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Spatial Analysis of Attrition Along the HIV Care Continuum in the Atlanta Metropolitan Area

By

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Epidemiology

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By

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B.S.
Pennsylvania State University
2013

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An abstract of
A thesis submitted to the Faculty of the
Rollins School of Public Health of Emory University
in partial fulfillment of the requirements for the degree of
Master of Science in Public Health
in Epidemiology
2015

Abstract

Spatial Analysis of Attrition Along the HIV Care Continuum in the Atlanta Metropolitan Area

By Brian M. Huylebroeck

Context Proper HIV management and prevention requires adherence to the HIV Care Continuum steps, which consist of diagnosis, linkage to care, retention in care, initiation of antiretroviral therapy, and achievement of viral suppression. Using spatial analysis to detect geographic hot spots of attrition from these steps may serve to identify how best to control the HIV epidemic.

Objective: To identify and describe geographic areas associated with poor engagement in HIV care in the metro-Atlanta area.

Design, Setting, and Participants: Surveillance data was extracted from Georgia Enhanced HIV/AIDS Reporting System for a retrospective cohort of persons diagnosed with HIV in 2010 and 2011 in Fulton, DeKalb, Gwinnett, Clayton, Douglas, and Cobb counties in Georgia, with follow-up to 2013 (n=2339). Spatial patterns of outcomes due to attrition along the HIV Care Continuum were analyzed using Hot Spot Analysis (Getis-Ord Gi*) in ArcGIS to identify geographic areas of significant, non-random clustering, known as hot spots. Logistic regression models were used to evaluate associations among hot spots, demographic factors, and each outcome.

Outcome Measurements: Outcomes of interest were: not linked to care, not linked to care within 90 days, not retained in care, and not virally suppressed.

Results: Of the 2339 persons in the sample, 2067 persons (88.4%) linked to care; 1295 persons (62.6%) linked to care within 90 days among those linked; 663 persons (32.1%) were retained in care among those linked; 326 persons (49.2%) were virally suppressed among those retained. Persons currently residing in geographic hot spots had higher odds to not link to care [adjusted odds ratio (AOR): 1.51 (95% confidence interval (CI) 1.04-2.21)], not link to care within 90 days [2.73 (1.28-5.83)], not retain in care [2.47 (1.43-4.26)], and not achieve viral suppression [2.72 (1.56-4.76)] than persons residing outside of hot spots in the follow-up period.

Conclusion: Spatial patterns associated with clustering of poor outcomes were found to be strong independent predictors of linkage to care, retention in care, and viral suppression in a 6-county section of the metro-Atlanta area. The findings provide further evidence for the use of spatial analyses as a tool for characterizing the HIV Care Continuum.

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Background

HIV/AIDS

The human immunodeficiency virus (HIV) is a sexually transmitted infection spread through contact with infected blood or from mother to child during pregnancy, childbirth, or breastfeeding (1). HIV destroys CD4 cells, an important part of the immune system, weakening the body's ability to fight opportunistic infections and leading to a chronic, life-threatening condition called acquired immunodeficiency syndrome (AIDS) (1). There is no cure for HIV, but treatment with antiretroviral therapy (ART) can limit virus levels and delay progression to AIDS (1). Controlling HIV with ART through viral suppression can allow for a normal life expectancy, prevent fatal opportunistic infections, and reduce the risk of transmitting HIV (1-4).

The Impact

The Centers for Disease Control and Prevention (CDC) estimate that in the United States about 50,000 people are diagnosed with HIV annually and that more than 1.2 million people are living with HIV (5). In addition, nearly 1 in 7 of those living with HIV are unaware of their infection (5). Some individuals may be at higher risk for acquiring HIV based on determinants such as race/ethnicity, age, sex, or engaging in health risk behaviors. For example, Blacks and Hispanics are disproportionately affected by HIV, with a rate of new infections among Blacks 7.9 times as high as the rate in Whites and the rate among Hispanics 3 times as high as the rate in Whites (6). Moreover, 31% of all new HIV infections in 2010 were in individuals aged between 25 and 34 years and 26% were in individuals aged between 13 and 24 years (6). Men who have sex with men (MSM) made up 63% of all new HIV infections and 78% of those among males in 2010, despite being only 4% of the male population (5, 7). Males also had 4.2 times the rate of new infection compared to females (6).

In 2011, Georgia ranked 5th out of 50 states for the number of new HIV diagnoses (8). Additionally, the Atlanta metropolitan area was ranked the city with the 5th highest number of

new HIV diagnoses in the United States in 2013 (9). Thus, Atlanta, Georgia has emerged as a center for the HIV epidemic in the United States.

The HIV Care Continuum

Initiating ART early increases survival rates of HIV-positive patients and acts as a preventive measure in reducing the risk of HIV transmission (10, 11). However, proper HIV management and prevention requires adherence to the HIV Care Continuum steps, which consist of diagnosis, linkage to care, retention in care, initiation of antiretroviral therapy, and achievement of viral suppression (11, 12). Attrition at each step of the HIV Care Continuum hinders the control of the HIV epidemic and perpetuates the chain of HIV transmission. In a study published in 2015, 91.5% of new HIV infections in 2009 were found to be attributable to persons not engaged in medical care, while less than 6% of new infections were attributable to people in care and receiving ART (13). Therefore, most of the new HIV infections in the United States may be prevented through early diagnosis and care, yet only 30% of United States citizens living with HIV had achieved viral suppression as of 2011 (14).

The CDC uses the HIV Care Continuum to identify prevention and care needs and to monitor the progress of the nation towards reaching the goals outlined in the National HIV/AIDS Strategy for the United States in July 2010 (15, 16). In an observed year, the proportion of people with HIV are tracked, using mandatory reported laboratory data, for the following: 1) diagnosis with HIV infection, 2) linkage to care, defined by visiting a health care provider within 90 days of diagnosis, 3) engagement or retention in care, defined by receiving medical care for the HIV infection, 4) prescription of ART, as documented in medical records, and 5) viral suppression, defined as an HIV-1 RNA viral load of <200 copies/mL (15). Monitoring engagement in each of the 5 steps of the HIV Care Continuum over time allows federal, state, and local health agencies to prioritize resources and funding for controlling the HIV epidemic (15).

The HIV Care Continuum model provides the framework for monitoring the progress of people living with HIV; however, state departments of public health are responsible for gathering the data that informs these metrics of care. The Georgia Department of Public Health produces HIV Care Continuum Surveillance Reports annually, utilizing the HIV/AIDS case surveillance data legally required to be reported (17). Since January 1, 2004, Georgia law has mandated that both health care providers and laboratories must report all HIV cases, including all subsequent tests indicative of an HIV infection, such as positive Western Blot results, all detectable and undetectable viral loads, all CD4 counts and percentages, and all viral nucleotide sequence results (18, 19). The 2012 report of the HIV Care Continuum among persons living with HIV in Georgia showed 54% minimally engaged in care (at least one CD4 count or viral load test in 2011), 38% retained in care (at least two CD4 counts or viral load tests at least 3 months apart in 2012), and 39% virally suppressed. (20). For comparison, an estimated 1.2 million people were living with HIV in the United States in 2011 and of those 40% were engaged in care and 30% achieved viral suppression (14). The same 2012 report provided data on the HIV Care Continuum among new diagnoses of HIV infection in Georgia in 2011 with 62% linked to care within 3 months of diagnosis, 66% minimally engaged in HIV care, 46% retained in care, and 45% virally suppressed (20).

More specifically, among new diagnoses of HIV infection within the Atlanta eligible metropolitan area (EMA) in 2011, 60% were linked to care within 3 months of diagnosis, 66% were engaged in care, 47% were retained in care, and 46% were virally suppressed (21). The Atlanta EMA includes Bartow, Paulding, Carroll, Coweta, Fayette, Spalding, Henry, Newton, Rockdale, Gwinnett, Walton, Barrow, Forsyth, Cherokee, Pickens, DeKalb, Fulton, Clayton, Cobb and Douglas counties (21). All of these estimates for the proportions of people engaged in each step of the HIV Care Continuum are relatively consistent, yet notable are the findings for the new diagnoses in 2011 being nearly identical for Georgia and the Atlanta EMA, which should

theoretically be expected as the majority of the HIV cases in Georgia are found in the Atlanta EMA (22). However, approximately 60% of all new diagnoses and of all persons living with HIV in Georgia can actually be attributable to a smaller geographic area than the 20-county Atlanta EMA by observing only five public health districts: 3-1 Cobb-Douglas, 3-2 Fulton, 3-3 Clayton (Jonesboro), 3-4 East Metro (Lawrenceville), and 3-5 DeKalb (22). These five districts are the heart of the HIV epidemic in Georgia.

Disparities in the HIV Care Continuum

While the previously stated findings show that there is substantial attrition along the HIV Care Continuum, these poor outcomes of care are exacerbated by demographic disparities. In the 2011 cohort of 1.2 million people living with HIV in the United States, linkage to care was lowest among persons aged 13-24 (73%) and among Blacks (76%) (14). In addition, persons in the groups 18-24, 25-34, and 35-44 years were less likely to be virally suppressed than persons 65 years or older (14). These disparities in care can be reflected in the Georgia 2012 HIV Care Continuum for adults and adolescents living with HIV as well, where viral suppression was lowest among Blacks (36%) and Hispanics (37%) compared to Whites (45%) (22). Persons in the 13-24 age groups also had lower proportions of people retained in care and virally suppressed compared to all other age groups (22). In Georgia, only 38% of Black males diagnosed in 2011 were virally suppressed as of March 2013 compared to Hispanic (56%) and White (54%) males (22). Among Black MSM diagnosed in 2011 in Georgia, persons aged 13-24 years had the lowest proportional viral suppression (26%) compared to 25-35 (35%), 35-44 (38%), 45-54 (47%), and 55+ years (36%) (22). Overall, Blacks, MSM, younger individuals, and males are less likely to remain on the HIV Care Continuum and to achieve viral suppression. These demographic disparities in the HIV Care Continuum correlate with disparities in HIV prevalence.

