Changepoint Detection Model based on Skew-Normal distributions for aCGH Data

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Abstract: In this paper we propose a changepoint detection procedure based on a skew normal distribution from the view of point of model selection. The detection procedure is constructed based on Schwarz information criterion (SIC) combined with the binary segmentation method for multiple changepoints detection purpose. Simulations are conducted to illustrate the performance of the proposed test. We apply the method to detect change points in the array Comparative Genomic Hybridization (aCGH) data set.

Keywords: Changepoint detection; Schwarz information criterion; Model selection; aCGH; Skew normal distribution.

1 Introduction

The skew normal distribution family is an extension of the normal distribution allowing the presence of skewness. Since Azzalini (1985) first studied various properties of this distribution family, it has been extensively investigated by many researchers in the past decades. Henze (1986) provided a probabilistic representation of the skew normal distribution family in terms of a normal random variable and a truncated normal random variable. Azzalini and Dalla Valle (1996) extended the univariate case to the multivariate case. Gupta and Chen (2004) gave another possible extension of the univariate skew normal model into the vector skew normal models. Recently, Ning and Gupta (2012) generalized the univariate extended skew normal distribution family to the matrix variate case by adopting the ideas from Chen and

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Gupta (2005) and Harrar and Gupta (2008). Ning (2013) extended the probabilistic representation of the univariate skew normal model to the matrix variate skew normal model, to name a few. Skew normal distribution is also applied widely in different fields such as finance and medical research due to its flexibility in modeling skewed data, for example, Chen et al. (2003), Figueiredo et al. (2010), Guolo (2013). The univariate standard skew normal distribution density is defined as

$$f_Z(z;\lambda) = 2\phi(z)\Phi(\lambda z), \tag{1.1}$$

where $\phi(\cdot)$ and $\Phi(\cdot)$ are the probability density function and the cumulative function of a standard normal distribution respectively. λ is called the shape parameter which is used to model the skewness of the data. We denote the random variable $Z \sim SN(\lambda)$. The corresponding general skew normal density function cooperating with the location and scale parameter is defined as

$$f_X(x;\mu,\sigma,\lambda) = \frac{2}{\sigma}\phi(\frac{x-\mu}{\sigma})\Phi(\lambda(\frac{x-\mu}{\sigma})), \tag{1.2}$$

where $x \in \Re$, μ is the location, σ is the scale and $\lambda \in \Re$ is the shape parameter. We denote the random variable $X \sim SN(\mu,\sigma,\lambda)$.

Changepoint problems have been received numerous attentions since Page (1954, 1955) who introduced a simple process to detect a single change (Chernoff and Zacks (1964), Gardner (1969), Hawkins (1992), Sen and Srivastava (1975), and Worsley (1979), Hsu (1977), Inclán (1993), Chen and Gupta (2012)). Csörgó and Horváth (1997) provided more details on parametric and nonparametric changepoint analysis. However, few work has been done in the direction of changepoint analysis for skew normal distribution family. Arellano-Valle et al. (2013) proposed a Bayesian approach for the changepoint detection but for at most one change in parameters of a skew normal distribution. In this paper, we will propose an information approach based on Schwarz information criterion (SIC) to detect possible multiple change points in the data. This paper is organized as follows. In Section 2, the method based on the SIC for the detection of the changes in location and scale parameters while holding shape parameter constant is proposed with corresponding adjustment to make the results more statistically convincing. Simulations are conducted in Section 3 to illustrate the performance of the proposed procedure under different settings with various sample sizes. The proposed method is applied to an array Comparative Genomic Hybridization (aCGH) data set for possible change point detection in Section 4. Discussion is provided in Section 5.

