

# USING SATSCAN<sup>TM</sup> SPATIAL-SCAN SOFTWARE WITH NATIONAL FOREST INVENTORY DATA: A CASE STUDY IN SOUTH CAROLINA

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**ABSTRACT.** The USDA Forest Service Forest Inventory and Analysis (FIA) program makes and keeps current an inventory of all forest land in the United States. To comply with privacy laws while at the same time offering its data to the public, FIA makes approximate plot locations available through a process known as perturbing (“fuzzing”) and swapping. The free spatial scanning software program SaTScan<sup>TM</sup> together with FIA data was used to examine the effects of this process and other arrangements of FIA data on the detection of hotspots of standing dead trees in South Carolina. Only 77.8%, 85.7%, and 66.7% of the hotspots identified in datasets with unaltered plot coordinates were observed when the coordinates were fuzzed, swapped, or both fuzzed and swapped, respectively. Aggregating plot-level data to census tract and county dampened the effect of fuzzing and swapping but resulted in the identification of fewer hotspots overall. Within the framework of forest health monitoring in which failing to identify a problem that truly exists can have serious repercussions, neither relying solely on fuzzed and swapped data nor aggregated data will suffice. The addition of buffer data to evaluate the stability of hotspots located near the study area boundary is recommended.

**Keywords:** FIA data, hotspot detection, point pattern analysis, SaTScan<sup>TM</sup>, spatial scan statistic.

## 1 INTRODUCTION

Spatial scan statistics are commonly used in epidemiology, criminology, and other fields to identify areas with an outbreak of disease, crime, or other unusual event commonly known as a “hotspot.” Hotspot detection relies on spatially-referenced point data and an algorithm that scans a geographical area and tests via a likelihood ratio whether the points inside the scanning window (usually a circle or ellipse) have a higher (or lower) rate of event occurrences than the points outside the scanning window. In addition to the underlying distribution of the phenomenon being investigated, the ability of spatial scan statistics to detect hotspots is dependent upon the location accuracy of the spatially-referenced point data and other input required by the scanning algorithm.

Spatial scan statistics have found recent, albeit somewhat limited, application to forestry, e.g., having been used to identify hotspots of forest fires (Orozco et al. 2012), oak regeneration (Fei 2010), forest fragmentation (Coulston and Riitters 2003, Riitters and Coulston 2005), insect and pathogen disturbances (Coulston and Riit-

ters 2003), and poor tree crown conditions (Bechtold and Coulston 2005). Unique among these applications were the studies by Bechtold and Coulston (2005) and Coulston and Riitters (2003) which employed the spatial scan statistic within the tiered forest health monitoring framework of the U.S. Forest Service (Riitters and Tkacz 2004). This framework consists of a detection tier, which is the routine and repeated, systematic sampling of the forest, and an evaluation tier which provides for intensive follow-up studies of irregularities observed in the detection tier. Together these activities seek to identify the extent and cause of deteriorating forest conditions that are occurring either subtly over a long period of time due to cumulative stresses or more rapidly due to specific stresses (Riitters and Tkacz 2004).

Ground surveys conducted by the Forest Inventory and Analysis (FIA) program of the Forest Service, U.S. Department of Agriculture, are a major source of data for forest health monitoring efforts in the United States. FIA has been conducting a forest inventory in the United States for over 80 years (USDA Forest Service 1992). Established initially by the McSweeney-McNary Forest

Research Act of 1928 (*P.L. 70-466*), the 1998 Agricultural Research, Extension, and Education Reform Act (*P.L. 105-185*) mandated FIA to annually report on the area of forestland; volume, growth, and removal of forest resources; and the health and condition of the resource across all lands, public and private (McRoberts et al. 2005, USDA Forest Service 1992). In addition to these annual reports, which are made available in both print and electronic formats, FIA also makes its raw inventory data available to the public. Standard inventory data such as tree height and diameter, forest type, stand age, etc., as well as information needed to make population estimates, are provided via the online FIA database accessible at <http://apps.fs.fed.us/fiadb-downloads/datamart.html> [Date accessed: February 26, 2016] (O’Connell et al. 2014).

Despite the plethora of data available through the online database, FIA is restricted from releasing exact plot locations by the 2000 Interior and Related Agencies Appropriations Act (H.R. 3423). To comply with this policy while at the same time offering its data to the public, FIA makes approximate plot locations available through a process known as perturbing and swapping (McRoberts et al. 2005). This process, also called “fuzzing and swapping,” perturbs the geographic coordinates of each plot location to within 1.6 km of its exact location and for a small proportion of the privately owned plots, exchanges the coordinates with other ecologically similar plots in close proximity (McRoberts et al. 2005). Except in unusual circumstances, coordinates are fuzzed and swapped within the same county or parish.

Several studies have examined the effect of fuzzing and swapping on the outcomes of different research questions and have shown that the process has varying effects. For example, studies that use FIA plot data in conjunction with satellite imagery or other spatially explicit data, e.g., digital terrain data, are affected most (Coulston et al. 2006, Prisley et al. 2009, Randolph 2015, Wang et al. 2011), whereas the effect is typically negligible for studies making estimates or building models for large areas (Gibson et al. 2014, Guldin et al. 2006, McRoberts et al. 2005, Prisley et al. 2009). Although many questions regarding the effect of fuzzing and swapping have been answered, questions continue to arise as new technologies are developed and used in conjunction with FIA data. Such is the case with spatial scan statistics. Thus, the objective of this study was to examine the effect of using various arrangements of FIA data to detect hotspots of standing dead trees in South Carolina with the free spatial scanning software program SaTScan<sup>1</sup> (Kulldorff and Information Management Services, Inc. 2015). The

first evaluation examines the effect of fuzzing, swapping, and fuzzing and swapping combined on the size, number, and location of hotspots of standing dead trees in South Carolina (Section 4). The second evaluation examines the effect of aggregating plot data to larger administrative units (census tract and county) as a way to minimize the effect of fuzzing and swapping (Section 5). Because edge effect, or boundary bias, is a concern for spatial analyses like hotspot detection (Gregorio et al. 2006, Van Meter et al. 2010), the third evaluation examines the stability of hotspots detected near the boundary of the study area (Section 6).