The Role of Spatial Analyses

Many contextual and lifestyle factors may be responsible for why these specific demographic groups are more likely to be infected with HIV and less likely to achieve viral suppression. Health outcomes are understood to be influenced by individual-level biological and behavioral factors, and they have been increasingly recognized to be influenced by contextual community-level factors (23-25). To understand how contextual influences affect health, a number of researchers have turned to the use of geographic information system (GIS) technology to map outcomes and perform spatial analyses to organize and visualize health data (26-30). Spatial analyses can be used to identify disparities in disease distribution or in access to resources, such as health care providers (31-33). In addition, GIS technologies provide methods to determine geographic clusters, or hot spots, where outcomes are concentrated (34).

One study in particular analyzed spatial patterns along the HIV Care Continuum to identify areas with poor care outcomes. Investigators from the Philadelphia Department of Public Health and the University of Pennsylvania studied the HIV Care Continuum in Philadelphia, PA using GIS technologies (29). For the study, they created four outcomes from the HIV Care Continuum steps (linkage to care, linkage to care within 90 days, retention in care, and viral suppression) and examined data for the residence at diagnosis for people diagnosed with HIV infection between 2008 and 2009 in Philadelphia, PA (29). Each study subject's set of outcomes were populated using laboratory result data provided at the date of diagnosis with follow-up to 2011, found in Philadelphia's Enhanced HIV/AIDS Reporting System (29). Spatial patterns were created using local cross K-functions, which calculate whether a case is significantly clustered or not with other cases using a radial distance band of which they used a 5000 foot distance (29). The result of the spatial analysis was the identification of four sets of geographic hot spots, one for each HIV Care Continuum outcome (29). No geographic overlap between hot spots from different HIV Care Continuum steps was exhibited (29). Overall, the study enrolled 1704 people and 82% were linked to care in the 24-month observation period, 75% were linked to care within

90 days of their diagnosis among those linked to care, 37% were retained in care among those linked to care, and 72% were virally suppressed among those retained in care (29). Using logistic regression, the relationships between each outcome variable and residence inside of a geographic hot spot were evaluated, controlling for age at diagnosis, sex at birth, race/ethnicity, transmission risk factor, insurance type, imprisonment, proximity to medical care, and receiving care from multiple care sites (29). The models showed that individuals residing in a hot spot had higher odds of not linking to care, not linking to care within 90 days, not being retained in care, and not being virally suppressed compared to persons residing outside of the hot spots (29). This study was the first of its kind to identify spatial patterns that were strong independent predictors of linkage to care, retention in care, and viral suppression (29).

Although the Philadelphia HIV Care Continuum study remains the only known published study that investigated spatial patterns of the HIV Care Continuum, other spatial analysis studies have been published in the area of HIV. A 2011 study from the New York City (NYC) Department of Health and Mental Hygiene performed spatial analysis on individuals newly diagnosed with HIV in NYC using United Hospital Fund neighborhoods in which they reside to function as their locations (28). Using ArcGIS 9.3, the NYC investigators created density maps of residences of new HIV diagnoses in 2007 in NYC using a distance diameter of one mile (28). The density surface maps of the newly diagnosed cases produced were able to be used to identify geographic areas where the HIV disease burden concentrated (28).

A different study from Duke University Medical Center in Durham, North Carolina (NC) was designed to evaluate whether or not GIS technologies could be used as strategy to locate subjects to screen for tuberculosis, syphilis, and HIV, through the identification of geographic hot spots of each of the diseases (27). The Duke University investigators overlaid maps with the densities of all three diseases in Wake County, NC from 2005-2007 and then proceeded to visually identify two areas with the highest density of all three diseases and were designated hot spots (27). Screening for all three diseases was then performed on eligible participants in clinics

located at the hot spots and found 8 participants with HIV infection, 3 with untreated syphilis, and 36 with latent tuberculosis infection (27). GIS-based screening was deemed an effective means of determining areas with a burden of disease (27).

Finally, a study from Emory University in Atlanta, Georgia assessed HIV prevalence in Atlanta at the census tract level and identified one large cluster of prevalent HIV cases using Kulldorff's spatial scan method (30). The cluster was located in central downtown Atlanta and contained 60% of the prevalent cases in the metro Atlanta area (30). The cluster was characterized by poverty, MSM, injection drug use and 42% of identified HIV service providers were located inside of the cluster (30). The spatial analyses determined that the burden of the HIV prevalent epidemic in metro-Atlanta is centralized (30).

Characterizing the Gaps in Care

GIS technologies can be used to characterize an epidemic and to identify geographic hot spots of the disease under investigation. As previously described, the spatial analysis of the HIV Care Continuum in Philadelphia was a novel approach to evaluate the attrition from care among persons diagnosed with HIV infection. Adapting the methods used in the Philadelphia study to analyze spatial patterns in other major cities may provide further insight into what factors influence poor care outcomes and how to prevent HIV-infected individuals from falling off the HIV Care Continuum. As one of the metropolitan areas most affected by the HIV epidemic in the United States, Atlanta, Georgia stands out as a leading choice on which to perform these spatial analyses. In addition, metro-Atlanta has disproportionately distributed HIV/AIDS care providers and poor spatial accessibility to care providers, thus the area needs further investigation of the gaps in care (35). As stated earlier, five public health districts bear the majority of the HIV burden in the Atlanta EMA and they consist of eight counties: Fulton, DeKalb, Gwinnett, Clayton, Douglas, Cobb, Rockdale, and Newton (22). With the exception of Rockdale and Newton counties, which have substantially lower prevalence data than the others, these counties

will form the geographic study area for these analyses (36). Using a geographic area that is more densely populated with cases will be more informative and reduce the hot spots created around singular, isolated cases (34). Therefore, we seek to identify geographic hot spots associated with poor engagement in the HIV Care Continuum among persons newly diagnosed with HIV infections in a 6-county Atlanta metropolitan area, consisting of Fulton, DeKalb, Gwinnett, Clayton, Douglas, and Cobb counties. Using spatial analysis to detect geographic hot spots of attrition along the HIV Care Continuum may serve to identify how best to control the HIV epidemic in metropolitan Atlanta.

Spatial Analysis of Attrition Along the HIV Care Continuum in the Atlanta Metropolitan Area

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ABSTRACT

Context Proper HIV management and prevention requires adherence to the HIV Care Continuum steps, which consist of diagnosis, linkage to care, retention in care, initiation of antiretroviral therapy, and achievement of viral suppression. Using spatial analysis to detect geographic hot spots of attrition from these steps may serve to identify how best to control the HIV epidemic.

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Conclusion: Spatial patterns associated with clustering of poor outcomes were found to be strong independent predictors of linkage to care, retention in care, and viral suppression in a 6-county section of the metro-Atlanta area. The findings provide further evidence for the use of spatial analyses as a tool for characterizing the HIV Care Continuum.

INTRODUCTION

Antiretroviral therapy (ART) is currently recommended for all people living with HIV (PLWH) to decrease HIV viral load, improve immune system function, prevent opportunistic infections, and reduce the risk of HIV transmission to others (2-4). The early initiation of ART can greatly improve individual survival and lead to HIV treatment as prevention (10, 11). However, proper HIV management requires adherence to a set of steps, which form the HIV Care Continuum: diagnosis, linkage to care, retention in care, initiation of ART, and achievement of viral suppression (14, 15). Poor engagement in care among HIV-infected individuals is associated with poor health outcomes, including increased mortality; thus assessing progress along the HIV Care Continuum can serve as a measurement to identify gaps in care (15, 37, 38).

Surveillance data from each step of the HIV Care Continuum has previously been evaluated by sex, age, race/ethnicity, and transmission risk category (13, 38-40). Evaluating the HIV Care Continuum based on these individual characteristics can and has revealed disparities among different age groups, race/ethnicity groups, risk groups, and sexes but there is limited data on whether geographic patterns of attrition along the continuum can be used to determine spatial disparities.

Atlanta, Georgia has emerged as a center for the HIV epidemic in the United States. Georgia ranked 5th out of the 50 states for the number of new HIV diagnoses in 2011 (8). Additionally, the Atlanta metropolitan area was ranked the city with the 5th highest number of new HIV diagnoses in the United States in 2013, based on estimated rates of infection (9). There are also issues of poor engagement in the HIV Care Continuum steps in Georgia. Among new diagnoses in the Atlanta EMA in 2011, 60% were linked to care within 3 months of diagnosis, 47% were retained in care, and 46% were virally suppressed (21). These poor outcomes of care are exacerbated by demographic disparities in the HIV Care Continuum. Blacks less likely to be linked, retained, or virally suppressed than Whites or Hispanics (21). Younger persons in the 13-

24 age range were less likely to be linked, retained, or virally suppressed than older persons, while linkage among men who had sex with men had the least amount of linkage, retention, and viral suppression (21).