2 Skew normal changepoint model

Let $x_1, \cdots x_n$ be a sequence of independent observations from a skew normal distribution $SN(\mu,\sigma,\lambda)$ with parameters (μ_1,σ_1,λ), (μ_2,σ_2,λ), $\cdots$, (μ_n,σ_n,λ), respectively. Assume that the shape parameter is constant but unknown and needs to be estimated. Consider testing the following hypotheses,

$$H_0 : \mu_1 = \mu_2 = \cdots = \mu_n = \mu; \quad \sigma_1 = \sigma_2 = \cdots = \sigma_n = \sigma, \tag{2.1}$$

where μ and σ are unknown, versus the alternative:

$$\begin{aligned} H_1 : \mu_1 = \cdots = \mu_{k_1} \neq \mu_{k_1+1} = \cdots = \mu_{k_2} \neq \cdots \neq \mu_{k_q+1} = \cdots = \mu_n, \\ \sigma_1 = \cdots = \sigma_{k_1} \neq \sigma_{k_1+1} = \cdots = \sigma_{k_2} \neq \cdots \neq \sigma_{k_q+1} = \cdots = \sigma_n, \end{aligned}$$

where $1 < k_1 < k_2 < \cdots < k_q < n$ are the unknown change point positions to be estimated and there are q unknown change points. In changepoint analysis, multiple change points detection can be dealt with the binary segmentation method proposed by Vostrikova (1981). Therefore, without loss of generality, we consider at most one change in the distribution. That is, we will test the following hypotheses: (2.1) versus

$$H_1 : \underbrace{\mu_1 = \mu_2 = \cdots = \mu_k}_{\mu_1} \neq \underbrace{\mu_{k+1} = \mu_{k+2} = \cdots = \mu_n}_{\mu_n} \tag{2.2}$$

$$\underbrace{\sigma_1 = \sigma_2 \cdots = \sigma_k}_{\sigma_1} \neq \underbrace{\sigma_{k+1} = \sigma_{k+2} = \cdots = \sigma_n}_{\sigma_n} \tag{2.3}$$

where $1 < k < n$, and k is the unknown position of the change point. The likelihood function for the above hypothesis is given as:

$$L_{H_0}(\mu, \sigma, \lambda) = \prod_{i=1}^{n} \frac{2}{\sigma} \phi(\frac{x_i - \mu}{\sigma}) \Phi(\lambda \frac{x_i - \mu}{\sigma}),$$

$$L_{H_1}(\mu_1, \mu_n, \sigma_1, \sigma_n, \lambda) = \prod_{i=1}^{k} \frac{2}{\sigma_1} \phi(\frac{x_i - \mu_1}{\sigma_1}) \Phi(\lambda \frac{x_i - \mu_1}{\sigma_1}) \prod_{i=k+1}^{n} \frac{2}{\sigma_n} \phi(\frac{x_i - \mu_n}{\sigma_n}) \Phi(\lambda \frac{x_i - \mu_n}{\sigma_n}).$$

The log-likelihood functions are:

$$\begin{aligned} l_{H_0}(\mu, \sigma, \lambda)) &= n \log 2 - n \log(\sigma) + \sum_{i=1}^{n} \left(\log \phi(\frac{x_i - \mu}{\sigma}) + \log \Phi(\lambda \frac{x_i - \mu}{\sigma}) \right), \\ l_{H_1}(\mu_1, \mu_n, \sigma_1, \sigma_n, \lambda) &= n \log 2 - k \log(\sigma_1) + \sum_{i=1}^{k} \left(\log \phi(\frac{x_i - \mu_1}{\sigma_1}) + \log \Phi(\lambda \frac{x_i - \mu_1}{\sigma_1}) \right) \\ &\quad - (n-k) \log(\sigma_n) + \sum_{i=k+1}^{n} \left(\log \phi(\frac{x_i - \mu_n}{\sigma_n}) + \log \Phi(\lambda \frac{x_i - \mu_n}{\sigma_n}) \right). \end{aligned}$$

To obtain the MLEs for $\mu,\ \mu_1,\ \mu_n,\ \sigma,\ \sigma_1,\ \sigma_n$ and λ, we take the derivative of the log-likelihood functions with respect to the parameters and set the equations equal to zero.

