Report
Spatial Analysis of Whiskey Fungus Testing for the Town of York, Maine

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Introduction:

The goal of the project described here was to determine whether and to what degree whiskey fungus contamination is escaping the Wiggly Bridge Distillery in York, ME. This report describes the mapping and spatial analysis portion of the project performed by the University of Maine at Machias GIS Service Center.

Methods:

Using ArcGIS Pro 3.1, 100 sample locations were generated in random locations within a 12 meter buffer of public roads within one statute mile of the Wiggly Bridge Distillery in York, Maine, and dispersed with at least 100 feet between points. Points generated in inaccessible locations were moved to the nearest accessible, public location, maintaining the minimum 100-foot distance. The points were assigned ID numbers and published to a web-based, mobile-friendly map application on ArcGIS Online for use in the field.

Field staff used the web-based map and their smartphone's location services to get as close as possible to each of the randomly generated points, then collected fungal samples. At each location, using an ArcGIS Survey123 app on their smartphones, field staff collected the coordinates for the actual sample location and entered key information about each test, including the Point ID, serial number of the fungal test, a description of the sample site, and a photo of the sampling location. Smartphones have a nominal locational precision of approximately 20 feet for horizontal coordinates. Elevations were not collected. Three samples were taken at 20 of the points for repeated measurements in the same locations to determine the reliability the testing.

Results of fungal testing were received from Hayes Microbial Consulting in a report in PDF format. The data for Baudoinia species (whiskey fungus) results for fungal spore estimates and mycelial estimates were copied to an Excel spreadsheet. The data showing actual sampling locations, associated information and photos were downloaded from the Survey123 app in geodatabase format. The attribute data was cleaned and any discrepancies between the two data sets (including errors in serial numbers) were noted in the entry for each point and reconciled.

To conduct the spatial analysis, the testing results spreadsheet was joined to the Survey123 data using the Point ID field as an index, and the resulting file was exported as a new feature class. Additional field were added to the attribute table to identify repeated samples, and they were assessed for variance to determine the degree of uncertainty among the results.

Two maps were created with the point layer symbolized with graduated sizes depicting the Baudoinia sp. spore range estimates and mycelial estimates.

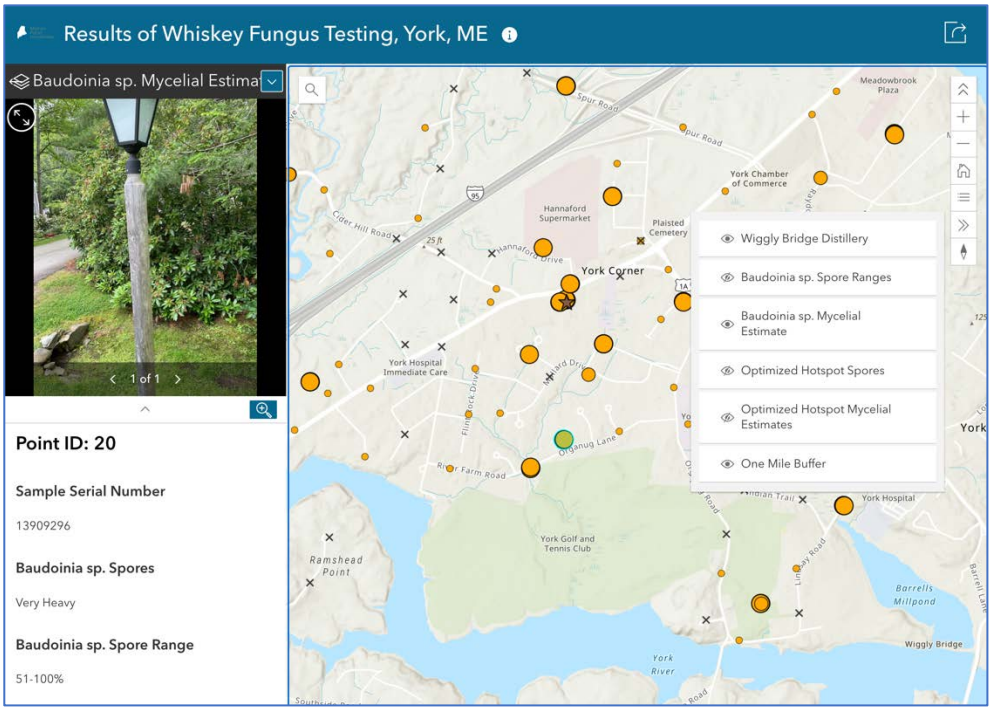
Once the point data was complete, statistical analysis was used to determine whether there is a spatial pattern in spore and mycelial distribution and to predict the distribution of spores and mycelia throughout the study area within one mile of the distillery. For all statistical analysis, the input values for the spore estimates were derived from the minimum of each reported range of spores detected (very heavy = 10,000, heavy = 1000, moderate = 100, light = 10, rare = 1, ND = 0). The input values for the mycelial estimates were derived by ranking the four ranges (many = 3, few = 2, trace = 1, ND = 0).

