Visualizing the changing distribution of blacklegged ticks and Lyme disease in New Brunswick

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Abstract

Understanding the spatial distribution of tick occurrences in the Maritime provinces is an essential prerequisite for raising public awareness of ticks and Lyme disease and, consequently, preventing the spread of the disease. During this collaborative project, a web-based geographic information system (GIS) was developed in order to make it possible for members of the public to view the spatial information collected by Dr. Vett Lloyd's lab at Mount Allison University. The displayed information encompassed geographic records of three species (*Dermacentor, Ixodes cookei, and I.* scapularis), gathered between 2012-16, as well as information about cases of canine Lyme disease. In the case of canine Lyme, a special hotspot analysis was conducted using a kernel density algorithm implemented in R and ArcGIS. This study also involved two sessions of preliminary user acceptability testing, conducted on August 3rd and August 16th, which will be used to make final changes to the information portal prior to public release and further formal assessment as part of my Honours Thesis. Feedback solicited during the user acceptability testing confirmed that the Mount Allison Tick Information Portal is an effective way to communicate the spatial patterns of ticks and Lyme disease, and will address an significant public information gap. It is anticipated that the information portal will raise public awareness and help to lower the risk of Lyme disease transmission via tick bites across the Maritimes.

Acknowledgements

- Canadian Lyme Disease Foundation
- Mount Allison University
- New Brunswick Environmental Network
- Lyme Research Network

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1.0 Introduction

In the temperate world, Lyme disease is the most commonly reported vector borne disease (Ogden et al, 2014, pp. 74). There is increasing public health and environmental risk with the expansion of suitable tick habitat throughout the Maritime provinces, Nova Scotia, New Brunswick and Prince Edward Island. Lyme disease is caused by the bacteria, *Borrelia burgdorferi* and is transmitted by ticks which acquire it while feeding on infected hosts such as rodents or birds (Ogden et al, 2014, pp. 74).

The Maritime provinces are increasingly at risk due to the expansion of the blacklegged tick in response to warmer temperatures. In time, once sufficient numbers of ticks and infected hosts co-occur, Lyme disease can become endemic in a given area. There are currently a number of recognized endemic areas in New Brunswick, such as the Saint John / Grand Bay area, and Grand Manan Island (Ogden et al. 2014). The average incidence of Lyme disease in New Brunswick from 2005-2012 (incidence being cases/100,000 people), was 0.27, in 2011 in Nova Scotia the incidence was 5.8 (Habegger, 2014).

There are some unique geographic properties that make up the Maritime provinces. Nova Scotia is made up of a rugged coastline, it has hills and low mountain ranges. Nova Scotia's mainland is also home to many freshwater lakes. The Appalachian mountain ranges continue up through New Brunswick. Throughout New Brunswick there are lowlands, rolling hills, and highlands. Nova Scotia and New Brunswick are both along the Bay of Fundy, known for its high tidal range. Prince Edward Island is low-lying, with some rolling hills (worldatlas.com, 2017). Ticks are often associated with and found in woodland habitats but can also be dispersed in a variety of neighbouring habitats by hosts such as rodents and birds

(Leighton et al, 2012). Many species of birds migrate through this region. The Maritime provinces have an abundance of suitable habitat for ticks to live and thrive.

There is an established body of literature which provides evidence that ticks are expanding their range northward. In 2012, Leighton and colleagues reported that *I. scapularis* has expanded its range to southern Canada [from the United States] and that expansion is increasing rapidly (Leighton et al., 2012). In the same study, degree days over 0^{o}C, a measure of energy availability, was the one of the most important variables in determining environmental suitability for ticks. This suggests that with increased climate warming, tick range expansion can only increase (Leighton et al., 2012). A current analysis recently conducted by Lieske and Lloyd (2017), based on point data of spring adult ticks recovered from 2014-16, shows that blacklegged ticks are widespread throughout southern New Brunswick, and the projections presented provided in that paper point to significant northward range expansion by 2080.

Geographic information systems are “automated systems for the capture, storage, retrieval, analysis, and display of spatial data” (Clarke et al,1996, pp.85). The use of GIS in visualizing spatial problems is extremely valuable. According to Clarke et al, geographic information systems are emerging as innovative and important parts of many public health projects (Clarke et al,1996, pp.85). Some of the advantages of using geographic information systems are the ability to handle tasks that are repetitive and comparing spatial data from different sources, and spatial areas, also speed and ability to compile large amounts of data (Moore and Carpenter, 1999). The use of GIS in this project was essential to be able to show visually the extent of tick distribution across the Maritime provinces. The map page on the website is the main focus of the Maritime tick information portal. It shows all tick occurrences submitted to Mount Allison University and gives the public the opportunity to visually see the distribution of ticks (Figure 1).

Identifying areas that are hotspots for ticks plays a key role in learning about distribution patterns throughout the province of New Brunswick as well as can help address questions concerning public health risk. It is valuable to be able to visualize these areas and there is potential benefit for policy makers, health professionals and increased awareness for the public. One of the difficulties with raw point data is that they can be difficult to understand across time and space and overwhelming because of quantity of points (Martin and Ralphs, 2013). According to the International Association of Crime Analysts, The National Institute of Justice outlines two general ways to identify a hotspot, using Geographic Information System (GIS) maps and applying statistical tests (Paynich, 2013).

Hot spot analysis has been used in many scientific studies, and has been greatly beneficial in the analysis of crime. It can help to signal presence or possibility of crime as well as indicate patterns of occurrence (Paynich, 2013). It has been performed with many different techniques, kernel density estimation just being one of many methods. Density estimation helps to approximate the concentration of tick occurrence and not just the number of occurrences happening in one specific area. It examines occurrences found within a specified search radius which works to estimate a cell density value (Paynich, 2013). Kernel density estimation (KDE) works in a similar way but instead of just adding up the occurrences within a specified radius, a kernel is also applied to every cell, this helps take into consideration intensity of events as a part of density estimation (Figure 2) (Paynich, 2013, Lin et al., 2010). Hotspot mapping is sensitive to some specific user-defined parameters such as type of estimation technique, method of interpolation, bandwidth, and cell size (Hart and Zandbergen, 2014, Paynich, 2013). This can affect the predictive accuracy of the maps and models created. Hotspot identification can also occur on various geographic levels, for example, addresses, blocks, neighborhoods, or even cities. KDE generalizes and smooths discrete data points so that a continuous surface area can be produced and visualized as a hotspot map (Hart and Zandbergen, 2014).

Studying the distribution of ticks and where range expansion is happening is of great importance to the Mount Allison University Lyme Research Network. Using location data gathered from the passive surveillance program, visualization of where ticks are located is accessible using GIS. According to Ogden and colleagues in 2014, it is of great importance to study the spatial distribution of ticks in Canada, because geographic occurrence defines where people acquire Lyme disease (Ogden et al, 2014, pp. 75). The purpose of the Maritime Tick Information Portal is to provide an accessible presentation of the point data received through passive surveillance at Mount Allison University. The data presented on the map page is point data, and each point represents a specific tick that has been submitted to the Lyme research network. Each tick is accompanied by data that tells the user what the *Borrelia* status is, what the life stage of the tick was and the species of tick it is. The study includes ticks submitted from passive surveillance from all three Maritime provinces: Nova Scotia, New Brunswick and Prince Edward Island. Specimens are submitted by physicians, veterinarians and the general public. These specimens are tested for Lyme disease in Dr. Lloyd's lab at Mount Allison University.

The purpose of this project is to gain a better understanding of spatial distribution of ticks throughout the Maritime provinces. Through creation and use of a web-based geographic information system, the distribution of ticks can be clearly seen and analyzed. The data was collected through passive surveillance and spans 2012-2016 and covers three main tick species, *Ixodes scapularis, Ixodes cookei, and Dermacentor sp.* The *Ixodes scapularis* tick, also commonly called the deer tick, is known to be the main vector that can transmit the *Borrelia* bacteria that causes Lyme disease. The purpose of this website is to make information about tick distribution in the Maritime provinces accessible to the public. Tick range expansion and Lyme disease occurrence has become an increasingly important public health problem.

The main objectives of this study are describing the current distribution of ticks throughout the Maritimes, identifying where Lyme disease occurs in dogs in New Brunswick ("hotspot analysis"), and determining whether web based GIS are effective ways in communicating spatial public health problems. The objectives are based around perceiving and communicating point patterns of ticks to the general public.

Ticks have increasingly become a cause for concern in the health world. It is important that citizens have access to the data that is being collected at Mount Allison University and are able to view tick occurrences that have been submitted in and around their communities.

2.0 Methods

2.1. Design Considerations for Implementation of the Web-based Information Portal

The creation of the web-based geographic information system (GIS), was hosted using ArcGIS server (ESRI 2017), with spatial information accessed and processed on the client-side by any ordinary web browser using the Java Script programming interface provided by ESRI (see https://developers.arcgis.com/javascript/ for more information). The information portal, which will eventually be hosted using the following proposed URL: http://www.maritimetickmaps.ca stands to be a highly effective means to communicate tick distribution in the Maritimes due to a combination of visual appeal as well as ease of access. Anyone with an internet connection and a web browser can access the information portal, and it was designed from the onset to dynamically reconfigure its appearance depending upon the user's platform. For instance, the main page icons rearrange themselves depending upon the size of the user's computer screen, such that it will work differently on a smartphone compared to a widescreen desktop monitor. The mapping pages are highly interactive, with users able to turn layers "on" or "off" in order to show or hide particular years worth of information. Each data point on the map can be individually clicked on to reveal information about the *Borrelia* status of that particular tick, as indicated by the results of the OspA and Flag B genetic testing. In addition to being able to zoom in and out of the map, users can change the "base map" layer from a street map view to an aerial image view, and can produce their own customized maps which they can print as a .pdf document. Other functions that make this web portal easy to use as an effective communication tool are clear instructions and descriptions, links to helpful resources and other websites such as the Lyme Research Network website and Dr. Vett Lloyds lab website.

