Application of a multidisciplinary One Health approach to understanding environmental drivers of the spatial distribution of vector-borne infectious diseases Jessie Barnett¹, Thomas Hart², Leigh Robertson¹, Jingtian Wang², Min-Ken Liao², John E. Quinn²

Introduction:

While much work has been done to understand micro-scale biological factors of infectious diseases, less has been done to understand macro-scale environmental drivers of disease emergence and spread. Here, we use land cover change to model distribution of ticks in the United States. In addition, we discuss the value of social media in collecting large-scale data sets.

Methods:

- We solicited tick submissions from veterinarians and pet owners via social media
- Comments from Facebook were coded with popular themes: personal, thankful, sharing, general, enthusiasm and questions (Fig. 2)
- We organized submitted ticks based on life stage, sex, and location

Results:

- Spring 2015 Facebook posts received: • April 15: 1,135 likes, 1236 shares,171 comments • June 16: 282 likes, 196 shares, 37 comments
- The most common reason for sharing was to share or express enthusiasm (Fig. 2)





Figure 1. Post on social media by Dr. Roark to encourage participation in the study.

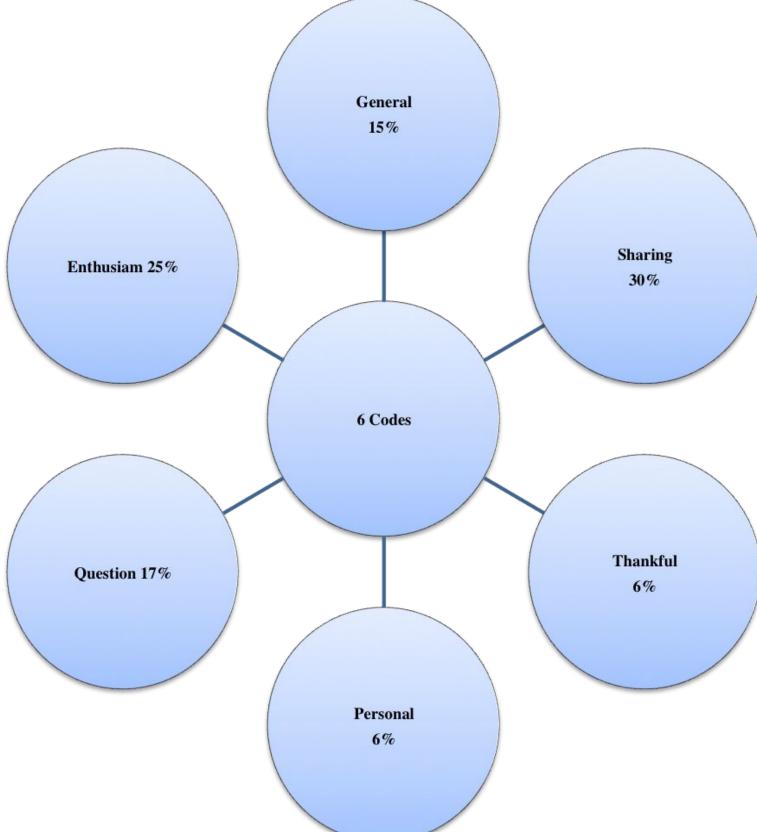
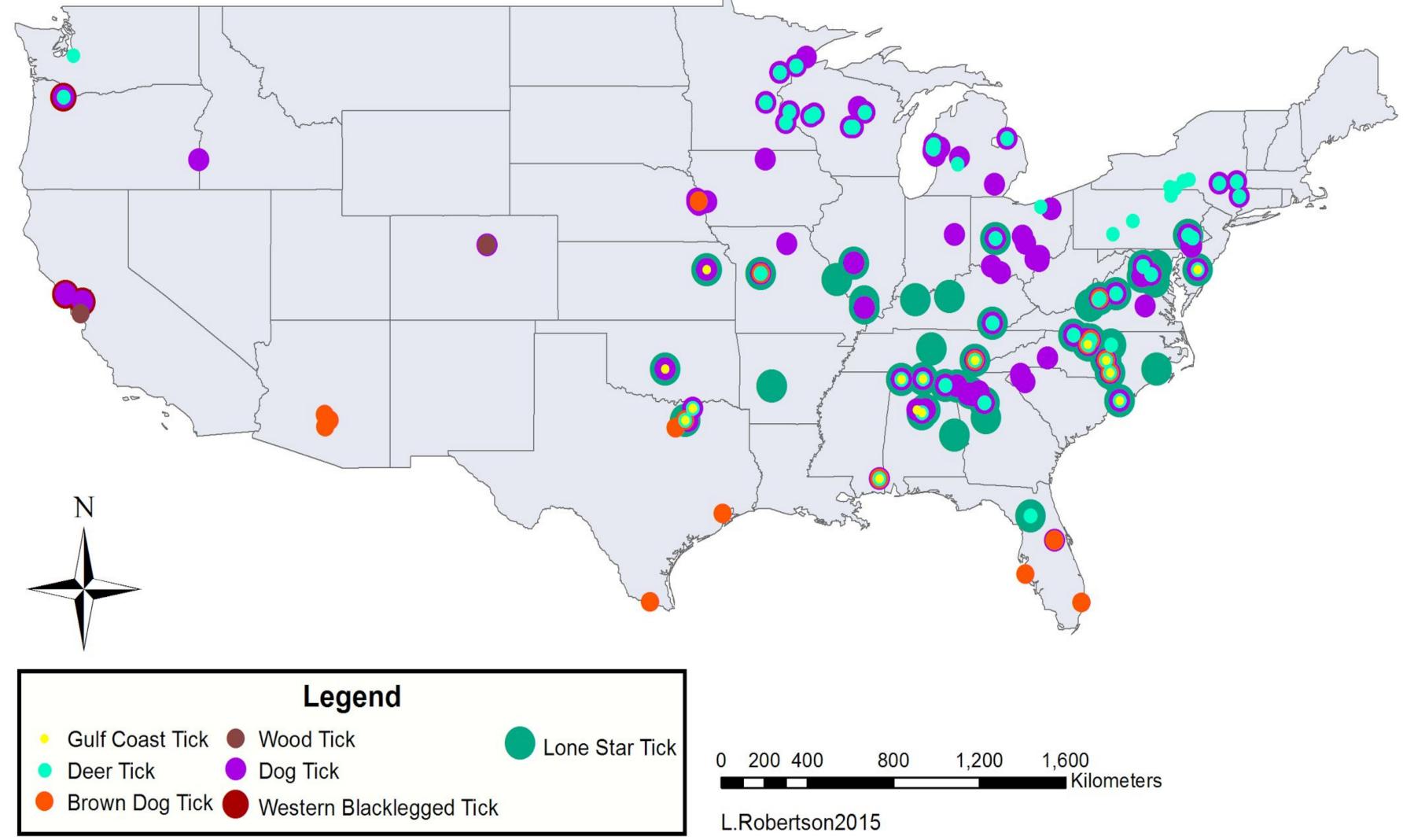
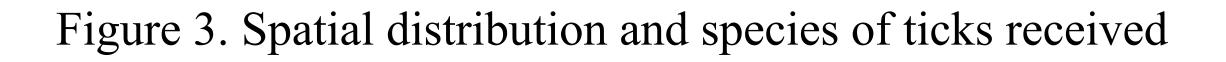


Figure 2. Facebook comments (n=237) were reduced to six thematic qualitative codes reflecting type and frequency of engagement.

• We detected the presence of bacteria using PCR with corresponding primers and RFLP and BLAST • We used macro-scale land use and land cover covariates to spatially analyze tick and infected tick occupancy patterns to better predict and understand drivers of tick vector disease spread.

