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Monitoring Hospital Outcomes Using Markov Chain Theory

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Abstract

Statistical tests based on the scan statistic are introduced for detecting possible increase in the occurrence of hospital events. The tests use a moving window and the theoretical aspects of the tests are investigated using Markov chain theory. The main objective of this study is to provide a powerful and easy-to-use statistical technique to assist the hospital staff in deciding whether the variation they observe is greater than usually expected under random variation. In this paper, we develop the test for Poisson data and apply the theory to monitor the occurrence of orthopaedic wound infection and Methicillin-Resistant *Staphylococcus Aureus* colonization. We find that this method is not only easy to use but also is sensitive in detecting the change in the process parameter.

1 Introduction

In the provision of health care in today's complex hospitals, collection of relevant data and their analyses should provide the opportunity for scientific methods to be used for the maintenance and improvement of health care. Our main concern is the study of variability that is associated with infections, colonizations of bacteria and mortality. Regardless of how well the events are monitored or how well the hospital personnel follow the standard

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procedures to reduce the occurrences of such events, inherent variation or natural variability will always exist. This natural variability is essentially an unavoidable cause, ie no preventive actions can be taken to avoid this variability, we refer to a stable system of chance causes [1]. Whenever only chance causes of variation are present in a system, then the system is said to be in statistical control.

We consider 'on-line' decision monitoring which enables us to detect where the variability in the data occur so that some investigation of the process can be made and corrective action can be taken to remove or reduce the sources of variability. In a prospective approach of 'on-line' monitoring, we need statistical techniques that can give a prompt signal of change from the state of statistical control.

One of the most useful or commonly used methods for 'on-line' monitoring of the quality of manufactured products in industry is the control chart. In addition to the classical Shewhart chart and various modifications, other frequently proposed control charts for use in industrial applications include the Cumulative Sum (CUSUM), CUSUM-Shewhart charts [2, 3, 4, 5, 6] and Exponentially Weighted Moving Average (EWMA) chart [7, 8, 9, 10, 11].

These control charts can be applied to 'on-line' monitoring of the occurrence of an event in the hospital. One basic difference between the manufacturing and medical environments is the 'product' to be controlled [12]. A patient is fundamentally different from a manufactured product. In monitoring an event, the input to the process, or factors that can affect the outcome, can be the equipment, management and control measures. The output or outcome of the process is the patient's condition. The intermediary steps of the process are standards and indicators. For example, when a patient undergoes an operation, the outcome of the operation can be affected by the operation equipment used or the expertise of the surgeon involved. Wound that may result from the operation can be classified according to a standard and the outcome is whether the wound is infected or not. Variation in the patient outcome is a function of variation in the inputs to the process and the standards or indicators used.

One of the difficulties faced by the hospital staff in using control charts for medical monitoring is the relative inexperience of hospital staff in formal quality control [12]. Although a control chart provides a graphical display so that the out-of-control situation

can be detected easily, the decision on whether the trend shown has been present for sufficient time for random variation to be unlikely for its occurrence has to be determined. This requires a test to determine whether the trend is due to a genuine change in the underlying occurrence rate. Some of these tests require calculation of a few values in order to determine whether the variation observed is greater than should occur due to random variation. Judgement on the suitability of these values is also required. Hospital staff who do not have a basic background in statistical quality control find that it is difficult to understand and judgement of suitable values is also difficult since techniques or decision making used in manufacturing must be modified for use in health care. There is also the possibility of misuse of control charts [13].

In a hospital, it is important to take early action or quickly be aware that a problem exists. Unlike manufacturing, where it is very expensive to stop a production line to search for a problem that may not exist, in the hospital the cost of this false alarm is unlikely to be great [14, 15, 16, 17]. Consequently, the usual practice of relying on the control chart three sigma limits in the manufacturing industry, is less suitable for hospital decision making. Furthermore, the results outside three standard deviations control limits will occur infrequently due to the generally small number of events occurring in the hospital setting.

It is crucial to develop a powerful and easy-to-use statistical technique to detect change in the rates of hospital events. What is needed is a method that could provide information to the hospital staff, in an easily understandable manner, on whether changes have occurred which are no longer consistent with being in control.

Here, we develop statistical tests based on the scan statistic which are easy to implement for detecting possible increases in the occurrences of certain hospital events. The tests use a moving window to calculate the value of a statistic. Theoretical aspects of the tests are investigated using Markov chain theory. We apply the scan statistic to the occurrence of orthopaedic wound infection and Methicillin-Resistant *Staphylococcus Aureus* (MRSA) colonization. Section 2 gives definition and algebraic expressions used througout this paper. The applications of the theory to data are discussed in Section 3.

