



# Expectation-based scan statistics for monitoring spatial time series data

Daniel B. Neill\*

*H.J. Heinz III College, School of Public Policy and Management, Carnegie Mellon University, 5000 Forbes Avenue, Pittsburgh, PA 15213, United States*

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## Abstract

We consider the simultaneous monitoring of a large number of spatially localized time series in order to detect emerging spatial patterns. For example, in disease surveillance, we detect emerging outbreaks by monitoring electronically available public health data, e.g. aggregate daily counts of Emergency Department visits. We propose a two-step approach based on the *expectation-based scan statistic*: we first compute the expected count for each recent day for each spatial location, then find spatial regions (groups of nearby locations) where the recent counts are significantly higher than expected. By aggregating information across multiple time series rather than monitoring each series separately, we can improve the timeliness, accuracy, and spatial resolution of detection. We evaluate several variants of the expectation-based scan statistic on the disease surveillance task (using synthetic outbreaks injected into real-world hospital Emergency Department data), and draw conclusions about which models and methods are most appropriate for which surveillance tasks.

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## 1. Introduction

Many applications require the monitoring of time series data in order to detect anomalous counts. A traditional application of time series monitoring is the use of statistical process control to ensure consistency in manufacturing: the process is measured regularly to ensure that the desired specifications (e.g. product

size and weight) remain within an acceptable range. More recently, time series monitoring has been used in a variety of event detection systems: crime surveillance systems (Gorr & Harries, 2003; Levine, 1999) detect emerging hot-spots of crime activity, disease surveillance systems (Sabhnani et al., 2005) monitor electronic public health data such as hospital visits and medication sales in order to detect emerging outbreaks, and environmental monitoring systems (Ailamaki, Faloutsos, Fischbeck, Small, & VanBriesen, 2003) detect abnormally high pollutant levels in the air, water, and soil.

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\* Tel.: +1 412 268 3885.

E-mail address: [neill@cs.cmu.edu](mailto:neill@cs.cmu.edu).

In all of these event detection applications, we wish to detect emerging spatial patterns as quickly and accurately as possible, enabling a timely and appropriate response to the detected events. As a concrete example, we focus on the task of detecting outbreaks of respiratory illness using hospital Emergency Department (ED) data. In this case, we can monitor the number of patients visiting the ED with respiratory symptoms in each zip code on each day. Each zip code  $s_i$  has a corresponding time series of daily counts  $c_i^t$ , and our goal is to detect anomalous increases in counts that correspond to an emerging outbreak of disease.

A variety of methods have been developed to monitor time series data and detect emerging anomalies. Control chart methods (Shewhart, 1931) compare each observed count to its expected value (a counterfactual forecast obtained from time series analysis of the historical data), and detect any observations outside a critical range. Cumulative sum methods (Page, 1954) and tracking signals (Brown, 1959; Trigg, 1964) aggregate these deviations across multiple time steps in order to detect shifts in a process mean. When extending these techniques to the simultaneous monitoring of multiple time series, we have several options (Burkom, Murphy, Coberly, & Hurt-Mullen, 2005). In the simplest, “parallel monitoring” approach, we monitor each time series separately and report any anomalous values. In the “consensus monitoring” approach, we combine the signals from multiple time series in order to achieve higher detection power. To detect anomalies that affect multiple time series simultaneously, we can either combine the outputs of multiple univariate detectors or treat the multiple time series as a single multivariate quantity to be monitored. For example, multivariate control charts (Hotelling, 1947) learn the joint distribution of a set of signals from historical data, and detect when the current multivariate signal is sufficiently far from its expectation.

We note, however, that none of these time series monitoring methods account for the *spatial* nature of the event detection problem. We expect events to be localized in space: if a given location is affected by the event, nearby locations are more likely to be affected than locations that are spatially distant. For example, disease outbreaks tend to affect spatially contiguous areas, either because of contagion

(e.g. human-to-human transmission) or because the cases share a common source (e.g. contaminated drinking water). Thus, we must consider alternate methods of monitoring spatial time series data, where we expect anomalies to affect the time series for some spatially localized subset of locations.

A typical approach to the monitoring of spatial time series data uses “fixed partitions”: we map the locations to a Euclidean space (e.g. using the longitude and latitude of each zip code centroid), partition the search space such that each location is contained in exactly one partition, and aggregate the counts for each partition into a single time series. We then monitor the time series for each partition separately, and report any anomalous counts. One challenge is deciding how to partition the search space: in the case of zip code level data, we could consider each zip code to be a separate partition, combine multiple adjacent zip codes in a single partition, or even aggregate all of the zip codes into a single time series. An alternative is to form an “ad-hoc partitioning” by identifying individual locations with high counts and using some heuristic to cluster these locations (Corcoran, Wilson, & Ware, 2003).

