PREPROCESSING RADAR SECONDARY DATA FOR SIGNAL DETECTION

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1. Introduction

In signal detection, one is interested in the problem of detection of a given radar signal s which is a complex vector in the presence of noise in transmission. The actual observed data Y may be a pure noise vector $\boldsymbol{n}$ or the signal s plus a noise vector $\boldsymbol{n}$. It is assumed that the noise follows a complex multivariate normal distribution with mean 0 and covariance matrix S. Statistically, the model can be described as $Y = s + \boldsymbol{n}$ where s is a specific signal and $\boldsymbol{n}$ is a noise random vector. The goal is to test the null hypothesis that $Y = \boldsymbol{n}$ versus the alternative hypothesis that $Y = s + \boldsymbol{n}$. Reed, Mallett and Brennan (1974) discussed an adaptive procedure for the above detection problem in which two sets of input data are used, which are called the primary and secondary data. A radar receives primary data Y_0 which may or may not contain a signal, and secondary data which are assumed to contain only noise, independent of and statistically identical to the noise components of the primary data. The goal is to test $H_0 : \mu = 0 \; versus \; H_1 : \mu = s$ where μ is the population mean of Y_0. Kelly (1986) used the likelihood ratio principle to derive a test statistic for the above hypothesis testing problem.

Chen and Wicks (1999) proposed a selection procedure which compares the covariance matrices of the secondary data with that of the primary data. It is used to identify and eliminate those observations that have different covariance structure from the secondary data. As described in Chen and Wicks (1999), this procedure can be applied prior to the step of estimating the covariance matrix of the secondary data in Kelly (1986).

2. The Selection Procedure

Let $Y_0 \sim CN_p(\mu, \Sigma)$ denote the primary data which is received by a receiver and is to be tested for a specific signal s where s ia a known vector. Let $Y_1, Y_2, \ldots, Y_n \sim CN_p(0, \Sigma)$ be the secondary data which is to be used to estimate the unknown covariance matrix Σ. The random vector Y_0 is independent of the secondary data. Let S denote n times the sample covariance matrix of the secondary data sample $Y_1, Y_2, \ldots Y_n$. Our goal is to test

(2.1) $$H_0 : \mu = 0 \quad versus \quad H_1 : \mu = s .$$

Kelly's likelihood ratio test statistic for (2.1) can be written as

(2.2) $$\eta = \frac{| s * S^{-1} Y_0 |^2}{(s * S^{-1} s)(1 + Y_0 * S^{-1} Y)} .$$

The null hypothesis is rejected for large observed η. It was shown in Kelly (1986) that under H_0, $\eta \sim Beta(1, n - p + 1)$, a Beta distribution with parameters 1 and $n - p + 1$.

Following Reed, Mallett, and Brennan (1974)'s structure of radar data, Kelly's test also assumes an i. i. d. sample $Y_1, Y_2, \ldots Y_n$ for the secondary data and an independently distributed primary data Y_0. Let $\pi_1, \pi_2, \ldots, \pi_k$ represent k p-variate complex normal populations $CN_p(m_i, \Sigma_i)$, i = 1, 2, ..., k, and let π_0 be a control p-variate complex normal population $CN_p(m_0, \Sigma_0)$. Those k populations are the resources of the k cells which may or may not have the same or similar covariance structures as the control population π_0 from which the secondary data are taken. Here "similarity" is defined in (2.3) and (2.4) and the paragraph after (2.4) later in this section. Thus, from each of the k experimental populations, only one observation is taken, and from the control population, n observations are taken. We assume that $m_i = 0$, i = 0, 1, 2, ..., k since the k experimental populations are the cells which are assumed to have zero mean. Let $l_{i,1} \geq l_{i,2} \geq \ldots \geq l_{i,p} > 0$ denote the ordered eigenvalues of $\Sigma_i \Sigma_0^{-1}$. We define the two disjoint and exhaustive subsets, Ω_G and Ω_B, of the set $\Omega = \{\pi_1, \pi_2, \ldots, \pi_k\}$, by using a pair of distance functions d_1 and d_2 defined as follows:

