0.3	0.436	0.03985342	0.3319606	0.08248407
0.4	0.530	0.04054580	0.2411582	0.06126349
0.5	0.647	0.03134863	0.1795267	0.06257280

β	Success Rate	MSE of μ_0	MSE of σ
0.0	0.839	0.1004419	0.05250117

3 Applications

3.1 Gene Expression Data

In this section, the SIC method and LRT method are applied to detect a gene expression pattern in yeast, *Saccharomyces cerevisiae*. The data set comes from the microarray experiments of Spellman et al. (1998) and the specific gene of consideration is the DAL5 gene (probe ID: YJR152W) from the CDC15 dataset. The gene is measured based on 24 equally time interval locations and the normalized log expression of this gene can be found on the yeast genome website `http://genome-www.stanford.edu/cellcycle`. This is the same data set that was analyzed using the Bayesian approach in Chen and Gupta (2007). During a certain duration of time, the DAL5 gene is known to play a necessary role in the allantoate transport system in *Saccharomyces cerevisiae* (Rai et al. (1987)). During this time period there is an increase in the normalized gene expression, known as an upregulation. Before and after this time period, the normalized gene expression is in a more steady state of fluctuation (Chen and Gupta (2007)).

To study if the gene expression is upregulated during a specific time frame, H_0 of model (2.1) for this data set is compared to H_1 of model (2.2) via the SIC and LRT methods. The sample size is $n = 24$.

Table 4: Success Rate of SIC Approach with $k_1 = 14$ and $k_2 = 29$

β	Success Rate	MSE of β	MSE of μ_1	MSE of σ
-0.5	0.995	0.02052970	0.1930485	0.05930814
-0.4	0.970	0.02483473	0.2122356	0.06426293
-0.3	0.892	0.02297933	0.2410995	0.05996529
-0.2	0.606	0.02789886	0.3272123	0.07265364
-0.1	0.277	0.03478356	0.4396052	0.10606755
0.1	0.279	0.04510367	0.5026791	0.08798779
0.2	0.610	0.03148258	0.3359006	0.07286485
0.3	0.863	0.02045753	0.2237819	0.05802576
0.4	0.962	0.02062928	0.1981439	0.05605714
0.5	0.991	0.02112470	0.1707105	0.05865338

β	Success Rate	MSE of μ_0	MSE of σ
0.0	0.836	0.1066133	0.05276508

Under H_1, $\min SIC(k_1, k_2)$ is 16.11332 for all (k_1, k_2) such that $1 < k_1 < k_2 < 24$, which is less than $SIC(24) = 40.82668$ under H_0. Therefore, we reject H_0 and conclude there is a linear upregulation trend in this gene expression pattern. This minimum is obtained for $k_1 = 11$ and $k_2 = 15$. Thus, $\hat{k}_1 = 11$ and $\hat{k}_2 = 15$. Hence, the SIC method estimates that the time of upregulation approximately lies between 11 and 15 in the time index.

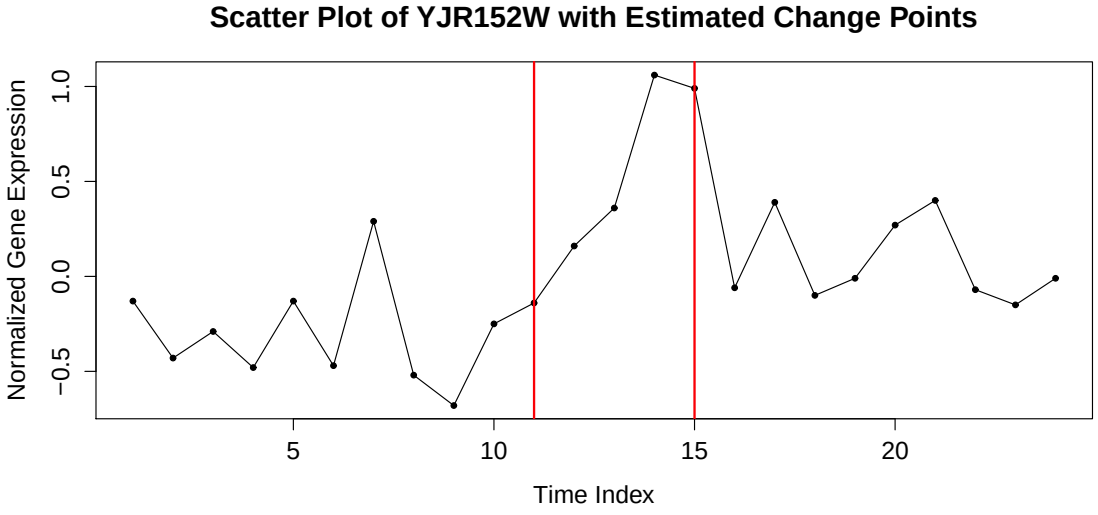

Figure 2: The plot of the gene expression of the DAL5 gene (probe ID: YJR152W)