## 2 SPATIAL SCAN

Hotspot detection was implemented with SaTScan<sup>TM</sup> version 9.4.2 (Kulldorff 2015, Kulldorff and Information Management Services, Inc. 2015). SaTScan works by imposing a scanning window of increasing size at each geographic point of data and testing via a likelihood ratio whether the points inside the scanning window have a higher (or lower) rate of event occurrences, i.e., cases, than the points outside the scanning window (Kulldorff 1997). The maximum size of the scanning window can be a percentage of the population at risk or a defined geographic distance. (The default setting is 50% of the population at risk.) For each scanning window, a likelihood ratio test statistic (LRTS) is calculated according to a specified probability model and the window corresponding to the maximum value of the calculated LRTS is identified as the most likely hotspot. Other hotspots follow in rank order according to the LRTS. Statistical significance of the hotspots is determined by Monte Carlo simulation that repeats the analysis for a user-specified number of random replications of the original data set under the null hypothesis of spatial randomness. (The default number of replications is 999.) The LRTSs for the hotspots are compared to the distribution of test statistics from the Monte Carlo simulation and if they exceed 95% of the values from the simulation they are considered significant at the 5% level.

For all analyses in this study, the null hypothesis was that the prevalence of standing dead trees in the scanning window was the same as the prevalence of standing dead trees outside the window, i.e., spatial randomness. The alternative hypothesis was that the prevalence of standing dead trees in the window was greater than expected under the null hypothesis. All runs of SaTScan were implemented as purely spatial scans under the Bernoulli probability model with a circular scanning window. The maximum size of the scanning window was defined as a percentage of the total population at risk, i.e., the

<sup>1</sup>SaTScan<sup>TM</sup> is a trademark of Martin Kulldorff. The SaTScan<sup>TM</sup> software was developed under the joint auspices of (i) Martin Kulldorff, (ii) the National Cancer Institute, and (iii)

Farzad Mostashari of the New York City Department of Health and Mental Hygiene.

combined total of standing dead and live trees (“cases” and “non-cases”, respectively) in the study area, and the number of replications for the Monte Carlo simulations was set to the default value. Only hotspots that were significant ( $\alpha = 0.05$ ) and not geographically overlapped by hotspots with higher LRTS values are discussed in the results. In all analyses, emphasis was placed on the difference between hotspots identified in two contrasting datasets rather than on the veracity of hotspots identified in any particular dataset.

### 3 FIA DATA

FIA plots are located across the United States in such a way that the sampling intensity is 1 plot per approximately 2,400 ha. The sampling frame used to locate each plot on the ground is based on a hexagonal tessellation of the United States with 1 plot randomly located within each hexagon (Reams et al. 2005). Each plot consists of four 7.32 m fixed-radius subplots on which trees  $\geq 12.7$  cm in diameter at breast height (d.b.h.) are measured. The cluster of subplots is arranged with 1 central subplot and 3 other subplots located 36.6 m from the central subplot at azimuths of 0, 120, and 240 degrees. Each plot is permanently monumented, georeferenced, and measured on a repeating cycle of between 5 and 10 years. All plots within a state are divided into spatially balanced “panels.” A single panel of plots is measured every year so that each state is completely measured once every 5 to 10 years on an ongoing basis. Although measurements are spread over multiple years, the inventories are dated with the year of the most recently collected panel of data. For this analysis, FIA data for inventory year 2012 were obtained from the FIA database for Georgia, North Carolina, and South Carolina (Fig. 1). Only fully forested plots with live or standing dead trees  $\geq 12.7$  cm d.b.h. were kept for the analyses (Table 1). According to FIA definitions, the bole of a dead tree must be at least 1.37 m in length

and lean less than 45 degrees from vertical in order for it to qualify as “standing dead” (USDA Forest Service 2012). Data from Georgia and North Carolina were only included in the evaluation of edge effect (Section 6).

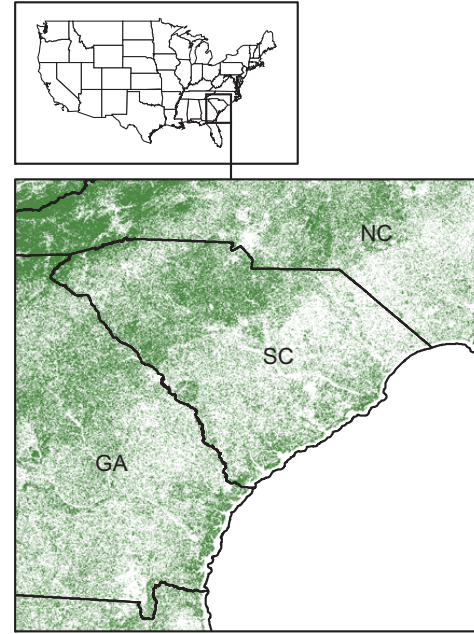


Figure 1: Location of forest and woody wetlands land cover (Homer et al. 2015) in the states of Georgia (GA), North Carolina (NC), and South Carolina (SC) in the southeastern United States.

### 4 FUZZING AND SWAPPING

Three datasets were compiled in order to evaluate the effect of FIA’s fuzzing and swapping procedure on the detection of hotspots of standing dead trees in South Carolina. First was a dataset in which all of the plot locations were the confidential geographic coordinates with no fuzzing and no swapping (hereafter referred to as “actual”). Second was a dataset in which the geographic coordinates were fuzzed but none were swapped (“fuzzed/nonswapped”). Third was a dataset like that available to the public in which all of the geographic coordinates were fuzzed and some were swapped (“fuzzed/swapped”). Among the plots used in this analysis, 18.5% had swapped geographic coordinates. For the scans in this analysis, the maximum size of the scanning window was set to 50% of the population at risk in South Carolina (Table 1).