To determine whether hotspot analysis would be statistically valid, the Spatial Autocorrelation (Global Moran's I) tool was used to determine whether spore concentrations and mycelia were statistically significant clustered. Since clustering was significant, an Optimized Hotspot Analysis was conducted to determine locations of points within statistically significant clusters.

To create a prediction of distribution, both variables were interpolated using Empirical Bayesian Kriging, a geostatistical spatial estimation tool. This method has been found to be the best for predictions distribution of airborne particulates such as fungal spores (Morillo et al., 2022) between sample locations. The interpolation produced a raster layer with a 5-meter cell size clipped to the one-mile buffer for each variable—spores and mycelia. The interpolated rasters were symbolized using a red-yellow-blue color scheme to signify "hot and cold" areas. The standard error rasters were symbolized using a red color gradient.

Results:

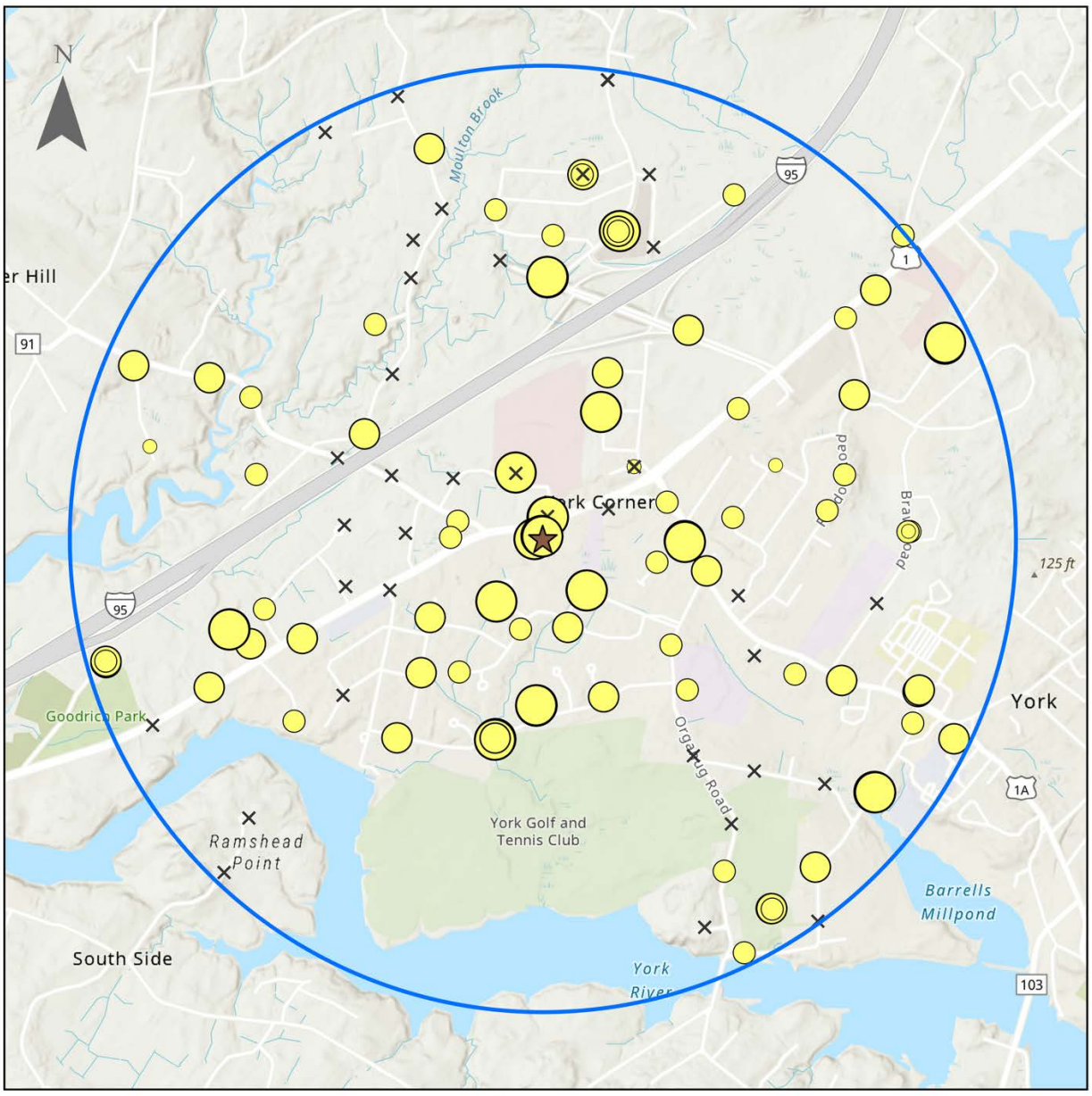
An interactive online map applications allows the user to explore the results of each sample and examine the results of the hotspot analysis. The interactive map can be accessed here:



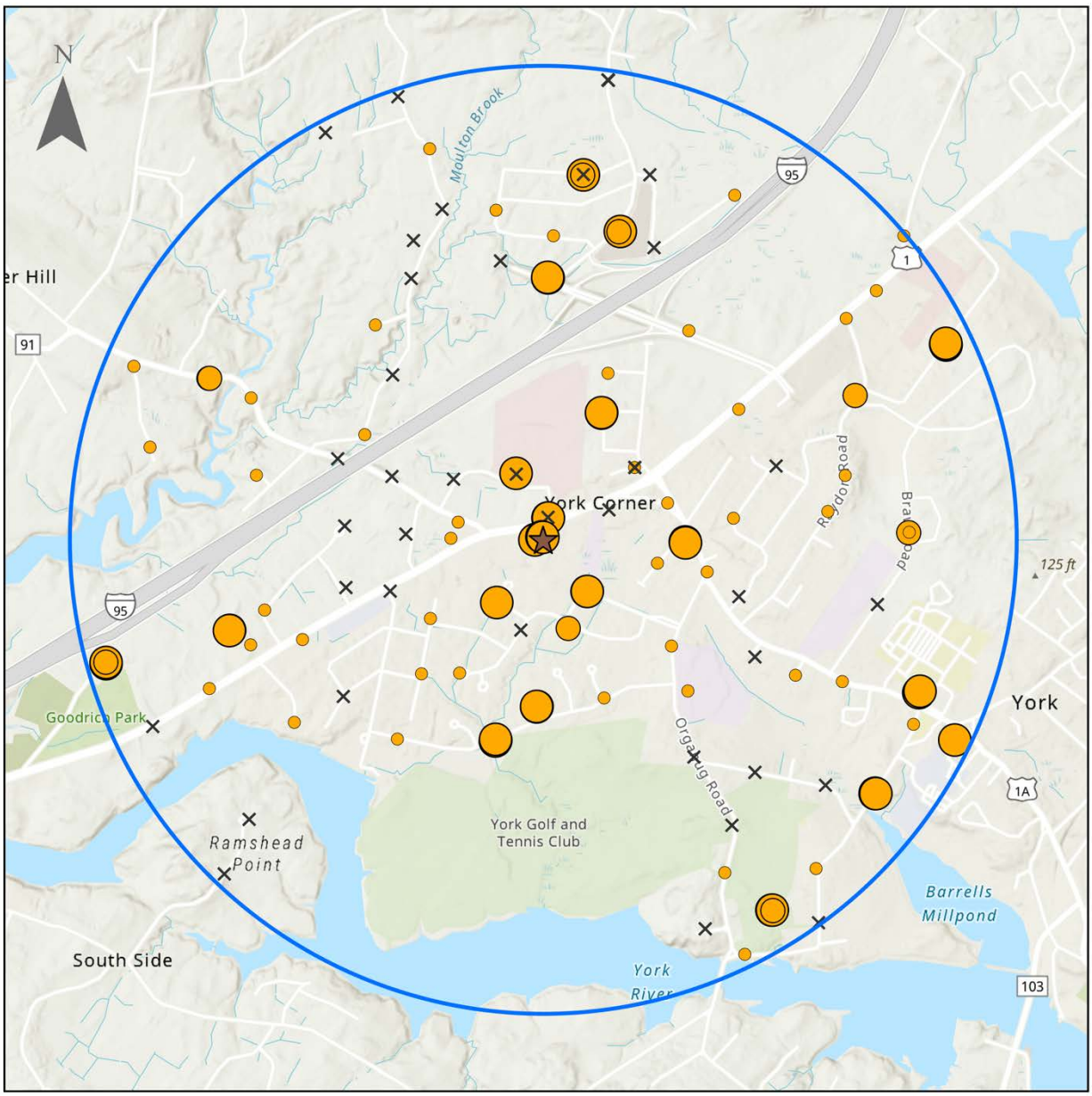
https://ums.maps.arcgis.com/apps/instant/attachmentviewer/index.html?appid=edc5ba49e15647d481b1c22e1963a52f.