2.2 Data Sources for Information Portal

The information portal consists of conventional web pages with textual information, as well as specialized map viewers. The conventional pages were intended to share information about the link between *Borrelia burgdorferi* and Lyme disease*,* guidelines for identifying ticks, background on the passive surveillance protocol used to gather tick specimens and assess *Borrelia* status, and links to the Lyme Research Network website and Dr. Vett Lloyds lab website (Appendix 1).

The map viewing tool provided the following functionality: (1) a basemap, either in the form of a street map with named streets, highways, and urban areas, or an aerial landcover image; (2) a layer selector tool, with an "eye" symbol that can be toggled by the user to either show or hide layers, including different years and species of ticks; (3) a legend tool which provides a key to the symbols for only the selected layers visible on the map, and is dynamically updated at any point the status of the selected layers changes; (4) an interactive feature identifier, which displays any associated information stored with a given tick point, including tick species, sex and life stage; and (5) an automated .pdf map generator users can use to produce custom maps they can be shared with friends and colleagues.

Data points originated as individual tick records submitted to Dr. Lloyd's tick monitoring program between 2012-16. The tick species included *Dermacentor*, *Ixodes cookei, and Ixodes scapularis.* Records associated with recent travel activity were screened out, as were tick records for which an approximate geographic position could not be ascertained. For instance, some tick specimens were accompanied by too little supporting information or too vague a geographic reference for geographic coordinates to be assigned. It is important to note that one final geoprocessing task was applied to all point locations prior to uploading to the server: easting and northing coordinates were randomized +/- 500m, resulting in an average "jiggle" of 750m to every point. This was done as a privacy protection measure for all individuals who have submitted ticks to the Mount Allison Lyme Research Network.

The website also includes predicted distribution maps of *I. scapularis* partially based on climate projections provided as part of the IPCC 5th Assessment Report. The details of the models used to generate the predicted occurrence maps are available in Lieske and Lloyd (2017). The two climate variables used in the Lieske and Lloyd (2017) models include degree days < 0^0C and mean annual precipitation (mm). Values for these two climate variables, downscaled to a 1-km resolution, were based on a carbon-stabilized future scenario (RCP 4.5), and a continual emissions growth scenario (RCP 8.5), for three future time periods: 2020, 2050, and 2080.

2.3 Preliminary User Acceptability Assessment

Two user acceptability sessions were held to gather feedback on the interpretability and ease-of-use of the information portal on August 3 and August 16, 2017. A two-page questionnaire was distributed to participants, who were presented with the “task” of identifying where tick locations are concentrated across the Maritimes and specifically New Brunswick (Appendix 3). Some questionnaires were completed fully, all questions answered and valuable feedback was given and taken into consideration when making changes to the information portal. Many other questionnaires were not fully completed but valuable conversations had, and all feedback was taken into consideration when making alterations to the online information portal.

2.4 Hotspot Analysis for Canine Lyme Disease Cases

A kernel density estimation (KDE) algorithm was applied to the canine Lyme disease points (Silverman 1986, ESRI 2017). done on occurrences of dogs that tested positive for Lyme disease in New Brunswick. This data is separate from the point data and analysis specifically focused on canine Lyme disease. The cluster analysis of canine Lyme disease used the statistical program R, to determine the kernel bandwidth and ArcGIS to perform the cluster analysis and to visually represent “hotspots” with contour lines. The ks library in R was used to determine the correct bandwidth needed to get an accurate representation of data in the set of dogs with Lyme disease. Once the correct bandwidth is known that measurement can be used in ArcMap to create a kernel density map of where the concentrations of dogs with Lyme disease are.

This research is not inclusive of all tick occurrences across all of the Maritime provinces. It specifically shows where people are submitting ticks to the Lyme Research Network at Mount Allison University. This does not mean that where there is no point data, there are no ticks. There could still be ticks present in these areas, but they have not been reported in this passive surveillance program.

The advantage of passive surveillance is that it provides a snapshot of the establishment of ticks across Canada through time, it gives a good indication of where people are finding ticks, either on themselves or on animals.

3.0 Results

3.1. Maritime Tick Information Portal

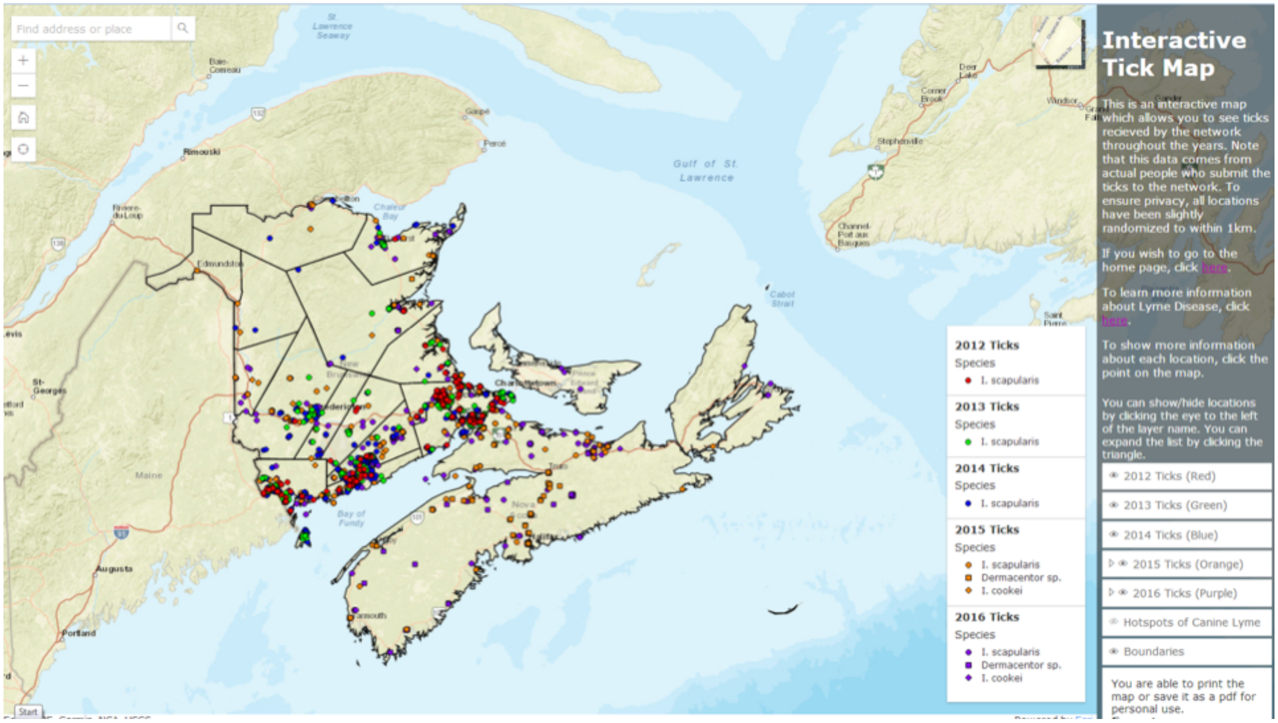
The central purpose of this website is to provide a way for the public to understand the current spatial distribution of ticks in the Maritimes, particularly New Brunswick. The Information Portal accomplishes this by displaying randomized points on the map, each of which represents a specimen voluntarily submitted by participating Veterinary clinics or members of the public to the tick testing program carried out by the Mount Allison Lyme Research Network and Dr. Vett Lloyd's lab. The information that can be extracted from the individual tick points includes where ticks have been submitted throughout, primarily New Brunswick, as well as Nova Scotia and Prince Edward Island. This point data can give evidence towards where ticks are concentrated across these provinces. Other information that can be derived from the individual tick points are species of tick that is found, as well as the sex and life stage of these specimens. With each tick occurrence, there is data for whether that specific tick was tested positive or negative for the *Borrelia* bacteria that can cause Lyme disease. These positives show the presence of the *Borrelia* bacteria, not necessarily a positive for the disease.

The map page has many functional features, such as switching between basemaps, users can view a street map or a with named streets, highways, and urban areas, or an aerial landcover image (Figure 3). Layers can be selected and turned on and off using the "eye" selector tool which enables users to show or hide layers based on years or different species of ticks for 2015 and 2016 (Figure 4). The legend tool is a useful feature for viewing a key to the symbols for the selected layers visible on the map. The legend is dynamic and updated when layers are turned on or off (Figure 5). Another useful feature is the interactive feature identifier, by clicking on specific points on the map users can find out more information about specific tick occurrences, such as tick species, life stage, sex and whether the tick was positive or negative for the *Borrelia* bacteria (Figure 6). Note that this is not an indication of Lyme disease in any individual. Along with the interactive features that make the map page functional for users, there is also an automated .pdf map generator, which allows users to produce custom maps that can be shared with friends and colleagues (Figure 7). This makes the data and information these maps provide accessible even when users may not have internet connections.

The maps created by the point data can be displayed by year – 2012-16 in the case of blacklegged ticks, or 2015-16 in the case of *Ixodes* cookei and *Dermacentor* sp. -- or all ticks at once. The default layer visible upon loading is the most recent 2016 records, for all three species, but users can interactively show or hide other years' data if they so desire by toggling the "eye" symbol in the layer list (Figure 4).

