Appendix: Calculating Test Statistics

Binary cumulative sum charts, based on the theory of sequential probability ratio tests, monitor a cumulative term that is incremented or decremented by certain amounts for each positive or negative result, respectively, in order to sequentially test between user-specified acceptable and unacceptable rates \((35,36)\) (Equation 1). In our application, the CUSUM statistic \(S_i\) is reduced at the time of each isolate by an amount \(D\), a calculated value that depends on the shift we wish to detect, and then increased by 1 for those isolates that are antibiotic resistant. The plotted statistic for the \(i\)th isolate, \(S_i\), and the control limit factors \(h_0\) and \(h_1\) are calculated as

\[
S_i = \begin{cases} 
S_{i-1} - D, & \text{if } X_i = 0 \\
S_{i-1} + 1 - D, & \text{if } X_i = 1 
\end{cases} = S_{i-1} + X_i - D, \tag{1}
\]

\[
h_0 = \frac{\ln \left( \frac{1 - \alpha}{\beta} \right)}{\ln \left( \frac{p_1}{p_0} \cdot \frac{1 - p_0}{1 - p_1} \right)}, \tag{2}
\]

\[
h_1 = \frac{\ln \left( \frac{1 - \beta}{\alpha} \right)}{\ln \left( \frac{p_1}{p_0} \cdot \frac{1 - p_0}{1 - p_1} \right)}, \tag{3}
\]

where \(X_i = 1\) if the \(i\)th isolate is resistant and 0 if it is not, the decrement \(D\) is computed as

\[
D = \frac{\ln \left( \frac{1 - p_0}{1 - p_1} \right)}{\ln \left( \frac{1 - p_0}{p_1} \cdot \frac{p_1}{1 - p_1} \right)},
\]

\(\alpha\) is the desired type I error rate, \(\beta\) is the desired type II error rate, \(p_0\) is the acceptable occurrence rate, \(p_1\) is the unacceptable occurrence rate that is desired to be detected, and \(S_0 = 0\) as a starting value.

The cumulative sum then is compared to nonconstant control limits that periodically are recalculated by subtracting \(h_0\) from and adding \(h_1\) to any \(S_i\) value that falls outside either limit, resulting in new limits until the next such violation and starting with lower control limit (LCL) = \(S_0 - h_0 = h_0\) and upper control limit (UCL) = \(S_0 + h_1 = h_1\). Values above the UCL indicate an outbreak, i.e., rejection of the hypothesis of \(p_0\) in favor of the hypothesis of \(p_1\), although contrary to traditional control charts values beneath the LCL here do not indicate a rate decrease but rather acceptance of \(p_0\) over \(p_1\).

For the moving average (MA) charts, the moving average for the \(i\)th isolate with a “window” of size \(w\) (varied in different test conditions), \(Y_{w,i}\), is calculated as
\[ Y_{w,i} = \begin{cases} \frac{X_i + X_{i-1} + \ldots + X_{i-w+1}}{w} = \frac{\sum_{j=i-w+1}^{i} X_j}{w}, & \text{for } i \geq w \\ \frac{X_i + X_{i-1} + \ldots + X_1}{i} = \frac{\sum_{j=1}^{i} X_j}{i}, & \text{for } i < w \end{cases} \] (4)

This result then is compared to estimated upper (UCL) and lower \( k \)-sigma control limits for the \( i \)th isolate, \( LCL_i \) and \( UCL_i \), with the standard deviation of the \( i \)th moving average, \( \sigma_{Y,w,i} \), estimated by using the conventional moving range (MR) control chart method for individual data that occur over time,

\[ \hat{\sigma}_{Y,w,i} = \frac{\hat{\sigma}_{X,i}}{\sqrt{\min(i,w)}} = \frac{MR_i / 1.128}{\sqrt{\min(i,w)}}, \] (5)

\[ MR_i = \frac{\sum_{j=2}^{i} |X_j - X_{j-1}|}{i-1}, \] (6)

\[ U\hat{C}L_i = \mu_i + k\hat{\sigma}_{w,i} = \overline{X}_i + k\frac{MR_i / 1.128}{\sqrt{\min(i,w)}}, \] and

\[ L\hat{C}L_i = \mu_i - k\hat{\sigma}_{w,i} = \overline{X}_i - k\frac{MR_i / 1.128}{\sqrt{\min(i,w)}}, \] (8)

all for \( i \geq 2 \), where \( i \) is the current total number of data points, \( X_i \) is the \( i \)th data value, \( w \) is the size of the moving average, and \( \overline{X}_i \) is the average of all data up to and including the \( i \)th data value. An MA value that exceeds its corresponding UCL will trigger an outbreak alert.