Figure 1 (left) shows a screenshot of the interactive, web-based map depicting results in four layers, including points representing test results for spores and mycelial estimates, as well as hotspot analysis results for both variables. Users may use the tools in the upper left to zoom and turn layers on and off.

Map 1 below shows the results of spore samples with graduated symbols.



Map 2 below shows the results of mycelial samples with graduated symbols.



Baudoinia sp. Mycelial Estimate

- ND
- Trace
- Few
- Many

Wiggly Bridge Distillery

One Mile Buffer

Feet

0 1,000

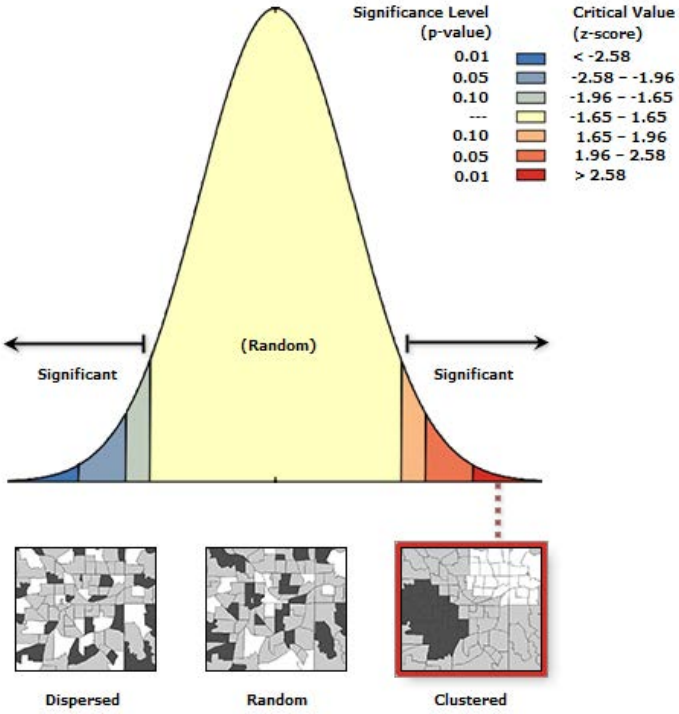


Figure 2 (left) is a graphical depiction of the output of the spatial autocorrelation analysis for spore sample results.