2 Motivation

We consider two distinct states of health and these are represented as binary 0, 1. We shall regard one of the states as 'success', denoted by 1 and the other as 'failure', denoted by 0. As an example, a patient could belong to either one or other of these two categories: infected or not infected, colonized or not colonized, dead or alive, and any one of two other states of health. Our data will either be the binary observations or a summary of these binary observations taken over a given period of time. For example, the state of infection of wounds after an operation can be denoted as 1 for 'infected' and 0 for 'not infected'. Obviously, such a dichotomy does not take into account the degree of infection. A summary of binary observations could be the daily number of patients infected by an organism in a ward or the weekly number of deaths in a hospital.

We use the concept of the scan statistic which was first investigated in detail by Naus [18]. The statistic can be computed by plotting the points on a line corresponding to the occurrence of events over time. First take a 'moving window' of length L, then we find the maximum sum of observations as the window scans the interval. Let us define S_m as the sum of the L observations, $Y_m, Y_{m+1}, \ldots, Y_{m+L-1}$, in the m^{th} window, for $m = 1, \ldots, T$, such that if the events occur at discrete times $t = 1, \ldots, T$, then we have $N = T - L + 1$. We can write $S_m = Y_m + \ldots + Y_{m+L-1}$. If we define a discrete scan statistic

$$Z_{N,L} \quad = \quad \max_{1 \leq m \leq N} S_m,$$

then the probability of the scan statistic exceeding a certain value A is denoted by $P(Z_{N,L} \geq A) = p(N, L, A)$. This probability can also be used as the 'p-value' for testing the null hypothesis of uniform occurrence of events. The 'p-value' is the smallest level of significance that would lead to rejection of the null hypothesis. This probability is calculated using the theory of Markov chains [19]. In this paper, we discuss a model which assumes that the process remains in equilibrium about a constant mean.

In the study of nosocomial infection surveillance, the assumption of the Poisson distribution of incidences or events frequency has been used since it provides a good model for data for the number of occurrences of a specified event in a given unit of time or space [20]. Detailed theoretical results are given in the **Appendix**.

3 Application to Wound Infection and MRSA Colonization

In this section, we discuss applications of the theory we have developed. Firstly, recall that we define $S_m = Y_m + \ldots + Y_{m+L-1}$ as the total number of events in a window of size L where m denotes the position of the start of the window. If events occur at discrete times $t = 1, \ldots, T$, then $m = 1, \ldots, N$ where $N = T - L + 1$. The discrete scan statistic is defined as $Z_{N,L} = \max_{1 \leq m \leq N} S_m$ and $p(N, L, A) = P(Z_{N,L} \geq A)$. However, since this study is done prospectively, T and N are not fixed. N increases as there are more observations included in the study. In other words the total number of events in the first L observations is denoted by $S_1 = Y_1 + \ldots + Y_L$ and $N = 1$. We then calculate $p(1, L, A)$. As another observation is included in the study, we can calculate $S_2 = Y_2 + \ldots + Y_{L+1}$. At this point, $N = 2$. We can continue this procedure until no more observations are left in the process or until we decide to stop the process and review it.

3.1 Orthopaedic Wound Infection Data

Our first application involves wound infection, see Morton et al [17]. In 1992, the Infection Control Service at the Princess Alexandra Hospital in Brisbane investigated whether Class 1 (clean) orthopaedic wound infections existed after 218 operations. The uninfected operation is labeled as zero and infection as one. The infections occurred after the following operations in the time order sequence:

30, 51, 53, 54, 113, 132, 170, 172 and 196.

The data suggest a cluster of events for operations 51 to 54. Morton et al [17] selected three per cent as the target rate for these operations. That is, approximately one infection is expected to occur in every 30 operations. The target rate of three per cent was selected because the Australian Council on Health Care Standards (ACHS) had indicated that the maximum rate for Class 1 surgery in major institutions should be 4.1 per cent, however, orthopaedic surgery rates are likely to be below the average for all surgery. A counted data CUSUM control chart and test introduced by Lucas [21] was used to detect common cause variation. The counted data CUSUM chart is designed to analyze count (Poisson) data but proportion (binomial) data can also be analyzed if the expected proportion of the events is small. In this case, the expected proportion of infections is $\frac{1}{30}$. To implement the

CUSUM test, the operations are grouped into blocks and each block has 30 operations. Morton et al [17] found that the change, from one to 3 infections which occurs in the second block, does not reach statistical significance. This is to say, the change was not sustained long enough to reach statistical significance.

Using the scan statistic, a window of 30 operations is selected, $L = 30$, therefore expecting one event to occur in the window. The window moves one step at a time. The start of the study is from the first operation. In line with the study carried out by Morton et al [17], the number of infections recorded in a window of 30 is assumed to be Poisson with mean 1. Recall that scanning these data from the first operation gives S_1. S_1 is the result of summing all the observations from the first operation to the 30^{th} operation and this gives $N = 1$ and $Z_{N,L} = Z_{1,30} = 1$. Using the results in the **Appendix** and the computer code, we calculate $p(N = 1, L = 30, A = 1)$ where this probability is equal to 0.64. For $N = 2, S_2 = 1$ and $Z_{2,30} = \max(S_1, S_2) = 1$. Then $p(2, 30, 1)$ is calculated. The same process is carried out for other values of N and we find that $p(N, 30, 1)$ increases with N. We continue this process until $N = 22$, when S_{22} becomes 2, giving $Z_{22,30} = 2$ and $p(22, 30, 2) = 0.47 > 0.05$ Thus the increase of infections to 2 cases in a window of size 30 does not reach statistical significance as $p(N, 30, 2)$ increases with N. Table 1 shows $p(N, 30, A)$ and N when $Z_{N,30}$ changes.