**4.1 Analysis** Three separate scans were made, one for each dataset (actual, fuzzed/nonswapped, and fuzzed/swapped). Hotspots were depicted as circles with radii equaling the distance from the plot at the center of the

Table 1: Number of live and standing dead trees observed on fully forested plots in select buffer zones surrounding South Carolina (SC).

| Geographic area        | Plots | Trees   |       |         |
|------------------------|-------|---------|-------|---------|
|                        |       | Live    | Dead  | Total   |
| SC only                | 1,742 | 46,473  | 1,899 | 48,372  |
| SC+6 km buffer         | 1,866 | 49,869  | 2,085 | 51,954  |
| SC+12 km buffer        | 1,967 | 52,670  | 2,217 | 54,887  |
| SC+18 km buffer        | 2,079 | 55,644  | 2,386 | 58,030  |
| SC+neighboring states* | 7,510 | 196,065 | 9,228 | 205,293 |

\*Georgia and North Carolina.

hotspot to the most distant plot included in the hotspot. Results were compared in a pairwise fashion:

- Actual vs. fuzzed/nonswapped, to observe the effect of fuzzing.
- Fuzzed/nonswapped vs. fuzzed/swapped, to observe the effect of swapping.
- Actual vs. fuzzed/swapped, to observe the effect of fuzzing and swapping combined.

For each pairwise comparison, geographically overlapping hotspot pairs were compared with an intersection-to-union area ratio ( $R_a$ ) calculated as

$$R_a = \frac{|X \cap Y|}{|X \cup Y|} \times 100$$

where X and Y represent the km<sup>2</sup> area of two geographically overlapping hotspots. Maximum  $R_a$ , i.e.,  $R_a = 1$ , occurs when overlapping clusters have identical center points and equal radii.  $R_a$  decreases from the maximum value and asymptotically approaches 0 as overlapping clusters diverge from one another in terms of size (radius) and/or center point location. Area calculations were made in ArcMap<sup>TM</sup> 10.3.1 (©ESRI 2015) under the Albers Equal Area Conic projection for North America. For some hotspots, the circular area extended beyond the border of South Carolina. In such cases, only the area within South Carolina was included in the  $R_a$  calculation.  $R_a$  was not calculated when one of the hotspots in an overlapping pair consisted of a single plot. The sensitivity of the scan to detect “true” hotspots was calculated as the percentage of hotspots detected in the base dataset also detected in the contrasting dataset. For the examination of the effect of fuzzing and the effect of fuzzing and swapping combined, the base dataset was the actual dataset. For the examination of the effect of swapping, the base dataset was the fuzzed/nonswapped dataset.

**4.2 Results** A total of 9 different regions, labeled A through I in Fig. 2, were identified as having hotspots of standing dead trees, but only regions A, C, D, E, G, and H were identified in all three datasets. Hotspots were identified in region B with the actual and fuzzed/nonswapped datasets, but not the fuzzed/swapped dataset. Hotspots were identified in regions F and I with the actual dataset only. Hotspots in regions C, D, E, and G were single-plot hotspots in each of the three datasets. The hotspots located in region A were the most likely hotspots in each dataset.

**4.2.1 Effect of Fuzzing** The scan based on the fuzzed/nonswapped dataset identified 2 fewer hotspots than the

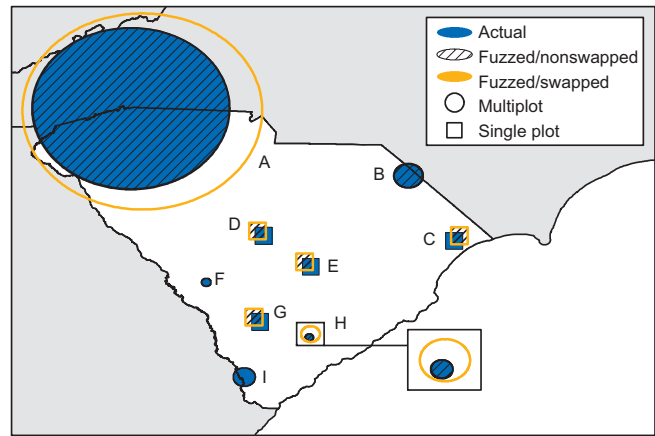


Figure 2: Hotspots of standing dead trees in South Carolina based on actual, fuzzed/nonswapped, and fuzzed/swapped plot coordinates. Single-plot locations are approximate. The letter A identifies the region with the most likely hotspot. The distance between single-plot locations within hotspot regions C, D, E, and G are exaggerated for visualization purposes.

scan based on the actual dataset (sensitivity = 77.8%), but had no effect on the total number of single-plot hotspots (Fig. 2). Located in region A (Fig. 2), the most likely hotspot in the fuzzed/nonswapped dataset (LRTS = 51.8) included 386 cases across 218 plots (Table 2) and compared favorably to the most likely hotspot in the actual dataset ( $R_a = 0.98$ ) (Table 3). Hotspots in regions C, D, E, and G (Fig. 2) were identical in terms of LRTS rank and plot composition, but their locations varied slightly due to the fuzzing procedure. Hotspots in regions B and H (Fig. 2) were also identical in terms of LRTS rank and plot composition, but were different in terms of location and area ( $R_a = 0.96$  and  $0.91$ , respectively) (Table 3).