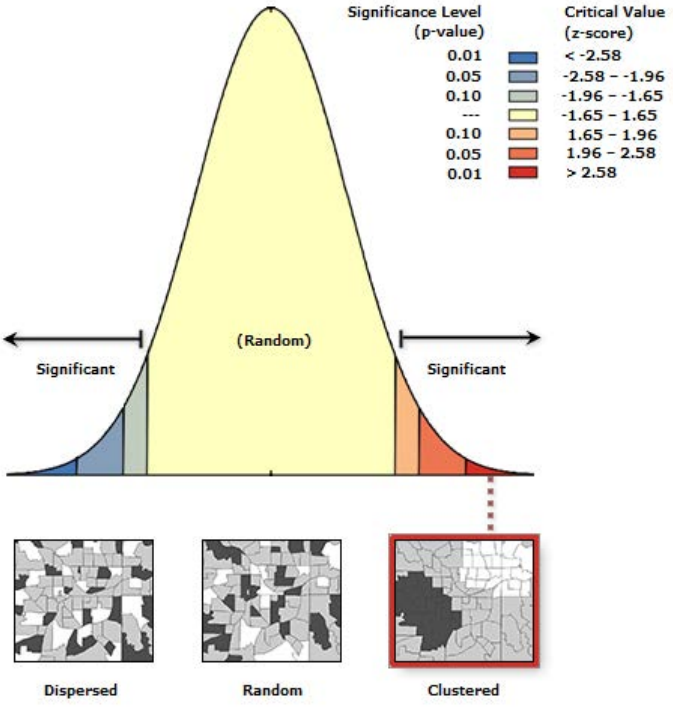
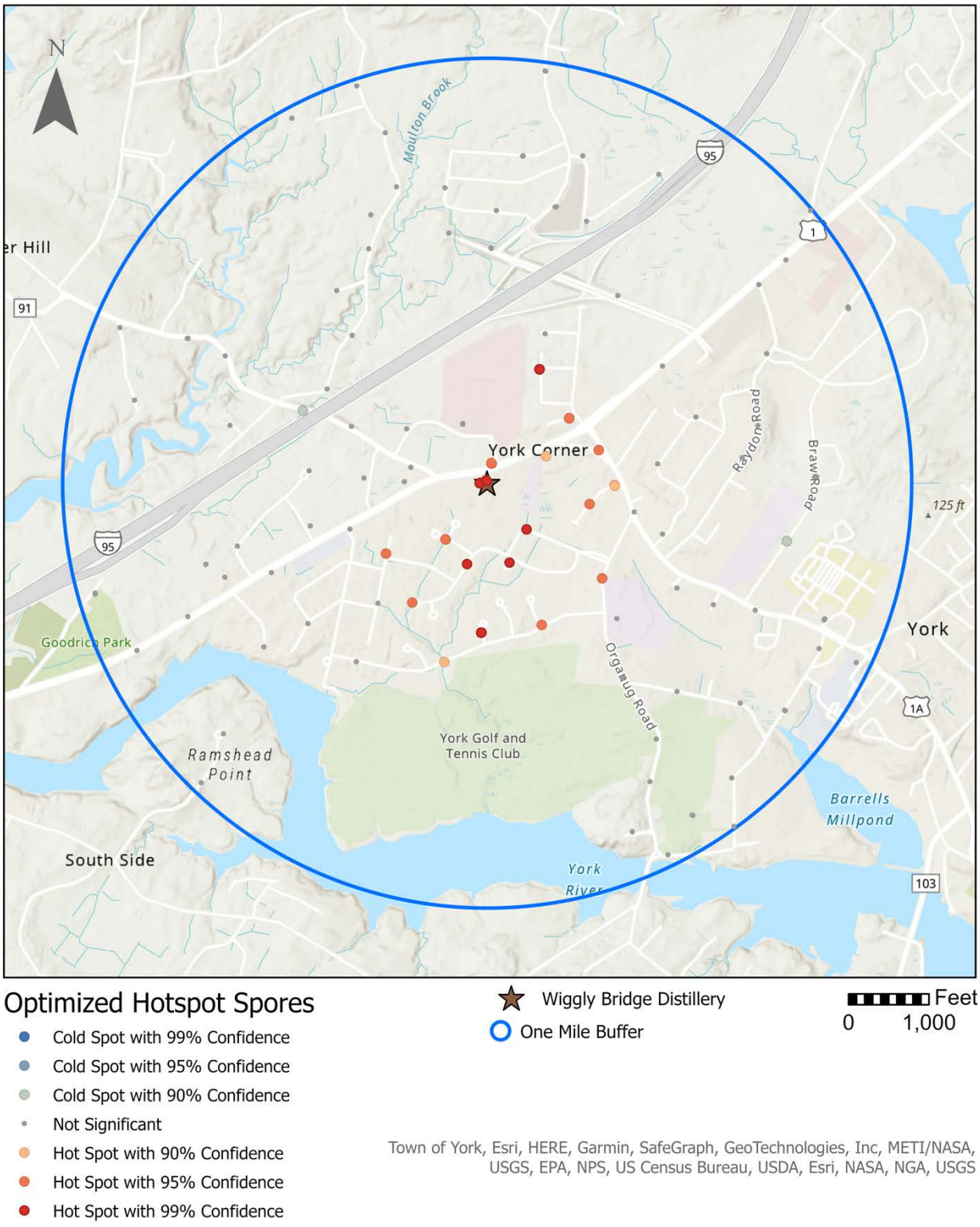


Figure 3 (left) is a graphical depiction of the output of the spatial autocorrelation analysis for mycelial sample results.