Any choice of partitioning scheme creates a set of potential problems, which we call the “curse of fixed partitions”. In general, we do not have *a priori* knowledge of how many locations will be affected by an event, and we wish to maintain high detection power whether the event affects a single location, all locations, or anything in between. A coarse partitioning of the search space will lose power to detect events that affect a small number of locations, since the anomalous time series will be aggregated with other counts that are not anomalous. A fine partitioning of the search space will lose power to detect events that affect many locations, since only a small number of anomalous time series are considered in each partition. Partitions of intermediate size will lose some power to detect both very small and very large events. Moreover, even if the partition size corresponds well to the event size, the fixed partition approach will lose power if the affected set of locations is divided between multiple partitions rather than corresponding to a single partition. While ad-hoc partitioning methods allow partitions to vary in size, the chosen set of partitions still may not correspond to

the actual set of locations affected, resulting in a loss of detection power.

Our solution to the “curse of fixed partitions” is a multi-resolution approach in which we search over a large and overlapping set of spatial regions, each containing some subset of the spatial locations, and find the most significant clusters of anomalous counts. Because we search over both large regions (coarse resolutions) and small regions (fine resolutions), this method has high power to detect both large and small clusters. Similarly, by searching over regions with varying shape, size, and duration, we can achieve high detection power for clusters with a wide range of spatial and temporal characteristics.

More precisely, we propose an “expectation-based scan statistic” approach with two distinct steps. First, we compute the “expected count” for each spatial location for each recent day of data. Each expected count is a counterfactual forecast assuming that no clusters are present, and is obtained from time series analysis of the historical counts for that spatial location. The second step is to detect space–time clusters, i.e. groups of nearby locations where the recent counts are significantly higher than expected. To do so, we develop a new variant of the spatial and space–time scan statistics (Kulldorff, 1997, 2001; Neill & Moore, 2005) which searches over space–time regions, compute a likelihood ratio statistic for each region, and detect the most significant clusters.

In the remainder of this paper, we describe the expectation-based scan statistic, and evaluate the performance of this method on the disease surveillance task. In Section 2, we present an overview of the expectation-based scan approach, and in Sections 3 and 4 we discuss each of the two steps (computing expected counts, and finding clusters with higher than expected counts) in detail. Finally, Sections 5 and 6 present and discuss our set of evaluations using hospital Emergency Department data, comparing several variants of the expectation-based scan and demonstrating large performance improvements as compared to traditional fixed partition and spatial scan approaches.

## 2. The expectation-based scan statistic

As noted above, the event detection problem requires us to monitor a set of spatially localized time

series in order to detect emerging spatial clusters of anomalous counts. We assume a given set of spatial locations  $\{s_i\}$ , where each location  $s_i$  corresponds to a point in Euclidean space. For example, in our disease surveillance task, each zip code is mapped to a two-dimensional space using the longitude and latitude of the zip code centroid. For each location  $s_i$ , we are given a time series of non-negative integer counts  $c_i^t$ , where  $t = 0$  represents the current time step and  $t = 1 \dots t_{\max}$  represent the historical data from 1 to  $t_{\max}$  time steps ago respectively. For example, each count  $c_i^t$  could represent the number of respiratory Emergency Department visits in zip code  $s_i$  on day  $t$ .

Given this data, our goal is to detect any spatial region where the recent counts are significantly higher than expected. More precisely, we define a set of “space–time regions”  $\mathbf{S}$ , where each region  $S \in \mathbf{S}$  contains a subset of spatial locations  $\{s_i : s_i \in S\}$ , and also has a time duration  $w(S)$ , meaning that the given set of spatial locations has been affected for the most recent  $w$  time steps ( $t = 0 \dots w - 1$ ). We search over space–time regions with durations  $w = 1 \dots W$ , where  $W$  is the “maximum temporal window size”; i.e., we are only interested in clusters that have emerged within the past  $W$  time steps.

The expectation-based scan statistic has two distinct steps: we first compute the “expected count” (or “baseline”)  $b_i^t$  for each spatial location  $s_i$  and each time step  $t = 0 \dots W - 1$ , and then detect space–time regions  $S$  with higher than expected counts. For the first step, each baseline  $b_i^t$  is a counterfactual estimate of  $c_i^t$  assuming the null hypothesis of no clusters, and is computed from the historical data in location  $s_i$  using some method of time series analysis. We must then find space–time regions  $S$  where the observed counts  $c_i^t$  are significantly higher than the expected counts  $b_i^t$ , for locations  $s_i \in S$  and time steps  $t = 0 \dots w(S) - 1$ .