$$\begin{aligned}
\frac{\partial l_{H_0}(\mu,\sigma,\lambda)}{\partial \mu} &= \sum_{i=1}^{n}\left(-\frac{1}{\sigma}\frac{\phi'(\frac{x_i-\mu}{\sigma})}{\phi(\frac{x_i-\mu}{\sigma})} - \frac{\lambda}{\sigma}\frac{\phi(\lambda\frac{x_i-\mu}{\sigma})}{\Phi(\lambda\frac{x_i-\mu}{\sigma})}\right) \\
&= \sum_{i=1}^{n}\left(\frac{(x_i-\mu)}{\sigma^2} - \frac{\lambda}{\sigma}\frac{\phi(\lambda\frac{x_i-\mu}{\sigma})}{\Phi(\lambda\frac{x_i-\mu}{\sigma})}\right) = 0,
\end{aligned} \tag{2.4}$$

$$\begin{aligned}
\frac{\partial l_{H_0}(\mu,\sigma,\lambda)}{\partial \sigma} &= \sum_{i=1}^{n}\left(-\frac{x-\mu}{\sigma^2}\frac{\phi'(\frac{x_i-\mu}{\sigma})}{\phi(\frac{x_i-\mu}{\sigma})} - \frac{\lambda(x-\mu)}{\sigma^2}\frac{\phi(\lambda\frac{x_i-\mu}{\sigma})}{\Phi(\lambda\frac{x_i-\mu}{\sigma})}\right) \\
&= \sum_{i=1}^{n}\left(\frac{(x_i-\mu)^2}{\sigma^3} - \frac{\lambda(x-\mu)}{\sigma^2}\frac{\phi(\lambda\frac{x_i-\mu}{\sigma})}{\Phi(\lambda\frac{x_i-\mu}{\sigma})}\right) = 0,
\end{aligned} \tag{2.5}$$

$$\frac{\partial l_{H_0}(\mu,\sigma,\lambda)}{\partial \lambda} = \sum_{i=1}^{n}\left(\frac{(x-\mu)}{\sigma}\frac{\phi(\lambda\frac{x_i-\mu}{\sigma})}{\Phi(\lambda\frac{x_i-\mu}{\sigma})}\right) = 0. \tag{2.6}$$

Similarly we have

$$\frac{\partial l_{H_1}}{\partial \mu_1} = \sum_{i=1}^{k}\left(-\frac{(x_i-\mu_1)}{\sigma_1^2} - \frac{\lambda}{\sigma_1}\frac{\phi(\lambda\frac{x_i-\mu_1}{\sigma_1})}{\Phi(\lambda\frac{x_i-\mu_1}{\sigma_1})}\right) = 0, \tag{2.7}$$

$$\frac{\partial l_{H_1}}{\partial \mu_n} = \sum_{i=1}^{n}\left(-\frac{(x_i-\mu_n)}{\sigma_n^2} - \frac{\lambda}{\sigma_n}\frac{\phi(\lambda\frac{x_i-\mu_n}{\sigma_n})}{\Phi(\lambda\frac{x_i-\mu_n}{\sigma_n})}\right) = 0, \tag{2.8}$$

$$\frac{\partial l_{H_1}(\mu_1,\mu_2,\sigma_1,\sigma_2,\lambda)}{\partial \sigma_1} = \sum_{i=1}^{k}\left(\frac{(x_i-\mu_1)^2}{\sigma_1^3} - \frac{\lambda(x-\mu_1)}{\sigma_1^2}\frac{\phi(\lambda\frac{x_i-\mu_1}{\sigma_1})}{\Phi(\lambda\frac{x_i-\mu_1}{\sigma_1})}\right) = 0, \tag{2.9}$$

$$\frac{\partial l_{H_1}(\mu_1,\mu_2,\sigma_1,\sigma_2,\lambda)}{\partial \sigma_n} = \sum_{i=k+1}^{n}\left(\frac{(x_i-\mu_n)^2}{\sigma_n^3} - \frac{\lambda(x-\mu_n)}{\sigma_n^2}\frac{\phi(\lambda\frac{x_i-\mu_n}{\sigma_n})}{\Phi(\lambda\frac{x_i-\mu_n}{\sigma_n})}\right) = 0, \tag{2.10}$$