On the other hand, the LRT test statistic is 20.48 and is obtained at $\hat{k}_1 = 11$ and $\hat{k}_2 = 15$ as well. Since 20.48 is greater than the empirical critical value of 15.39, there is enough evidence to overthrow H_0 in favor of H_1, and the LRT approach agrees with the SIC

approach. Figure 2 displays the data and the change location estimates $\hat{k}_1$ and $\hat{k}_2$. Chen and Gupta (2007) estimated the upregulation to be between 11 and 14 via a Bayesian approach. Furthermore, The MLE estimators for β, μ, and σ when $\hat{k}_1 = 11, \hat{k}_2 = 15$ are computed by the formulas in (2.4) are $\hat{\beta} = 0.3105$, $\hat{\mu}_1 = -0.1294$, and $\hat{\sigma}_1 = 0.277$.

3.2 Predator versus Prey Data

Wolves and moose are a good example of predator versus prey systems and in such systems, information regarding population changes are important to know. In this section, the SIC and LRT approaches are applied to the populations of wolves and moose living in Isle Royale National Park, USA throughout the years 1959 to 2011. The data and general information are obtained from Vucetich and Peterson (2012).

To study if the population of each animal is increasing during a specific time frame and then abruptly decreased, the hypotheses of H_0 (2.1) and H_1 (2.2) are assessed by the SIC and LRT methods. The sample size for each animal is $n = 53$, which corresponds to the 53-year time frame. The tests are done separately for each animal. The results are displayed in Figure 3, Figure 4, and Table 5.

Table 5: The output of SIC and LRT testing procedures for wolf and moose counts.

	SIC		LRT						
	SIC(53)	$SIC(\hat{k}_1, \hat{k}_2)$	W_n	critical value	$\hat{k}_1$	$\hat{k}_2$	β	μ_1	σ
Wolf	332.03	281.62	54.38	14.92	13	22	3.15	20.63	5.08
Moose	745.89	677.66	72.20	12.31	28	38	146.02	825.81	213.09

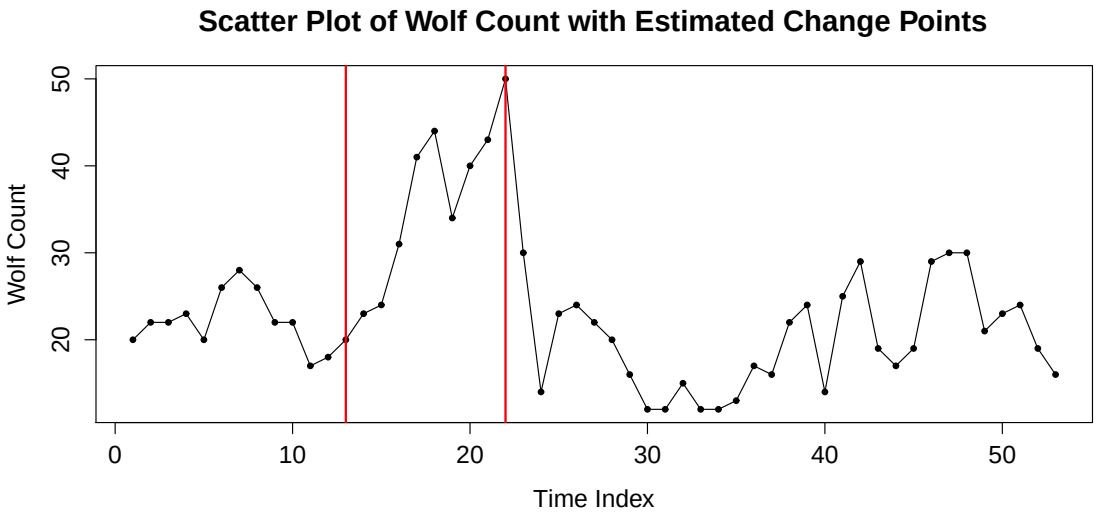

Figure 3: The plot of the wolf count through 1959 to 2011)