To do so, we develop a likelihood ratio test based on the spatial and space–time scan statistics. The spatial scan statistic, first presented by Kulldorff and Nagarwalla (1995) and Kulldorff (1997) and extended to space–time data by Kulldorff, Athas, Feuer, Miller, and Key (1998) and Kulldorff (2001), is commonly used in the public health community for purposes ranging from the detection of bioterrorist attacks (Neill, 2006) and emerging infectious

diseases (Mostashari, Kulldorff, Hartman, Miller, & Kulasekera, 2003) to the identification of environmental risk factors for breast cancer (Kulldorff, Feuer, Miller, & Freedman, 1997) and childhood leukemia (Hjalmar, Kulldorff, Gustafsson, & Nagarwalla, 1996). Here we apply the generalized spatial scan framework described by Neill and Moore (2005). We first define generative models of the data under  $H_0$ , the null hypothesis of no clusters, and under  $H_1(S)$ , the alternative hypothesis assuming a cluster in some space–time region  $S$ . We then compute the likelihood ratio statistic  $F(S)$  for each space–time region  $S \in \mathbf{S}$ . The likelihood ratio is defined as the ratio of the data likelihoods under the alternative and null hypotheses:

$$F(S) = \frac{\Pr(\text{Data} \mid H_1(S))}{\Pr(\text{Data} \mid H_0)}$$

If the null or alternative hypotheses have any free parameters, we compute the likelihood ratio using the maximum likelihood estimates of each parameter:

$$F(S) = \frac{\max_{\theta_1(S) \in \Theta_1(S)} \Pr(\text{Data} \mid H_1(S), \theta_1(S))}{\max_{\theta_0 \in \Theta_0} \Pr(\text{Data} \mid H_0, \theta_0)}$$

The regions with the highest values of the likelihood ratio statistic are those which are most likely to have been generated under the alternative hypothesis (cluster in space–time region  $S$ ) instead of the null hypothesis of no clusters. However, because we are maximizing the likelihood ratio over a large number of regions, we are very likely to find many regions with high likelihood ratios even when the null hypothesis is true. Thus we must choose a threshold value  $F_{\text{thresh}}$  based on the acceptable false positive rate, and report all space–time regions  $S$  with  $F(S) > F_{\text{thresh}}$ .

The detection threshold  $F_{\text{thresh}}$  can be calibrated in one of two ways. The traditional approach (Kulldorff, 1997) is to perform randomization testing: we generate a large number of replica datasets under the null hypothesis and compute the distribution of the maximum region score under the null. Then, for a given false positive rate  $\alpha$ ,  $F_{\text{thresh}}$  is the  $100(1 - \alpha)$  percentile value of the null distribution. An alternative is to use the empirical distribution of maximum region scores from a large amount of historical data, again using the  $100(1 - \alpha)$  percentile value from this distribution. Neill (2007) compared these two

approaches on real-world Emergency Department and over-the-counter medication sales data, and concluded that randomization testing tends to be oversensitive (producing false positive rates of up to 40% for  $\alpha = 0.05$ ), and that the empirical approach tends to achieve higher detection power. Nevertheless, randomization testing may be a useful alternative to the empirical approach when only a limited amount of historical data is available.

### 3. Time series forecasting

A variety of time series analysis methods may be used to compute counterfactual forecasts  $b_i^t$  for each spatial location  $s_i$ , using the time series of historical counts  $c_i^t$ . We compute these baselines (expected counts) for each of the past  $W$  days, where  $W$  is the maximum temporal window size, then search over space–time regions with time durations up to  $W$ . Here we consider eight different time series analysis methods: four simple “moving average” methods, two “day-of-week adjusted moving average” methods, and two methods that account for both day-of-week and seasonality. Letting  $t = 0$  represent the current day’s counts, and  $t > 0$  represent the historical counts from  $t$  days ago, the 28-day moving average (MA28) is defined as follows:

$$b_i^t = \frac{1}{28} \sum_{u=t+1 \dots t+28} c_i^u$$

The 7-day, 14-day, and 56-day moving averages are defined analogously, and we compare all four of these methods in our evaluation below. While such methods may be sufficient for datasets without seasonal or day-of-week trends, datasets with these trends may require more complex forecasting methods. The simple moving average may be adjusted for day of the week by estimating the proportion of counts  $\beta_i^j$  occurring in each location  $s_i$  on each day of the week ( $j = 1 \dots 7$ ). Then when we predict the baseline value for a given location on a given day, we choose the corresponding value of  $\beta_i^j$  and multiply our estimate by  $7\beta_i^j$ . We distinguish between “local” and “global” methods of adjusting for day of the week, where the local method computes  $\beta_i^j$  using only counts from location  $s_i$ , and the global method computes  $\beta_i^j$  using the global aggregate counts  $g_t = \sum_i c_i^t$ . Using 12

weeks of historical data, we can compute the  $\beta_i^j$  for the local (MALD) and global (MAGD) methods respectively:

$$\text{MALD: } \beta_i^j = \frac{\sum_{t=j, j+7, \dots, j+77} c_i^t}{\sum_{t=1, \dots, 84} c_i^t},$$

$$\text{MAGD: } \beta_i^j = \frac{\sum_{t=j, j+7, \dots, j+77} g_t}{\sum_{t=1, \dots, 84} g_t}.$$