(2.3) $$d_1(\Sigma_i, \Sigma_0) = l_{i,1};\ d_2(\Sigma_i, \Sigma_0) = l_{i,p}$$

(2.4) $$\Omega_B = \{\pi_i \mid d_2^* \leq d_2(\Sigma_i, \Sigma_0) \text{ or } d_1(\Sigma_i, \Sigma_0) \leq d_1^*\}, \Omega_G = \Omega - \Omega_B,$$

where $d_1^* < d_2^*$ are pre-assigned positive real numbers which are used to define similar and dissimilar populations. A population is considered similar to a control population when the distance measures are close to unity. Our goal is to separate the populations obtained from the guard cells into two disjoint subsets, S_G and S_B. The separation is correct if $S_G \subset \Omega_G$, meaning that all populations included in selected subset S_G have similar covariance structure as the control population. We require a procedure R that will satisfy the probability requirement that Pr(the seperation is correct| R) = Pr(CS| R) $\geq$ P*, where P* satisfies 2^{-k} < P* < 1.

The procedure R defined in Chen and Wicks (1999) is as follows.

Procedure *R*: For each population π_i (i = 1, 2, ..., k), we first compute $T_i = (x_i^H S^{-1} x_i)/n$

where x_i's are the data vectors from experimental cells, x_i^H is the conjugate transpose of x_i, and S is the sample covariance matrix associated with population π_0. Then we partition the set of populations $\Omega = \{\pi_1, \pi_2, \ldots, \pi_k\}$ into two subsets S_G and S_B. The subset S_G consists of those populations π_i with $c \leq T_i \leq d$ where c and d are chosen such that the probability requirement P(CS) $\geq$ P* is satisfied and $S_B = \Omega - S_G$.

To implement the procedure with a pre-determined probability requirement P*, Chen and Wicks (1999) have shown that constants c and d have to satisfy the following integral equation:

(2.5) $$\min_{\Omega} \text{P(CS)} = \min_{0 \leq m \leq k} \text{P}(T_i < c,\ i = 1, \ldots, m;\ T_j > d,\ j = m+1, \ldots, k) \geq \min_{0 \leq m \leq k} \{1 - m\text{P}(T_i > c) - (k-m)\text{P}(T_i < d)\}$$

$$= \min_{0 \leq m \leq k} \{1 - m(1 - F_{2p,2(n-p+1)}(\frac{(n-p+1)}{p}\frac{c}{d_1^*})) - (k-m) F_{2p,2(n-p+1)}(\frac{(n-p+1)}{p}\frac{d}{d_2^*})\}$$

where $F_{2p,2(n-p+1)}$ is the distribution function of an F distribution with $2p$ and $2(n-p+1)$ degrees of freedom. We also define $T_0 \equiv 0$ and $T_{k+1} \equiv 0$.

3. Simulation Study and An Example

Example: Five test (or guard) cells are to be examined and to be compared with a sample of secondary cells. Each cell π_i is represented by a 20 $\times$ 1 random vector x_i from a multivariate complex normal distribution with mean 0 and covariance matrix Σ_i. The covariance matrix of

the secondary cells is denoted by Σ_0. The five test cells come from normal populations with covariance matrices Σ_i such that

$\Sigma_1\Sigma_0^{-1}$ = diag (2.8, 6.7, .06, .05, .08, .07, .06, .05, 1.68, .09, 11.7, 9.6, .05, .08, .07, .06, .05, .08, .07, .06);