Health outcomes are influenced by individual-level biological and behavioral factors and have been increasingly recognized to be influenced by contextual community-level factors (23-25). To understand how contextual influences affect health, a number of researchers have turned to the use of geographic information system (GIS) technology to map outcomes and perform spatial analyses to organize and visualize health data (26-29). Spatial analyses can be used to identify disparities in disease distribution or in access to resources, such as health care providers (31-33). In addition, GIS technologies provide methods to determine geographic clusters, or hot spots, where outcomes are concentrated (34). Detecting geographic hot spots, or clustering, of attrition from steps along the HIV Care Continuum may serve to identify how best to prioritize and allocate resources to where gaps in the HIV Care Continuum are located and to assist in monitoring progress in specific areas.

In coordination with investigators from the Georgia Department of Public Health (GDPH) and Emory University, the aim of this study is to identify geographic areas associated with not linking to care, not linking to care within 90 days, not being retained in care, and not achieving viral suppression. Building on the methodology of Eberhart et al., who sought to identify areas related to the same set of outcomes in Philadelphia, this study evaluates these unsuccessful care outcomes based on the framework of the HIV Care Continuum for people newly diagnosed with HIV infections in 2010 and 2011 in a 6-county metro-Atlanta area using GIS technology (29).

METHODS

Data Source and Study Population

Analyses were performed on data extracted from the Georgia Enhanced HIV/AIDS Reporting System (eHARS), a browser-based database that is used to collect and manage HIV/AIDS case surveillance data for reporting to the CDC. Georgia legally requires both health care providers and laboratories to report all HIV cases, including all subsequent tests indicative of an HIV infection, such as all detectable and undetectable viral loads and all CD4 counts and percentages (18, 19). In addition, healthcare facilities are required to report to the GDPH any changes to patient information (i.e. name, address, and/or gender), any change in clinical status (i.e. AIDS status or AIDS-defining clinical conditions), and any new patients entering care in their facility (19). Death data on persons diagnosed with HIV infections is also ascertained from the Social Security Administration's Death Master File, the National Death Index, and Georgia's State Office of Vital Records (18). As a result, the Georgia eHARS is the most comprehensive database of information on HIV/AIDS cases for use in these analyses.

The Atlanta Eligible Metropolitan Area (EMA) incorporates 20 counties in north Georgia, including Bartow, Paulding, Carroll, Coweta, Fayette, Spalding, Henry, Newton, Rockdale, Gwinnett, Walton, Barrow, Forsyth, Cherokee, Pickens, DeKalb, Fulton, Clayton, Cobb, and Douglas counties (21). This study will focus on a 6-county area of the Atlanta EMA, including Fulton, DeKalb, Gwinnett, Clayton, Douglas, and Cobb counties. The city of Atlanta resides in Fulton County with small extension east into DeKalb County. The study population was selected based on their year of diagnosis, residential address at diagnosis, and current residential address in order to locate HIV cases in the 6-county metro-Atlanta area of interest. The current addresses of cases diagnosed in 2010 and 2011 were used as proxies for addresses at diagnosis as there was not a sufficient percentage of valid addresses at diagnosis that could be assigned to spatial locations for analysis. Therefore, the criteria for inclusion were as follows: 1) a

valid, new HIV diagnosis in 2010 or 2011, 2) a Georgia address located in Fulton, DeKalb, Gwinnett, Clayton, Douglas, or Cobb County at the time of diagnosis and currently, and 3) a vital status of living or dead after the 24-month observation period. Individuals excluded from analysis had invalid or insufficient current address data or an address at a correctional facility at the time of diagnosis or as their current address.

Outcome and Predictor Variables

Information on age, sex at birth, race/ethnicity, and HIV transmission risk was collected for each case. Age at diagnosis was separated into categories: <25, 25-45, and >45 years. Race/ethnicity was categorized as non-Hispanic white, non-Hispanic black, Hispanic, or other/unknown. Transmission risk was categorized as heterosexual contact only, male-to-male sexual contact (MSM), injection drug use (IDU), and other/no identified risk (NIR)/no reported risk (NRR). Any case with IDU as an HIV transmission risk in combination with any other risk was grouped into the IDU category. Cases who were classified as MSM & heterosexual contact were grouped into the MSM category. Perinatal exposure was grouped into other/NIR/NRR.

Outcome variables were determined using the HIV Care Continuum, which defines the necessary stages for PLWH to achieve viral suppression (15). These stages were adapted for this analysis into 4 steps that reflect poor outcomes: 1) not linked to care, in the follow-up period, 2) not linked to care within 90 days of diagnosis, 3) not retained in care, and 4) not achieved viral suppression. The categorization of the outcome variables was chosen in accordance with the methodology of Eberhart et al. Linkage to care was defined as post-diagnosis documentation of 1 or more CD4 count or viral load test results (29). Linkage to care within 90 days was defined as having 1 or more CD4 count or viral load test results in the first 90 days after diagnosis, based on the difference in time between the date of diagnosis and the date of the first laboratory test result (29). Retention in care was defined as completion of at least 1 comprehensive HIV medical care visit in each 6-month period of a 24-month measurement period with a minimum of 60 days

between medical visits, as described by the National Quality Forum Medical Visit Frequency Measure (29, 42). The beginning of the 24-month measurement period was marked as the date of first linkage to care. CD4 count and/or viral load test results were used to approximate the completion of comprehensive HIV medical care visits (29). Viral Suppression was defined as documentation of a HIV-1 RNA viral load <200 copies/mL at the end of the 24-month measurement period ±120 days, to detect virally suppressed individuals receiving viral load testing at 4 month intervals (29). Following study population selection with the inclusion and exclusion criteria, HIV Care Continuum markers for the outcome variables were calculated, and predictor variables and address data were pulled using SAS 9.3 (SAS Institute Inc., Cary, NC) (Appendix A). The data was divided into four distinct datasets for each outcome step with each having a denominator that is a subset of a previous step: 1) the linkage to care dataset, containing all eligible persons in the study population, 2) the linkage to care within 90 days dataset, containing all eligible persons sans those not linked to care, 3) the retention in care dataset, containing all eligible persons sans those not linked to care, and 4) the viral suppression dataset, containing all eligible persons sans those not retained in care.

Mapping and Spatial Analysis

Current residential address data extracted from the eHARS database was geocoded, using ArcMap in ArcGIS 10.2 (ESRI, 2014) and an address locator provided by the GDPH Spatial Analysis & GIS Team, into geographic coordinates that could be projected onto a map of the 6-county metro-Atlanta area of interest. Spatial data was projected onto the XY coordinate system NAD 1983 Georgia Statewide Lambert (US Feet). Analyses on these coordinates were performed using the ArcGIS Spatial Statistics and Spatial Analyst tools for analyzing spatial distributions and patterns.

Hot Spot Analysis (Getis-Ord Gi*) is a mapping cluster tool that calculates the Getis-Ord Gi* statistic, which is a z-score accompanied by a p-value, for each weighted feature in the input

dataset (34, 43). The tool examines each set of spatial coordinates for a feature and its location in relation to neighboring features to determine whether high or low values spatially cluster into statistically significant hot spots or cold spots (34, 43). With the Hot Spot Analysis tool, incident data must be aggregated prior to analysis to provide weight to point data, so coincident points were combined into sums of cases at each unique location for both sides of an outcome using the Collect Events tool in ArcMap (43, 44). To distinguish between persons engaged in HIV Care Continuum steps and persons not engaged in the steps, sums of cases engaged at coincident locations were converted to negative values of -1 or less while sums of cases not engaged had positive values of 1 or greater. Each sum of cases represents either one feature or a set of features in the dataset, but we will refer to a set of features as simply a feature from now on. For the purposes of this study, non-engagement in the HIV Care Continuum outcomes was being evaluated to locate hot spots of persons not engaged. A hot spot is defined by a feature with a high, positive value that is surrounded by other features with high, positive values (34, 43). If the local sum of these features and neighboring features is very different from the expected local sum when compared proportionally to the sum of all features and this difference is too large to be present in a random distribution of the same values, then these features are assigned statistically significant z-scores (34, 43). Statistically significant, positive z-scores translate into a hot spot of high values, whereas statistically significant, negative z-scores indicate a cold spot of low values (34, 43). No clear spatial clustering is present where features have a z-score near zero (34, 43). In addition, these calculations may assign high z-scores to features with low values and vice versa based on the level of spatial clustering present (34, 43). Thus, not all cases within a hot spot may contribute to the hot spot. Spatial relationships among features were conceptualized based on a fixed distance band of 25,000 ft., which is a distance that ensures that each feature has at least one neighboring feature. Neighboring features within this 25,000 ft. distance receive a spatial weight of 1, while features outside of this distance band receive a spatial weight of 0, and these weights are used in the computations of the Gi* statistic for each target feature (34, 43).

Evaluating each of the four distinct outcome datasets in the Hot spot Analysis (Getis-Ord Gi*) tool yielded four sets of z-scores and p-values that were then interpolated to a continuous (or predicted) raster surface using an inverse distance weighted (IDW) interpolation technique available in the ArcGIS Spatial Analyst extension. IDW interpolation uses a linearly weighted combination of a set of sample points to predict measurements for all locations in a raster dataset, essentially assigning values to unmeasured locations based on the surrounding measured values (45). IDW interpolation assumes that a feature's influence decreases with distance from its location, thus this distance is weighted by a function of inverse distance (45). After all input measurements and predicted measurements are assigned to locations, the values are smoothed into an interpolated surface raster (45). We input the Hot Spot Analysis results into the IDW interpolation tool, with the Gi* z-scores used as the magnitude value for each point, resulting in a raster surface that displayed the predicted shape of hot spots on the extent of the 6-county map. The interpolated surface raster was then overlaid with contour lines, which connect locations of equal value within the raster, and converted into enclosed polygons thereby emphasizing areas of statistical significance that represent the hot spots of the HIV Care Continuum outcomes (46).