- We received 5,782 ticks from seven species between May and July, 2015 (Figs. 3 & 4)
- Ticks came primarily from three regions; midwest, southeast, and northeast (Fig. 3)
- We found spotted fever group *Rickettsia* species such as *R. rickettsia*, *R. amblyommii*, *R.* monacensis, R. montanensis and R. parkeri, Rickettsia massiliae, Rickettsia rhipicephali.
- *Rickettsia* sp. were detected in 50.0% of **Southeastern** ticks.





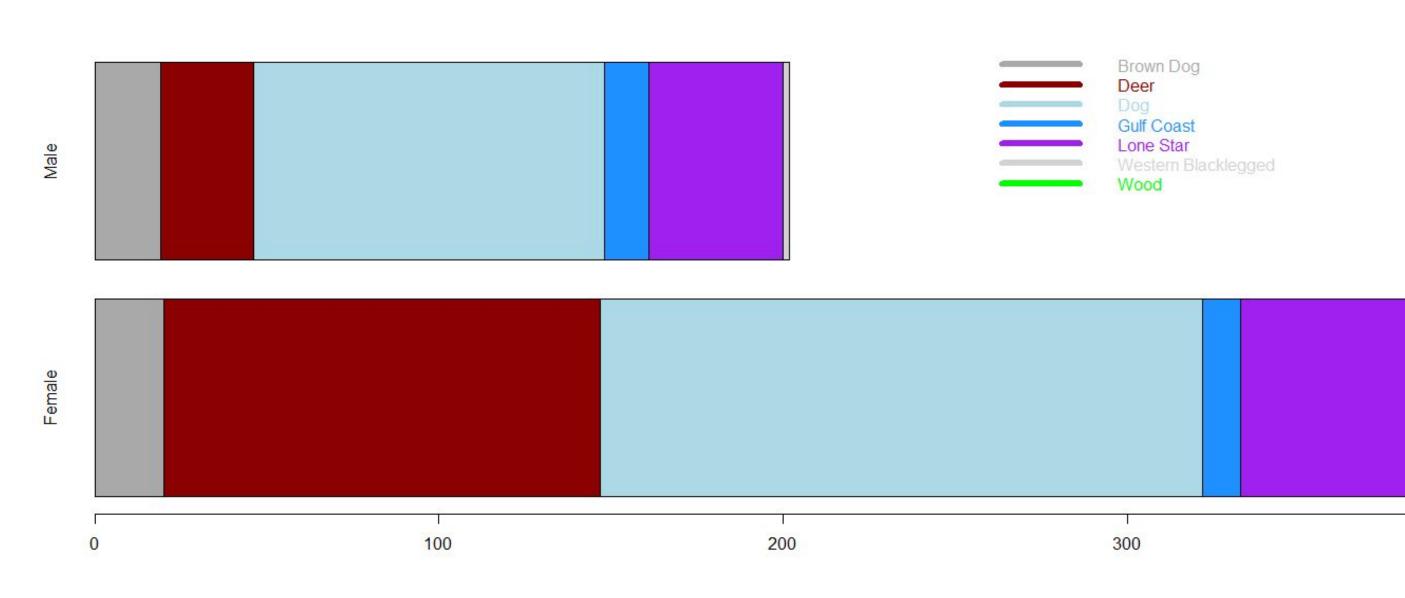