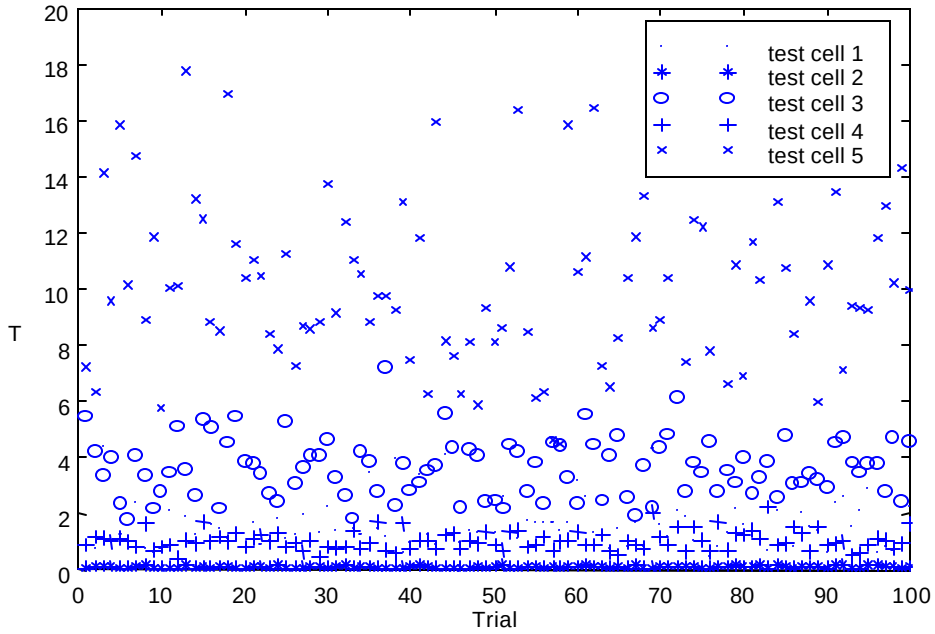
$\Sigma_2\Sigma_0^{-1}$ = diag (.1, .1, …, .1);

$\Sigma_3\Sigma_0^{-1}$ = diag (1.2, 2.5, 3.1, .8, 2.3, 5.4, 3, 2.9, 6.1, 3.3, 5.3, .5, .9, 7.3, 1.7, 5.5, 2.3, 3.1, 6.4, 5.5);

$\Sigma_4\Sigma_0^{-1}$ = I; $\Sigma_5\Sigma_0^{-1}$ = diag (10, 10, …, 10).