Using the Generate Near Table tool in ArcMap, distances were calculated between individual points, representing cases in the denominator for each outcome, and the closest "hot spot" polygon for specified outcomes (47). The generated tables of distances were then joined to each population, and a distance of 0 was considered to denote that a person was within the hot spot in question.

The geographic distribution of the cases diagnosed with HIV infection in 2010 and 2011 in the 6 counties was depicted using the Kernel Density tool and major HIV/AIDS medical care providers were geocoded to show their distribution for comparison purposes (48, 49).

Statistical Analysis

Statistical analyses on the predictor, exposure, and outcome variables were produced in SAS 9.3 (SAS Institute Inc., Cary, NC). Bivariate statistics and Pearson chi-square tests were used to describe the included and excluded datasets and the differential engagement in the 4 outcomes. Four multivariable logistic regression models were fit to assess the relationship between residing in a geographic hot spot and the outcomes of interest related to each set of hot spots, controlling for age at diagnosis, sex at birth, race/ethnicity, and transmission risk as potential confounders (Appendix B). Confounding was evaluated in each model, but no reduced models gave meaningfully better precision to the results than the fully controlled models. Adjusted odds ratios (AORs) with 95% confidence intervals (CIs) were generated, with a p-value <0.05 considered statistically significant.

RESULTS

In 2010 and 2011, 2592 people were newly diagnosed with HIV in Fulton, DeKalb, Gwinnett, Clayton, Douglas, and Cobb counties and met the inclusion criteria (Table 1). Excluded from those identified were 253 people (10%) who had invalid or insufficient current address data (N=180) or had an address at a correctional facility at the time of diagnosis or as their current address (N=73).

For the 2339 included persons, 80.5% were male, 76.4% were black, and 52.8% were between 25 and 45 years old at the time of diagnosis. The majority of HIV transmission risk factors were other/NIR/NRR (44.4%), followed by MSM (42.7%). Excluded persons were determined to not be statistically significantly different from included persons in our analytic sample. Among all eligible diagnoses, 2067 persons (88.4%) were linked to care (Table 2). Among all of those linked to care, 1295 persons (62.6%) were linked to care within 90 days and 663 persons (32.1%) were retained in care. Among those retained in care, 326 persons (49.2%) were virally suppressed. Overall, only 13.9% of the 2339 persons included in the analysis met the

study criteria for linked to care, retained in care, and viral suppression during the 24-month follow-up period. Age at diagnosis, race/ethnicity, and residing in a geographic hot spot were each found to be significantly associated with each of the outcomes of interest, according to the Pearson chi-square tests. Transmission risk was significantly associated with linkage to care during the observation period and linkage to care within 90 days. Sex at birth was not observed to have an association with any one the four outcomes.

Spatial Patterns

The 6-county metro-Atlanta area of interest, shown in Figure 1 as a reference, contains 492 census tracts. Figure 2 shows the geographic distribution of the 2010 and 2011 HIV infection diagnoses in the 6 counties. Figure 3 shows the distribution of major HIV/AIDS care providers. Figures 4-7 show the areas identified as geographic hot spots for each of the 4 outcomes.

HIV-infected persons diagnosed in 2010 and 2011 were observed to concentrate in counties with the highest populations and in the most densely populated areas of those counties, explicitly in the center of Fulton County and most of DeKalb County (Figure 2). The distribution of major HIV/AIDS medical care providers also follows a similar pattern, with a dense concentration of care facilities in the city of Atlanta in the center of Fulton County (Figure 3).

Hot spots associated with persons not linking to care were found to be in southern Fulton Co. on the border of Clayton Co., in southeastern DeKalb Co., and in small areas in central Gwinnett Co. and Douglas Co. (Figure 4). These hot spots included 45 census tracts. Hot spots associated with not linking to care within 90 days are smaller and more spread out, including an area between DeKalb Co. and Gwinnett Co., and small areas in west and south DeKalb Co., south of Atlanta in Fulton Co., and in northwest Gwinnett Co. near the border of Fulton Co. (Figure 5). These hot spots included 19 census tracts. Hot spots for not being retained in care included a large area in Cobb Co. that extends into Fulton Co. and a few smaller, scattered areas in

southeastern Fulton Co. (Figure 6). These hot spots included 25 census tracts. Hot spots associated with not achieving viral suppression were located in a large area in central DeKalb Co., in a large area extending from Fulton Co. to Clayton Co., and in small areas in central Cobb Co. and central Fulton Co. (Figure 7). These hot spots included 64 census tracts. A total of 128 unique census tracts were identified to include the geographic hot spots out of a total of 492 census tracts contained in the 6-county area.

Considering only hot spots with radial distances over 1,250 ft., we observed three instances of overlapping hot spots that were created from different outcomes. First, a large hot spot associated with non-linkage to care overlapped another large hot spot associated with not achieving viral suppression in southern Fulton Co., on the border of Clayton Co. (Figures 4 and 7). More overlapping was observed between a large hot spot associated with non-linkage to care and a large hot spot associated with no viral suppression in the center of DeKalb Co. (Figures 4 and 7). The final instance of overlapping occurred with the large hot spot associated with non-linkage to care in central DeKalb Co. and a couple of small hot spots associated with not linking to care within 90 days (Figures 4 and 5).

Logistic Regression Models

Logistic regression models were fit to assess the relationship between residing in the geographic hot spots and the outcomes of interest related to each set of hot spots (Table 3).

Model 1 – Not Linked to Care

A model was fit to assess the relationship between not linking to care and residing in geographic hot spots of non-linkage to care, controlling for age at diagnosis, sex at birth, race/ethnicity, and transmission risk. Persons currently residing inside of the geographic hot spots had higher odds of not linking to care during a 24-month observation period than persons residing outside of those hot spots [AOR: 1.57 (95% CI: 1.04-2.38)]. Blacks had higher odds of non-

linkage than Whites to not be linked. Persons under 25 years old at diagnosis had a higher odds of non-linkage than persons over 45 years old at diagnosis No significant differences were detected between sexes at birth, between known transmission risks, or between Hispanics and Whites.

Model 2 – Not Linked to Care Within 90 Days

A model was fit to assess the relationship between not linking to care within 90 days and residing in geographic hot spots of non-linkage to care within 90 days, controlling for age at diagnosis, sex at birth, race/ethnicity, and HIV transmission risk. Persons currently residing inside of geographic hot spots had higher odds of not linking to care within 90 days than persons residing outside of the identified hot spots [AOR: 3.13 (95% CI: 1.18-8.32)]. Blacks had higher odds than Whites for non-linkage within 90 days, while persons less than 25 years old at diagnosis had higher odds for non-linkage within 90 days compared to those older than 45 years. Additionally, individuals with MSM or other/NIR/NRR as their transmission risk compared with those with heterosexual contact only as their transmission risk had higher odds for not linking to care within 90 days. No differences were observed by sex at birth.

Model 3 – Not Retained in Care

A model was fit to assess the relationship between not being retained in care and residing in geographic hot spots of non-retention in care, controlling for age at diagnosis, sex at birth, race/ethnicity, and HIV transmission risk. Among those linked to care, individuals currently residing inside of geographic hot spots had higher odds of not being retained in care compared to those outside of those locations [AOR: 1.99 (95% CI: 1.07-3.68)]. Blacks and other races/ethnicities had higher odds of non-retention in care than Whites, while younger individuals had higher odds of the same effect compared to those older than 45 years at diagnosis. No significant differences were detected by transmission risk or sex at birth.

Model 4 – Not Virally Suppressed

A model was fit to assess the relationship between not achieving viral suppression and residing in geographic hot spots of non-achievement of viral suppression controlling for age at diagnosis, sex at birth, race/ethnicity, and HIV transmission risk. Among those retained in care, persons currently residing in the geographic hot spots had higher odds of not achieving viral suppression compared to persons residing outside of those hot spots [AOR: 2.92 (95% CI: 1.59-5.36)]. In regards to not being virally suppressed, Blacks had a higher odds than Whites, and persons between 25 and 45 years old and persons under 25 years old at diagnosis had a higher odds than persons over 45 years old at diagnosis. No differences were observed by transmission risk or sex at birth.

DISCUSSION

Among those diagnosed with HIV infections in 2010 and 2011, we identified 2339 individuals who met our inclusion and exclusion criteria. Of those in our cohort, 88% were linked to care within the first 24 months of their diagnosis. Among those linked to care, 63% were linked to care within 90 days of their diagnosis and 32% were retained in care during the 24 months observed. Approximately 49% of those retained in care achieved viral suppression. Overall, only 14% of those 2339 selected individuals met the criteria for being linked to care, being retained in care, and achieving viral suppression during the 24-month follow-up period. For comparison, the GDPH reports that among adults and adolescents diagnosed with HIV infections in 2011 in the Atlanta EMA, 60% were linked to care within 3 months of diagnosis, 47% were retained in care, and 46% were virally suppressed (21). Our outcome for “linkage to care” pertains to having at least 1 viral load test after diagnosis during the 24-month observation period, whereas the GDPH does not directly produce estimates for this outcome. Although our estimate for linkage to care within 90 days was consistent with the HIV Care Continuum surveillance data,

we suspect that our estimates for retention at 32% and overall viral suppression at 23% differ from the estimates produced by the GDPH due to the differences in the inclusion of persons diagnosed in 2010 and 2011 in our cohort compared to only 2011 in the GDPH cohort, the differences in follow-up periods, which can determine when the most recent viral load test occurred for purposes of defining viral suppression, and differences in the definition of "retention in care" between our estimates. The GDPH defined retention in care as 2 or more CD4 or viral load results at least 3 months apart, 4 to 15 months after diagnosis, whereas we defined retention in care as at least 1 CD4 or viral load result in each 6-month period of the 24-month measurement period with a minimum of 60 days between test results (21). Our decision to define retention in care in this manner was to remain consistent with the methodology of Eberhart et al.