The number of infections increases to 3 when the window shifts for the 24^{th} time $(N = 24)$ and the corresponding $p(N, L, A) = p(24, 30, 3) = 0.19$. $Z_{N,L} = Z_{25,30} = 4$ when $N = 25$ and $p(N, L, A) = p(25, 30, 4) = 0.059$, showing that the scan statistic gives a marginally significant result. The decision at $N = 25$ might be to stop the process and review it. However, in this context, it remains an open question as how this information could be used in decision making. For example, how small should $p(N, L, A)$ be for a decision to be made? We should note that, after $N = 31$, no other cluster of infections occurs that gives the scan statistic larger than 4.

Since the probability of the scan statistic exceeding a certain value A becomes less sensitive as N increases, it is wise to investigate the probability when $N = 1, p(1, L, A)$ first since if $p(1, L, A)$ is not significant, then for any N, $p(N, L, A)$ is not significant. Let us calculate $p(1, L, A)$ for $A = 2, 3$ and 4, giving $p(1, 30, 2) = 0.28$, $p(1, 30, 3) = 0.086$ and $p(1, 30, 4) = 0.021$. This is to say that, regardless of where the starting point of the

analysis, if one infection is expected in 30 operations, there would have to be a cluster of 4 infections in a window for the change to reach statistical significance.

Using the scan statistic, we discover that there is a maximum of 4 infections in a window of 30 operations instead of 3, as was found by Morton et al [17]. This is because the scan statistic moves the window one step at a time. On the other hand, Morton et al [17] grouped the operations into nonoverlapping blocks of 30.

3.2 MRSA Colonization

An outbreak of the Methicillin-Resistant *Staphylococcus Aureus* (MRSA) is the expression used when there is a significant increase in the rate of MRSA colonization and/or infection in a given facility [22]. At the University of California Davis Medical Center (UCDMC), an MRSA outbreak was defined as more than 4 cases reported per month [23]. The threshold of four cases represents the average number of new MRSA cases per month this University had since 1983. On the other hand, another study [24] defined an outbreak as more than 20% of the patients being colonized. Note that these studies did not use statistical methods to prove that the increases in the counts observed are statistically significant. In what follows we use statistical technique to determine the increase we are seeing is significant.

We consider a set of data that recorded the occurrences of MRSA colonizations daily from 1 July 1993. The data were obtained from the Princess Alexandra Hospital, Queensland, Australia. According to Morton et al [16], the rate of colonization which is expected to occur is 8 per week. This gives a rate of $\frac{8}{7} = 1.14$ colonization events per day. Firstly, let us investigate daily events with a window of 7 days. 7 days is chosen as the size of the window to avoid day of the week effects. An investigation on the daily data reveal that there is one day in each week where no events occur and it is suggested that the day when the occurrence of MRSA colonizations was not recorded until the next working day. Figure 1 shows the daily occurrences of MRSA colonizations for the first 100 days from 1 July 1993. The highest MRSA colonizations within this period occurred on the 17 August 1993 (day 48) where there are 7 colonized patients.

We start the analysis from 1 July 1993 and let the window of 7 days moves one day at a time. Assuming that the events follow a Poisson process with $\mu = \frac{8}{7}$, then when $N = 1$, $Z_{N,L} = Z_{1,7} = 14$ and $p(N, L, A) = p(1, 7, 14) = 0.049$. In other words, if the expected rate

of colonizations is 8 per week and if the observed number of colonizations in a week is 14 cases, then we see that the change observed shows a significant result. The decision might be to stop the process and alert the hospital staff about the significant change observed.

Suppose that the next analysis is carried out starting from 6 July 1993 (day 6), because, if we start the analysis before this date, then the values of $p(N, L, A)$ are less than 0.05, and thus the process should be stopped. We observe that there are 9 cases of colonizations when the window shifts for the first time when the analysis restarts on 6 July 1993. The corresponding $p(1, L, A) = p(1, 7, 9) = 0.49$. When $N = 2$, $Z_{N,L} = Z_{2,7} = 10$ and so $p(N, L, A) = p(2, 7, 10) = 0.40$. Table 2 shows N and $p(N, 7, A)$ when $Z_{N,7}$ changes as the window scans through the data. A maximum of 16 colonizations can be observed in the 7-day window. This occurs on day 69 when $N = 40$. Continuing the analysis for day 70 onward, we find that $p(N, L, A)$ becomes larger for fixed $A = 16$. Day 69 should be investigated further in order to make a conclusion since as N gets larger, $p(N, L, A)$ increases for fixed A and L. As noted earlier, we should investigate $p(1, L, A)$. We find that $p(1, 7, 13) = 0.088$, $p(1, 7, 14) = 0.049$, $p(1, 7, 15) = 0.025$ and $p(1, 7, 16) = 0.012$. We can conclude that an increase from the expected 8 to more than 14 colonization cases gives a significant result, if we take 0.05 as the level of significance.