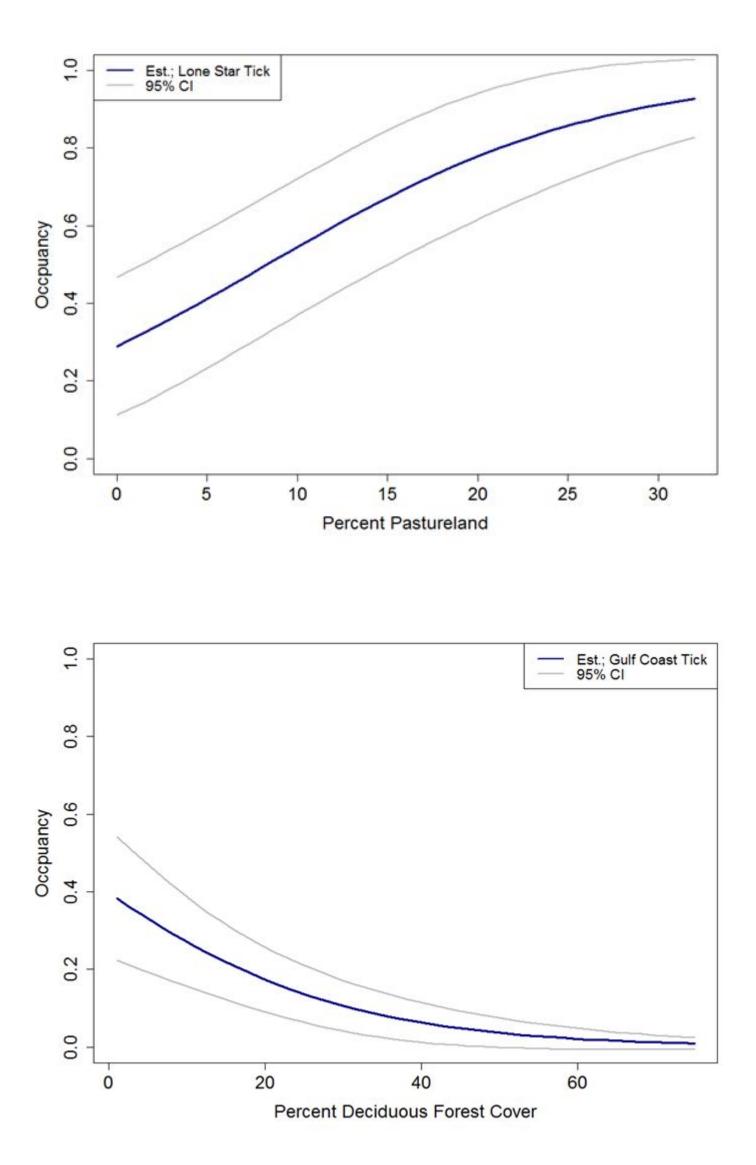
Figure 4. Proportion of species and gender of ticks received



Results:

Land Cover Classification	Casar, NC	Clarkston, GA
OpenWater	0.12	0.96
TotalDevelopedArea	10.61	68.65
DeciduousForest	44.21	12.49
EvergreenForest	8.24	12.29
MixedForest	2.09	0.54
TotalForest	54.54	25.32
Shrub	4.44	0.60
Grassland	4.23	1.35
Pastureland	25.06	1.42
Cultivated Crops	0.24	0.00

• The sample areas of interest showed variety in the heterogeneity of land cover types (Figs. 5 & 6).