The majority of cases in our cohort were male (80.5%), black (76.4%), between 25 and 45 years old (52.8%), and had a transmission risk that was other/NIR/NRR (44.4%). The majority of PLWH in metro-Atlanta in 2011 were male (79%), black (62%), between 25 and 45 years old (46%), MSM among males (76%), and heterosexual among females (72%) (50). Therefore, our cohort is relatively consistent with GDPH HIV surveillance estimates of adults and adolescents living with HIV in metro-Atlanta in 2011, except for the transmission risks (50). The discrepancies in our findings for transmission risk compared to the GDPH estimates can be attributed to the difference in approach to missing data. As a substantial amount of data is reported to the GDPH without an identified risk factor, the GDPH uses multiple imputation (MI), a statistical adjustment approach for assigning plausible values to replace missing data (51). The GDPH uses MI on the transmission risk categories thereby reducing the proportion of cases with NIR and NRR as transmission risks and increasing other risks (51). MI is the recommended CDC methodology; however, MI methods make assumptions that cannot be assessed for validity (51). As the relationships between the HIV Care Continuum outcomes and the risks of cases listed as NIR or NRR may fundamentally differ from the relationships between the outcomes and the

assigned risks through MI, this study decided to not use MI to account for missing risk factor data, and instead reports only the raw data (51).

Using sex, age, race/ethnicity, and transmission risk group to predict attrition at each step of the HIV Care Continuum has been studied previously, but few used geographic factors as predictors (29, 37, 52). Building on the methodology of Eberhart et al., this study attempted to use the spatial relationship of cases associated with negative outcomes to identify geographic hot spots that can predict outcomes along the HIV Care Continuum. Residing in geographic hot spots was independently associated with all four outcomes. Overall, we found that each set of geographic hot spots contained between 19 and 64 census tracts, which summed to 128 unique census tracts (26.0% of all tracts in the 6-county area) and accounts for some overlapping between hot spots. The overlap between hot spots observed in three instances may suggest that individual-level factors and community-level factors that affect these outcomes may be similar across the stages of the HIV Care Continuum in the areas where hot spots are overlapping; however, other hot spots that do not exhibit geographic overlap may imply the same factors do not explain all of the differences responsible for poor outcomes. Individual-level and community-level factors that may impact the HIV epidemic for persons residing in the geographic hot spots include poverty, education, discrimination, social stigma, crime and incarceration rates, limited public transportation options, limited access to social services, and housing stability issues (53-59).

Although the 128 unique census tracts associated with all of the geographic hot spots represent 26.0% of all census tracts in the area and contain 31.9% of our all HIV-infected persons in our cohort, the geographic hot spots themselves contain only 19.5% of the cohort. Based on the number of census tracts intersecting our hot spots, the high density of cases in the smaller geographic area may indicate a higher burden of HIV and the need for increased treatment and preventative services; however, these census tracts cover a much larger area than the hot spots we

identified. Thus, the identified hot spots may be better representative of the total area impacted by the burden of poor outcomes in the HIV Care Continuum than the census tracts in which the hot spots reside. Proximity to care was not assessed directly, but we observed that the majority of the hot spots were located in areas where major HIV/AIDS medical care providers (Figure 3) were within 5 miles, which may suggest that distance to care is not a major factor in determining whether an individual engages in care. However, without assessing individual travel distance to HIV/AIDS medical care providers, we cannot determine whether proximity to care is associated with any of the four outcomes. Evaluation of proximity to care, with consideration to issues of insurance plans and ability to pay for care, deserves further investigation.

Using the multivariable logistic regression models, we found that residing in a geographic hot spot resulted in having higher odds for having a poor outcome at each step of the HIV Care Continuum compared to not residing in a hot spot. Independent of residing in a hot spot, the odds of Blacks not being engaged in care or achieving viral suppression was higher than the odds for Whites at each step of the continuum. For a person younger than 25 years at the time of their HIV diagnosis, the odds of not being linked to care within 90 days, retained in care, or virally suppressed were higher than the odds for a person older than 45 years old, adjusting for residence in a hot spot. The same holds true for the odds of persons between 25 years old and 40 years old not being retained in care or achieving viral suppression compared to persons older than 45 years old at diagnosis. In addition, the odds of MSM being not linked to care within 90 days were higher than the odds of heterosexual persons. These findings for disparities in level of care for Blacks, younger persons, and MSM are consistent with other published estimates of progress along the HIV Care Continuum (2, 41, 60, 61). Among Blacks and MSM, lower levels of care may be influenced by factors that include poverty, stigma, discrimination, and lack of health insurance (61, 62). Further research needs to be performed to evaluate how other individual-level

factors and community-level factors may be predictors of treatment failure for persons in these hot spots.

The findings in this study are subject to at least six limitations. First, we used current residential address data as a proxy for residential address data at diagnosis, yet we suspect that this decision may partially account for migration, as those diagnosed in the 6-county area are more likely to have received care in the 6-county area if they currently reside in the area. However, this means that any subject with an invalid or insufficient current address data was dropped from analysis. Second, we excluded individuals with an address at a correctional facility at the time of diagnosis or as their current address. The exclusion of incarcerated populations was performed because their clustering is non-random and would represent a source of bias in the Hot Spot Analyses. Additionally, populations in correctional facilities have different access to HIV treatment compared to the general population. Third, this study did not use MI methods to assign transmission risk factors to cases without identified risk factors, thus our results for transmission risks could be found altered after MI. Fourth, we could not evaluate ART use or account for possible underreporting of CD4 or viral load results as the data was extracted from routine HIV surveillance. Although law mandates that HIV viral loads are reported, we cannot fully account for missing laboratory reports and incomplete reporting, and there is uncertainty for portions of the population for which laboratory data may be missing. Without the key laboratory data used to determine engagement in care or achievement of viral suppression in the 24-month follow-up period, persons may have been classified as having poor outcomes. Fifth, since our sample population was newly diagnosed in 2010 and 2011 and follow-up was to 2013, not all of these individuals may have been eligible for ART according to Department of Health and Human Services ART treatment guidelines from 2011 (63). Sixth, areas with less case density can influence the Hot Spot Analysis calculations, resulting in small, isolated hot spots, which can reflect the “clustering” of one or two cases with poor outcomes within 25,000 ft. of each other.

These small hot spots can be created as an artifact of the lack of surrounding case density due to the cohort selection. However, small hot spots may also be indicative of significant clustering of many coincident cases in a small, yet densely populated area. Determining the difference between small hot spots created from areas with less, surrounding case density and hot spots created from areas with more, surrounding case density can be accomplished through comparison with the kernel density of cases diagnosed in 2010 and 2011, as seen in Figure 2.

In summary, we identified spatial patterns that were strong independent predictors for attrition along the HIV Care Continuum, as defined by linkage to care, retention in care, and viral suppression. The methods used herein to analyze these outcomes can be used to identify the demographics and geographic location of cases not engaged in care or not virally suppressed, allowing for more specifically targeted interventions. Future studies should focus on other individual-level factors and community-levels factors that may influence HIV Care Continuum loss within the cohort, such as health insurance, proximity to care services, crime levels, infrastructure, access to public services, and housing stability. In this study, we provided further evidence for the use of spatial analyses to evaluate the HIV Care Continuum. The importance of properly allocating resources and interventions to the areas where improvement is most needed cannot be understated in managing the HIV epidemic, thus the detection of geographic hot spots of poor care outcomes will likely prove to be critical in enhancing linkage to care, retention in care, and viral suppression.

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TABLES

Table 1. Characteristics of Persons Diagnosed With HIV Infection in Metropolitan Atlanta† by Inclusion in the Analysis Sample, 2010-2011.

Characteristics	Included n=2339 (%)	Excluded n=253 (%)	χ^2	*P*
Age at diagnosis (yrs)			1.31	0.52
>45	542 (23.2)	65 (25.7)		
25-45	1235 (52.8)	134 (53.0)		
<25	562 (24.0)	54 (21.3)		
Sex at birth			0.04	0.84
Female	456 (19.5)	48 (19.0)		
Male	1883 (80.5)	205 (81.0)		
Race/Ethnicity			0.78	0.86
White	310 (13.2)	31 (12.2)		
Black	1786 (76.4)	198 (78.3)		
Hispanic	166 (7.1)	15 (5.9)		
Other/Unknown	77 (3.3)	9 (3.6)		
Transmission risk			5.65	0.13
Heterosexual Contact	247 (10.6)	22 (8.7)		
MSM	999 (42.7)	94 (37.1)		
IDU	55 (2.3)	5 (2.0)		
Other/NIR/NRR	1038 (44.4)	132 (52.2)		

MSM: male-to-male sexual contact; IDU: injection drug use; NIR: no identified risk; NRR: no risk reported; Significance at $P < 0.05$, Pearson chi-square test

† Metropolitan Atlanta: Fulton, DeKalb, Gwinnett, Clayton, Douglas, and Cobb counties

Table 2. Engagement at Each Step of the HIV Care Continuum among a Sample of Persons Diagnosed with HIV Infection in Metropolitan Atlanta† by Select Characteristics, 2010-2011.