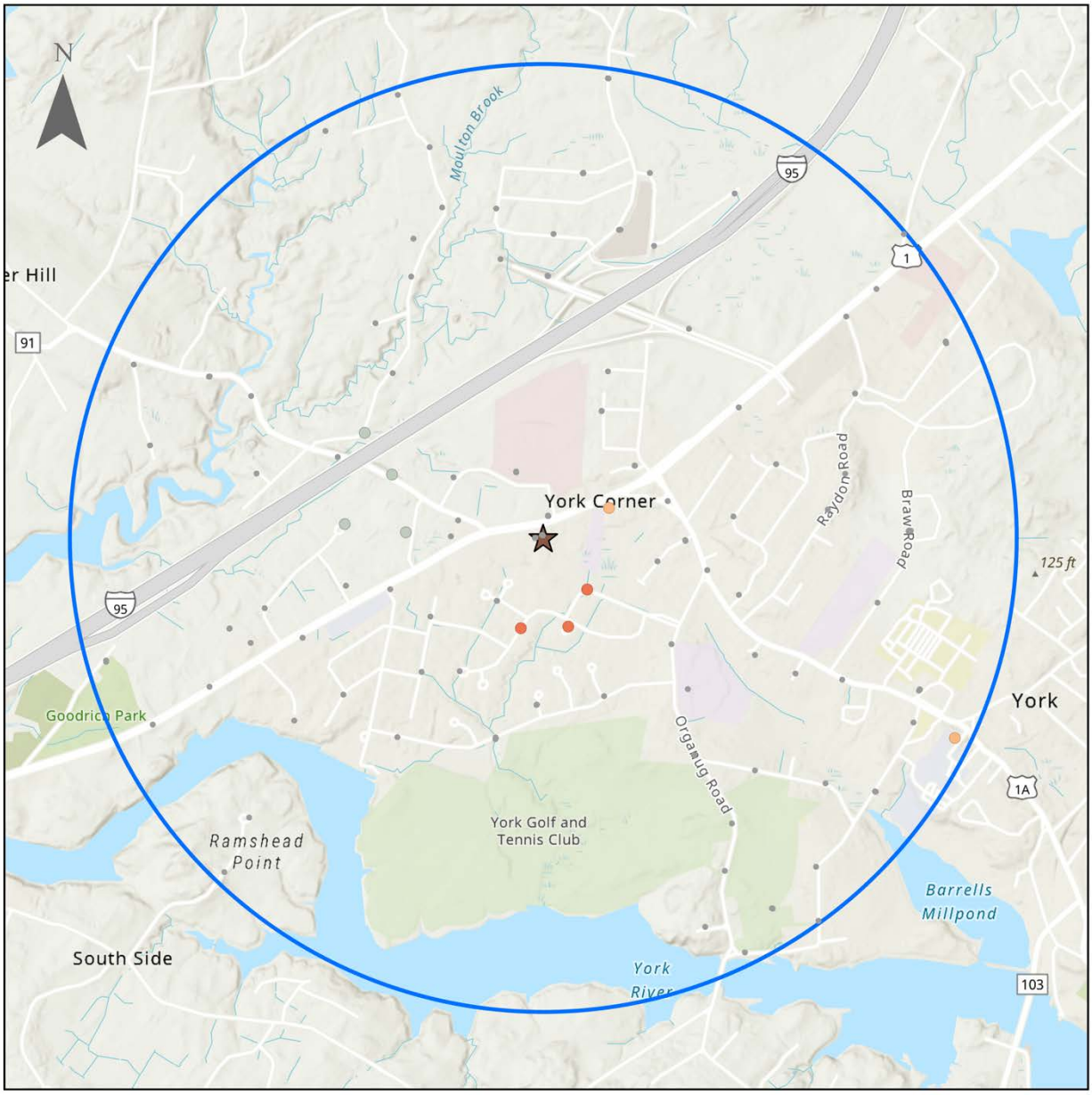
Results of spatial autocorrelation analysis of spore samples show a very high degree of clustering. Given the z-score of 7.93 and the p-value < 0.0001, there is a less than 1% likelihood that this clustered pattern could be the result of random chance. Similarly, spatial autocorrelation analysis of mycelial samples also shows a high degree of clustering. Given the z-score of 8.33 and the p-value < 0.0001, there is a less than 1% likelihood that this clustered pattern could be the result of random chance.

Hotspot analysis shows that the clusters are centered on the Wiggly Bridge Brewery.

Map 3 below shows the results of the optimized hotspot analysis for the spore samples with highly significant clusters centered on the brewery.