**4.2.2 Effect of Swapping** The scan based on the fuzzed/swapped dataset identified 1 less hotspot than the scan based on the fuzzed/nonswapped dataset (sensitivity = 85.7%), but had no effect on the total number of single-plot hotspots (Fig. 2). Located in region A (Fig. 2), the most likely hotspot in the fuzzed/swapped dataset (LRTS = 51.8) included 611 cases across 382 plots (Table 2) and compared moderately to the most likely hotspot in the fuzzed/nonswapped dataset ( $R_a = 0.66$ ) (Table 3). Hotspots in regions C, D, E, and G (Fig. 2) were identically located. Though located in the same general region H, the hotspot identified in the fuzzed/swapped dataset varied considerably in terms of geographic area from the one identified in the fuzzed/nonswapped dataset ( $R_a = 0.18$ ) (Table 3).

Table 2: Descriptive statistics for selected hotspots of standing dead trees in South Carolina based on plot data with actual geographic coordinates, fuzzed/nonswapped geographic coordinates, and fuzzed/swapped geographic coordinates. A case is defined as a standing dead tree.

| Coordinates       | Hotspot* | Number of plots | LRTS <sup>†</sup> | Number of cases | Radius (km) |
|-------------------|----------|-----------------|-------------------|-----------------|-------------|
| Actual            | A        | 224             | 53.1              | 396             | 95          |
| Actual            | B        | 6               | 10.8              | 14              | 14          |
| Actual            | H        | 2               | 11.2              | 16              | 4           |
| Fuzzed/nonswapped | A        | 218             | 51.8              | 386             | 94          |
| Fuzzed/nonswapped | H        | 2               | 11.2              | 16              | 4           |
| Fuzzed/swapped    | A        | 382             | 51.8              | 611             | 115         |
| Fuzzed/swapped    | H        | 5               | 13.3              | 16              | 9           |

\*Illustrated in Fig. 2.

<sup>†</sup>Likelihood ratio test statistic.

Table 3: Intersection-to-union ratio ( $R_a$ ) of the geographically overlapping multiplot hotspots illustrated in Fig. 2.

| Hotspot                                     | $R_a$ |
|---------------------------------------------|-------|
| Effect of fuzzing*                          |       |
| A                                           | 0.98  |
| B                                           | 0.96  |
| H                                           | 0.91  |
| Effect of swapping <sup>†</sup>             |       |
| A                                           | 0.66  |
| H                                           | 0.18  |
| Effect of fuzzing and swapping <sup>‡</sup> |       |
| A                                           | 0.67  |
| H                                           | 0.20  |

\* Actual vs. fuzzed/nonswapped.

<sup>†</sup> Fuzzed/nonswapped vs. fuzzed/swapped.

<sup>‡</sup> Actual vs. fuzzed/swapped.

#### 4.2.3 Effect of Fuzzing and Swapping Combined

The scan based on the fuzzed/swapped dataset identified 3 fewer hotspots than the scan based on the actual dataset (sensitivity = 66.7%), but had no effect on the total number of single-plot hotspots (Fig. 2). Located in region A (Fig. 2), the most likely hotspot in the actual dataset ( $LRTS = 53.1$ ) included 396 cases across 224 plots (Table 2) and compared moderately to the most likely hotspot in the fuzzed/swapped dataset ( $R_a = 0.67$ ) (Table 3). The single-plot hotspots in regions C, D, E, and G (Fig. 2) were identical in terms of plot composition, but their locations varied slightly due to the fuzzing procedure. Though located in the same general region H, the hotspot identified in the actual dataset varied considerably in terms of geographic area from the one identified in the fuzzed/swapped dataset ( $R_a = 0.20$ ) (Table 3).

**4.3 Discussion** The FIA process of fuzzing and swapping plot geographic coordinates provided to the public is necessary for protecting landowner privacy. From the outset, it was determined that the act of fuzzing alone was not sufficient to meet the confidentiality requirements required by law (Guldin et al. 2006). Thus, the second step of exchanging the coordinates of ecologically similar plots was added. The decision to add swapping in order to improve confidentiality was evident in this study, for fuzzing alone only minimally effected the spatial scan outcome. That is, the geographic location of individual hotspots identified in the actual dataset was much more similar to hotspots identified in the fuzzed/nonswapped dataset than to hotspots identified in the fuzzed/swapped dataset ( $R_a > 0.90$  vs.  $R_a < 0.68$ ).

As observed in other studies (Coulston et al. 2006, Prisley et al. 2009, Wang et al. 2011), using the publicly available FIA data, i.e., fuzzed/swapped data, carries with it risks that may be unacceptable for certain investigations. Typically within the forest health monitoring framework, a high rate of false positives is accepted as the cost of not overlooking a serious problem (Riitters and Tkacz 2004). Accepting such is particularly warranted when resources are available to investigate and either confirm or nullify a suspected hotspot (e.g., Bechtold and Coulston 2005, Randolph et al. 2009). No false positives were identified in the fuzzed/swapped dataset; however, there were 3 false negatives. Though this was a moderate rate of success, failing to identify a forest health problem when one actually exists can have serious repercussions. Thus, if the goal is to identify all possible hotspots for further investigation, using fuzzed/swapped data with SaTScan would not suffice.

## 5 DATA AGGREGATION

Aggregating FIA data to a coarser spatial scale prior to implementing a spatial scan would eliminate many

Table 4: Descriptive statistics for hotspots of standing dead trees in South Carolina based on census tract and county aggregations of individual plot data. A case is defined as a standing dead tree.

| Aggregation  | Coordinates        | Hotspot        | Number of locations | LRTS* | Number of cases |
|--------------|--------------------|----------------|---------------------|-------|-----------------|
| Census tract | Actual             | A <sup>†</sup> | 85                  | 50.9  | 439             |
| Census tract | Fuzzed and swapped | A <sup>†</sup> | 85                  | 49.8  | 444             |
| Census tract | Fuzzed and swapped | B <sup>‡</sup> | 1                   | 9.4   | 10              |
| County       | Actual             | A <sup>‡</sup> | 14                  | 46.6  | 673             |

\*Likelihood ratio test statistic.