If we consider the data starting from 1 July 1993, letting the window move until 13 September 1993 will find a maximum sum of 16 colonizations in the 7-day window. The window shifts 45 times and the resulting p-value is 0.15. This indicates the increase in colonization to 16 cases does not show a significant result, however the process should be stopped and restarted. To explain this we note that, if the window has shifted number of times and then an increase in frequency of events occurs, then this increase has to be larger for a given statistical significance than if the frequency increase had occurred after a few window shifts. That is, for given A and L, $p(N, L, A) > p(N + N_1, L, A)$ for $N_1 > 0$. To see how the rate of occurrence selected affects the result, let us select different values of μ. Table 2 shows $p(N, L, A)$ corresponding to $\mu = \frac{8}{7}, 1$ and $\frac{6}{7}$. It shows the sensitivity, in terms of $p(N, L, A)$, of the results as the expected rate is decreased from $\frac{8}{7}$ to $\frac{6}{7}$.

A possible criticism of the analysis using daily data are that daily rates are not constant. We have already noted that one day has $\mu = 0$ whereas $p(N, L, A)$ is calculated assuming they are. Another approach is to group the MRSA colonizations into weekly rates and this

overcomes some of these objections. Weekly MRSA occurrences are shown in Figure 2. Starting the analysis on 1 July 1993 and choosing the window size, L, as two weeks, then when $N = 1, Z_{N,L} = 22$. The corresponding $p(N, L, A) = p(1, 2, 22) = 0.15$ when the expected number of colonizations per week is 8. The maximum value of $Z_{N,L}$ occurs when the window of two weeks moves 9 times ($N = 9$) and $p(9, 2, 23) = 0.36$. In this analysis, we fail to detect a significant increase in the first week of the analysis which we detected earlier in the analysis using a 7-day window. This may be due to the small number of occurrences in the second week, giving a smaller value of $Z_{N,L}$. If the expected values are 7 or 6 per week, the corresponding $p(1, 2, 22)$ are 0.052 and 0.011, respectively. Hence, reducing the number of expected occurrences to 6 or 7 weekly gives significant results.

Suppose we choose L to be three weeks and start the analysis from 1 July 1993. We find that $Z_{N,L} = 33$ for all N. The probability of the maximum possible sum when $N = 1$, $p(1, 3, 33)$, equal 0.076 if the expected value is 8 per week, giving a marginally significant result. This merely demonstrates the problems associated with significance values or p-values obtained from hypothesis testing procedures. It is strongly suggested that the window size is fixed at the start, otherwise the p-value is affected by multiple looks at the data.

4 Conclusion

In this paper, we developed a scan statistic for discrete data, and its probability distribution is obtained using Markov chain theory. We take a window that moves one step at a time and find the maximum sum of the observations as the window scans the interval. Although we can use the method developed in this paper retrospectively as well as prospectively, the emphasis is on the prospective approach. We assumed that the process is stationary and we developed an 'in control' test.

This method has been applied to the orthopaedic wound infection data and the MRSA colonization data. We find that a window that moves one step at a time through the observations is likely to detect clusters of events that cannot be detected by grouping the events in blocks. Hence this method is more sensitive in detecting clusters of events.

The window size and the number of events expected to occur in an interval have

to be predetermined and this can be done using historical information or externally set standards. The scan statistic can be made somewhat simplistic to understand by choosing the window size so that one event is expected to occur per window length. Such a choice might give the scan statistic approach more appeal to health care workers and therefore its adoption. For example, if one infection is expected in a window of thirty operations, the window size can be chosen to be 30. Consideration of window size can also depend on the context of use. A warning is required as soon as possible when a significant increase is found. It is strongly suggested that the window size is fixed at the start, otherwise the p-value is affected by the multiple looks at the data.

The only shortcoming of the scan statistic obtained using the Markov chain theory is that it depends on N, the number of window shifts. The probability of the scan statistic, $p(N, L, A)$, becomes less sensitive as N increases. Therefore we suggest the statistic is reset to start afresh or a fixed number of shifts is analyzed each time. The window shift number, N, should be small and it is wise to investigate $p(1, L, A)$ since if $p(1, L, A)$ does not show a significant result, then for any N, the $p(N, L, A)$s are not significant.

We recommend that the scan statistic developed in this paper can also be used retrospectively as it guards against overzealous 'data mining' to discover significant results. However, the cost of a false positive may be less prospectively than retrospectively.