Preliminary feedback from two sessions of user acceptability testing, conducted on August 3rd and August 16, 2017, in Fredericton, New Brunswick at a Lyme disease support group with approximately 15 people present and in Sackville New Brunswick, with approximately 7 students respectively, indicated that these maps effectively communicate the spatial pattern of Maritime ticks. A few moments viewing of the maps shows the tendency for ticks to be concentrated in denser, more settled areas such as north of Saint John and along the Kennebecasis River Valley, as well as in the vicinity of Fredericton, Moncton and Dieppe, the Tantramar area near the Town of Sackville. While not explicitly stated on any of the pages of the Information Portal, the implication is that volunteered ("passive") recoveries of tick specimens is biased towards (1) locations with denser human populations, and (2) originate from individuals sufficiently motivated or concerned to go through the trouble of completing a tick submission form and submitting a specimen to Mount Allison University for testing.

The website provides links to information and resources on Lyme disease and ticks in Canada as well as future projections on where ticks will be based on climate models from the Intergovernmental Panel on Climate Change (IPCC), RCP 4.5 and 8.5 in 2020, 2050 and 2080 (Lieske and Lloyd, 2017). The information on this site is not meant to be the only source of information on ticks and Lyme disease. Its purpose is to provide spatial information about ticks that have been submitted. This website will be updated so that new tick submissions will be shown on the map page of the Maritime tick information portal.



Interactive Tick Map

This is an interactive map which allows you to see ticks recieved by the network throughout the years. Note that this data comes from actual people who submit the ticks to the network. To ensure privacy, all locations have been slightly randomized to within 1km.

If you wish to go to the home page, click here.

To learn more information about Lyme Disease, click here.

To show more information about each location, click the point on the map.

You can show/hide locations by clicking the eye to the left of the layer name. You can expand the list by clicking the triangle.

You are able to print the map or save it as a pdf for personal use.

***Figure 1**: Map from the Maritime tick information portal showing all ticks submitted to Mount Allison University through the passive surveillance program for testing at Dr. Vett Lloyds lab.*

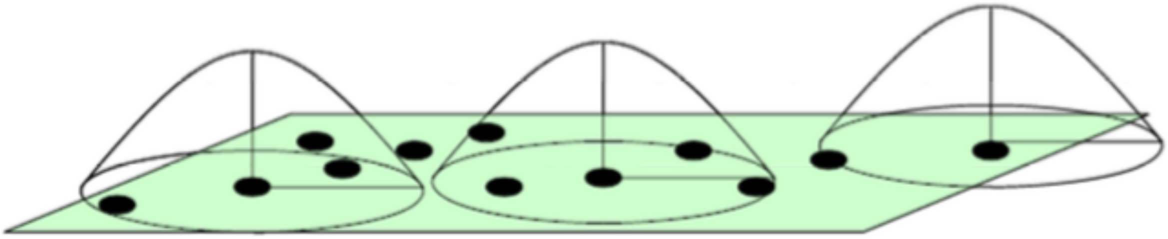
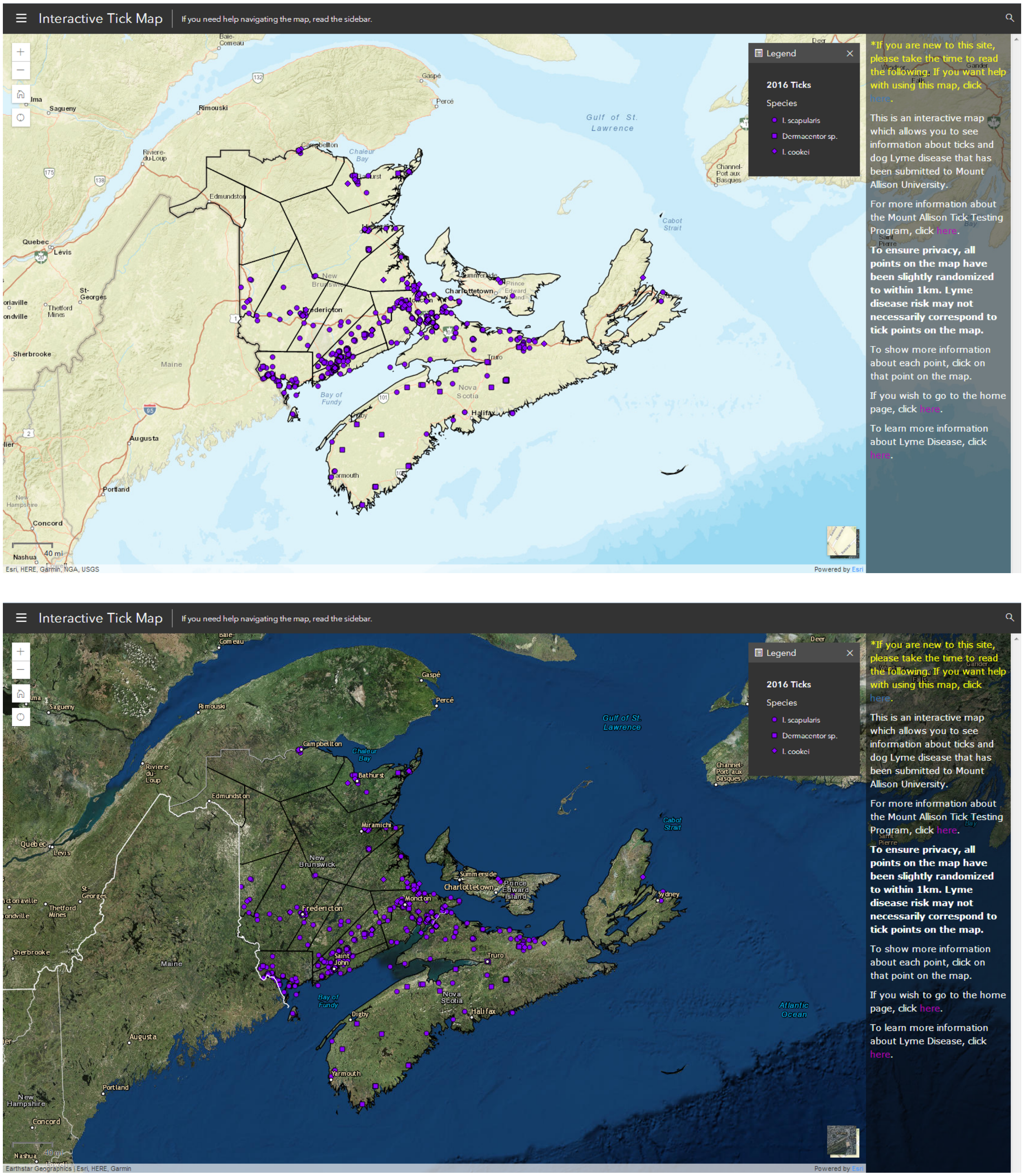


***Figure 2:** Diagram from Martin, K., & Ralphs, M. (2013). Showing the visualization of the kernel smoothing process.*



Interactive Tick Map

If you need help navigating the map, read the sidebar.

*If you are new to this site, please take the time to read the following. If you want help with using this map, click here.

This is an interactive map which allows you to see information about ticks and dog Lyme disease that has been submitted to Mount Allison University.

For more information about the Mount Allison Tick Testing Program, click here.

To ensure privacy, all points on the map have been slightly randomized to within 1km. Lyme disease risk may not necessarily correspond to tick points on the map.

To show more information about each point, click on that point on the map.

If you wish to go to the home page, click here.

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Figure 3: *Comparison of basemaps, street map view and aerial image view.*