<sup>†</sup>Illustrated in Fig. 6.<sup>‡</sup>Illustrated in Fig. 5.

concerns about plot confidentiality; however, as seen in the field of human epidemiology, aggregating data to administrative units such as county, zip code, or census tract can negatively affect hotspot detection rates (Jeffrey et al. 2009, Olson et al. 2006, Ozonoff et al. 2007). This is because data aggregation can incongruently alter the concentration of events or cases relative to background population levels. This is particularly the case when a hotspot crosses the artificial, administrative boundary by which the aggregations are defined. Though FIA makes every effort to work with partners wishing to use actual geographic coordinates in analyses that require them<sup>2</sup>, such requests take time to be approved and fulfilled. Data aggregation might be an alternative to using actual plot coordinates for spatial scan applications if hotspots present at the plot-level can be successfully identified within the aggregated data. Thus, this section explores how well hotspots identified at the plot-level are identified at coarser spatial scales and if the same level of agreement can be achieved by basing the aggregations on the fuzzed/swapped dataset as on the actual dataset.

**5.1 Analysis** Plot-level counts of standing dead trees (cases) and live trees (non-cases) were respectively summed by census tract and county. The census tract aggregation was completed twice, once with the actual dataset and secondly with the fuzzed/swapped dataset (Section 4). County-level aggregations needed to be done only once because plots were fuzzed and swapped within counties. The respective sums were assigned to the geographic coordinates of the census tract centroid or county centroid. Centroids were determined with the calculate geometry function in ArcMap<sup>TM</sup> 10.3.1 (©ESRI 2015). Spatial scans were implemented with the maximum size of the scanning window set to 50% of the population at risk in South Carolina (Table 1). Results from the scans based

on the aggregated data (actual dataset) were compared visually to the plot-level scan (actual dataset) (Section 4) through a geographic information system (GIS) overlay. Results from the two census-tract aggregations were compared to one another with the intersection-to-union area ratio ( $R_a$ ) (Section 4.1). For this calculation of  $R_a$ , the area of each hotspot equaled the total area of all census tracts included in the hotspot.

## 5.2 Results

**5.2.1 Census tract and county aggregations** Only 1 hotspot was identified when the plot-level data (actual dataset) were aggregated to census tract (Fig. 3). This hotspot included 439 cases and 85 census tracts (Table 4), and excluded tracts roughly corresponding to the Interstate-85 corridor and cities of Greenville and Spartanburg. Likewise, only 1 hotspot was identified when the plot-level data were aggregated to county (Fig. 3). This hotspot included 673 cases and 14 counties (Table 4). Both the census tract hotspot and the county hotspot coincided geographically with the most likely hotspot identified in the plot-level data (Fig. 3). The coarser the aggregation, the greater the effect on the detection of hotspots (Ozonoff et al. 2007). Thus, as expected, the extent of the census tract hotspot more closely resembled the extent of the plot-level hotspot than did the county-level hotspot. Eight of the 9 hotspot regions identified in the plot-level data were not identified in either aggregated dataset (sensitivity = 11.1%).

**5.2.2 Effect of fuzzing and swapping** Two significant hotspots were identified when the census tract aggregation was based on the fuzzed/swapped dataset (Fig. 4). The most likely hotspot, labeled A in Fig. 4, included 444 cases and 85 census tracts (Table 4). The second hotspot, labeled B in Fig. 4, included 10 cases and only 1 census tract (Table 4). The geographical similarity between the most likely hotspot detected in the fuzzed/swapped aggregation and the only hotspot identified in the actual aggregation was high ( $R_a = 0.98$ ) (Fig. 4). If the ag-

<sup>2</sup>More information about this type of arrangement can be obtained by contacting FIA Spatial Data Services (<http://www.fia.fs.fed.us/tools-data/spatial/index.php>) [Date accessed: February 1, 2017].



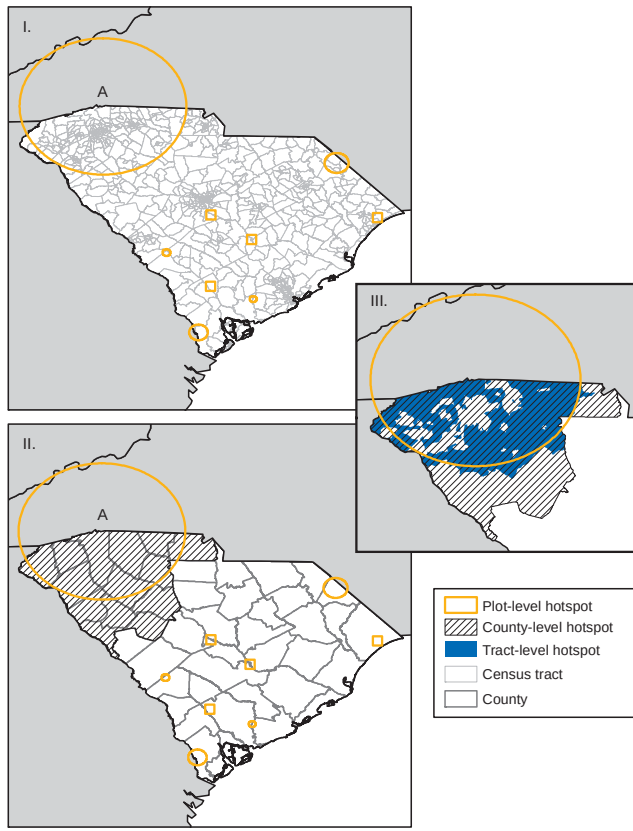


Figure 3: Hotspots of standing dead trees in South Carolina based on individual plot data (actual coordinates) and plot data (actual coordinates) aggregated to census tract (I) and county (II). Inset (III) highlights the extent of geographical overlap of the plot-, census tract-, and county-level hotspots. Single-plot locations (shown as squares) are approximate. The letter A identifies the region with the most likely hotspot.