The global adjustment for day of the week assumes that weekly trends have a constant and multiplicative effect on counts for each spatial location. The local adjustment assumes that each spatial location displays different weekly trends, and thus accounts for space by day-of-week interaction. On the other hand, we expect the global estimates to display less variance since they rely on larger counts to estimate the day-of-week proportions.

Finally, we consider two other methods of time series forecasting, both of which account not only for day-of-week trends but for seasonal trends as well. The multiplicative Holt–Winters’ (HW) method is a commonly used extension of exponential smoothing that also adjusts dynamically for cyclical day of the week effects and for linear trends (e.g. those due to seasonal variation in counts); it was shown to be highly effective for temporal biosurveillance by [Burkom, Murphy, and Shmueli \(2007\)](#). The Holt–Winters’ forecasts are calculated from the counts  $c_i^t$  by iterating the following three equations for the smoothed value  $S_t$ , trend component  $T_t$ , and day-of-week component  $I_t$ , from  $t = 84$  to  $t = 1$  (the day before the current day  $t = 0$ ):

$$S_t = \alpha \frac{c_i^t}{I_{t+7}} + (1 - \alpha)(S_{t+1} + T_{t+1})$$

$$T_t = \beta(S_t - S_{t+1}) + (1 - \beta)T_{t+1}$$

$$I_t = \gamma \frac{c_i^t}{S_t} + (1 - \gamma)I_{t+7}.$$

Then each day’s expected count is given by the one-step-ahead, day-of-week adjusted estimate,  $b_i^t = (S_{t+1} + T_{t+1})I_{t+7}$ . For our comparison, we used fixed values of  $\alpha = \beta = \gamma = 0.1$ ; these were not optimized, but achieved adequate performance in preliminary studies on a different public health dataset.

Finally, the “current day” (CD) method was used to derive baseline estimates for the space–time permutation statistic ([Kulldorff, Heffernan, Hartman, Assuncao, & Mostashari, 2005](#)). This method assumes that counts are independently distributed in space and time, and thus the expected count  $b_i^t$  for a given location  $s_i$  on a given day  $t$  is equal to the total number of cases on day  $t$  multiplied by the fraction of cases occurring in location  $s_i$ :

$$b_i^t = \frac{\sum_i c_i^t \sum_t c_i^t}{\sum_i \sum_t c_i^t}.$$

This method focuses on detecting space–time interaction, and thus it does not detect purely spatial or purely temporal clusters. As noted by [Neill, Moore, Sabhnani, and Daniel \(2005b\)](#), this method uses the current day’s aggregate count to estimate the current day’s counts, and may lose power to detect spatially large clusters. On the other hand, by conditioning on the aggregate count, CD can produce accurate baseline estimates even in the presence of strong temporal trends due to day of the week, seasonality, or holidays.

#### 4. Detecting space–time clusters

The primary advantage of the scan statistic approach is that, rather than detecting individual counts  $c_i^t$  that are higher than expected, it integrates information over multiple spatial locations  $s_i$  and multiple time steps  $t$  to detect space–time clusters with higher than expected counts. Unlike typical methods that use a fixed partition of the search space, the level of aggregation need not be determined in advance. Instead, we search over a large set of space–time regions with varying sizes, shapes, and temporal durations. This process can be visualized as moving a “space–time window” around the search area, allowing the size, shape, and duration of this window to vary, and detecting any window which contains anomalously high counts. As noted above, we choose a set of search regions  $\mathbf{S}$ , where each region  $S \in \mathbf{S}$  contains a set of spatial locations  $\{s_i : s_i \in S\}$ , and also has a temporal duration  $w(S)$ . For the alternative hypothesis  $H_1(S)$ , representing a cluster in region  $S$ , we assume that the locations  $s_i \in S$  have been affected for the most recent  $w(S)$  time

steps. Under the null hypothesis  $H_0$ , no locations are affected. For notational simplicity, we let  $c_i^t \in S$  denote the set of counts in region  $S$ , i.e. those counts  $c_i^t$  such that  $s_i \in S$  and  $t = 0 \dots w(S) - 1$ . For each region  $S$  under consideration, we evaluate the likelihood ratio score  $F(S) = \frac{\Pr(\text{Data} | H_1(S))}{\Pr(\text{Data} | H_0)}$ , comparing the counts  $c_i^t \in S$  to their expected values  $b_i^t$ . We now consider the choice of search regions, and the computation of the likelihood ratio statistic, in more detail.