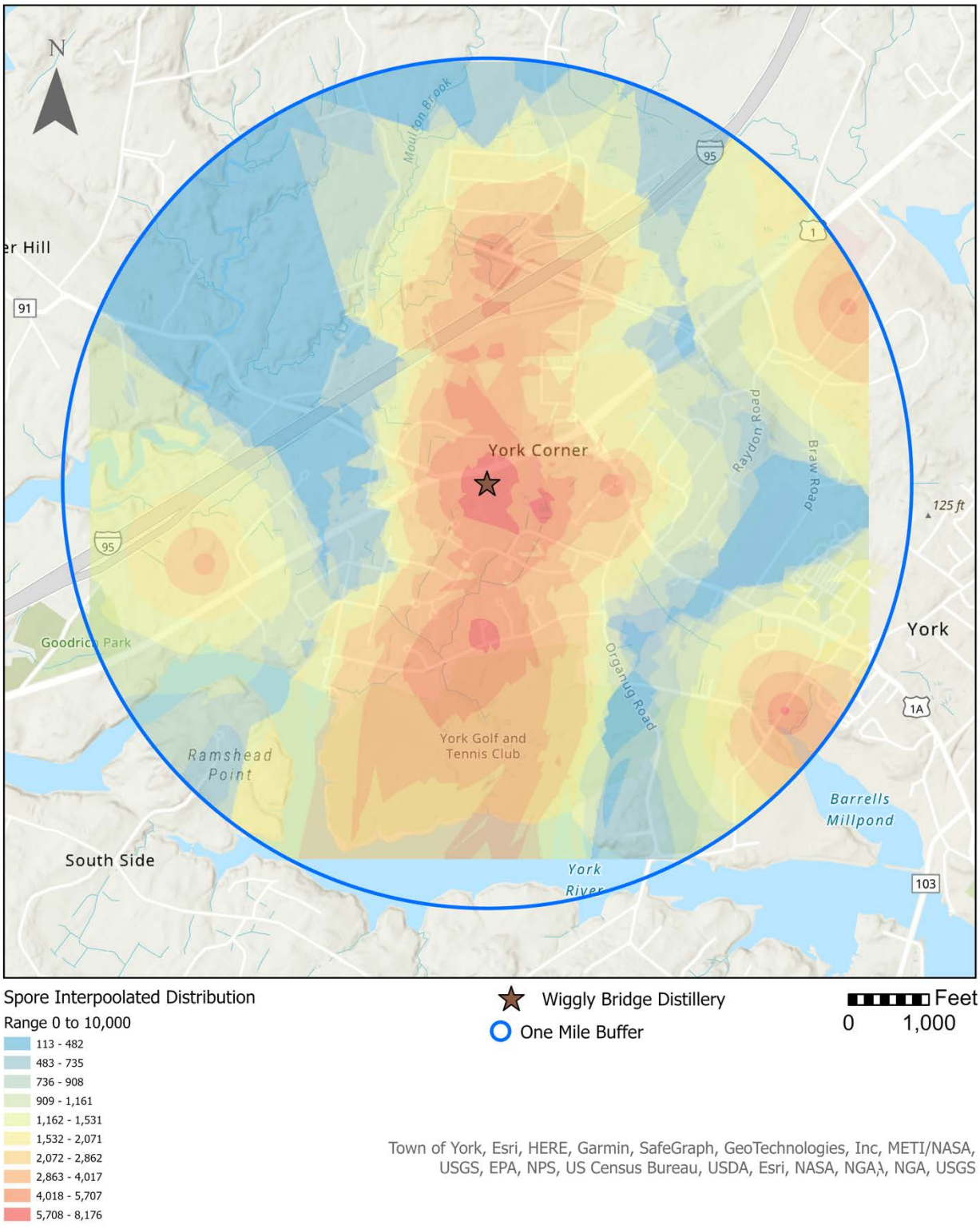


Map 4 below shows the results of the optimized hotspot analysis for the mycelial samples with significant clusters centered on the brewery.

