



## Using spatial analysis to estimate depopulation for Native American populations in northeastern North America, AD 1616–1645

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### ABSTRACT

Eight years ago, [Ramenofsky et al. \(2003\)](#) characterized the discussion of the impact of Old World diseases on Native American populations as almost exclusively historical in nature. They specifically argued for the application of more evolutionary, genetic, and epidemiological theory to research into this topic. We agree with their assessment and further suggest that such research would greatly benefit from spatial analyses of disease spread as well. Using trend surface analysis of existing ethnohistorical and archaeological data pertaining to population sizes and disease events, we examine the spatiotemporal dimensions of 17th century depopulation in northeastern North America. The subsequent results allow us to predict possible depopulation rates for populations with very little demographic data. Further, our use of biological, historical, and cultural data to interpret the results represents an attempt to provide a more complex explanation for the variability in cultural survivability across the region and several possible avenues for productive future research. We believe research like this can significantly improve our understanding of how Old World diseases affected historic Native American populations and cultures and continue to impact them today.

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### Introduction

Determining the magnitude of depopulation from the introduction of Old World diseases among Native American societies has many benefits, from helping us to understand cultural development, to providing information that may be helpful for understanding current demographic patterns in Native American communities, and to helping us understand disease transmission and effects among human populations. There currently exists a significant amount of data, albeit highly variable in accuracy and precision, on pre- and post-contact Native American population sizes, depopulation rates, and the timing of Old World disease events. However, large geographic, demographic, and temporal gaps exist in the data when viewed on regional scales. There is a need to fill in those gaps to better understand the variability of depopulation and the nature of disease spread. With more complete data, we may be able to synthesize and analyze population and disease patterns in more detail.

[Ramenofsky et al. \(2003\)](#) contended that discussions of pre-contact populations and the impact of Old World diseases on Native American populations have tended to focus on historical questions and have yet to adequately examine the complex set of cultural

and biological factors that were likely influencing depopulation rates. [Thornton \(1997\)](#) similarly critiqued the lack of demographic theory being applied to this area of research. We agree with these assessments and further suggest that this topic would benefit greatly from spatial analyses of existing population data in order to explore spatial trends in the data and even possibly predict population losses among groups with no current data.

Our first goal for this research is to simply map what we currently know about the population distributions and depopulation (i.e. percentage of population lost) for 17th-century Native American societies in northeastern North America. We will use this information to examine spatial trends in the depopulation—something that has yet to be done. Our second goal is to use spatial interpolation to determine depopulation for groups in northeastern North America with no current population information. This will fill in the gaps in our current information and help us to better understand the nature of depopulation in this region. To accomplish this goal, we map 17th-century population distributions and existing historic and archaeological depopulation data to examine simple spatial patterning in depopulation rates and analyze existing historic and archaeological data using kriging, a spatial interpolation method, in order to predict depopulation rates. Our final goal is to use our results and existing historic and archaeological population data to begin discussions about the cultural, biological, and historical factors that may have influenced depopulation rates among Native American groups. To accomplish the final goal, we

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use current hypotheses about host immune function and genetic variability, cultural information from these groups, and historical information from the region to explore possible causes of observed patterns of depopulation in the Northeast.

## Background

The reduction of Native American populations during the sixteenth through nineteenth centuries was culturally and demographically devastating and has had lasting effects among Native American societies. As a result, numerous researchers, including archaeologists, paleodemographers, and historians, have been interested in gaining a better understanding of this phenomenon. Although warfare, slavery, and other mistreatments were causes, introduced Old World diseases were responsible for the overwhelming majority of deaths (Black, 1991). As such, these diseases have rightfully been the focus of research into the details of Native American depopulation. In this body of work, researchers have used numerous methods for estimating depopulation percentages and rates from disease. These have included the use of historical data (e.g. Dobyns, 1966, 1983; Kroeber, 1939; Palkovich, 1985; Thornton, 1987, 1997; Ubelaker, 1976, 1988), archaeological data (e.g. Jones, 2010a, 2010b; Snow, 1995a, 2001; Warrick, 2008), and combinations of both (Ramenofsky, 1987). To date, there have been almost no attempts to estimate depopulation figures or explore existing data using spatial analysis techniques.