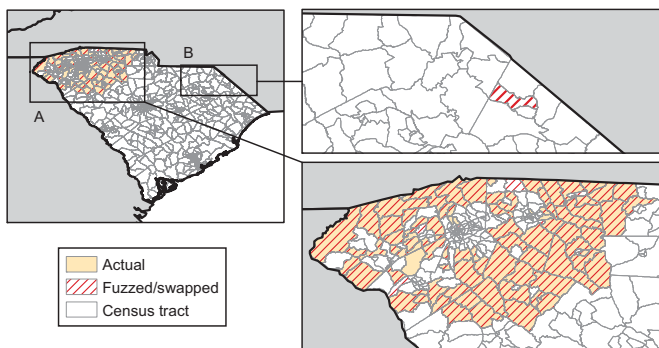


Figure 4: Hotspots of standing dead trees in South Carolina based on plot data aggregated to census tract using actual geographic coordinates and fuzzed/swapped geographic coordinates. The letter A identifies the region with the most likely hotspot.

gregation to census tract based on the actual dataset is considered to represent true hotspots, then the aggregation based on the fuzzed/swapped dataset resulted in 1 false positive.

**5.3 Discussion** A high number of false negatives was observed when the scans based on the aggregated data were compared to the scans based on the plot-level data. This occurred at both scales of aggregation, county and census tract, and for both sets of geographic coordinates, actual and fuzzed/swapped. Though one hotspot was consistently identified across all scans, the rate of success was too low to recommend relying solely on aggregated data for forest health monitoring purposes. Nonetheless, aggregating data from precise locations may sometimes be profitable despite the occurrence of false negatives. Jeffrey et al. (2009) showed that the power to detect hotspots was highest with precise locations and disturbances that were confined to small regions of the study areas or those that affected a large portion of the population, but they also observed that aggregation could improve the ability to detect weak signals if the level of aggregation was equal to, or smaller than, the spatial disturbance. Weak signals may represent areas with an emerging problem and could be important with regard to forest health monitoring. Because the distribution of risk is not known *a priori*, utilizing multiple levels of aggregations in addition to the precise locations could be beneficial for identifying forest health problems. In so doing, a decision must be made about which plot coordinates to use for aggregations smaller than the county-level. As seen here, the geographical similarity between the census tract aggregations was exceptionally high for the most likely cluster ( $R_a = 0.96$ ) and a considerable improvement over what was observed at the plot-level ( $R_a = 0.67$ ). Nevertheless, the false positive hotspot reveals the uncertainty that can arise when fuzzing/swapping moves plots from one aggregation unit and into another. Ideally then, aggregations to units smaller than county should be made with actual geographic coordinates.

## 6 EDGE EFFECT

Geopolitical or other boundaries unrelated to the phenomenon being investigated can pose a problem for hotspot detection if the population of interest extends beyond the boundary for which data are available. Such spatial censoring can introduce bias near the boundaries and affect overall inferences drawn from analyses (Gregorio et al. 2006, Van Meter et al. 2010). Two solutions to this problem have been posited. The first is a reduction of the maximum allowable size of the scanning window (Gregorio et al. 2006, Loha et al. 2012, Perez et al. 2005).

The second is the inclusion of data from a buffer zone around the area of interest (Bechtold and Coulston 2005, Sadler et al. 2011, Van Meter et al. 2010). The former minimizes the chance that hotspots will reach or extend beyond the boundary of the study area whereas the latter maximizes full estimation of hotspots within the study area.

Choosing a scanning window size that is too large may produce hotspots that are too large to be useful or hide small, homogeneous hotspots within larger, heterogeneous ones; choosing a size that is too small may produce results that miss large hotspots (Chen et al. 2008, Fotheringham and Zhan 1996). Likewise, an exceedingly large buffer area may alter the overall spatial distribution of risk and unduly influence detection of hotspots within the interior of the study area. This is especially true if the risk in the buffer area is different from the risk in the area of interest. Two questions that follow from these different approaches, to what size should the scanning window be reduced and what size buffer area is appropriate, are addressed here.

**6.1 Analysis** An initial, baseline scan was made using the default SaTScan value for the maximum size of the scanning window, i.e., 50% of the total population at risk. Only data from South Carolina (Table 1) were included in the baseline scan. Plot locations were based on the confidential, i.e., actual, geographic coordinates (Section 4).

**6.1.1 Scanning window size** To address the question regarding the maximum size of the scanning window, SaTScan was run with maximum scanning window sizes equal to 5%, 15%, 25%, and 33% of the population at risk, i.e., the total number of live and standing dead trees in South Carolina (Table 1). Hotspots identified with these four scanning window sizes were compared to hotspots identified in the baseline scan on the basis of geographical overlap with the intersection-to-union area ratio ( $R_a$ ) (Section 4.1). Area calculations were made in ArcMap<sup>TM</sup> 10.3.1 (©ESRI 2015) under the Albers Equal Area Conic projection for North America. Hotspots were depicted as circles with radii equaling the distance from the plot at the center of the hotspot to the most distant plot included in the hotspot. For some hotspots, the circular area extended beyond the border of South Carolina. In such cases, only the area within South Carolina was included in the  $R_a$  calculation.  $R_a$  was not calculated when one of the hotspots in an overlapping pair consisted of a single plot.

**6.1.2 Buffer area size** To address the question about buffer size, the study area was expanded to include data from 4 buffer areas around South Carolina: (a) within

6-km, (b) within 12-km, (c) within 18-km, and (d) in all neighboring states, i.e., Georgia and North Carolina. The 6-, 12-, and 18-km buffer distances were selected to approximately include the nearest, 2 nearest, and 3 nearest bands of FIA plots, respectively. For these additional scans, the maximum size of the scanning window was set to 50% of the respective population at risk (Table 1). Hotspots identified with each of the scans were compared to hotspots identified in the baseline scan on the basis of geographical overlap with the intersection-to-union area ratio ( $R_a$ ) (Section 4.1). Hotspots were depicted as circles with radii equaling the distance from the plot at the center of the hotspot to the most distant plot included in the hotspot.  $R_a$  calculations excluded the area of hotspots extending beyond the South Carolina state boundary and were made only when both hotspots in the overlapping pair consisted of multiple plots.