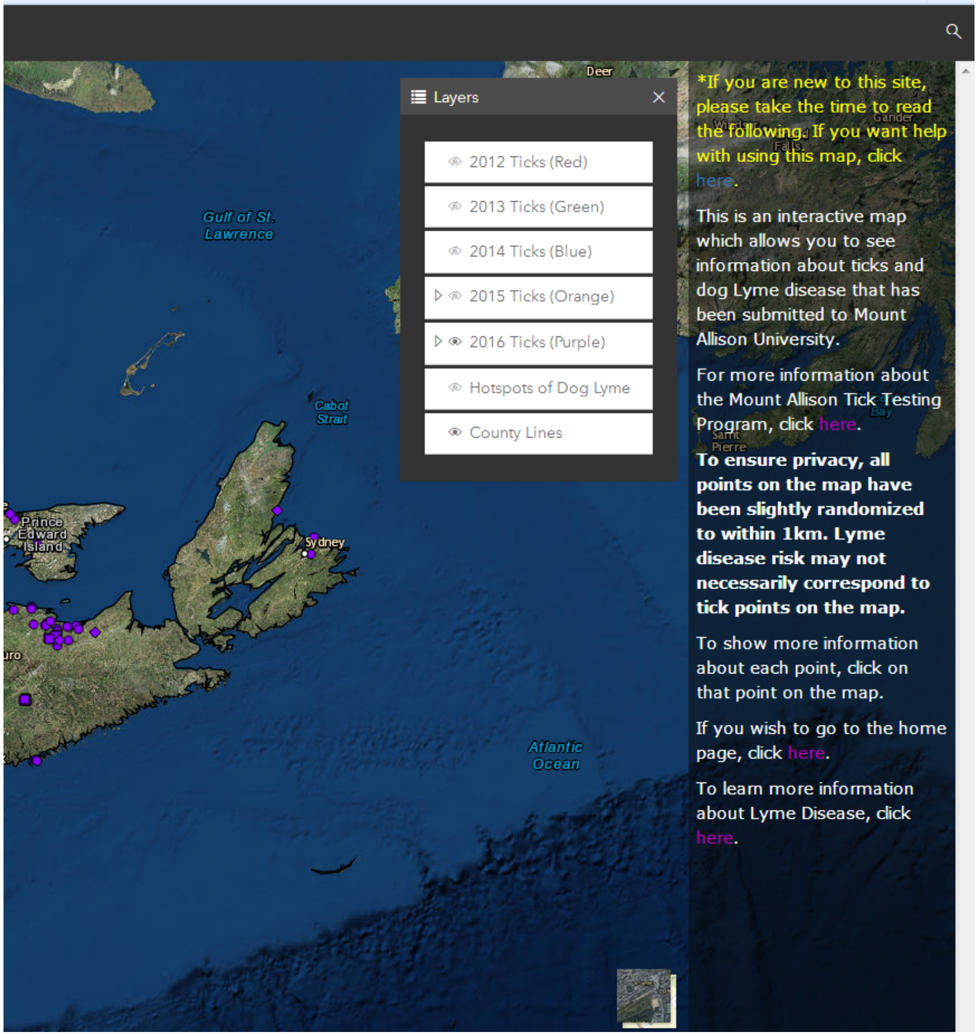

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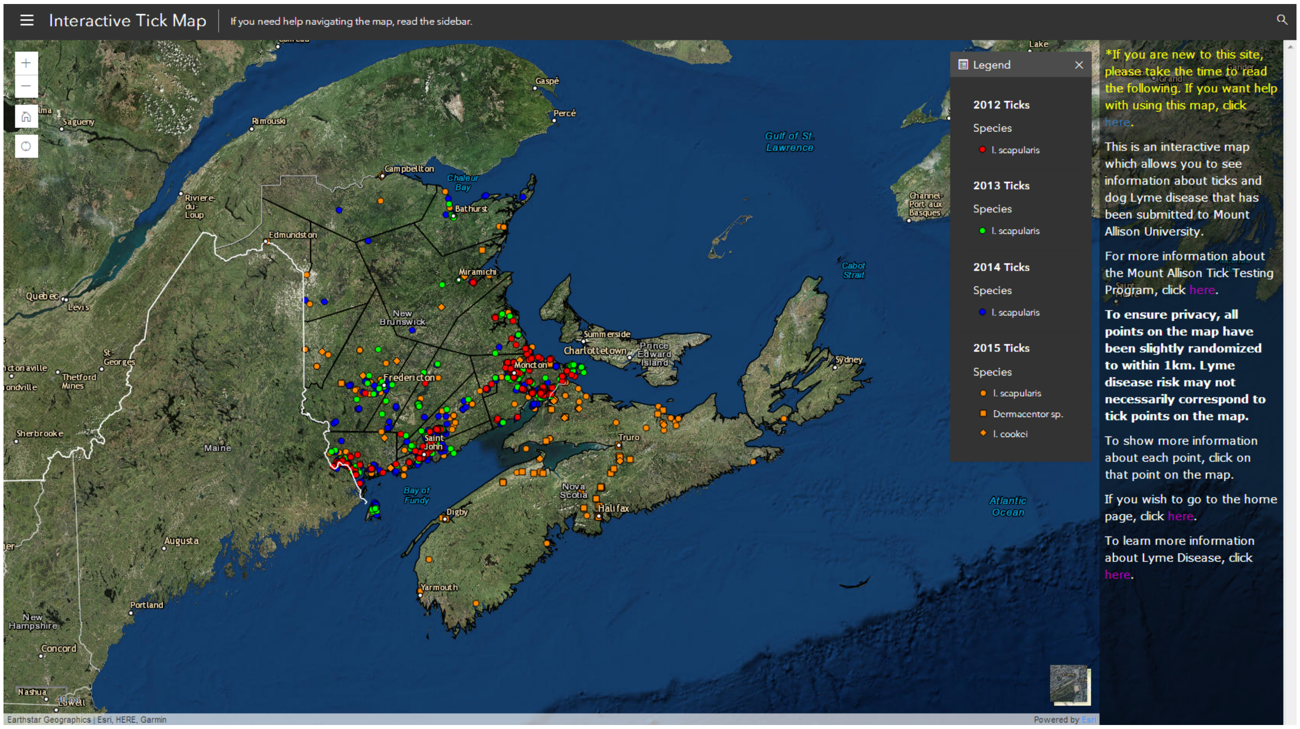
Figure 4: *Map page showing layer selector tool, the "eye" is the selector button, used to show and hide layers.*



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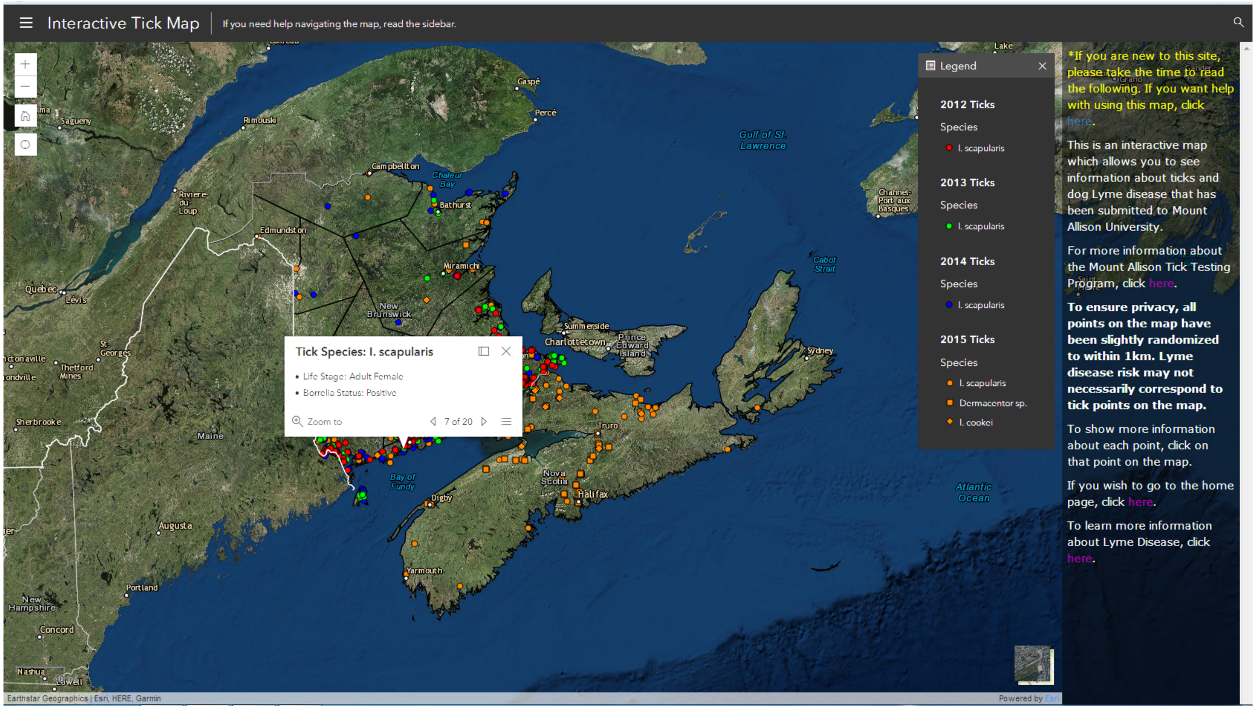
If you wish to go to the home page, click here.

To learn more information about Lyme Disease, click here.

Figure 5: *Map page showing dynamic legend feature on right had side of the map. The legend shows a key to which layers are currently in view on the map.*



Tick Species: I. scapularis

- Life Stage: Adult Female
- Borrelia Status: Positive

*If you are new to this site, please take the time to read the following. If you want help with using this map, click here.

This is an interactive map which allows you to see information about ticks and dog Lyme disease that has been submitted to Mount Allison University.

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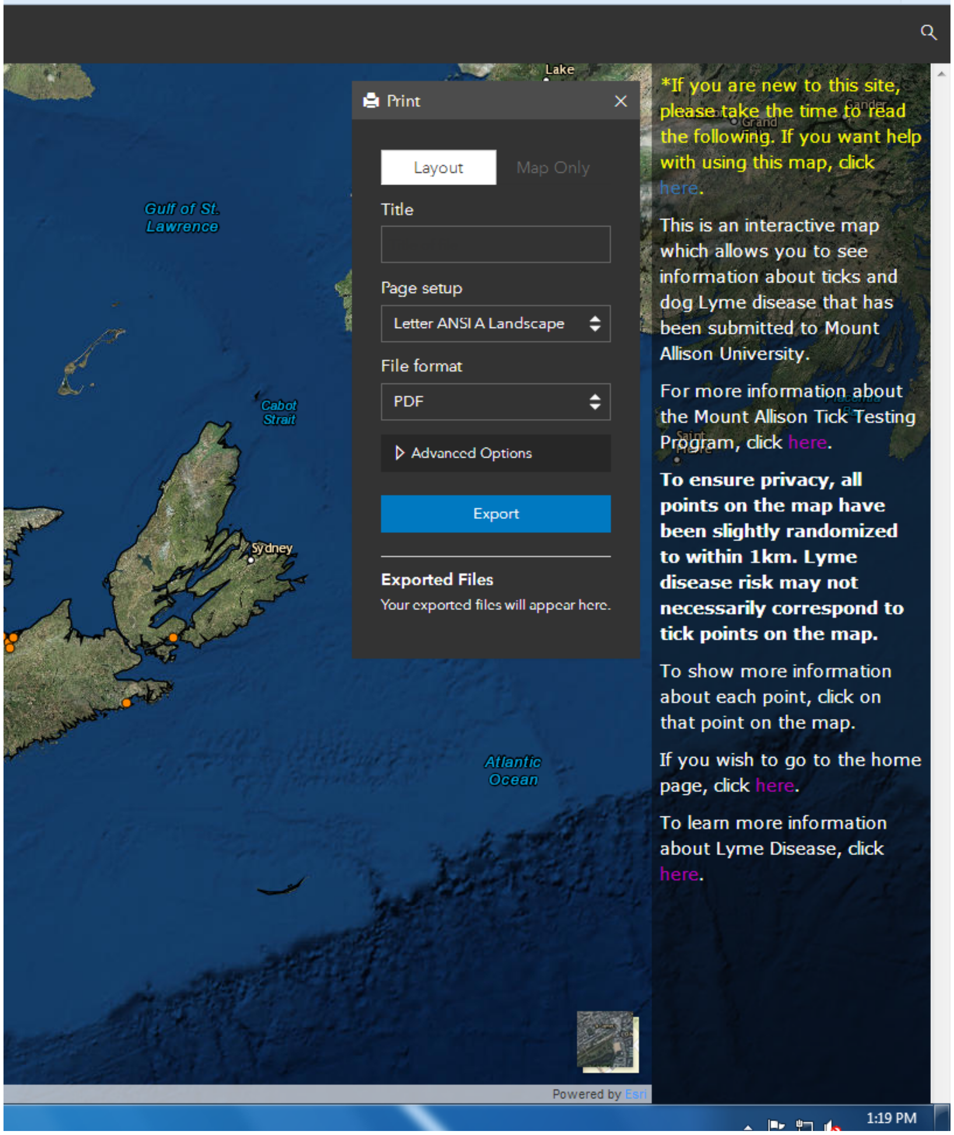
To show more information about each point, click on that point on the map.