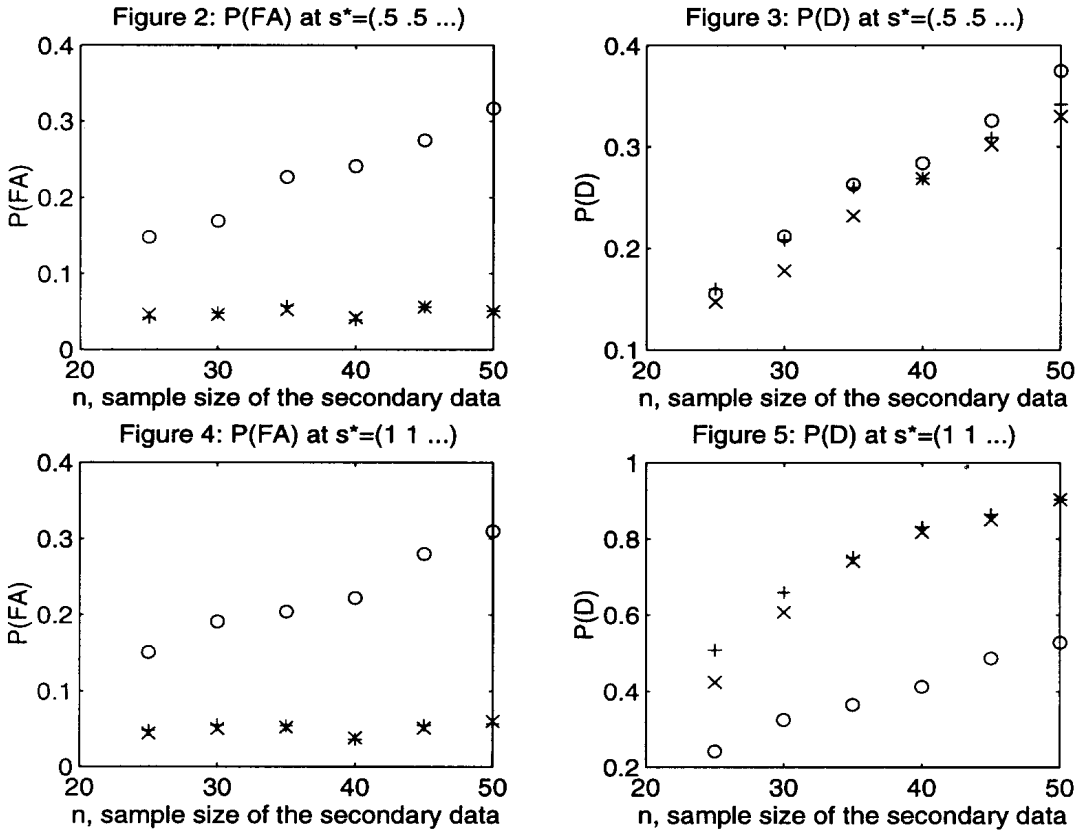
Suppose we want to eliminate the test cell p_i if either the largest eigenvalue of $\Sigma_i\Sigma_0^{-1}$ is smaller than or equal to d_1^* = .1 or the smallest eigenvalue of $\Sigma_i\Sigma_0^{-1}$ is larger than or equal to d_2^* = 10. Then by choosing c = .2 and d = 5, we find from a computing algorithm for (2.5), for the case k = 5, p = 20, d_1^*/c = ½, and d_2^*/d = 2, that the required sample size is n = 39 for the secondary data to achieve P* = .90. We simulated 100 trials of x_i (i = 1, …, 5) and S from the multivariate complex normal populations with mean 0 and with respective covariance matrices satisfying the above conditions. Then for each trial, we calculate the test statistic $T_i = x_i^H S^{-1} x_i / n$. The results are plotted in Figure 1 at the end of the paper. From the definition of Procedure R given in Section 2, Cell p_i is retained if .2 < T_i < 5. It is clear from the figure that Cell 4 is always retained. Cell 2 and Cell 5 are always eliminated. Cell 1 and Cell 3 are retained most of the times. Notice that Cell 4 is a perfect cell while Cell 1 and Cell 3 are both considered good cells.

Fig 1: 100 trials of T for 5 test cells x and a sample covariance S from n=39 secondary cells



In our next simulation illustrations, we show, in Figures 2 to Figure 5, the probability of the false alarm (P(FA)) and the probability of the detection (P(D)) when Kelly 's adaptive detection algorithm is applied to three different data sets. The first data set is the perfect data set where all the observations in the secondary data are simulated from the same multivariate complex normal distribution as the primary data. The second data set is the contaminated data set

where the secondary data includes some observations that were obtained from simulation of various multivariate complex normal distributions whose covariance matrices are significantly different from the covariance matrix of the primary data. The third data set is the screened data set which consists of those observations that were originally in the contaminated data set and were retained in the secondary data after our procedure *R* has been applied. We consider the following cases: *n*, the sample size of the secondary data, = 25, …, 50; p = 20; and s = (.5, …., .5)* and (1, …, 1)*. The level of significance is set at .05 for all the cases considered. In Figures 2-5, the 'o''s are for the contaminated data set. The 'x's are for the perfect data set, and the '+''s are for the screened data set. It is clear from the illustrations that Kelly's algorithm does not provide a constant false alarm rate (CFAR) for the contaminated data set and it always gives CFAR for the perfect data set and screened data set.



'o': the contaminated data set; 'x': the perfect data set; '+': the screened data set.

References

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