## 6.2 Results

**6.2.1 Effect of scanning window size** The hotspots identified with a maximum scanning window set to 50% of the population at risk were identical to the hotspots identified with a maximum scanning window of 33%, 25%, and 15% of the population at risk. Therefore, only the results for the 5% scanning window are shown in contrast to the results for the 50% scanning window.

A total of 9 significant hotspots were identified with the 50% scanning window and 11 with the 5% scanning window. The only difference between the two scans occurred in the region of the most likely hotspots where the 5% scanning window detected 3 hotspots and the 50% scanning window detected only 1 (Fig. 5). The most likely hotspot (LRTS = 53.1) identified with the 50% scanning window, labeled A in Fig. 5, included 396 cases across 224 plots extending up to 95 km from the hotspot center. The most likely cluster (LRTS = 42.33) identified with the 5% scanning window was a single-plot (labeled B in Fig. 5) consisting of 19 cases. The two other hotspots identified with the 5% scanning window in this region, labeled C and D (Fig. 5.), overlapped hotspot A with  $R_a$  values of 0.43 and 0.02, respectively (Table 5).

**6.2.2 Effect of buffer zones** The number of significant hotspots in South Carolina decreased as the size of the buffer area increased, ranging from 9 significant hotspots with no buffer to 4 significant hotspots when data from all neighboring states were included (Fig. 6). The number of single-plot hotspots remained at 4 as the buffer size increased until data from all neighboring states were included, at which point only 3 single-plot hotspots were identified (Fig. 6). For the state-only and buffer-added scans, the most likely hotspot was located in the same geographic area, labeled A in Fig. 6. The



Table 5: Descriptive statistics for selected hotspots of standing dead trees in South Carolina based on a maximum scanning window size of 50% of the population at risk (hotspot A) and 5% of the population at risk (hotspots B, C, and D). A case is defined as a standing dead tree.

| Hotspot* | Number of plots | LRTS <sup>†</sup> | Number of cases | Radius (km) | Ra <sup>‡</sup> |
|----------|-----------------|-------------------|-----------------|-------------|-----------------|
| A        | 224             | 53.1              | 396             | 95          | -               |
| B        | 1               | 42.3              | 19              | -           | -               |
| C        | 85              | 27.3              | 153             | 42          | 0.43            |
| D        | 23              | 18.6              | 64              | 30          | 0.02            |

\*Illustrated in Fig. 5.

<sup>†</sup>Likelihood ratio test statistic.

<sup>‡</sup>Intersection-to-union ratio with hotspot A.

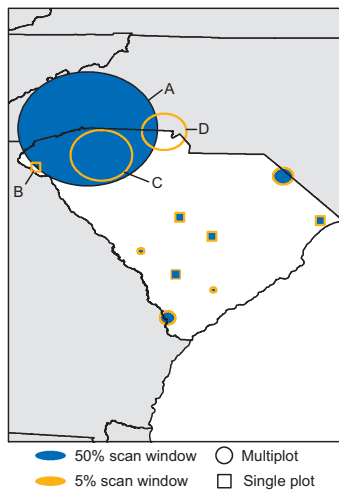


Figure 5: Hotspots of standing dead trees in South Carolina based on two scanning window sizes, 50% of the population at risk and 5% of the population at risk. Single-plot locations are approximate.

hotspots located in this region increased in area and number of cases as the size of the buffer area increased (Table 6). Similarity between the most likely hotspot in the South Carolina-only scan and the most likely hotspot in the buffer-added scans was approximately the same for buffers of size 6-km, 12-km, and 18-km:  $R_a = 0.95$ ,  $0.94$ , and  $0.94$ , respectively (Table 6). The similarity between the South Carolina-only scan and the scan with data from South Carolina, Georgia, and North Carolina was lowest of all ( $R_a = 0.63$ ) (Table 6).

Two hotspots located near the border of South Carolina, labeled B and C in Fig. 6, were not significant once data in the buffer zones were included in the spatial scan. Hotspot D, located toward the interior of the state, was not detected with buffers >12-km, and hotspots E and F in the interior were not detected when data from Georgia and North Carolina were included (Fig. 6).

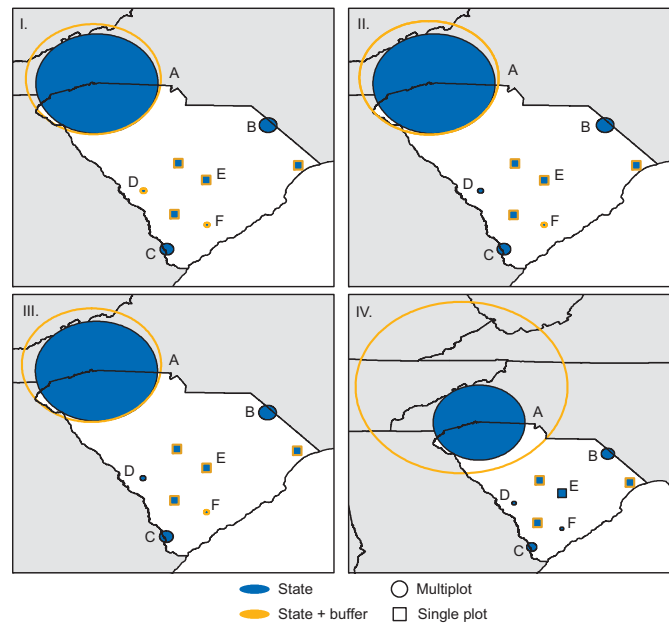


Figure 6: Hotspots of standing dead trees in South Carolina based on data from South Carolina plus data in a buffer area of size 6 km (I), 12 km (II), 18 km (III), and all neighboring states (IV). Single-plot locations are approximate.