#### 4.1. Search regions

Our set of search regions  $\mathbf{S}$  was determined by mapping the spatial locations (e.g. zip code centroids) to a uniform  $N \times N$  grid, and then searching over all rectangular regions on the grid. In this case, each space–time region  $S \in \mathbf{S}$  can be defined by five integers  $(x_{\min}, y_{\min}, x_{\max}, y_{\max}, w)$ , representing the  $x$  and  $y$  coordinates of the top left and bottom right grid cells, and the time duration, respectively. All combinations of  $0 \leq x_{\min} \leq x_{\max} < N$ ,  $0 \leq y_{\min} \leq y_{\max} < N$ , and  $1 \leq w \leq W$  were considered. Thus, the total number of search regions increases linearly with the maximum window size  $W$ , and proportional to the fourth power of the grid size  $N$ . For each region  $S$ , the score  $F(S)$  can be calculated from the counts  $c_i^t \in S$  and baselines  $b_i^t \in S$ . Neill and Moore (2004) and Neill, Moore, and Sabhnani (2005a) demonstrated that these scores can be found in a computationally efficient manner, calculating the aggregate count  $\sum c_i^t$  and aggregate baseline  $\sum b_i^t$  for each rectangular region  $S$  in constant time, and then using these sufficient statistics to calculate the score  $F(S)$ . For large grid sizes, further computational speedups can be gained by using the *fast spatial scan* (Neill & Moore, 2004; Neill, Moore, Pereira, & Mitchell, 2005) to find the highest scoring clusters without an exhaustive search.

We note that this approach considers a wide range of region sizes, varying from individual  $1 \times 1$  cells to the entire  $N \times N$  grid, and thus has high power to detect both small and large clusters. Similarly, it considers regions ranging from squares to highly elongated rectangles, and thus has high power to detect both compact and elongated clusters. Finally, by allowing the cluster duration (i.e. the window size  $w$ ) to vary, it has high power to detect both rapidly and gradually emerging clusters.

#### 4.2. The expectation-based Poisson (EBP) statistic

As noted above, we must evaluate the likelihood ratio score  $F(S) = \frac{\Pr(\text{Data} | H_1(S))}{\Pr(\text{Data} | H_0)}$  for each spatial region  $S \in \mathbf{S}$ , and report the highest scoring regions. To do so, we must choose models of how the data is generated, both under the null hypothesis  $H_0$  (assuming that no clusters are present) and under the set of alternative hypotheses  $H_1(S)$ , each representing a cluster in some region  $S$ .

We assume that each count  $c_i^t$  has been drawn from a Poisson distribution. This is a common assumption in the epidemiological literature: individual cases can be specified as the realization of a Poisson point process (with spatially varying intensity based on the population at risk), and thus the aggregate count in each spatial area is Poisson distributed. We allow the Poisson means to vary over both space and time: under the null hypothesis  $H_0$  of no clusters, we assume that each count  $c_i^t$  has been drawn with mean equal to the expected count  $b_i^t$ . As discussed in Section 3, these baselines are learned from the historical data for location  $s_i$  by time series analysis. Under the alternative hypothesis  $H_1(S)$ , we assume that each count  $c_i^t \in S$  has been drawn with mean equal to the product of the expected count  $b_i^t$  and some constant  $q_i^t$ , which we call its *relative risk*. Thus, we wish to search for regions  $S$  where the relative risks  $q_i^t$  are greater than 1. We make the further simplifying assumption that the relative risks are uniform over region  $S$  ( $q_i^t = q$  for all  $c_i^t \in S$ ), and thus we expect a constant multiplicative increase in counts in the affected region.

As noted above, we wish to determine whether any space–time region  $S$  has significantly higher than expected counts. Under our model assumptions, where each count  $c_i^t \in S$  has been drawn from a Poisson distribution with mean proportional to the baseline  $b_i^t$  times the uniform relative risk  $q$ , this question simplifies to determining whether any region  $S$  has  $q > 1$ . Thus, we test the null hypothesis  $H_0$  against the set of alternative hypotheses  $H_1(S)$ , where:

$$H_0: c_i^t \sim \text{Poisson}(b_i^t) \text{ for all spatial locations } s_i \text{ and time steps } t.$$

$$H_1(S): c_i^t \sim \text{Poisson}(qb_i^t) \text{ for all } c_i^t \in S, \text{ and } c_i^t \sim \text{Poisson}(b_i^t) \text{ for all } c_i^t \notin S, \text{ for some } q > 1.$$