	Linkage to Care, n = 2339			Linkage Within 90 Days Among Those Linked, n = 2067			Retention in Care among Those Linked, n = 2067			Viral Suppression Among Those Retained, n = 663		
Predictors	Yes, n (%)	No, n (%)	*P*	Yes, n (%)	No, n (%)	*P*	Yes, n (%)	No, n (%)	*P*	Yes, n (%)	No, n (%)	*P*
Total	2067 (88.4)	272 (11.6)		1295 (62.6)	772 (37.4)		663 (32.1)	1404 (67.9)		326 (49.2)	337 (50.8)	
Age at diagnosis (yrs)			*			*			*			*
>45	481 (88.7)	61 (11.3)		312 (64.9)	169 (35.1)		189 (39.3)	292 (60.7)		110 (58.2)	79 (41.8)	
25-45	1112 (90.0)	123 (10.0)		733 (65.9)	379 (34.1)		358 (32.2)	754 (67.8)		175 (48.9)	183 (51.1)	
<25	474 (84.3)	88 (15.7)		250 (52.7)	224 (47.3)		116 (24.5)	358 (75.5)		41 (35.3)	75 (64.7)	
Sex at birth												
Female	414 (90.8)	42 (9.2)		274 (66.2)	140 (33.8)		138 (33.3)	276 (66.7)		66 (47.8)	72 (52.2)	
Male	1653 (87.8)	230 (12.2)		1021 (61.8)	632 (38.2)		525 (31.8)	1128 (68.2)		260 (49.5)	265 (50.5)	
Race/Ethnicity			*			*			*			*
White	294 (94.8)	16 (5.2)		204 (69.4)	90 (30.6)		140 (47.6)	154 (52.4)		87 (62.1)	53 (37.9)	
Black	1545 (86.5)	241 (13.5)		937 (60.6)	608 (39.4)		438 (28.3)	1107 (71.7)		188 (42.9)	250 (57.1)	
Hispanic	154 (92.8)	12 (7.2)		105 (68.2)	49 (31.8)		62 (40.3)	92 (59.7)		37 (59.7)	25 (40.3)	
Other/Unknown	74 (96.1)	3 (3.9)		49 (66.2)	25 (33.8)		23 (31.1)	51 (68.9)		14 (60.9)	9 (39.1)	
Transmission risk			*			*						
Heterosexual Contact	236 (95.5)	11 (4.5)		176 (74.6)	60 (25.4)		86 (36.4)	150 (63.6)		42 (48.8)	44 (51.2)	
MSM	924 (92.5)	75 (7.5)		548 (59.3)	376 (40.7)		299 (32.4)	625 (67.6)		135 (45.2)	164 (54.8)	
IDU	52 (94.5)	3 (5.5)		36 (69.2)	16 (30.8)		18 (34.6)	34 (65.4)		7 (38.9)	11 (61.1)	
Other/NIR/NRR	855 (82.4)	183 (17.6)		535 (62.6)	320 (37.4)		260 (30.4)	595 (69.6)		142 (54.6)	118 (45.4)	
Located in Hot Spot			*			*			*			*
No	1919 (88.9)	239 (11.1)		1289 (62.9)	759 (37.1)		650 (32.6)	1346 (67.4)		310 (51.6)	291 (48.4)	
Yes	148 (81.8)	33 (18.2)		6 (31.6)	13 (68.4)		13 (18.3)	58 (81.7)		16 (25.8)	46 (74.2)	

MSM: male-to-male sexual contact; IDU: injection drug use; NIR: no identified risk; NRR: no risk reported;
* Significance at $P < 0.05$, Pearson chi-square test
† Metropolitan Atlanta: Fulton, DeKalb, Gwinnett, Clayton, Douglas, and Cobb counties

Table 3. Multivariable Logistic Models of Engagement at Each Step of the HIV Care Continuum for a Sample of Persons Diagnosed with HIV Infection in Metropolitan Atlanta†, 2010-2011.

	Not Linked to Care, n=2339		Not Linked to Care Within 90 Days, n = 2067		Not Retained in Care, n = 2067		Not Virally Suppressed, n = 663	
Predictors	AOR (CI)	*P*	AOR (CI)	*P*	AOR (CI)	*P*	AOR (CI)	*P*
Age at diagnosis (yrs)								
>45	1.0 (Ref)		1.0 (Ref)		1.0 (Ref)		1.0 (Ref)	
25-45	0.96 (0.69-1.35)		0.92 (0.73-1.16)		1.36 (1.08-1.72)	*	1.46 (1.00-2.12)	*
<25	1.66 (1.14-2.43)	*	1.45 (1.10-1.92)	*	1.85 (1.37-2.49)	*	2.12 (1.27-3.55)	*
Sex at birth								
Female	1.0 (Ref)		1.0 (Ref)		1.0 (Ref)		1.0 (Ref)	
Male	1.47 (0.97-2.23)		0.77 (0.56-1.06)		1.05 (0.75-1.48)		0.89 (0.50-1.60)	
Race/Ethnicity								
White	1.0 (Ref)		1.0 (Ref)		1.0 (Ref)		1.0 (Ref)	
Black	2.79 (1.63-4.76)	*	1.38 (1.05-1.82)	*	2.16 (1.65-2.81)	*	1.86 (1.23-2.82)	*
Hispanic	1.60 (0.73-3.52)		1.09 (0.71-1.68)		1.29 (0.86-1.93)		0.92 (0.37-2.32)	
Other/Unknown	0.72 (0.20-2.55)		1.11 (0.64-1.93)		1.92 (1.11-3.32)	*	0.92 (0.37-2.32)	
Transmission risk								
Heterosexual	1.0 (Ref)		1.0 (Ref)		1.0 (Ref)		1.0 (Ref)	.
MSM	1.12 (0.53-2.41)		2.44 (1.56-3.80)	*	1.08 (0.70-1.68)		1.48 (0.70-3.11)	
IDU	1.03 (0.26-3.99)		1.64 (0.81-3.31)		1.18 (0.59-2.34)		2.15 (0.67-6.86)	
Other/NIR/NRR	3.60 (1.79-7.26)	*	2.16 (1.45-3.22)	*	1.38 (0.93-2.04)		1.07 (0.55-2.09)	
Located in Hot Spot								
No	1.0 (Ref)		1.0 (Ref)		1.0 (Ref)		1.0 (Ref)	
Yes	1.57 (1.04-2.38)	*	3.13 (1.18-8.32)	*	1.99 (1.07-3.68)	*	2.92 (1.59-5.36)	*

MSM: male-to-male sexual contact; IDU: injection drug use; NIR: no identified risk; NRR: no risk reported; AOR: adjusted odds ratio; CI: 95% confidence interval; Ref: reference group;

* Significance at $P < 0.05$, compared to reference group, Wald chi-square test

† Metropolitan Atlanta: Fulton, DeKalb, Gwinnett, Clayton, Douglas, and Cobb counties

FIGURES

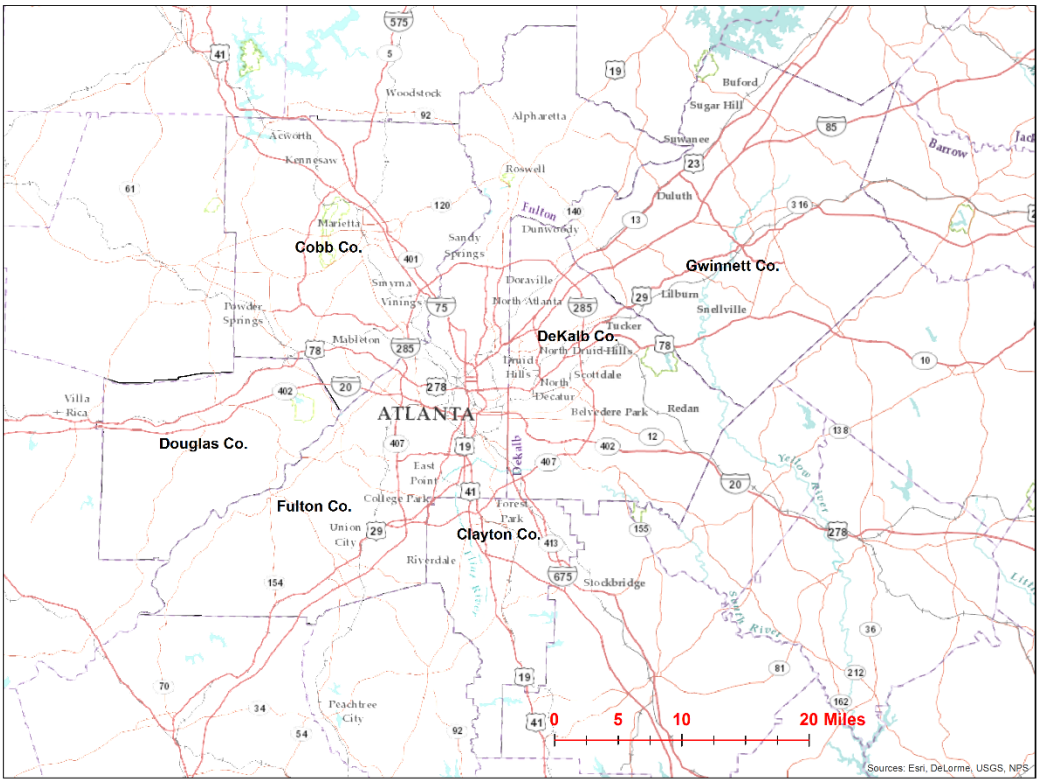

Figure 1. Reference map of the Atlanta metropolitan area.[1]

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[1]Map created using ArcGIS® software by Esri. ArcGIS® and ArcMap™ are the intellectual property of Esri and are used herein under license. Copyright © Esri. All rights reserved. For more information about Esri® software, please visit www.esri.com.