Pre- and post-contact Native American populations in the Northeast present perhaps the best cases for examining existing depopulation patterns with new methods. Demographic archaeological research on Iroquoian-speaking populations, such as the Haudenosaunee and Wendat (Jones, 2010a, 2010b; Snow, 1995a, 1995b; Snow and Starna, 1989; Warrick, 2008), has produced an empirically based population dataset for several populations for the periods just prior to and around the time of the arrival of Europeans. For other groups in the region, population data in the form of total counts, warrior counts, and impacts of diseases come from historical texts dating to the very earliest 17th century interactions between Europeans and Native Americans through the 18th century (for examples see Jameson, 1909, p. 141; Thwaites, 1959, vol. 7: p. 87, vol. 8: p. 43, vol. 12: pp. 263–265; Winthrop, 1908, vol 1: pp. 111–114). However, there are a small but significant number of populations in the region that have little or no population data. These include the Erie, Wenro, Neutral, Susquehannock, Kennebec, Munsee, and Naragansett–Pekanoket. These gaps have made discussing large-scale patterns of disease spread and depopulation in the region difficult. However, this type of dataset with several reliable sources of population data and a few gaps is almost ideal for using spatial interpolation methods to estimate depopulation rates for those groups with no relevant data. Interpolation methods use trends in existing data to estimate values for holes in the dataset. Datasets with more data will produce more accurate estimated values. Once these gaps are filled, the depopulation data for the Northeast will be one of the more complete population datasets for the continent. Such a dataset would allow us to explore the biological, cultural, and historical factors behind the depopulation trends in much more detail than has been possible in the past.

While a great deal of research has gone into producing pre- and post-contact Native American population numbers, there have been far fewer attempts to explain the patterns of the diseases and other causes that gave rise to these numbers. In addition to generating new depopulation data, we attempt to build on the small number of influential studies that sought to explain the depopulation patterns. Black (1991) discussed the role of human genetic diversity in disease virulence, particularly within native

South American populations, which tend to be relatively homogeneous. Such host homogeneity can increase the virulence of a disease, because a pathogen that has infected and adapted to one host is thereafter preadapted to individuals who are genetically similar to the original host. There have been few attempts to apply Black's findings to other results.

Ramenofsky (1990) examined differential survivability as a result of Old World diseases for groups in the Southeast using a selectionist approach (i.e. Darwinian evolution). She developed a model based largely on settlement location and type and how characteristics, such as sedentism and distance to major waterways, would impact survivability of a group. Her work introduces several possible explanations for differential depopulation rates among groups in the same region. Like Black's work, little follow-up research has been done to test her hypotheses. Below, we discuss our results in reference to Ramenofsky's model.

Thornton et al. (1991) sought to bring a more complex demographic approach to the discussion of depopulation. They noted that it is an oversimplification to talk solely of mortality. We must take into account, in particular, fertility patterns before and after disease events in order to fully understand the overall depopulation rate that is observed. For example, they noted that a population with a 1% growth rate could completely recover from a 40% loss in population within 35 years (Thornton et al., 1991, p. 37). While we do not specifically address fertility below, it is important to keep their findings in mind when discussing depopulation rates.

Specifically in the Northeast where our research focuses (region and cultures shown in Fig. 1), it appears that Old World diseases had drastic negative impacts on Native American populations only after protracted contact with Europeans (Jones, 2010a, 2010b; Snow, 1995a, 1995b; Snow and Starna, 1989; Warrick, 2008). Snow and Lanphear (1988) sought to explain early results using modern knowledge of the virulence and vectors of transmission of smallpox, the most likely disease to have first struck Northeastern groups. They hypothesized that adults on the initial voyages to North America would have begun the journey with immunity to smallpox, as otherwise the disease would have burned itself out during the voyage. Only when a significant number of possible hosts (i.e. children) were present on boats could the disease infect and spread among susceptible individuals and thus be maintained on the long voyage. Although speculative, this is one of the only attempts to determine disease vectors and their role in the timing of diseases.

Using a different approach, Milner et al. (2001) and Milner and Chaplin (2010) sought to explain differential disease impacts and depopulation through first-level spatial analyses of the geographic ranges of Late Prehistoric cultures in eastern North America. First-level spatial statistics are the initial observations of patterns, and these two studies identified a clustered pattern of settlement that included significant areas of uninhabited space across the eastern portion of the continent. The authors proposed that these uninhabited areas acted as barriers to disease spread, preventing pandemics.

All of these studies were informative and represented the beginning of a wave of analyses that sought to move beyond numbers to explain the patterns of depopulation. Unfortunately, many of these studies (aside from Milner and associates' work) are over 20 years old. Few studies have sought to continue this approach over the last decade.

## Methods

Information about the spatial distribution of early 17th-century Native American populations in the Northeast came from existing publications, which are listed in Table 1, and archaeological survey

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