Computing the likelihood ratio, and using the maximum likelihood estimate for the parameter  $q$  (the

uniform relative risk for region  $S$ ), we obtain the following expression:

$$F(S) = \frac{\max_{q>1} \prod_{c_i^t \in S} \Pr(c_i^t \sim \text{Poisson}(qb_i^t))}{\prod_{c_i^t \in S} \Pr(c_i^t \sim \text{Poisson}(b_i^t))}.$$

Plugging in the equations for the Poisson likelihood, and simplifying, we obtain:

$$\begin{aligned} F(S) &= \frac{\max_{q>1} \prod_{c_i^t \in S} e^{-qb_i^t} (qb_i^t)^{c_i^t} / (c_i^t)!}{\prod_{c_i^t \in S} e^{-b_i^t} (b_i^t)^{c_i^t} / (c_i^t)!} \\ &= \max_{q>1} \prod_{c_i^t \in S} e^{(1-q)b_i^t} q^{c_i^t} = \max_{q>1} e^{(1-q)B} q^C, \end{aligned}$$

where  $C$  and  $B$  are the total count  $\sum c_i^t$  and total baseline  $\sum b_i^t$  of region  $S$ , respectively. We find that the value of  $q$  that maximizes the numerator is  $q = \max(1, \frac{C}{B})$ . Plugging in this value of  $q$ , we obtain:

$$F(S) = \left(\frac{C}{B}\right)^C e^{B-C}$$

if  $C > B$ , and  $F(S) = 1$  otherwise. Because  $F(S)$  is a function only of the sufficient statistics  $C$  and  $B$ , this function is efficiently computable: we can calculate the score of any region  $S$  by first calculating the aggregate count and baseline, and then applying the function  $F$ .

### 4.3. Comparison to Kulldorff’s statistic

The spatial scan statistic was originally presented by Kulldorff (1997) in a purely spatial setting, where we are given a single count  $c_i$  and baseline  $b_i$  for each spatial location  $s_i$ . Later work (Kulldorff, 2001; Kulldorff et al., 1998) extended this approach to the space–time scan statistic, where we are given the counts  $c_i^t$  and baselines  $b_i^t$  for each time step  $t$ . In these settings, the baselines  $b_i^t$  are given, and are assumed to represent the population of each location  $s_i$ . Under the null hypothesis of no clusters, we assume a spatially uniform incidence rate  $q_i^t = q_{all}$ , and thus we expect the counts  $c_i^t$  to be proportional to the baselines  $b_i^t$ . Under the alternative hypothesis  $H_1(S)$ , we assume that the incidence rate is higher inside the region than outside. Kulldorff’s statistic can also be used in

our expectation-based scan statistic framework, where the baselines are expected counts learned from time series analysis of historical data. In this case, the null hypothesis  $H_0$  assumes a constant relative risk  $q_{all}$ , and the alternative hypothesis  $H_1(S)$  assumes a higher relative risk inside region  $S$  than outside ( $q_{in} > q_{out}$ ).

More precisely, Kulldorff’s statistic assumes that each count  $c_i^t$  is generated independently from a Poisson distribution with mean proportional to the expected count  $b_i^t$  times the relative risk  $q_i^t$ . Furthermore, we assume that the relative risk is uniform both inside the region ( $q_i^t = q_{in}$  for all  $c_i^t \in S$ ) and outside the region ( $q_i^t = q_{out}$  for all  $c_i^t \notin S$ ). Then we test the null hypothesis  $H_0$  against the set of alternative hypotheses  $H_1(S)$ , where:

$H_0$ :  $c_i^t \sim \text{Poisson}(q_{all}b_i^t)$  for all locations  $s_i$  and time steps  $t$ , for some constant  $q_{all}$ .

$H_1(S)$ :  $c_i^t \sim \text{Poisson}(q_{in}b_i^t)$  for all  $c_i^t \in S$ , and  $c_i^t \sim \text{Poisson}(q_{out}b_i^t)$  for all  $c_i^t \notin S$ , for some constants  $q_{in} > q_{out}$ .

In this case, the alternative hypothesis has two free parameters ( $q_{in}$  and  $q_{out}$ ) and the null hypothesis has one free parameter ( $q_{all}$ ). Computing the likelihood ratio, and using the maximum likelihood parameter estimates  $q_{in} = \frac{C_{in}}{B_{in}}$ ,  $q_{out} = \frac{C_{out}}{B_{out}}$ , and  $q_{all} = \frac{C_{all}}{B_{all}}$ , we obtain the following expression for the likelihood ratio:

$$F(S) = \left(\frac{C_{in}}{B_{in}}\right)^{C_{in}} \left(\frac{C_{out}}{B_{out}}\right)^{C_{out}} \left(\frac{C_{all}}{B_{all}}\right)^{-C_{all}}$$

if  $\frac{C_{in}}{B_{in}} > \frac{C_{out}}{B_{out}}$ , and  $F(S) = 1$  otherwise. In this expression,  $C_{in}$  and  $B_{in}$  are the total count  $\sum c_i^t$  and total baseline  $\sum b_i^t$  inside region  $S$ ,  $C_{out}$  and  $B_{out}$  are the total count and baseline outside region  $S$ , and  $C_{all}$  and  $B_{all}$  are the total count and baseline everywhere. A detailed derivation of Kulldorff’s statistic is provided by Kulldorff (1997) and Neill (2006).