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APPENDIX

Let the independent $Y_1, Y_2, Y_3, \ldots$ take on non-negative integer values where $Y_m \sim \text{Poisson}(\mu)$, $m = 1, 2, \ldots$. Consider a sum, S_m of L values and define

$$\begin{aligned} S_m &= Y_m + Y_{m+1} + \cdots + Y_{m+L-1} \\ S_{m-1} &= Y_{m-1} + Y_m + \cdots + Y_{m+L-2} \\ T_m &= Y_m + Y_{m+1} + \cdots + Y_{m+L-2} \end{aligned} \tag{1}$$

where S_m is the sum of L observations in the m^{th} window, $S_m = T_m + Y_{m+L-1}$ and $S_{m-1} = T_m + Y_{m-1}$ and m can take values from 1,...,N, where N is the maximum number of window shifts. The distribution of S_m can be Poisson which arise from the sum of L independent Poisson variable.

Since S_m is the sum of the observations in the m^{th} window, it depends on the outcome of the directly preceding one, S_{m-1}, but is conditionally independent of the outcomes of all former trials. The event S_m can also be called the state of the system. To see this, we need to investigate $P(S_m|S_1, \ldots, S_{m-1})$. We see that S_m is defined in terms of S_{m-1} only and Y_{m+L-1} which is assumed independent of the Y_js, for $j < m+L-1$. Thus S_m depends only on S_{m-1} and not any $S_{m-2}, \ldots, S_1$. Thus $P(S_m|S_1, \ldots, S_{m-1}) = P(S_m|S_{m-1})$. For a homogeneous Markov chain of the first order, the transition probabilities can be written as

$$P(S_m = j|S_{m-1} = i) = p_{ij},$$

say, and are independent of m.

Using the conditional partition formula, the transition probabilities for the moving window can be written as follows:

$$P(S_m = j|S_{m-1} = i) = \sum_k P(S_m = j|S_{m-1} = i, Y_{m-1} = k)P(Y_{m-1} = k|S_{m-1} = i).$$

Since $S_{m-1} = T_m + Y_{m-1}$, the event

$$\begin{aligned} \{S_{m-1} = i, Y_{m-1} = k\} &= \{T_m + Y_{m-1} = i, Y_{m-1} = k\} \\ &= \{T_m = i - k, Y_{m-1} = k\}. \end{aligned}$$

From equation (1), we know that $S_m = T_m + Y_{m+L-1}$. Also

$$\begin{aligned} P(Y_{m-1} = k | S_{m-1} = i) &= \frac{P(Y_{m-1} = k, S_{m-1} = i)}{P(S_{m-1} = i)} \\ &= \frac{P(T_m = i - k, Y_{m-1} = k)}{P(S_{m-1} = i)}, \end{aligned}$$

thus giving

$$\begin{aligned} P(S_m = j | S_{m-1} = i) &= P(Y_{m+L-1} = j - i + k | T_m = i - k, Y_{m-1} = k) \\ &\quad \times \frac{P(T_m = i - k, Y_{m-1} = k)}{P(S_{m-1} = i)} \end{aligned}$$

and, since Y_{m+L-1}, T_m and Y_{m-1} are independent, then

$$P(S_m = j | S_{m-1} = i) = \sum_k P(Y_{m+L-1} = j - i + k) \frac{P(Y_{m-1} = k, S_{m-1} = i)}{P(S_{m-1} = i}$$

Then it follows that $S_m \sim$ Poisson$(L\mu)$ and $T_m \sim$Poisson$[(L-1)\mu]$. Hence for Poisson data, the transition probabilities can be found to be equal to

$$P(S_m = j | S_{m-1} = i) = \sum_{k=\max(0, i-j)}^{i} \binom{i}{k} \frac{(L-1)^{i-k} e^{-\mu} \mu^{j-i+k}}{L^i (j - i + k)!} \tag{2}$$

$i, j = 0, 1, \ldots$.

The probability distribution for each random variable S_m can be determined if the initial probability distribution, $\mathbf{p_0} = [P(S_0 = 0), P(S_0 = 1), \ldots]$, and the transition probabilities of a Markov chain are known. We would like to know whether, after a sufficiently long period of time, the system settles down to a condition of statistical equilibrium, where the state occupation probabilities are independent of the initial conditions. If so, then there is an equilibrium probability distribution $\mathbf{p}$ and $\mathbf{p}$ satisfies the following infinite system of linear equations:

1. $\mathbf{p} = \mathbf{p}$P where P$= [p_{ij}]$ has an infinite number of rows and columns and the vector $\mathbf{p} = [P(S_0 = 0), P(S_0 = 1), \ldots]$ and

2. the sum of the elements in $\mathbf{p}$ is equal to one.