$$\begin{aligned}
\frac{\partial l_{H_1}(\mu_1,\mu_2,\sigma_1,\sigma_2,\lambda)}{\partial \lambda} &= \sum_{i=1}^{k}\left(\frac{(x-\mu_1)}{\sigma_1}\frac{\phi(\lambda\frac{x_i-\mu_1}{\sigma_1})}{\Phi(\lambda\frac{x_i-\mu_1}{\sigma_1})}\right) \\
&+ \sum_{i=k+1}^{n}\left(\frac{(x-\mu_n)}{\sigma_n}\frac{\phi(\lambda\frac{x_i-\mu_n}{\sigma_n})}{\Phi(\lambda\frac{x_i-\mu_n}{\sigma_n})}\right) = 0.
\end{aligned} \tag{2.11}$$

We solve equations (2.4) to (2.11) to obtain the MLEs for $\mu,\ \sigma,\ \mu_1,\ \mu_n,\ \sigma_1,\ \sigma_n$ and λ. However, there are no explicit forms for the solutions to these equations, thus the numerical approach (R package *sn*, version 0.4-7 by Azzalini, 2011) will be applied to obtain the MLEs for these parameters. Let $\hat{\mu},\ \hat{\sigma},\ \hat{\mu}_1,\ \hat{\mu}_n,\ \hat{\sigma}_1,\ \hat{\sigma}_n\ \hat{\lambda}$ represent the MLE for $\mu,\ \sigma,\ \mu_1,\ \mu_n,\ \sigma_1,\ \sigma_n$ and λ respectively. Under the null hypothesis, the SIC model is given by,

$$SIC_t(n) = -2\log L(\hat{\mu}, \hat{\sigma}, \hat{\lambda}) + t\log n, \tag{2.12}$$

where $t = 3$ is the number of parameters in the model under H_0. Under the alternative hypothesis, the SIC model is given by

$$SIC_t(k) = -2\log L(\hat{\mu}_1, \hat{\mu}_2, \hat{\sigma}_1, \hat{\sigma}_n, \hat{\lambda}) + t\log n, \tag{2.13}$$

where $t = 5$ is the number of parameters in the model under H_1. We choose $[\log n] \leq k \leq n - [\log n]$ so that we have sufficient number of observations to obtain MLEs of parameters. Thus we reject the null hypothesis if

$$SIC_t(n) > \min_{[\log n]\leq k\leq n-[\log n]} SIC_t(k),$$

and $\hat{k}$ is the estimated change point location such that

$$SIC_t(\hat{k}) = \min_{[\log n]\leq k\leq n-[\log n]} SIC_t(k).$$

Theorem 2.1. Under the null hypothesis, for all $x \in \mathbb{R}$,

$$\lim_{n\to\infty} P[a(\log n)\lambda_n - b(\log n) \leq x] = \exp\{-2e^{-x}\}, \tag{2.14}$$

where $a(\log n) = (2\log\log n)^{1/2}$, $b(\log n) = 2\log\log n + \log\log\log n$, and

$$\lambda_n^2 = \max_{[\log n]\leq k\leq n-[\log n]} \left\{ 2\log L(\hat{\mu_1}, \hat{\mu_2}, \hat{\sigma_1}, \hat{\sigma_2}, \hat{\lambda}) - 2\log L(\hat{\mu}, \hat{\sigma}, \hat{\lambda}) \right\}.$$

As pointed by Chen and Gupta (2012), the small difference between $\min_k SIC_t(k)$ and $SIC_t(n)$ may be resulted from data fluctuation and in fact there is no change point. Therefore, we follow the idea by Chen and Gupta (2012) to introduce a significance level α and the corresponding critical value c_α. We conclude there is a change point if

$$SIC_t(n) > \min_{[\log n]\leq k\leq n-[\log n]} SIC_t(k) + c_\alpha, \tag{2.15}$$

where c_α can be computed by

$$1 - \alpha = P\left[SIC_t(n) < \min_{[\log n]\leq k\leq n-[\log n]} SIC_t(k) + c_\alpha | H_0 \right]. \tag{2.16}$$