If you wish to go to the home page, click here.

To learn more information about Lyme Disease, click here.

Figure 6: *Map page showing the interactive feature identifier.*



Title

Page setup: Letter ANSI A Landscape

File format: PDF

Exported Files
Your exported files will appear here.

*If you are new to this site, please take the time to read the following. If you want help with using this map, click here.

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Figure 7: *PDF map generator. Used to print and share data provided on the map page.*

3.2. Hotspot Analysis of Ticks and Lyme Disease

Data for the spatial analysis of canine Lyme disease came from research conducted at Mount Allison University in 2013/14 (November 2013 to March 2014, and June to October 2014) for the province of New Brunswick. With the assistance of 21 veterinary hospitals, serum samples were collected from dogs throughout New Brunswick (Lieske and Lloyd, 2017). One hundred samples were collected from each of the 7 health districts, with clinics deciding which dogs to submit for further analysis. Some dogs were excluded because they had been vaccinated for *Borrelia* in the past year, did not go outside, or were unable to be used for blood collection (too old, small, or aggressive) (Lieske and Lloyd, 2017). Consent was acquired from dog owners and information on risk exposure gathered. All samples were tested at Mount Allison University, and results were returned to clinics so that owners could be notified of the findings (Lieske and Lloyd, 2017). The data from these tests was used for spatial analysis, matching location and positive cases of Lyme disease found in dogs.

The kernel smoothing (ks) package of Duong (2017) was used for kernel density estimation (KDE) of the spatial locations of the canine Lyme cases. KDE is a powerful tool for visualizing distribution of data points, and is an ideal way to highlight clusters or concentrations of point data (Duong, 2017). The ks package uses “diagonal and unconstrained data-driven bandwidth matrices for kernel density estimation” through cross-validation, and can be applied to data with as many as 6 dimensions (Duong, 2017). Given that our data consisted of points with a Cartesian-style georeferencing system (eastings, northings), we used 2-dimensions but averaged the two estimated kernel bandwidth distances to define a single fixed kernel width in ArcGIS (ESRI 2017).

Kernel estimation is one of the most commonly used methods to estimate the density for data analysis, and is defined by the following general equation:

$$\hat{f}(\boldsymbol{x};\mathbf{H}) = n^{-1}\sum_{i=1}^{n} K_{\mathbf{H}}(\boldsymbol{x} - \boldsymbol{X}_i)$$

(Duong, 2017).

The definition of a kernel estimator is that it serves to sum the 'bumps' created by individual observations at that particular point. In the case of a univariate measurement, an observation could be an instance of a particular data value, but in a geographical context, an observation indicates the occurrence of a particular point in space (Silverman, 1986, pp. 76). The variable K is the kernel function, which determines the shape of the 'bump', and H is the bandwidth, which defines the scale or width over which 'bumps' are summed to define the overall density at that location (Duong, 2017 and Silverman, 1986).

The kernel smoothing (ks) package in R (Duong 2017) generated an estimated kernel bandwidth of 23,782.685m (or 23.8 km, see Table 1). The estimate kernel bandwidth is the average of the two output bandwidths. The script used can be seen in Appendix 4. The ks package has functions to plot the dog Lyme data and the estimated bandwidth. This plot, seen in figure 9 shows the Easting and Northing coordinates with lines showing the clusters of occurrences of dogs with Lyme disease (Figure 10).

The resulting KDE map identified concentrations of canine Lyme disease, with the intended purpose of highlighting areas which appear to pose elevated risk for *Borrelia* transmission. While the resulting hotspots indicated where Lyme disease cases are concentrated in dogs, we also expect this to be associated with an elevated risk of transmission to humans as well. It is intended that this information, once the system is made live, will assist physicians, policy makers, and the general public better understand where ticks and Lyme disease occur, and encourage the development and adoption of prevention and monitoring measures (Prasannakumar et al., 2011). As indicated in Figures 8 and 9, there were some clearly visible concentrations of dog Lyme disease cases, which generally corresponded to areas with large number of tick recoveries (Figure 8 and 9). Clusters were visible in the southern areas of New Brunswick, as well as in smaller pockets further north~~.~~ (Figure 9). The largest areas of concentration are Tantramar, Saint John, and Miramichi. The smaller concentrations are around Fredericton, and the northwestern regions of the provinces (Figures 8 and 9).