We note that the assumptions made by Kulldorff’s statistic are very different from the assumptions made by EBP, resulting in a substantially different likelihood ratio statistic. EBP expects the counts  $c_i^t$  to be equal to the baselines  $b_i^t$  under the null hypothesis, not just proportional to the baselines, since in this case the baselines represent expected counts. Under the alternative hypothesis  $H_1(S)$ , Kulldorff’s statistic compares the relative risks inside and outside the region, while EBP ignores the counts outside the

region and simply compares the relative risk inside the region to 1. Assuming that we can accurately estimate the expected count (under the null hypothesis of no clusters) in each spatial location, and that we are interested in detecting any regions with higher than expected counts, the EBP statistic is a more natural model representation. Additionally, Kulldorff's statistic will lose power to detect spatially large clusters. Let us consider the extreme case where a cluster causes a uniform multiplicative increase in counts over the entire search region. In this case, we would have  $q_{in} = q_{out} = q_{all} \gg 1$ : Kulldorff's statistic would be entirely unable to detect this increase, while EBP would easily detect it. On the other hand, Kulldorff's statistic has the advantage of being more robust to misestimation of global trends such as day-of-week and seasonality, since the parameter  $q_{all}$  automatically adjusts for the case when all estimates are incorrect by a constant multiplicative factor. Thus, it is an open question as to which methodology will work better in real-world time series monitoring scenarios.

## 5. Evaluation

To evaluate the detection performance of the expectation-based scan statistic in the disease surveillance domain, we obtained one year of Emergency Department data from Allegheny County, Pennsylvania. Daily counts of the number of patient records with respiratory chief complaints were aggregated at the zip code level, and thus each count  $c_i^t$  represented the number of respiratory ED visits for a given zip code  $s_i$  for a given day  $t$ . The ED dataset contains data for 88 distinct Allegheny County zip codes from January 1, 2002 to December 31, 2002. The first 84 days of data were used for baseline calculations only, giving us 281 days of count data for evaluation. The total number of respiratory ED visits in Allegheny County ranged from 5 to 62 cases per day, with a mean of 32.58 cases and standard deviation of 7.60 cases. To test for day-of-week trends in the data, we performed a one-way ANOVA using the aggregate daily count as the dependent variable and day of the week as the independent variable. This analysis revealed that counts tend to be significantly higher on Mondays than on other days of the week. Similarly, ANOVA analysis using month of the year as the independent variable revealed that

counts tend to be significantly higher during the winter months (November through March) and significantly lower during the summer months (May through August). These results suggest the potential value of using more complex time series forecasting methods that can account for day-of-week and seasonal trends, and we consider several such methods in Section 5.3.

To evaluate the detection power of our methods, we used a semi-synthetic testing framework, injecting simulated outbreaks of disease into the real-world data. In the biosurveillance domain, outbreak simulation is commonly used to evaluate detection methods because of the scarcity of available, labeled data from real-world outbreaks. Simulation also allows us to precisely evaluate the effect of different parameters (such as the size, shape, and temporal progression of the outbreak) on each method's detection performance; as we observe below, many of these parameters have substantial effects on the relative performance of different methods. Simulation of outbreaks is an active area of ongoing research in biosurveillance, and several recently developed methods (Buckeridge et al., 2004; Wallstrom, Wagner, & Hogan, 2005) show great promise for producing realistic outbreak scenarios. Finally, we note that the expectation-based scan statistic method has been evaluated retrospectively on the 2000 gastroenteritis outbreak which occurred in Walkerton, Ontario, and was able to detect the outbreak two days before the first public health response (Davies, for the ECADS partners and collaborators, 2006; Neill, 2006). However, data from a single outbreak is insufficient to draw detailed conclusions about the relative performance of different methods.