Thus, from (2.15) we have,

$$
\begin{aligned}
1-\alpha &= P\left[SIC(n) < \min_{[\log n]\le k\le n-[\log n]} SIC(k) + c_\alpha | H_0\right] \\
&= P\left[SIC(n) - \min_{[\log n]\le k\le n-[\log n]} SIC(k) < c_\alpha | H_0\right] \\
&= P\left[\max_{[\log n]\le k\le n-[\log n]} (SIC(n) - SIC(k)) < c_\alpha | H_0\right] \\
&= P\left[\max_{[\log n]\le k\le n-[\log n]} \left(-2(\log L(\hat{\mu},\hat{\sigma},\hat{\lambda}) - \log L(\hat{\mu_1},\hat{\mu_n},\hat{\sigma_1},\hat{\sigma_n},\hat{\lambda})) - 2\log n\right) < c_\alpha | H_0\right] \\
&= P\left[\lambda_n^2 < 2\log n + c_\alpha | H_0\right] \\
&= P\left[0 < \lambda_n^2 < 2\log n + c_\alpha | H_0\right] \\
&= P\left[0 < \lambda_n < (2\log n + c_\alpha)^{\frac{1}{2}} | H_0\right] \\
&= P\left[-b(\log n) < a(\log n)\lambda_n - b(\log n) < a(\log n)(2\log n + c_\alpha)^{\frac{1}{2}} - b(\log n) | H_0\right] \\
&= P\left[(a(\log n)\lambda_n - b(\log n) < a(\log n)(2\log n + c_\alpha)^{\frac{1}{2}} - b(\log n)\right] \\
&- P\left[a(\log n)\lambda_n - b(\log n) < -b(\log n)\right].
\end{aligned}
$$

Now with the approximation in Theorem 2.1. we solve c_α as follows.

$$
\begin{aligned}
&1-\alpha \cong \exp\left\{-2\exp\left\{a(\log n)(2\log n + c_\alpha)^{\frac{1}{2}} - b(\log n)\right\}\right\} - \exp\left\{-2\exp\left\{b(\log n)\right\}\right\} \\
&\Rightarrow\ 1-\alpha + \exp\left\{-2\exp\left\{b(\log n)\right\}\right\} \cong \exp\left\{-2\exp\left\{a(\log n)(2\log n + c_\alpha)^{\frac{1}{2}} - b(\log n)\right\}\right\} \\
&\Rightarrow\ \log\log\left[1-\alpha + \exp\left\{-2\exp\left\{b(\log n)\right\}\right\}\right]^{-\frac{1}{2}} \cong a(\log n)(2\log n + c_\alpha)^{\frac{1}{2}} - b(\log n) \\
&\Rightarrow\ c_\alpha \cong \left[\frac{-1}{a(\log n)}\log\log\left[1-\alpha + \exp\left\{-2\exp\left\{b(\log n)\right\}\right\}\right]^{-\frac{1}{2}} + \frac{b(\log n)}{a(\log n)}\right]^2 - 2\log n
\end{aligned}
$$

Adjusted critical values for different value of sample size with given nominal values are given in Table 1 in Appendix.

3 Simulations

In this section, simulations are conducted to illustrate the performance of the proposed testing procedure for different changes in location and scale parameters. We perform 1000 simulations under $SN(\mu,\sigma,1)$ with different change point location k, sample sizes, $n = 100, 150$ and 200 and location and scale parameters $(\mu_1 = \sigma_1) = 1, 2, 3$ and $(\mu_n = \sigma_n) = 2, 3, 4, 5, 6$. We notice that as the difference between the parameters increases, the power of the test also increases. For example, with sample size $n = 100$, $k = 20$, the power is 0.597 for $(\mu_1, \sigma_1/\mu_n, \sigma_n) = (1, 2)$, while the power is 0.917 for $(\mu_1, \sigma_1/\mu_n, \sigma_n) = (1, 4)$. Through all simulations, Type

I error is well controlled within a give significance level $\alpha = 0.05$. The results are listed in Table 2 in Appendix.