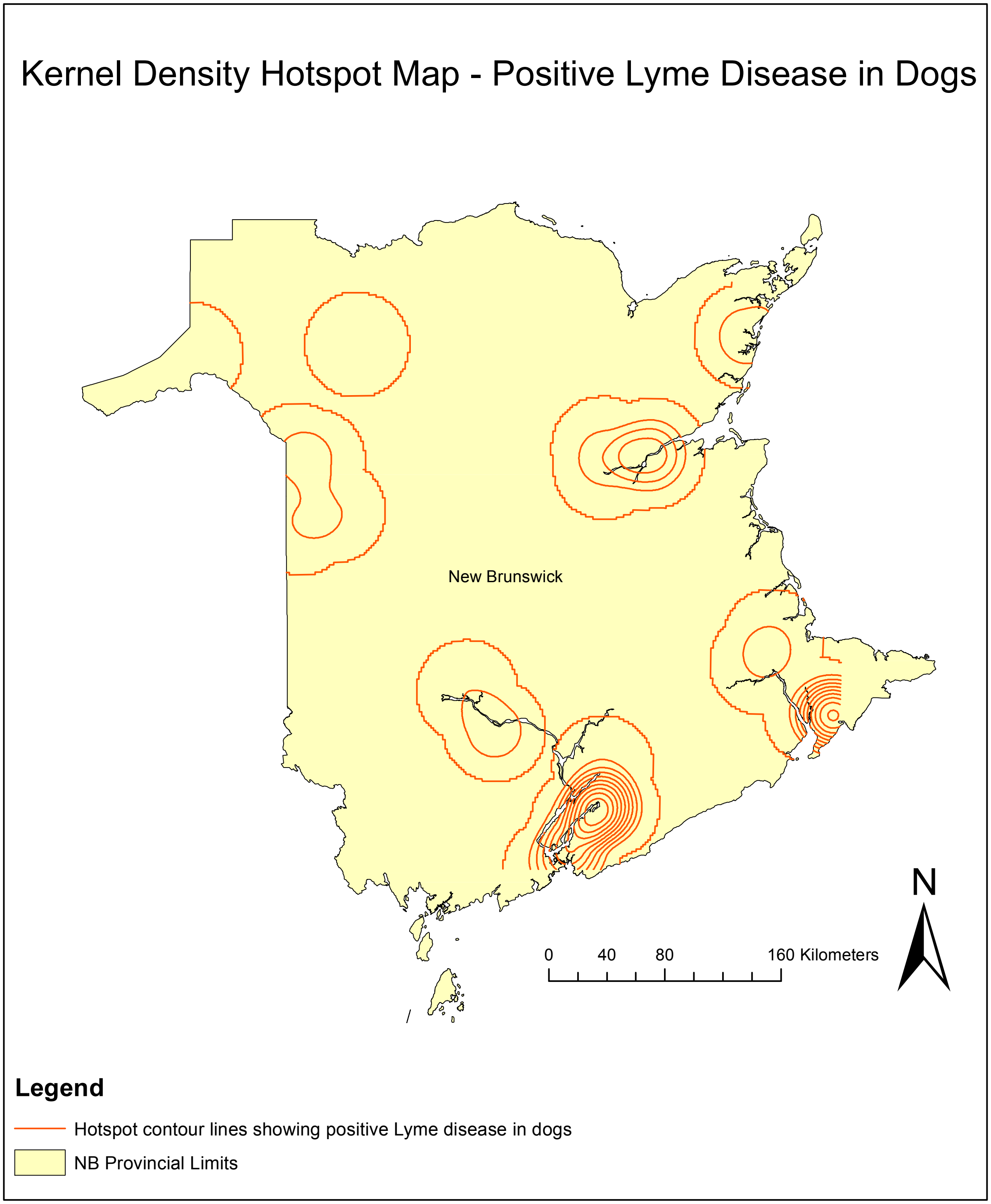


***Figure 8**: Map showing the kernel density hot spot map of positive Lyme disease in dogs.*

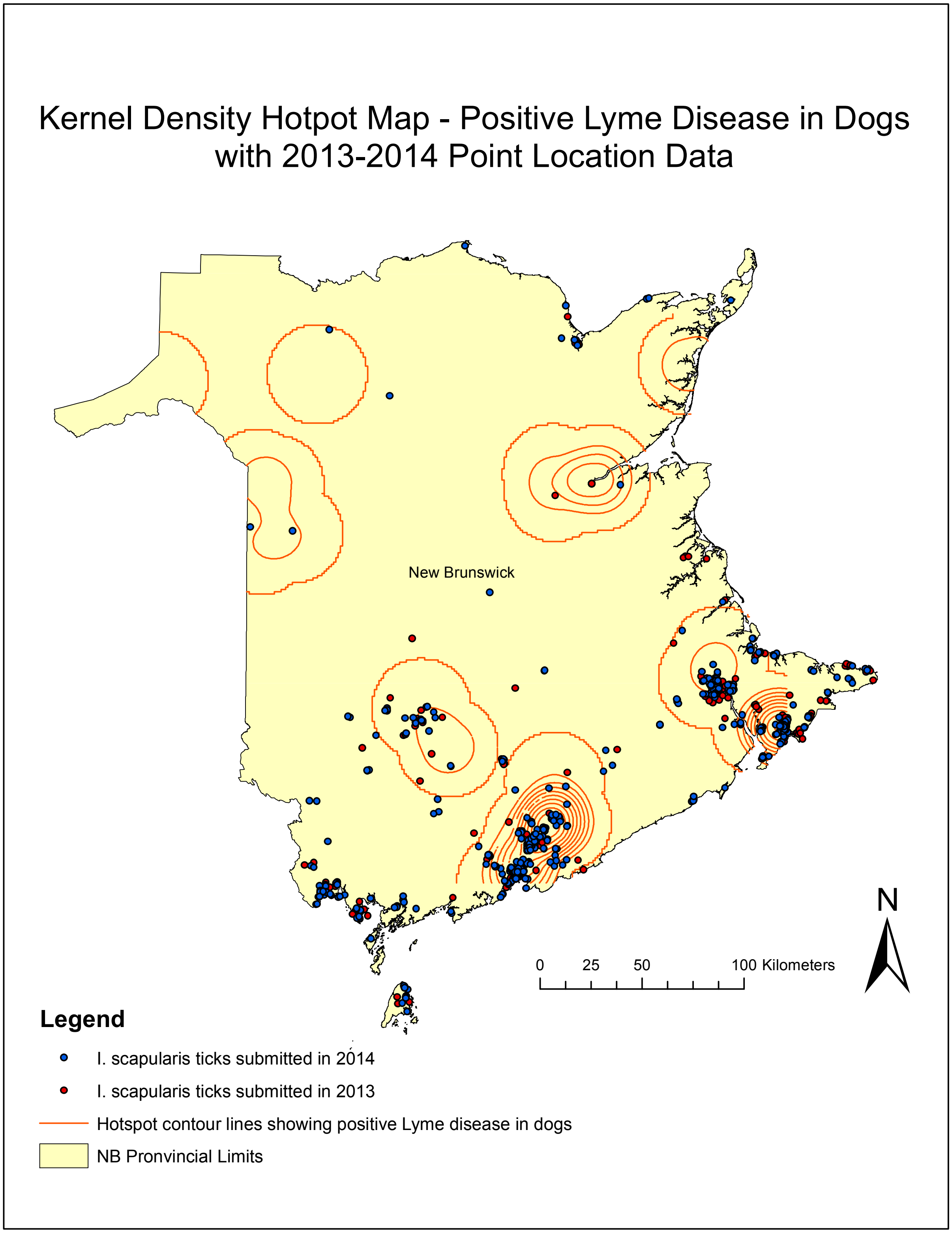


Figure 9: *Map showing kernel density hotspot of positive Lyme disease in Dogs, layered with 2013 and 2014 point occurrence data of ticks.*

Table 1*: Output from kernel bandwidth estimator from R.*

	[,1]	[,2]
[1,]	22393.05	0.00
[2,]	0.00	25172.32

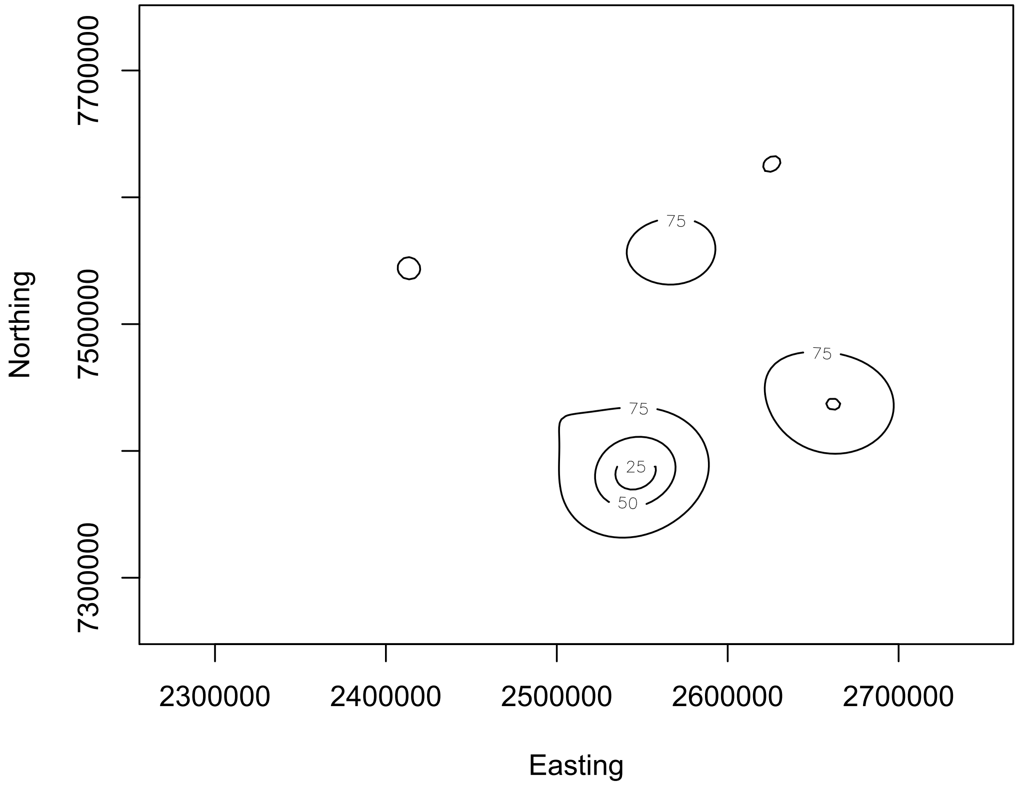


Figure 10: *plot(fhat) from kernel smoothing using Duongs ks package.*

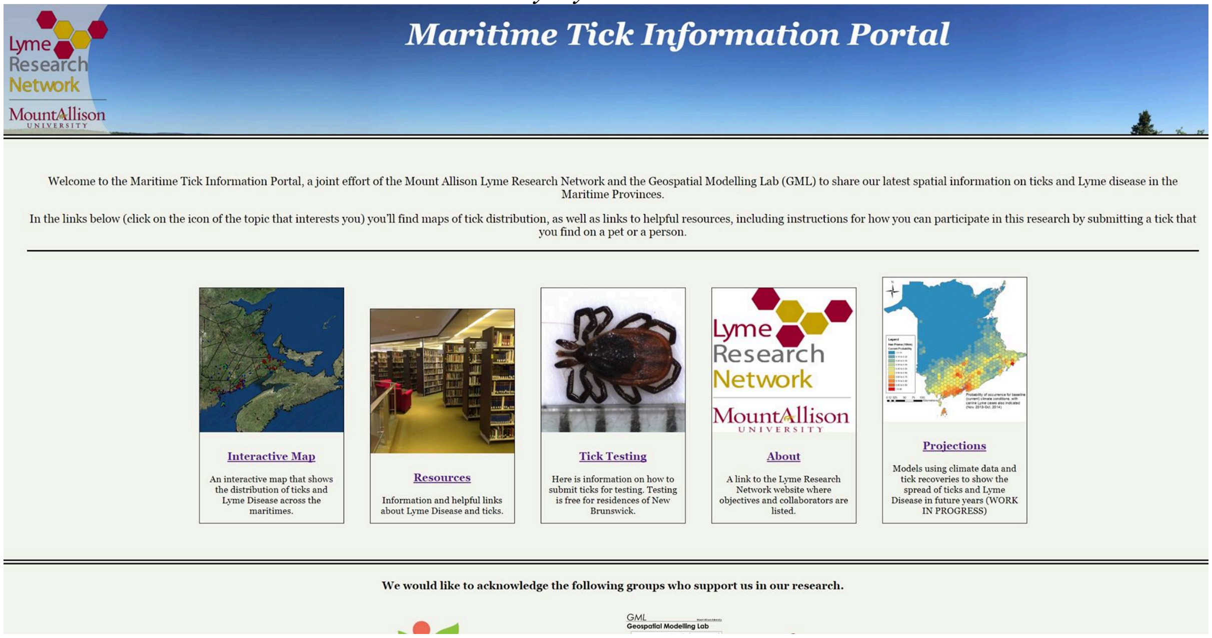
The use of ArcGIS and kernel smoothing in R is effective in appropriately visualizing the "hotspots" of Lyme disease in dogs in New Brunswick. Creating maps to help public view where dogs have been affected with Lyme disease is a helpful tool to get information out about these important public health problems. The kernel smoothing in R was an effective tool to use to get the appropriate bandwidth to create the maps.

