Scalable Detection of Anomalous Patterns with Connectivity Constraints

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Detect any emerging events (i.e. outbreaks of disease) Pinpoint the affected areas

Biosurveillance

(Kulldorff, 1997; Neill and Moore, 2005)



Scan over multiple regions to detect where counts are higher than expected

Aggregate the individual counts from each location within a region $C = \sum_{s} c_{i}^{t}$ and $B = \sum_{s} b_{i}^{t}$

Determine *anomalousness* of region with a scoring function

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

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

(Kulldorff, 1997; Neill and Moore, 2005)



Scan over multiple regions to detect where counts are higher than expected

Aggregate the individual counts from each location within a region

Circles

Choose a center location \boldsymbol{s}_{c} and its k nearest neighbors

Find the circle that maximizes the score function of the aggregated counts and baselines

Expectation-Based Scan Statistics

(Kulldorff, 1997; Neill and Moore, 2005)



Power to Detect

Circles are useful for detecting tightly clustered outbreaks

However, they lose power to detect abnormally shaped clusters

Affected locations

Un-affected locations contributing to region score

Expectation-Based Scan Statistics



Create an adjacency graph of the locations and score *connected subsets*

Increase power to detect non-circular clusters

Upper Level Set Scan Statistic (ULS) Patil & Taillie, 2004 Uses a heuristic to determine high scoring connected subsets Is not guaranteed to find the highest scoring connected subset

Flexible Scan statistic (FlexScan)

Tango & Takahashi, 2005

Naively scores all connected subsets Infeasible for regions of >30 locations

Connectivity Constraints

(Neill, 2008)

PROBLEM:	The number of subsets grows exponentially
	with the size of the region 2^{N}

This makes it computationally infeasible for regions with more than ~30 locations

SOLUTION:	Exploit a property of scoring functions to rule out subsets that cannot obtain the highest score	
This reduction in the search space allows for exact and efficient calculation of the highest scoring		

unconstrained subset

EXTENSION:	Use this same property for exact and efficient calculation of the highest scoring
	connected subset

Subset Scanning

(Neill, 2008) We wish to maximize a scoring function

$$F \, \mathbf{S} = F \left(\sum_{s_i \in S} c_i, \sum_{s_i \in S} b_i \right)$$

over all possible subsets, S

Sort the locations according to a priority function

For example,

$$G(s_i) = \frac{c_i}{b_i}$$

Works for expectation-based Poisson (EBP)





Some Quick Intuition... (Neill, 2008)

If the kth priority location is contained in the optimal subset and if removing the higher priority adjacent location the subset must also be in the optimal subset.

C=41 B=3 LTSS with Connectivity Constraints

We represent groups of subsets as a string of 0's, 1's, and ?'s

Priority	4	ſ	2	Л	F	6
Ranking	Ŧ	2	3	4	5	0
Bit	1	0	0	1	2	2
String	Ŧ	0	0	T	ŗ	ſ
The above bit string represents						

The above bit string represents 4 possible subsets: {1,4} {1,4,5} {1,4,6} {1,4,5,6}

A Naïve approach would search all 2^N subsets and is computationally infeasible

6 3 4 5 6 3 4 2 3 4 5 2 5 6 ? ? ? ? ? ? ? ? 1 ? ? ? ? ? ? ? ? ?? ? ? ? ? ? 0 0 1 ? ? ?? 0 ?

GraphScan Algorithm

2

?

1

0

0

Û

1

1

0

0

0

0

 S_1

 S_2

S₃

S₄

S₅

S₆

3

?

?

0

4

?

?

1

5

?

?

?

6

?

?

?

Seed nodes have higher priority than all of their neighbors

We can rule out bit strings whose highest priority node is not a seed node

Seed nodes provide starting locations for the following depth first search

GraphScan Algorithm: Seeds

GraphScan Algorithm: Propagation

Q

U

E

U

Ε

1

2

1

Notice that 3 can be removed and not disconnect the subset

Provably sub-optimal by LTSS Property

5

1

6

1

0

GraphScan Algorithm: Propagation

1

1

0

Q U E U E

1

2 is the lowest priority record that can be removed without disconnecting the subset

1

7 1

However, 2 is not low enough to rule out this subset (compared to 4)

GraphScan Algorithm: Backtrack

Ε

U E

Priority	Count	Baseline
1	9	1
2	7	1
3	9	3
4	3	1
5	3	3
6	1	1
7	2	3
8	1	2

2 and 6 have combined priority of

2 and 6 may be removed simultaneously without disconnecting the subset $\frac{7+1}{1+1} = \frac{8}{2}$ still not lower than 4's $\frac{3}{1}$ priority

GraphScan Algorithm: Backtrack

Priority	Count	Baseline
1	9	1
2	7	1
3	9	3
4	3	1
5	3	3
6	1	1
7	2	3
8	1	2

E U E

2,6, and 5 may be removed simultaneously without disconnecting the subset

2, 6, and 5 have combined priority of $\frac{7+1+3}{1+1+3} = \frac{11}{5} = 2.2$

lower than 4's $\frac{3}{1}$ priority.

GraphScan Algorithm: Backtrack

If the domain provides *spatial* information, we may use both proximity and connectivity constraints simultaneously Forming a neighborhood of the 'k nearest neighbors'

Proximity Constraints

Two years of admissions from 10 different Allegheny County Emergency Departments

The patient's home zip code is used to tally the counts at each location (node)

Only consider patients from within Allegheny County

Evaluation: Emergency Department Data

Run time analysis for FlexScan and GraphScan with and without Branch and Bounding. The x-axis denotes the "neighborhood size" as various values of k.

Evaluation: Run Times

Semi-synthetic injects were created by artificially increasing the observed counts in selected zip codes. Zip codes adjacent to rivers were selected as an example of realistic yet abnormally-shaped cluster.

Compare performance on detection power and time to detect for a fixed false positive rate of 1 per month.

Evaluation: Injects

Average detection time and detection power for outbreaks along the rivers.

Results

Average run time on random graphs

Run time performance of GraphScan on randomly generated Erdos-Renyi graphs of varying size and edge probability. Labeled data points mark the proportion of graphs where run time exceeded a 1-hour threshold.

Results: Random Graphs

This work provides...

Theoretical framework for ruling out connected subsets that are provably suboptimal according to the LTSS property

Practical implementation of LTSS with connectivity constraints through the GraphScan Algorithm

GraphScan has shown...

Extremely large speed improvements over FlexScan, while still guaranteeing to identify the highest scoring connected subset

Using connected subsets can increase detection power for irregularly shaped disease clusters

Conclusions