Figure 2. Kernel Density of Persons Diagnosed with HIV in Metro-Atlanta, 2010-2011.

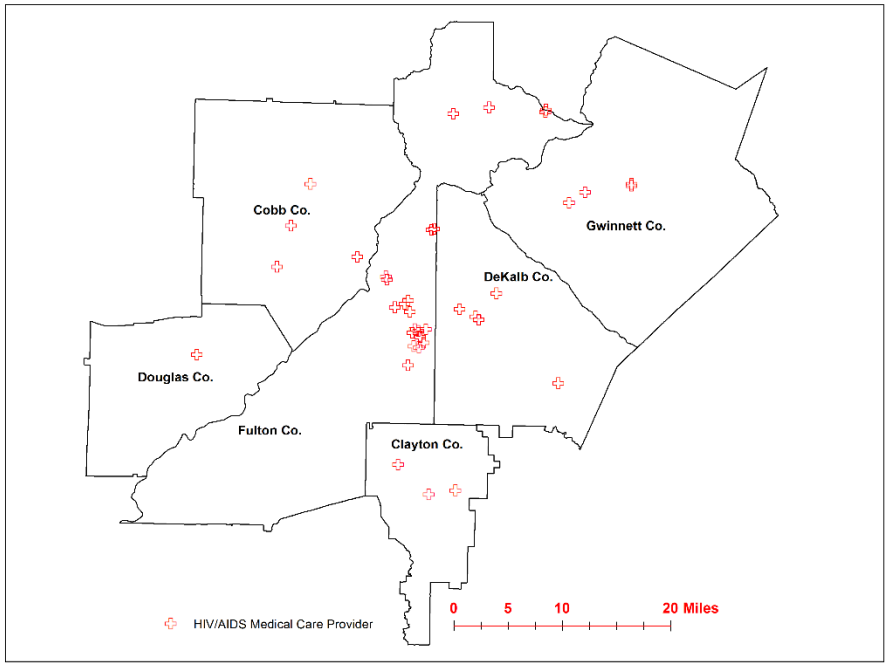

Figure 3. Geographic Distribution of Major HIV/AIDS Medical Care Providers in Metro-Atlanta.

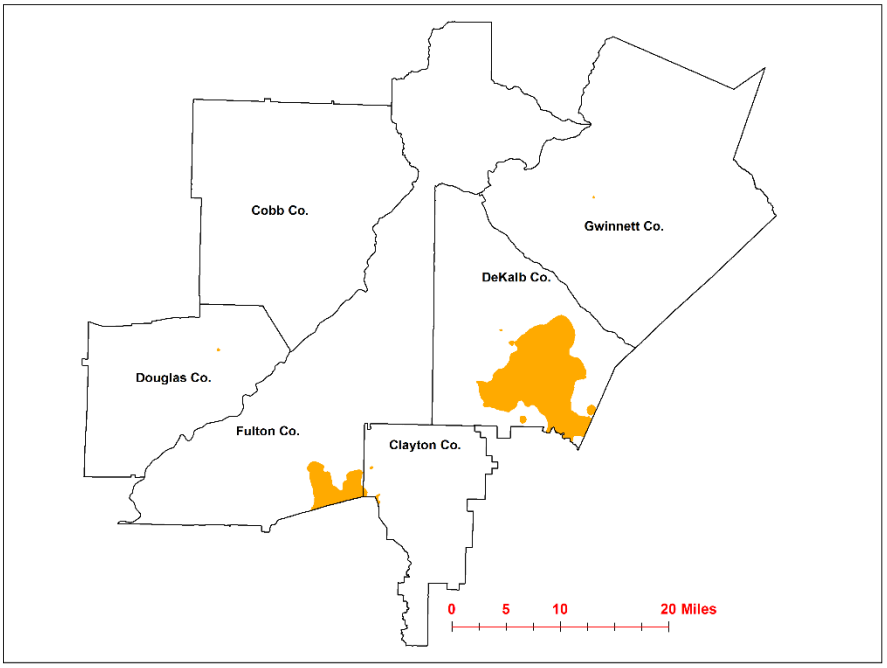

Figure 4. Geographic Hot Spots Associated with Not Linking to Care in Metro-Atlanta, 2010-2011.

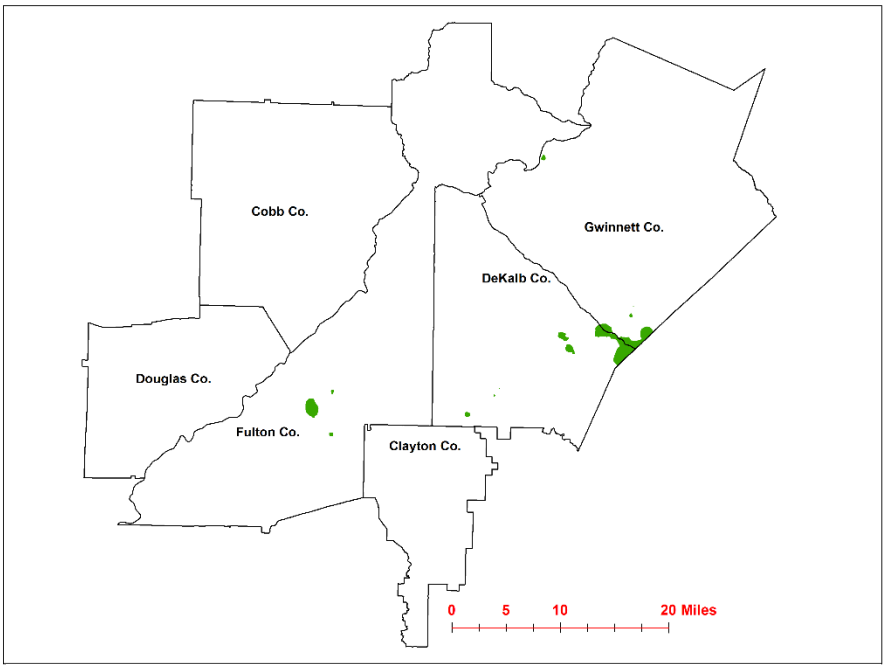

Figure 5. Geographic Hot Spots Associated with Not Linking to Care within 90 Days in Metro-Atlanta, 2010-2011.

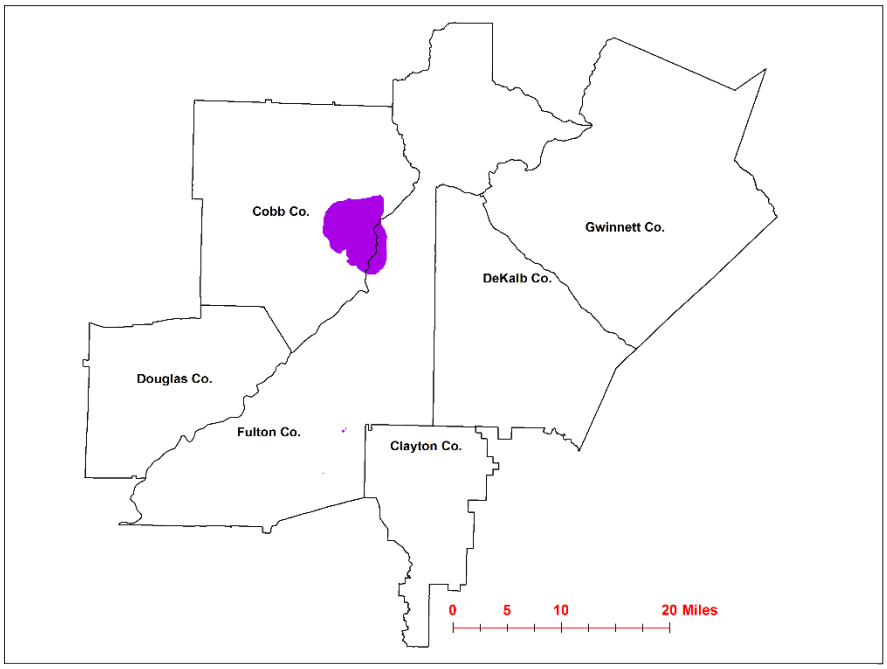

Figure 6. Geographic Hot Spots Associated with Not Retaining in Care in Metro-Atlanta, 2010-2011.