The two methods agree in selecting 1971 as the beginning of the upward trend in wolf count and in selecting 1980 as the year before the drastic decrease. Between 1971 and 1980,

the methods estimate the average rate to be $\hat{\beta} = 3$ wolves per year. Furthermore, both methods estimate moose count to increases from 1986 until 1996 at an estimated average rate of $\hat{\beta} = 146$ moose per year. Interestingly, Vucetich and Peterson (2012) mention that "in 1980 the wolf population crashed when humans inadvertently introduced a disease, canine-parvovirus," and "in 1996, the moose population collapsed during the most severe winter on record and an unexpected outbreak of moose ticks." Hence, the results agree with Vucetich and Peterson (2012) and give further insight on the average growth rate of wolf and moose counts. Furthermore, the results suggest the moose count started a major increase in 1986 which is after the wolf count's drastic decreased.

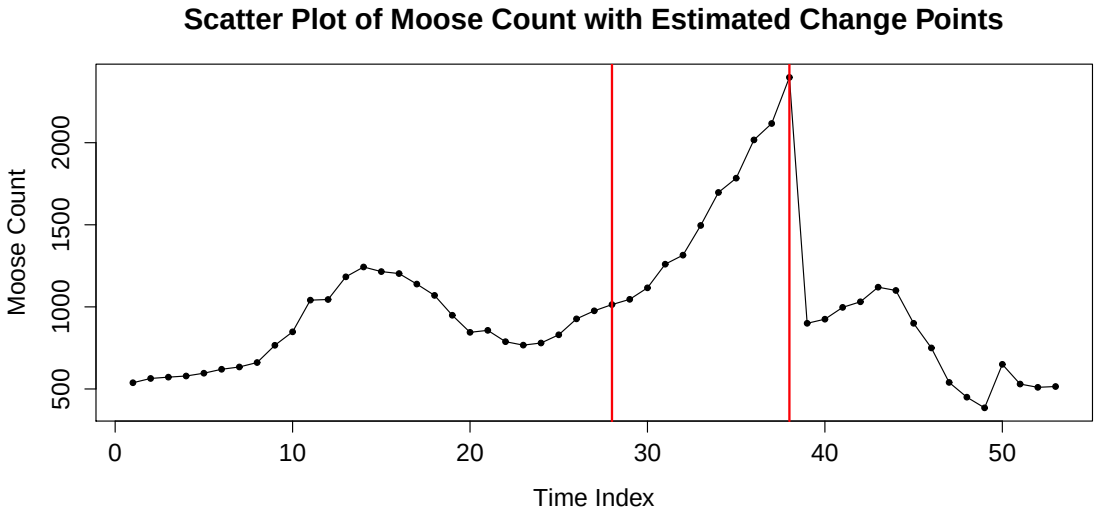

Figure 4: The plot of the moose count through 1959 to 2011)

4 Discussion

In this paper, the smooth-abrupt change-point (SACP) model is investigated. Particularly, the approaches based on the likelihood ratio test (LRT) and the Schwarz information criterion (SIC) are proposed. Simulations conducted under different SACP model settings indicate the reasonable performance of both approaches in detecting the changes in terms of the control of Type I error and the power. The proposed methods are applied to gene expression data and predator versus prey data to reveal possible abrupt changes in a linear trend. With the testing results, we conclude that a SACP model is appropriate to describe both data.

From the simulations, as we mentioned in previous sections, we observe that the SIC method performs more sensitive to the changes between small slopes β with the same sign than the LRT method does. We suspect that the sensitivity of the SIC method may vary when some component which affects the model complexity of SIC is altered. For instance, when we use the model selection criterion to analyze a change point problem, the change locations are possible components which may affect the complexity of the model. When the changes are either close to the beginning or to the end of the data, it could

cause some redundant parameters in the parameter space as Chen et al. (2006) pointed out. Consequently, it may affect the complexity of the model since it is usually measured in terms of the dimensionality of the parameter space. Therefore, we are curious about whether the variety of the complexity of the SACP model could affect the sensitivity of the SIC method when the slopes are relatively small. One possible direction for us to explore is that we may alter the locations of changes in data and investigate the magnitude of changes of the sensitivity under such scenarios analytically and numerically.

In our work, we only consider a change with a linear pattern and extensively use the normal assumption. Future work could be expanded to nonlinear patterns with various parametric assumptions or nonparametric assumptions. Further, other epidemic models can be considered, but the corresponding theoretical results remain to be justified.

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