**6.3 Discussion** To minimize the influence of scanning window size on the interpretation of SaTScan results, Chen et al. (2008) recommended repeating the scan with multiple window sizes and calculating a reliability score for each location included in the analysis. Calculated as the ratio of the number of scans for which location  $i$  is within a significant hotspot to the total number of scans, this score measures the stability of hotspots reported by multiple scans and helps identify a hotspot’s core. In this study, all of the hotspots except hotspot A (Fig. 6) remained unchanged as the maximum size of the scanning window was reduced from 50% of the population at risk to 5% of the population at risk. Therefore, reliability scores

Table 6: Descriptive statistics for hotspots in region A (Fig. 6) of South Carolina (SC) based on plot data from select buffer zones. A case is defined as a standing dead tree.

| Geographic area                      | Number of plots* | LRTS <sup>†</sup> | Number of cases* | Radius (km) | Ra <sup>‡</sup> |
|--------------------------------------|------------------|-------------------|------------------|-------------|-----------------|
| SC only                              | 224              | 53.1              | 396              | 95          | -               |
| SC + 6 km buffer                     | 238              | 69.2              | 420              | 105         | 0.95            |
| SC + 12 km buffer                    | 240              | 88.5              | 422              | 108         | 0.94            |
| SC + 18 km buffer                    | 240              | 102.8             | 422              | 108         | 0.94            |
| SC + neighboring states <sup>§</sup> | 417              | 604.3             | 643              | 216         | 0.63            |

\*Plots and cases outside of SC are excluded.

<sup>†</sup>Likelihood ratio test statistic.

<sup>‡</sup>Intersection-to-union ratio with hotspot A identified with the SC-only dataset.

<sup>§</sup>Georgia and North Carolina.

were deemed unnecessary. Nevertheless, the approach highlighted 3 areas within hotspot A (B, C, and D in Fig. 5) that might be considered core areas and as such could be prioritized for follow-up study. Likewise, the addition of buffer data identified 2 hotspots that are likely artifacts of spatial censoring (B and C in Fig. 6) and could be given low priority in a follow-up study.

A buffer area of 6- to 12-km was sufficient to see changes in the hotspots near the study area boundary. However, whether or not 6- to 12-km should be considered a standard buffer width when using SaTScan to monitor state-level forest health with FIA data was not tested specifically. In general, the size of the buffer area should be chosen carefully, with consideration given to the nature of the resource and disturbance phenomenon under investigation. With FIA’s national sampling framework, buffer data are available for all areas except those along the international borders.

Altering the maximum size of the scanning window and adding buffer data are not equivalent forms of evaluating edge effects, yet both provide valuable insight into the location and stability of hotspots centered near the boundary of a study area. Subsequently, both tactics may be of use in exploratory analyses such as might be employed within the forest health monitoring framework. It should be noted, however, that selecting hotspots for reporting should not be based on multiple scans utilizing different maximum scanning window sizes unless  $p$ -values are adjusted to account for multiple testing (Han et al. 2016).

## 7 SUMMARY

Detecting hotspots of forest fires, insect and disease outbreaks, or other unusual occurrences within the forested landscape is an essential aspect of monitoring forest health in the same way that detecting outbreaks of human disease is an essential part of monitoring public health. Spatial scan statistics have emerged as a promis-

ing exploratory tool for identifying such hotspots at a variety of spatial scales. The utility of these statistics depends upon the location accuracy of the georeferenced forest inventory data and other input required by the scanning algorithms. In this study, SaTScan was used to identify hotspots of standing dead trees in South Carolina based on national forest inventory data collected by the FIA Program. The effect of three factors on identified hotspots were investigated: the FIA fuzzing and swapping procedure, data aggregation, and edge data.

Overall, this study demonstrated what Gregorio et al. (2006) called the “conditional nature of spatial analyses” whereby the size, number, and location of identified hotspots are influenced by the study area size, scanning parameters, and geographical precision of the input data, in addition to the underlying geographic distribution of risk. In all cases, the most likely hotspot of standing dead trees in South Carolina was located in the same general area. Yet it was evident that the FIA process of fuzzing and swapping plot coordinates affected the location, size, and composition of hotspots identified at both the plot and census tract levels. Though aggregating data to census tract dampened the effect of the fuzzing and swapping procedure, numerous hotspots went undetected when the data were aggregated on the basis of both the actual and fuzzed/swapped geographic coordinates. Hotspots that are detectable at the plot-level but not at the census tract level may be areas of considerable concern if they represent areas where problems are beginning to develop. As such, relying solely on spatial scans based on census tract aggregations is not a suitable practice for forest health monitoring.

This study considered only one application of SaTScan to FIA data: that of looking for hotspots of standing dead trees in a single state with a circular scanning window under the case/non-case Bernoulli model. Results may not be representative of all hotspot detection investigations utilizing FIA data and SaTScan or other spatial scan methods. Additional studies in other ar-

areas of the United States or with other variables under different statistical models might produce different conclusions, particularly regarding the effects of fuzzing and swapping. This is because swapping is only done for privately owned forested plots and between such plots with similar forest characteristics in the same county or parish (Gibson et al. 2014). Thus, the effect of using data with fuzzed/swapped geographic coordinates that was observed in this study may be different in areas with large public land holdings or with variables that are closely tied to the characteristics on which swapping decisions are based, e.g., forest type. In addition, the underlying size of the affected area, i.e., the size of the “true” hotspot, should also be considered. Geographically large hotspots will be less influenced by the swapping procedure than smaller hotspots because the swapping is more likely to occur from within the larger areas than from without (Lister et al. 2005). These factors were not tested directly in this study but could be addressed in a power study using simulated or semisynthetic data in which the distribution of risk is precisely known and controlled (Olson et al. 2006, Ozonoff et al. 2007).

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