4.0 Conclusions

The creation of the web-based GIS, used as part of the Maritime tick information portal, is an effective way to communicate important public health information. The website provides key information including maps and other resources about ticks and Lyme disease in the Maritime Provinces. The analysis of Lyme disease in dogs using kernel density estimation is a simple way to show the public the principal locations where Lyme disease is affecting dogs in New Brunswick and by extension, places where people are at risk, too. These projects compiled into the Maritime tick information portal, as part of the Mount Allison University Lyme Research Network, will be integrated into a larger project as part of an Undergraduate Honours, based on assessing the impact of web mapping tools for communicating community awareness of ticks and Lyme disease in southeastern New Brunswick. This study will involve focus groups to measure the risk awareness of individuals. Future directions for this work could include but should not be limited to, looking at kernel density estimation for each year, determining where ticks are and if hotspots are becoming larger as the years progress, doing a maxent analysis on predictor layers seeing if environmental variables such as degree days, river density, distance to coast and forest density have an impact of where hotspots of ticks are located. This will also continue with community awareness projects and assessment of risk within the community primarily in southeastern New Brunswick.

Appendices

Appendix 1: *Image of Main Page of the Maritime Tick Information Portal. Showing all of the current pages and links to other helpful resources such as Dr. Vett Lloyds lab page and the Mount Allison University Lyme Research Network Website.*



Welcome to the Maritime Tick Information Portal, a joint effort of the Mount Allison Lyme Research Network and the Geospatial Modelling Lab (GML) to share our latest spatial information on ticks and Lyme disease in the Maritime Provinces.

In the links below (click on the icon of the topic that interests you) you'll find maps of tick distribution, as well as links to helpful resources, including instructions for how you can participate in this research by submitting a tick that you find on a pet or a person.

An interactive map that shows the distribution of ticks and Lyme Disease across the maritimes.

Information and helpful links about Lyme Disease and ticks.

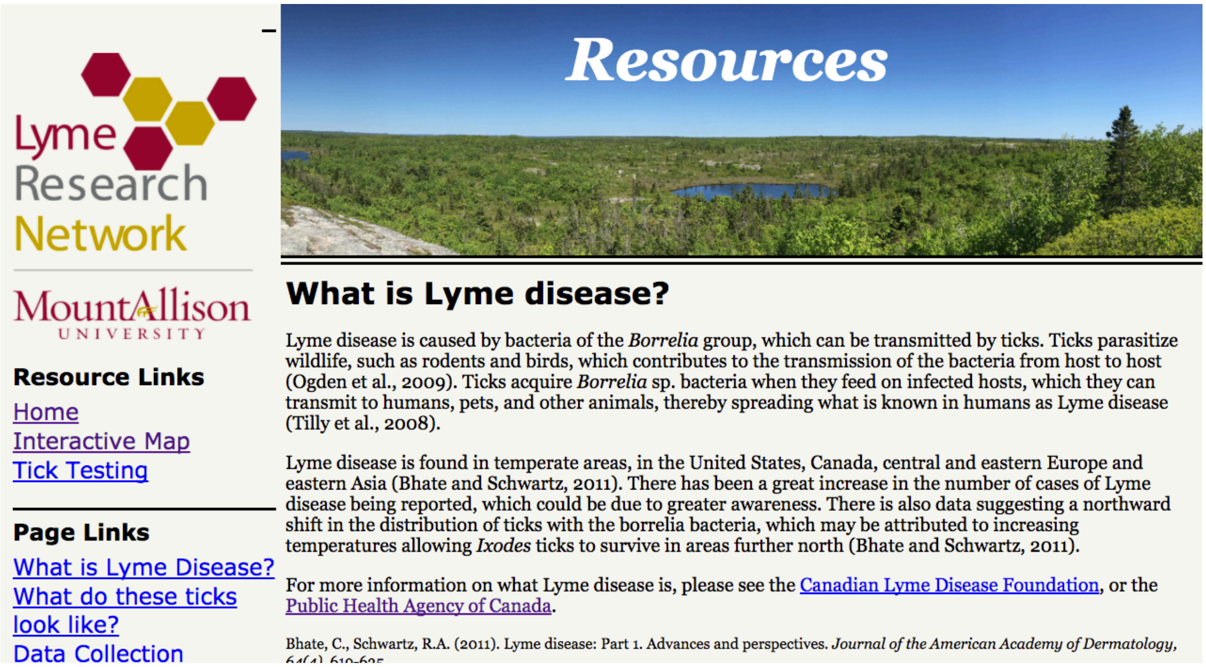
Here is information on how to submit ticks for testing. Testing is free for residences of New Brunswick.

A link to the Lyme Research Network website where objectives and collaborators are listed.

Models using climate data and tick recoveries to show the spread of ticks and Lyme Disease in future years (WORK IN PROGRESS)

We would like to acknowledge the following groups who support us in our research.

Appendix 2: *Image of the Resources page, providing users with more information and helpful links about Lyme disease and ticks.*



What is Lyme disease?

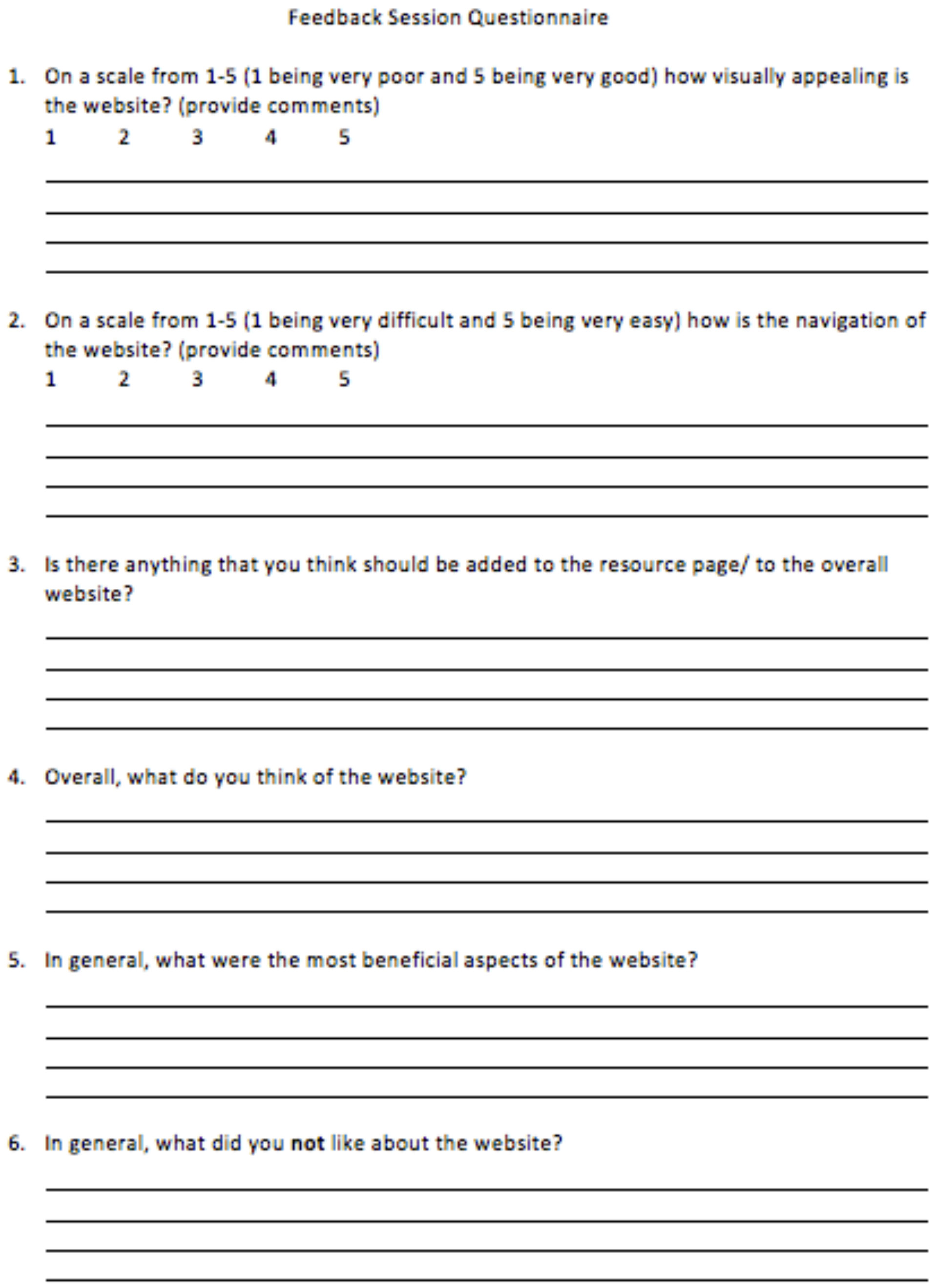
Lyme disease is caused by bacteria of the *Borrelia* group, which can be transmitted by ticks. Ticks parasitize wildlife, such as rodents and birds, which contributes to the transmission of the bacteria from host to host (Ogden et al., 2009). Ticks acquire *Borrelia* sp. bacteria when they feed on infected hosts, which they can transmit to humans, pets, and other animals, thereby spreading what is known in humans as Lyme disease (Tilly et al., 2008).