The transition matrix, P, has an infinite number of rows and columns since the state space for Poisson distribution ranges from 0 to ∞. The transition matrix is obtained by

calculating the transition probabilities $p_{ij} = P(S_m = j | S_{m-1} = i)$ where

$$\mathrm{P} = \begin{pmatrix} p_{00} & p_{01} & p_{02} & \cdots & p_{0j} & \cdots \\ p_{10} & p_{11} & p_{12} & \cdots & p_{1j} & \cdots \\ p_{20} & p_{21} & p_{22} & \cdots & p_{2j} & \cdots \\ \vdots & \vdots & \vdots & \cdots & \vdots & \cdots \end{pmatrix}. \tag{3}$$

and

$$\begin{aligned} \mathbf{p} &= [P(S_0 = 0), P(S_0 = 1), \ldots, P(S_0 = L), \ldots] \\ &= \left[e^{-L\mu}, \quad L\mu e^{-L\mu}, \quad \frac{(L\mu)^2 e^{-L\mu}}{2!}, \quad \frac{(L\mu)^3 e^{-L\mu}}{3!}, \quad \ldots \right]. \end{aligned} \tag{4}$$

We know that $\mathbf{p}$ is the stationary distribution as it is the marginal distribution for S_m for all m.

We develop a test for the system being 'in control'. To recap, a process or system is said to be 'in control' if only chance causes of variation are present in a process. In the control chart studies, to see whether a process is 'in control', data pertaining to the process are plotted on a control chart. If data conform to a pattern of random variation within the control limits, then the process is said to be 'in control' at a level equal to the mean line on the chart. In the hospital, we are only concerned with the upper control limit, A, with the smallest possible being as good as possible, so that the test can be based upon $S_m < A$ for $m = 1, \ldots, N$. Note that

$$P(S_m < A, m = 1, \ldots, N) \to 0$$

as $N \to \infty$ for $A = 1, 2, \ldots, L-1$. We wish to find the probability of $S_m < A$ for $m = 1, \ldots, N$ for given A and N. To do this, we consider the following.

Define $\{S_m^*, m = 1, 2, ...\}$ to be a new chain derived from S_m by taking A to be an absorbing state where A is the maximum possible sum in any window of length L. If a process enters an absorbing state, then the process can never leave that state. It is 'absorbed' into that state [19]. In general, a state of a Markov chain is absorbing if the one-step transition probability between that state and itself is equal to 1. That is, state A is absorbing if $p_{AA} = 1$. If m_1 is the first occasion that S_m equals or exceeds the value

A, then define S_m^* by

$$S_m^* = \begin{cases} S_m & m = 1, 2, \ldots, m_1 - 1 \\ A & m = m_1, m_1 + 1, \ldots . \end{cases}$$

Also let P^* be the probability transition matrix of S_m^*.

The event $\{S_m < A, m = 1, \ldots, N\}$ is equivalent to $m_1 \geq N + 1$, using the definition above. The complement of $\{m_1 \geq N + 1\}$ is $\{m_1 \leq N\}$. Now the event $\{m_1 \leq N\}$ occurs if and only if $S_N^* = A$. To see this, trivially if $m_1 \leq N$ then $S_N^* = A$, by definition. If $S_N^* = A$ then certainly $m_1 \leq N$. Thus,

$$\begin{aligned} P(S_m \geq A, \text{for some } m, m = 1, \ldots, N) &= P\left(\max_{1 \leq m \leq N} S_m \geq A\right) \\ &= 1 - P\left(\max_{1 \leq m \leq N} S_m \leq A - 1\right) \\ &= 1 - P(S_m \leq A - 1, m = 1, \ldots, N) \\ &= 1 - P(S_m < A, m = 1, \ldots, N) \\ &= 1 - P(m_1 \geq N + 1), \text{from above} \\ &= P(m_1 \leq N) \\ &= P(S_N^* = A). \end{aligned}$$

The required probability of the random variable S_N^* is $P(S_N^* = A)$ and is given by the last element of the vector $\mathbf{p_N}$. The quantities of $\mathbf{p_N}$ are called the N-step transition probabilities. Thus given the initial probabilities $\mathbf{p_0} = [P(S_0^* = 0), \ldots, P(S_0^* = A - 1), P(S_0^* = A)]$ and the matrix of transition probabilities P, we can find the N-step transition probabilities to be $\mathbf{p_N} = \mathbf{p_{N-1}}\mathrm{P}$ and on iteration, we obtain $\mathbf{p_N} = \mathbf{p_{N-2}}\mathrm{P}^2 = \ldots = \mathbf{p_0}\mathrm{P}^N$. $P(S_N^* = A)$ is also the probability of the scan statistic $Z_{N,L}$ exceeding A, denoted by $p(N, L, A)$.

$\mathrm{P}^* = [p_{ij}^*]$ is a transition matrix for S^* and it is derived from P as follows:

$$\begin{aligned} p_{ij}^* &= P(S_m^* = j | S_{m-1}^* = i) \\ &= \begin{cases} P(S_m = j | S_{m-1} = i) & i < A, j < A \\ 1 & i = A, j = A \\ 1 - \sum_{j'=0}^{A-1} P(S_m = j' | S_{m-1} = i) & i < A, j = A \end{cases} \end{aligned}$$

for $i, j = 0, \ldots, A$.