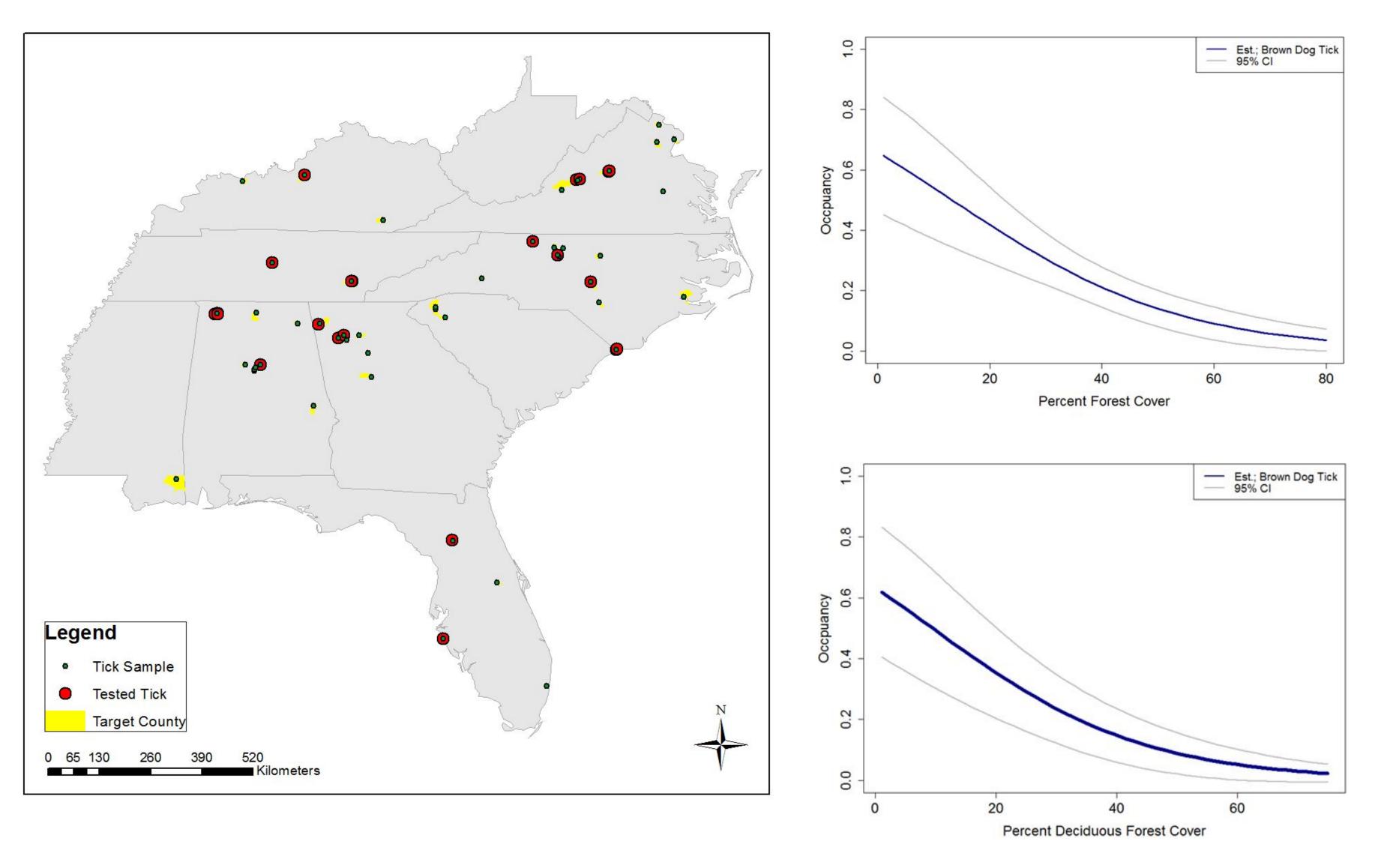


Figure 7. GLM results and overview map of the test area of interest with sample locations (US SE)

of three species (Fig. 7)

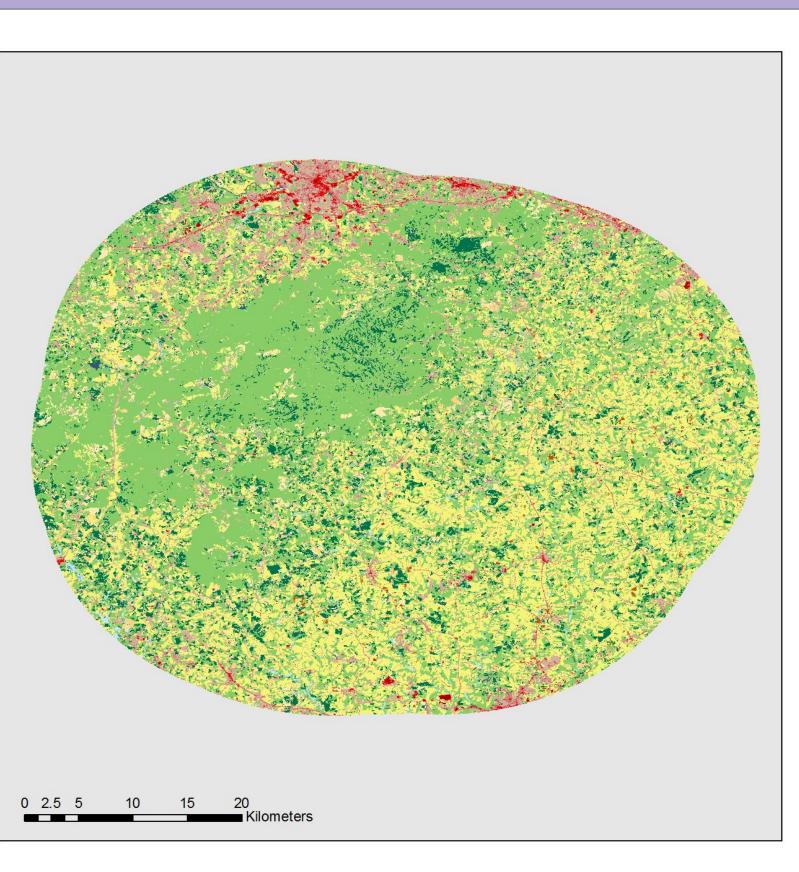
Discussion and Future Directions:

Though still preliminary, this project demonstrates the value of interdisciplinary research for public health, the capacity of social media for data collection, the need for regional scale spatial analysis, and widespread presence of *Rickettsia* spp. Further steps in this project will focus on other vector borne diseases and spatially explicit risk maps. Ultimately, achieving optimal health requires collaborative, integrated, and multidisciplinary approaches to better predict infectious disease

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¹Furman Earth and Environmental Science, ²Furman Biology





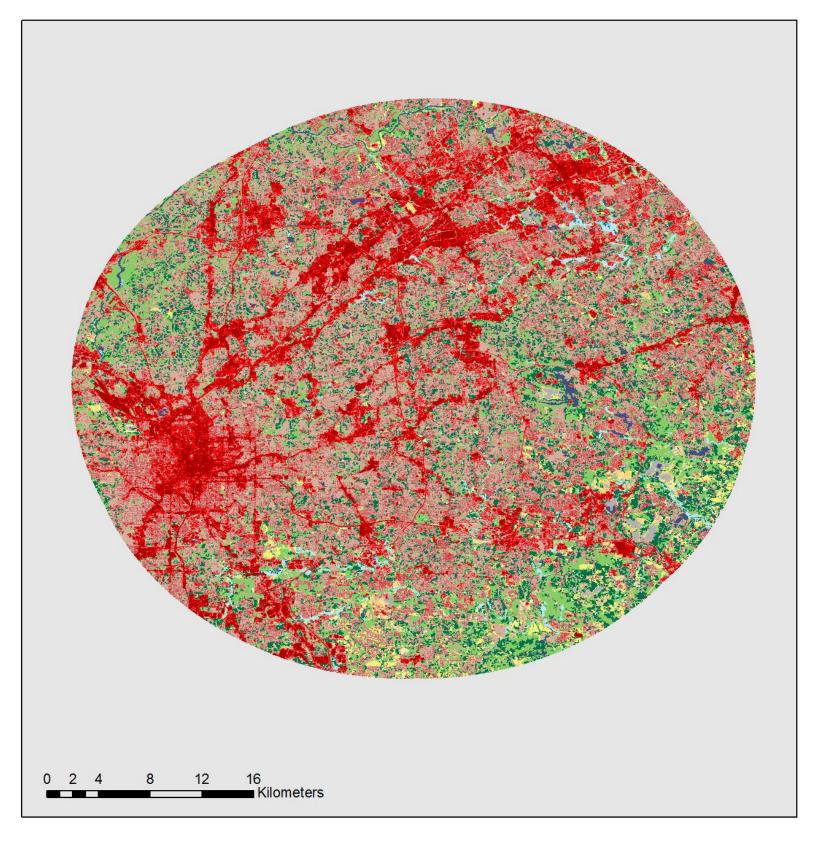


Figure 5. Buffer sample Clarkston, GA

• Using tick species presence data, we were able to identify land cover types as covariates that best predicted occupancy