We considered a simple class of circular outbreaks with a linear increase in the expected number of cases over the duration of the outbreak. More precisely, our outbreak simulator takes four parameters: the outbreak duration  $T$ , the outbreak severity  $\Delta$ , and the minimum and maximum number of zip codes affected,  $k_{min}$  and  $k_{max}$ . Then for each injected outbreak, the outbreak simulator chooses the start date of the outbreak  $t_{start}$ , the number of zip codes affected  $k$ , and the center zip code  $s_{center}$  uniformly at random. The outbreak is assumed to affect zip code  $s_{center}$  and its  $k - 1$  nearest neighbors, as measured by the distance between the zip code centroids. On each day  $t$  of the outbreak,  $t = 1 \dots T$ , the outbreak simulator

injects  $\text{Poisson}(tw_i\Delta)$  cases into each affected zip code, where  $w_i$  is the “weight” of each affected zip code, set proportional to its total count  $\sum_t c_i^t$  for the entire dataset, and normalized so that the total weight equals 1 for each injected outbreak. Using this simple outbreak simulator, we performed three simulations of varying size: “small” injects affecting 1–10 zip codes, “medium” injects affecting 10–20 zip codes, and “large” injects affecting all zip codes in Allegheny County. We used  $\Delta = 3$ ,  $\Delta = 5$ , and  $\Delta = 10$  for small, medium, and large injects respectively. We used a value of  $T = 7$  for these outbreaks, and thus outbreaks were assumed to be one week in duration. An additional simulation of a “gradual” outbreak affecting 10–20 zip codes, with  $T = 28$  and  $\Delta = 1$ , was used to evaluate scan statistics with varying temporal window sizes, as discussed below. For each of these simulations, we considered 1000 different, randomly generated outbreaks.

For each combination of method and outbreak size, we computed the method’s proportion of outbreaks detected, and the average number of days to detection, as a function of the allowable false positive rate. To do this, we first computed the maximum region score  $F^* = \max_S F(S)$  for each day of the original dataset with no outbreaks injected (as noted above, the first 84 days of data are excluded, since these are used to calculate baselines for our methods). Then, for each injected outbreak we computed the maximum region score for each outbreak day, and determined the proportion of the days for which the original dataset had higher scores. Assuming that the original dataset contains no outbreaks, this is the proportion of false positives that we would have to accept in order to have detected the outbreak on day  $t$ . For a fixed false positive rate  $r$ , the “days to detect” for a given outbreak is computed as the first outbreak day ( $t = 1 \dots 7$ ) with the proportion of false positives less than  $r$ . If no day of the outbreak has the proportion of false positives less than  $r$ , the method has failed to detect that outbreak: for the purposes of our “days to detect” calculation, these are penalized proportional to the length of the outbreak, and thus are counted as 14 days to detect for a 7-day outbreak. The tradeoff between the false positive rate and average days to detection for a given method can be visualized as an Activity Monitoring Operating Characteristic (AMOC) curve (Fawcett & Provost, 1999), or we can

compare detection times for a fixed false positive rate such as 1 false positive per month. In either case, a lower detection time for a given false positive rate corresponds to improved detection performance.

A secondary performance measure is the method’s *spatial detection accuracy*, which measures its ability to precisely pinpoint the set of locations affected by an outbreak. For a given day of a simulated outbreak, we define the “true outbreak region”  $S_{true}$  as the set of locations with injected cases, and we define the “detected region”  $S^*$  as the region with the highest score,  $S^* = \arg \max_S F(S)$ . Then the *spatial precision* is defined as the ratio of correctly detected locations to all detected locations,  $\frac{\#\{s_i \in S^* \cap S_{true}\}}{\#\{s_i \in S^*\}}$ . Similarly, the *spatial recall* is defined as the ratio of correctly detected locations to all correct locations,  $\frac{\#\{s_i \in S^* \cap S_{true}\}}{\#\{s_i \in S_{true}\}}$ . For each simulated outbreak, we compute the precision and recall at the midpoint of the outbreak (e.g. day 4 of a 7-day outbreak), and average the precision and recall measures over all outbreaks for a given simulation. Finally, we compute the *F-measure* (harmonic mean of precision and recall), as an aggregate measure of the method’s spatial detection accuracy.

### 5.1. Comparison of the scan statistic and fixed partition approaches

In our first set of experiments, we compared the scan statistic method to the traditional “fixed partition” method of time series surveillance. We considered a range of grid sizes from  $N = 1$  to  $N = 32$ . For each grid size, we evaluated the performance of the scan statistic (searching over all rectangular regions on the grid, with sizes varying from  $1 \times 1$  to  $N \times N$ ) and the fixed partition approach (treating each grid cell as a separate time series, and thus searching over  $1 \times 1$  regions only). As noted above, the mapping of zip codes to grid cells was performed using the zip code centroids, and thus each rectangular region on the grid was assumed to correspond to the set of zip codes with centroid coordinates contained in that rectangle. A 1-day temporal window ( $W = 1$ ) was used for all of these runs. We used a 28-day moving average (MA28) to compute expected counts, and the EBP statistic to detect clusters. For each of the three simulations discussed above (assuming small, medium, and large outbreaks respectively), we





