We need to determine $\mathbf{p_N} = \mathbf{p_0}(\mathrm{P}^*)^N$ where P^* is a $(A+1) \times (A+1)$ transition matrix. To set up the new chain with an absorbing state at A, the initial distribution, $\mathbf{p_0}$, is defined by

$$P(S_0^* = j) \quad = \quad \frac{e^{-L\mu}(L\mu)^j}{j!} \quad j = 0, \ldots, A-1$$

and the last element of $\mathbf{p_0}$ is given by

$$P(S_0^* = A) \quad = \quad 1 - \sum_{j=0}^{A-1} P(S_0^* = j)$$

since the sum of the elements in each row in P should be equal to 1. The transition matrix of S_m^*, written as P^*, is an $(A+1) \times (A+1)$ matrix,

$$\mathrm{P}^* = \begin{pmatrix} p_{00} & p_{01} & p_{02} & \cdots & p_{0j} & \cdots & q_{0A} \\ p_{10} & p_{11} & p_{12} & \cdots & p_{1j} & \cdots & q_{1A} \\ p_{20} & p_{21} & p_{22} & \cdots & p_{2j} & \cdots & q_{2A} \\ \vdots & \vdots & \vdots & \cdots & \vdots & \cdots & \vdots \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}.$$

where

$$q_{iA} = 1 - \sum_{j=0}^{A-1} p_{ij}, \quad i = 0, 1, \ldots, A-1.$$

To calculate $P(S_N^* = A)$, we use the FORTRAN program which is available from the first author.

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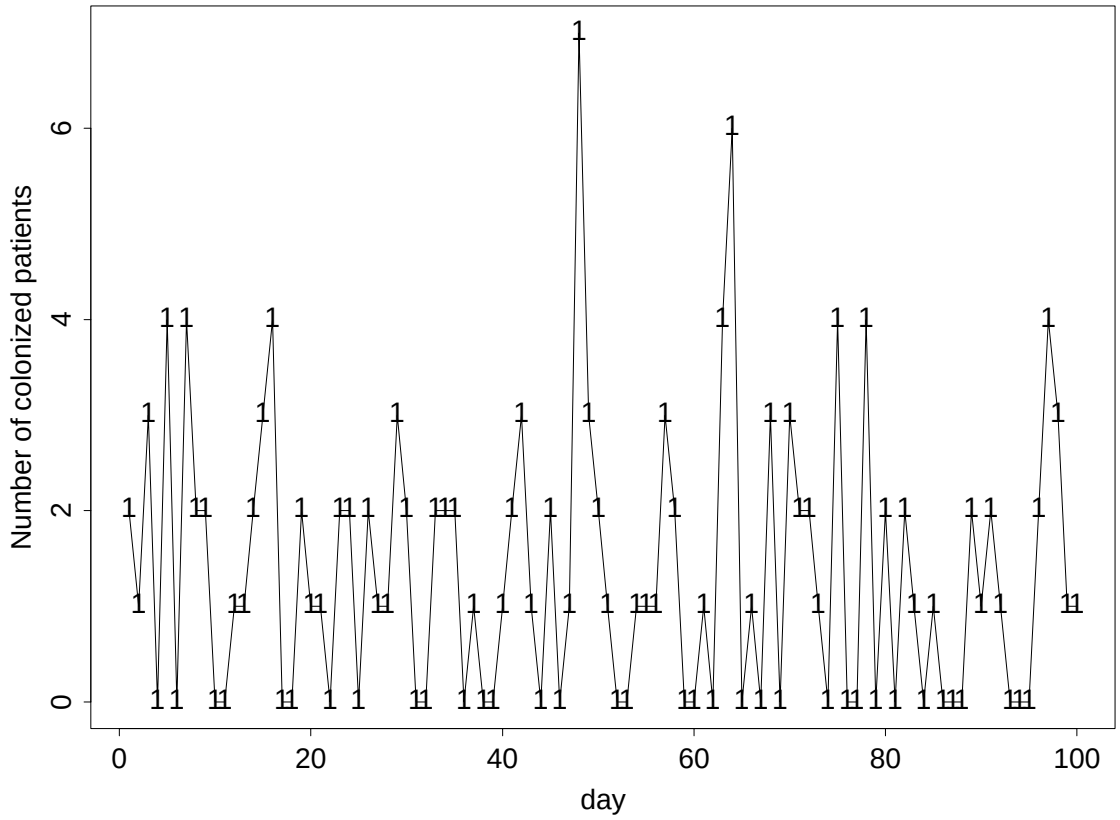

Figure 1: Daily occurrences of MRSA colonizations for the first 100 days starting from 1 July 1993.