Lyme disease is found in temperate areas, in the United States, Canada, central and eastern Europe and eastern Asia (Bhate and Schwartz, 2011). There has been a great increase in the number of cases of Lyme disease being reported, which could be due to greater awareness. There is also data suggesting a northward shift in the distribution of ticks with the borrelia bacteria, which may be attributed to increasing temperatures allowing *Ixodes* ticks to survive in areas further north (Bhate and Schwartz, 2011).

For more information on what Lyme disease is, please see the Canadian Lyme Disease Foundation, or the Public Health Agency of Canada.

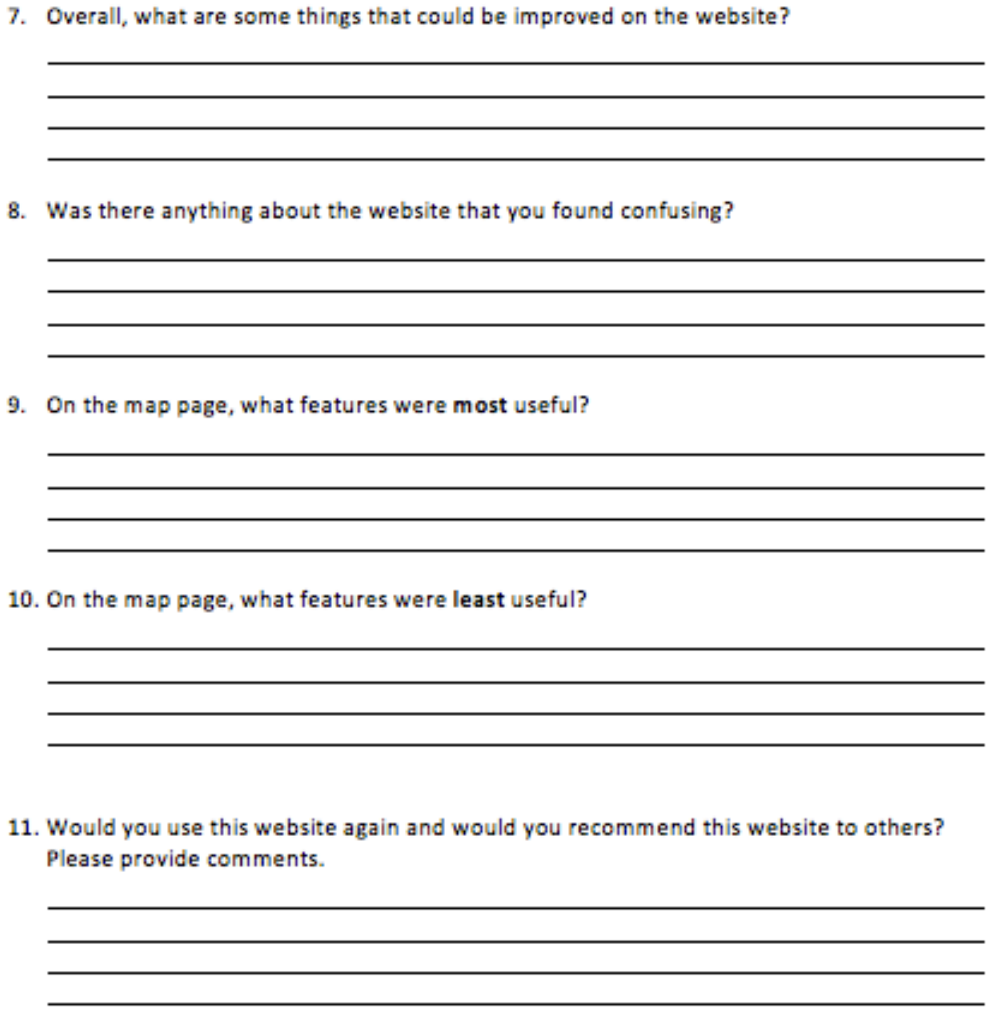
Bhate, C., Schwartz, R.A. (2011). Lyme disease: Part 1. Advances and perspectives. *Journal of the American Academy of Dermatology,*

Appendix 3: *Feedback questionnaire, used in two sessions on August 3rd and August 16th. For usability testing to make adjustments to the web portal.*



Feedback Session Questionnaire

1. On a scale from 1-5 (1 being very poor and 5 being very good) how visually appealing is the website? (provide comments)
   1 2 3 4 5
2. On a scale from 1-5 (1 being very difficult and 5 being very easy) how is the navigation of the website? (provide comments)
   1 2 3 4 5
3. Is there anything that you think should be added to the resource page/ to the overall website?
4. Overall, what do you think of the website?
5. In general, what were the most beneficial aspects of the website?
6. In general, what did you **not** like about the website?



7. Overall, what are some things that could be improved on the website?

8. Was there anything about the website that you found confusing?

9. On the map page, what features were **most** useful?

10. On the map page, what features were **least** useful?

11. Would you use this website again and would you recommend this website to others? Please provide comments.

Appendix 4: *Kernel smoothing package script in R*

```
#
# Author:               Anna Jamieson
# Date:                 July 24, 2017
# Purpose:      Learning ks package in R - to determine kernel bandwidth to work with in
ArcGIS
# NOTES:
#
#

#Load all relevant libraries
library(ks)
library(maptools)
```

```
library(rgdal)

#Load data set
#CanineLyme_2015.txt - use data tab in R commander, text file, comma deliminated

#Basic map loading
map.aoi = rgdal :: readOGR("NB_Boundary.shp")
# Print a preliminary "map"
plot(map.aoi)
points(x=df$Easting, y=df$Northing)

#generating random number plot, using ks library, example stuff
set.seed(8192)
samp <- 200
mus <- rbind(c(-2,2), c(0,0), c(2,-2))
Sigmas <- rbind(diag(2), matrix(c(0.8, -0.72, -0.72, 0.8), nrow=2), diag(2))
cwt<-3/11
props <- c((1-cwt)/2, cwt, (1-cwt)/2)
x <- rmvnorm.mixt(n=samp, mus=mus, Sigmas=Sigmas, props=props)
plot(x)

Hpi2 <- Hpi.diag(x=x)
Hpi2
fhat.pi2 <- kde(x=x, H=Hpi2)
fhat.pi2
plot(fhat.pi2)
points(x)

############################################
Kernel smoothing using Duongs ks package
############################################

doglyme <- df[,c("Easting", "Northing")]
doglyme
bw.diag <- Hpi.diag(x=doglyme)
bw.diag
       [,1]          [,2]
[1,] 501448761     0
[2,] 0             633645514

#Square root bw.diag, to get actual bandwidth information
sqrt(bw.diag)
       [,1]         [,2]
[1,] 22393.05     0.00
[2,] 0.00         25172.32
```

```
#Create kde object
fhat <- kde(x=doglyme, H=bw.diag)
plot(fhat)
```

Works Cited

Clarke, K.C., McLafferty, S.L., Tempaiski, B.J. (1996). On Epidemiology and Geographic Information Systems: A review and Discussion of Future Directions. *Emerging Infectious Diseases, 2(2).*

Duong, T. (2017). ks: Kernel density estimation for bivariate data.

ESRI. (2017). ArcGIS Desktop 10.5.1. Environmental Systems Research Institute, Redlands, California.

Hapbeggar, Simon. (2014). Lyme Disease in Canada: An Update on the Epidemiology. *National Collaborating Centre for Infectious Diseases*.

Hart, T.C. & Zanbergen, P.A. (2014). Kernel density estimation and hotspot mapping: Examining the influence of interpolation method, grid cell size, and bandwidth on crime forecasting. *Policing An Internation Jounral of Police Strategies and Management.*

Leighton, Patrick A., Koffi, J.K., Pelcat, Y., Lindsay, L.R., & Ogden, N.H. (2012) Predicting the speed of tick invasion: an empirical model of range expansion for Lyme disease vector Ixodes scapularis in Canada. *Journal of Applied Ecology*.

Lieske, D.J. and V. Lloyd. 2017. Combining public participatory surveillance and occupancy modelling to predict the distributional response of Ixodes scapularis to climate change. In review.

Lin, Y.P., Chu, H.J., Wu, C.F., Chang, T.K., & Chen, C.Y. (2010) Hotspot Analysis of Spatial Environmental Pollutants Using Kernel Density Estimation and Geostatistical Techniques. *International Journal of Environmental Research and Public Health, 8,* 75-88.

Martin, K., & Ralphs, M. (2013). Using kernel methods to visualize crime data. *Office for National Statistics, UK.*

Moore, D.A., & Carpenter, T.E. (1999). Spatial Analytical Methods and Geographic Information Systems: Use in Health Research and Epidemiology. *Epidemiologic Reviews, 21(2).* 143-161

Ogden, N.H., Koffi, J.K., Pelcat Y., & Lindsay L.R. (2014). Environmental risk from Lyme disease in central and eastern Canada: a summary of recent surveillance information. *Public Health Agency of Canada, Canada Communicable Disease Report*, 40(5).

Paynich, R. (2013). Identifying High Crime Areas. *Standards, Methods, & Technology (SMT) Committee White Paper 2013-02. International Association of Crime Analysts (IACA).*

Prasannakumar, V., Vijith, H., Charutha, R., & Geetha, N. (2011). Spatio-Temporal Clustering of Road Accidents: GIS Based Analysis and Assessment. *Procedia Social and Behavioral Sciences 21,* 317-325.

R Core Team. 2017. R: a language and environment for statistical computing. R Foundation for Statistical Computing, https://www.R-project.org.

Silverman, B.W. (1986). Density Estimation for Statistics and Data Analysis. *Chapman and Hall/CRC.*

World Atlas (2017)

http://www.worldatlas.com/webimage/countrys/namerica/province/peizland.htm#page