4 Application to Biomedical Data

We applied the proposed detection procedure to detect the change points in "the array Comparative Genomic Hybridization" (aCGH) data set, see Snijders et al.(2001) for more details. We consider the Chromosome 4 of the fibroblast cell line GM13330. This chromosome consists of 167 genomic positions on which log base 2 ratio of the intensities were recorded. Using the test criteria in (2.15), we compute the SIC for all the genomic positions. The values of $SIC_t(n) = -55.86854$ and $\min_{6\leq k\leq 163} SIC_t(k) = SIC_t(150) = -301.2888$. We observe that $SIC_t(n)$ is larger than $\min SIC_t(k)$, even larger that $\min SIC_t(k) + c_\alpha$ after adjustment. Therefore we reject the null hypothesis and conclude that there is a change point. The estimated changepoint position is $k = 150$. Binary segmentation method is applied for possible multiple change points and it turns out that there is no more change point. The graphs of the SIC values and the log base 2 ratio of the fibroblast cell are given in Figure 1. We observe that the change point is visible in Figure 1 at the 150^{th} position. This result matches the one obtained by Chen and Gupta (2012).

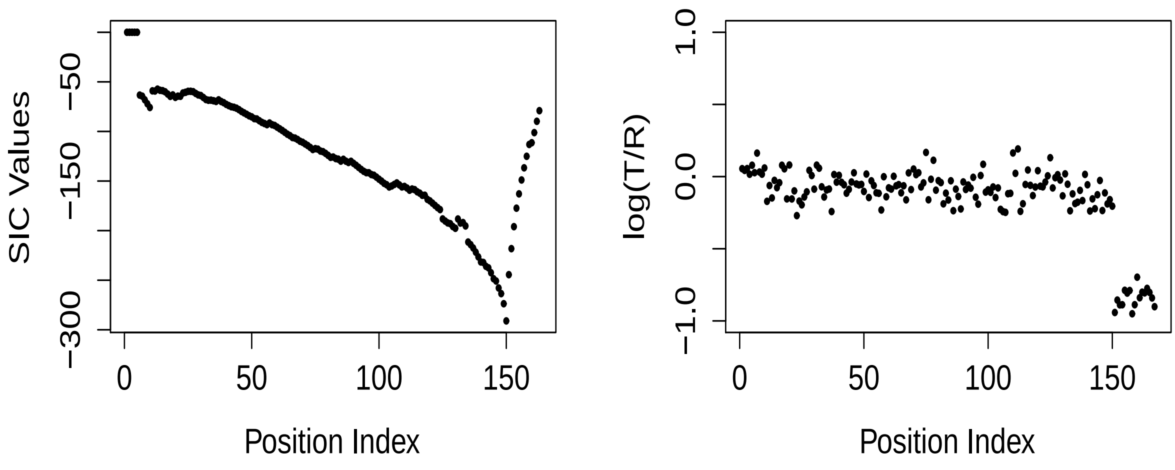

Figure 1: Left: The SIC values for every locus on chromosome 4 of the fibroblast cell line GM13330; Right: Chromosome 4 of the fibroblast cell line GM13330.

5 Discussion

Skew normal distribution family is an important distribution family which is an extension of normal distribution family and is more flexible in fitting data especially for skewed data. In this paper, we investigate changeppoint problem for this distribution family. We propose a testing procedure based on Schwarz information criterion (SIC) to avoid possible complicated derivation of asymptotic properties of test statistic such as likelihood ratio test statistic. Multiple change points scenario is dealt with the binary segmentation method. Another advantage of using information approach based procedure is that we can estimate the change point locations simultaneously while concluding the existence of change points. Simulation results under different settings indicate the good performance of the proposed method. A biomedical data has been used to illustrate the detection procedure. The extension of this method to the multivariate case with changes in a fraction of parameters will be studied in our future work.