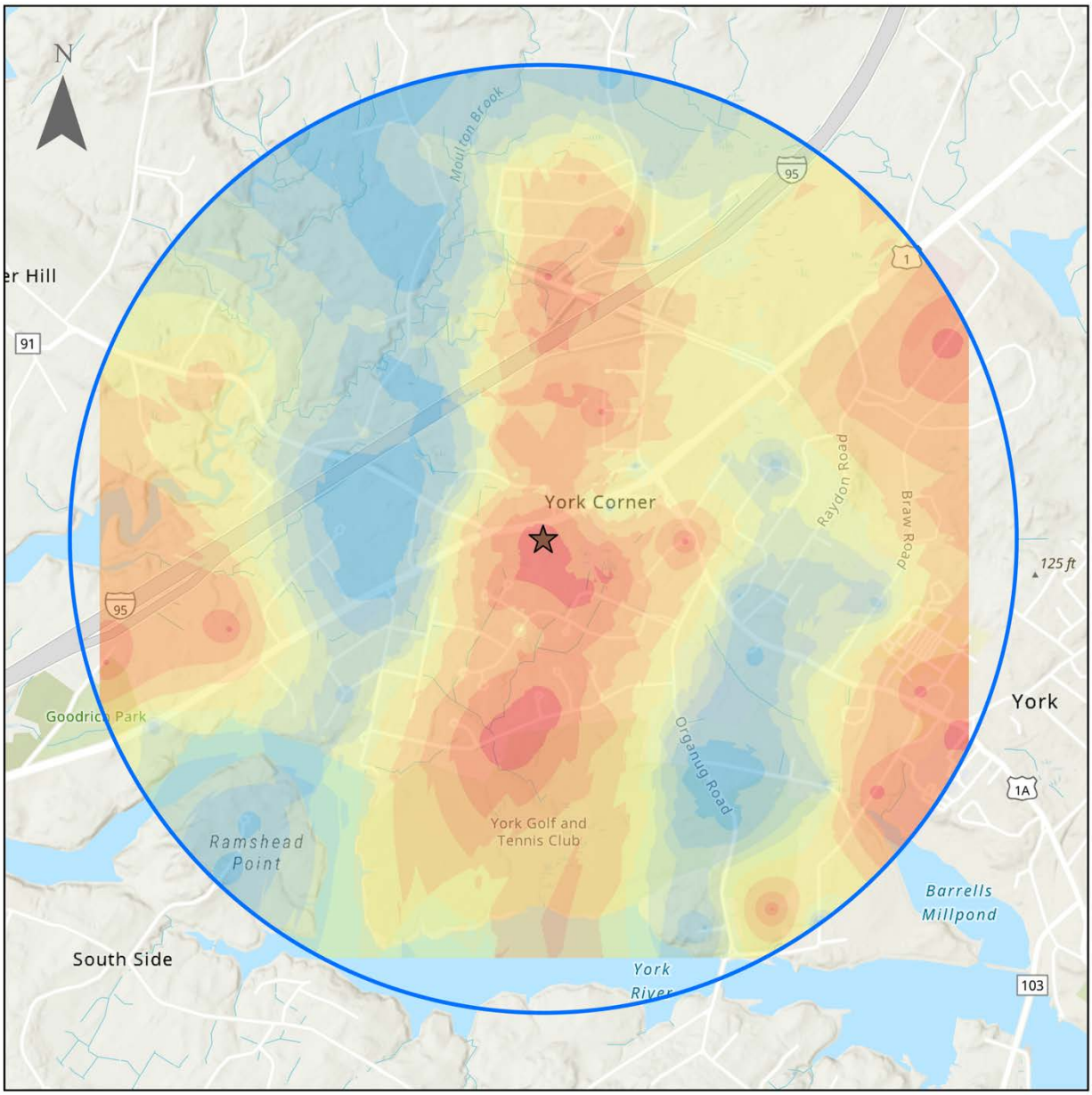


Results of the interpolation predict a roughly north/south pattern of distribution of spores and mycelia, based on the sampled data.

Map 5 below shows the results of the Empirical Bayesian Krige interpolation for the spore samples.



Map 6 below shows the results of the Empirical Bayesian Krige interpolation for the mycelial samples.



Conclusion:

The statistical analysis showed a significant cluster of whiskey fungus spores and mycelia centered on the distillery. Based on the spatial analysis, it is highly likely that the distillery is the source of this cluster. There is a somewhat statistically significant hotspot of mycelia outside the area surrounding the distillery to the southeast; it is impossible to determine if the distillery is source of this additional cluster.

Works Cited

Morillo, M. C., Martínez-Cuevas, S., García-Aranda, C., Molina, I., Querol, J. J., & Martínez, E. (2022). Spatial analysis of the particulate matter (PM10) an assessment of air pollution in the region of Madrid (Spain): Spatial interpolation comparisons and results. *International Journal of Environmental Studies*, 1–11. https://doi.org/10.1080/00207233.2022.2072585