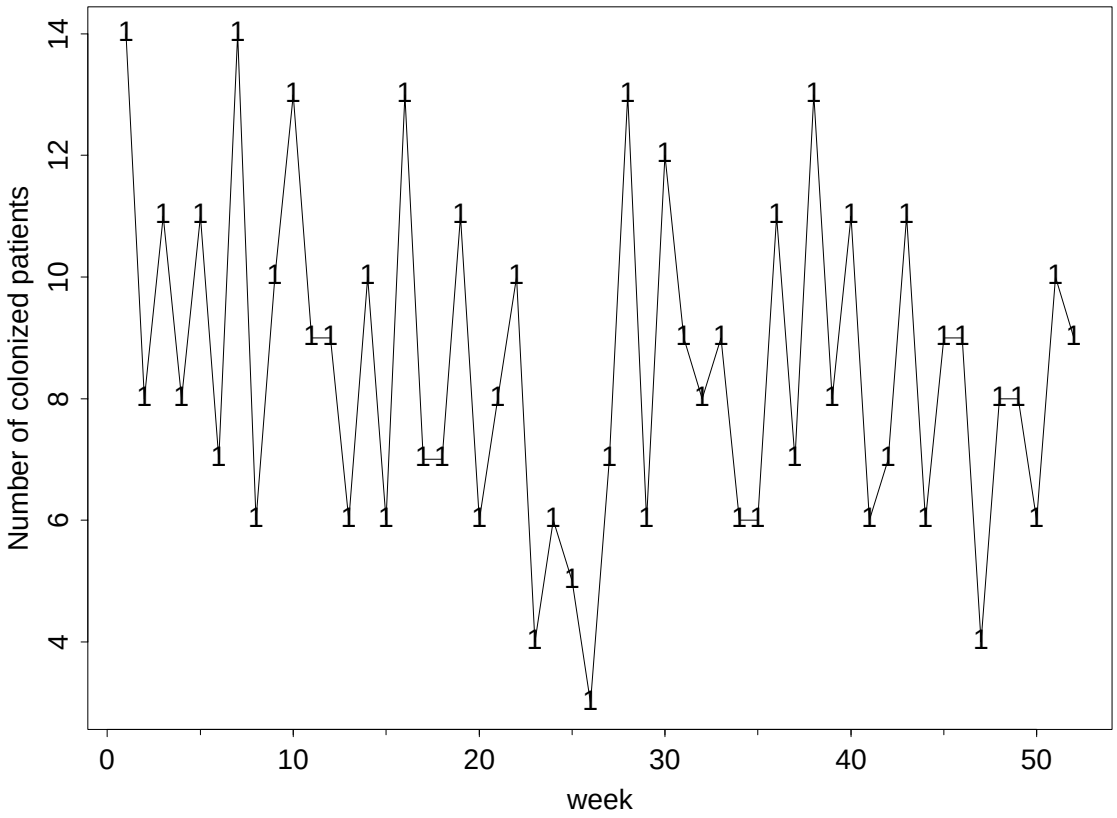

Figure 2: Number of MRSA colonizations weekly starting from 1 July 1993.

Table 1: Scan statistic p-values, $p(N, L, A) = P(Z_{N,L} \geq A)$, for the orthopaedic wound infection data with a window size L of 30 operations. N is the number of window shifts, $Z_{N,L} = \max_{1 \leq m \leq N} S_m$ and S_m gives number of infections for operations $m, \ldots, m + L - 1$.

N	$Z_{N,30}$	$p(N, L, A)$
1	1	0.6442
$\vdots$	$\vdots$	$\vdots$
21	1	0.8173
22	2	0.4653
23	2	0.4724
24	3	0.1922
25	4	0.0587

Table 2: Values of the probability, $p(N, 7, A)$, of the scan statistic $Z_{N,7}$ exceeding A, calculated from MRSA colonization data with a window of 7 days with different values of μ. N is the number of window shifts, $Z_{N,7} = \max_{1 \le m \le N} S_m$ and $S_m = Y_m + \ldots + Y_{m+6}$ and Y_i is the number of colonizations per day.

		$p(N, 7, A)$ at		
N	$Z_{N,7}$	$\mu = \frac{8}{7}$	$\mu = 1.0$	$\mu = \frac{6}{7}$
1	9	0.4864	0.3371	0.1988
2	10	0.4042	0.2596	0.1385
⋮	⋮	⋮	⋮	⋮
4	10	0.4879	0.3268	0.1819
5	11	0.3807	0.2313	0.1137
⋮	⋮	⋮	⋮	⋮
7	11	0.4363	0.2724	0.1374
8	12	0.3224	0.1798	0.0788
⋮	⋮	⋮	⋮	⋮
36	12	0.6999	0.4708	0.2409
37	14	0.3622	0.1760	0.0617
38	14	0.3690	0.1799	0.0632
39	15	0.2318	0.0958	0.0281
40	16	0.1329	0.0468	0.0115