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Appendix

Table 1: Critical values with α and Sample size n

n	α=0.01	α=0.025	α=0.05	α= 0.1
10	23.07060	15.99423	11.31283	7.168499
11	22.52369	15.69148	11.13858	7.087391
12	22.10831	15.44547	10.98893	7.010367
13	21.76289	15.23288	10.85445	6.935751
14	21.46347	15.04386	10.73120	6.863355
15	21.19818	14.87308	10.61709	6.793235
16	20.95987	14.71714	10.51070	6.725433
17	20.74363	14.57361	10.41098	6.659935
18	20.54582	14.44062	10.31712	6.596686
19	20.36366	14.31671	10.22843	6.535604
20	20.19494	14.20073	10.14437	6.476595
21	20.03788	14.09171	10.06445	6.419556
22	19.89103	13.98886	9.988275	6.364386
23	19.75319	13.89152	9.915503	6.310986
24	19.62336	13.79911	9.845834	6.259258
25	19.50068	13.71117	9.779008	6.209112
26	19.38444	13.62728	9.714797	6.209112
27	19.27401	13.54708	9.652998	6.113227
28	19.16885	13.47026	9.593433	6.067332
29	19.06850	13.39655	9.535943	6.022706
30	18.97255	13.32569	9.480385	5.979285
35	18.54758	13.00757	9.227490	5.778242
40	18.19266	12.73666	9.007971	5.599685
45	17.88832	12.50071	8.813923	5.439112
50	17.62215	12.29170	8.639973	5.293224
55	17.38579	12.10408	8.482294	5.159545
60	17.17331	11.93387	8.338068	5.036173
65	16.98042	11.77811	8.205151	4.921615
70	16.80384	11.63453	8.081879	4.814683
80	16.49016	11.37717	7.859242	4.620012
90	16.21778	11.15145	7.662302	4.446292
100	15.97721	10.95041	7.485684	4.289397
120	15.56699	10.60421	7.179053	4.014778
140	15.22548	10.31289	6.918813	3.779721
150	15.07403	10.18286	6.802049	3.673718
160	14.93309	10.06140	6.692662	3.574131
180	14.67758	9.840132	6.492633	3.391355
200	14.45073	9.642588	6.313270	3.226777
300	13.59074	8.885006	5.619338	2.584701

Table 2: Power Simulation for $SN(\mu, \sigma, \lambda)$ with n = 100, 150, 200

n=100		$\mu_1 = \sigma_1/\mu_n = \sigma_n$	2	3	4	5	6
	k=20	1	0.597	0.783	0.917	0.930	0.933
		2	0.050	0.240	0.530	0.740	0.780
		3	0.250	0.050	0.353	0.760	0.653
	k=50	1	0.597	0.820	0.927	0.967	0.957
		2	0.050	0.300	0.643	0.757	0.830
		3	0.433	0.050	0.220	0.407	0.603
	k=75	1	0.723	0.923	0.933	0.987	0.977
		2	0.050	0.397	0.693	0.883	0.883
		3	0.038	0.050	0.693	0.543	0.570
n=150	k=50	1	0.603	0.860	0.907	0.930	0.960
		2	0.050	0.435	0.790	0.753	0.840
		3	0.300	0.050	0.593	0.437	0.697
	k=75	1	0.690	0.787	0.940	0.953	0.970
		2	0.050	0.443	0.623	0.737	0.827
		3	0.293	0.050	0.257	0.487	0.617
	k=120	1	0.650	0.867	0.930	0.967	0.970
		2	0.050	0.200	0.630	0.800	0.867
		3	0.180	0.050	0.300	0.480	0.603
n=200	k=20	1	0.490	0.810	0.903	0.940	0.950
		2	0.050	0.307	0.597	0.710	0.813
		3	0.423	0.050	0.177	0.477	0.760
	k=50	1	0.603	0.860	0.907	0.930	0.960
		2	0.050	0.443	0.790	0.753	0.840
		3	0.250	0.050	0.593	0.437	0.697
	k=100	1	0.600	0.790	0.890	0.950	0.970
		2	0.050	0.397	0.680	0.800	0.893
		3	0.278	0.050	0.516	0.677	0.780