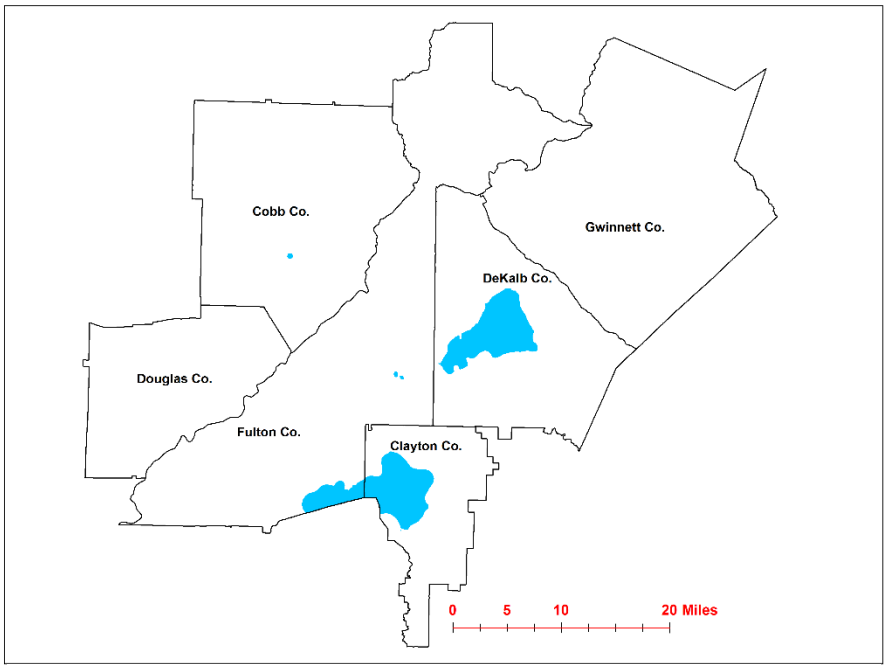

Figure 7. Geographic Hot Spots Associated with Not Achieving Viral Suppression in Metro-Atlanta, 2010-2011.

SUMMARY, PUBLIC HEALTH IMPLICATIONS, POSSIBLE FUTURE DIRECTIONS

The analyses in this study produced four important findings. First, we provided evidence of demographic disparities in different stages of the HIV Care Continuum for a cohort of persons diagnosed with HIV infections in metropolitan Atlanta in 2010 and 2011. Second, we provided further evidence for the use of spatial analysis tools to characterize the HIV epidemic and to locate geographic hot spots, where there are potentially a greater need for outcome-focused interventions that target non-engaged populations and assist them in achieving viral suppression. Third, we identified four spatial patterns, based on the clustering of poor outcomes within 25,000 ft., that were strong independent predictors of being not linked to care, not linked to care within 90 days, not retained in care, and not virally suppressed in Fulton, DeKalb, Gwinnett, Clayton, Douglas, and Cobb counties in Georgia. Fourth, we observed three instances of overlap between geographic hot spots created from different HIV Care Continuum outcomes, which may suggest that the individual-level and community-level factors that influence health may be affecting the poor outcomes similarly in each stage of the HIV Care Continuum represented in the overlap. In other words, the contextual influences of the geographic area represented in the overlap may be responsible for both poor outcomes being clustered in that location.

Although this study suggests that geographic clustering can estimate an HIV patient's odds of not being engaged in care or achieving viral suppression, this information should be taken with a healthy level of skepticism and understanding. The spatial patterns presented herein are specific to the cohort of person newly diagnosed with HIV infection in 2010 and 2011 and specific to the radial distance of 25,000 ft. specified for the Hot Spot Analysis. Notably, the hot spots that we described can change slightly or greatly depending on the size of the distance bands used as a search radius for neighboring features, and this change in spatial patterns provides different ways to characterize the HIV epidemic. How one chooses an appropriate distance band for the spatial patterns depends on what one knows about the phenomena under investigation and

on what distance will promote clustering. Therefore, geographically-tailored HIV interventions using spatial clustering to inform resource allocation or infrastructure planning should modify their spatial analyses to fit the problem in question. For instance, a community-based organization seeking to re-engage persons living with HIV who are not linked to care in a Douglas County, where case density is low, would probably need to evaluate a recent cohort of cases within a distance greater than 20,000 ft. to ensure every case as at least one neighbor. Although we did not observe much clustering of outcomes among newly diagnosed persons in Douglas County in this study, the stated analysis may produce different results with a different cohort. The spatial analysis possibilities are nearly limitless and the information that can be learned from these analyses have the possibility to be used programmatically.

Furthermore, important information may be overlooked if geographic clusters of good outcomes, or cold spots in this study, are not assessed. We did not evaluate or present results on cold spots in this study, but they did exist in opposition to the hot spots. What may be the most interesting facet of the geographic cold spots are how individual-level and community-level factors in these areas influence cases towards good outcomes along the HIV Care Continuum. If we can determine what influences differ between the hot spots and the cold spots, we may gain a better understanding of how to control the HIV epidemic in the hot spots of poor care outcomes. In addition, studying the change in geographic clustering from one cohort of annual diagnoses to the next may provide an interesting time series of how these hot spots are moving or if they are moving across the metropolitan Atlanta area. The implications of hot spots moving throughout the area are difficult to determine without knowing how they move though. For instance, if the hot spots move substantially and randomly on an annual basis, then controlling HIV with geographically-tailored interventions may be implausible. However, this sporadic movement is not likely without major shifts in population density and in individual engagement in care. The stability of hot spots as been assessed for tuberculosis previously, and over four years there was

no change in the location of the hot spots for incident tuberculosis case clustering (27). Therefore, if HIV hot spots act similarly to incident tuberculosis hot spots, then we are likely to find small, gradual movement or no movement in hot spots from year to year, meaning over time interventions could maintain relatively stable locations in areas where they are most needed.

Our finding of overlapping hot spots has possible implications for narrowing down the individual-level and community-level factors to the issues that have the greatest influence on a poor care outcome. For instance, if poor access to care is common in the overlapping area between the hot spot associated with persons not linked to care and the hot spot associated with persons not achieving viral suppression, then improving public transportation options or opening a new clinic in the area may resolve both issues. The fact of the matter is that spatial patterns are tools to be used to locate areas where further analysis is appropriate.

Evaluation of cases residing in geographic hot spots, controlling for age, sex at birth, race/ethnicity, and transmission risk, was informative as a preliminary analysis; however, assessing and adjusting for more individual-level and community-level factors may improve upon the validity of our results. Therefore, further research is needed on the effects of health insurance, proximity to care services, crime levels, contextual infrastructure, access to public services, and housing stability in the geographic hot spots identified in this study. With an increased understanding of the contextual influences affecting poor care outcomes in these hot spots, we seek to increase the impact of HIV prevention efforts in the metropolitan Atlanta area.

APPENDICES

Appendix A. SAS Code for Sample Selection, Variable Creation, and Data Extraction.

```
/*create lab (care) and address (geo) data by person for spatial
analysis of care continuum outcomes using frozen year-end
datasets*/

/*revised for use with current eHARS datasets (changed lab test
codes and var names)*/

/*written by Michael Eberhart (michael.eberhart@phila.gov)*/

/*updated by Brian Huylebroeck for use in "Spatial Analysis of
Attrition Along the HIV Care Continuum
in the Atlanta Metropolitan Area"*/

/*location of ehars data*/
libname docs
'H:\Share Drive\eharsdatasets\END_OF_YEAR\EOY_DOCUMENT';
libname p
'H:\Share Drive\ehars datasets\END_OF_YEAR\EOY_ANALYSIS_PERSON';

options nofmterr;


**create temp dataset of selected variables from person
dataset******;
data persons;
    set p.person
          (keep=ehars_uid
                    dob
                    expo_categ
                    hiv_categ
                    hiv_aids_dx_dt
                    dx_status
                    stateno
                    status_flag
                    aids_categ
                    birth_sex
                    dod
                    hiv_aids_age_yrs
                    hiv_aids_age_mos
                    race
                    vital_status
                    aids_dx_dt
                    hf_name1
                    af_name1
                    hiv_dx_dt
                    cur_street_address1
                    cur_street_address2
```

```
                    cur_city_name
                    cur_county_name
                    cur_state_cd
                    cur_zip_cd
                    cur_county_fips
                    rsd_street_address1
                    rsd_street_address2
                    rsd_city_name
                    rsd_zip_cd
                    rsd_state_cd
                    rsd_county_name
                    rsd_county_fips
                    rsd_city_fips
                    prison
                    );
run;


***** Select valid hiv cases diagnosed in 2010 and 2011 ********;

data rsd_1011; set persons;
IF stateno ne ' '; * delete missing stateno;
IF status_flag in ('A' 'W');*valid cases;
IF hiv_categ in ('1','2'); *include all cases that meet the case
defination;
IF '20100101' le hiv_aids_dx_dt le '20111231'; *diagnosed in 2010
and 2011;
IF rsd_state_cd='GA'; *residence at dx in GA;
IF cur_state_cd='GA'; *current residence in GA;
IF rsd_county_FIPS in ('121', '063', '089', '067', '097', '135');
*residence at dx in Atlanta 6-county area;
IF cur_county_FIPS in ('121', '063', '089', '067', '097', '135');
*current residence in Atlana 6-county area;
IF vital_status eq '1' or dod gt '20121231';*alive or deceased
AFTER end of observation period;
RUN;


*****************lab data for cases ***************************;
* only cd4 and vl (for in-care and suppression analyses);
proc sql;
create table labdocs as
select *
from docs.document as d left join docs.lab as l
on d.document_uid=l.document_uid
where d.ehars_uid in
(select ehars_uid from rsd_1011)and (l.lab_test_cd in ("EC-014"
"EC-015" "EC-016" "EC-017"))
and substr(l.sample_dt,1,4) in ('2010'
'2011','2012','2013','2014');
quit;
```

```
/*Delete dups*/
proc sort data=labdocs nodupkey out=labdocs2 dupout=dups;
by ehars_uid sample_dt lab_test_cd result;
run;
/*Sort data by uid and sample_dt*/
proc sort data=labdocs2; by ehars_uid sample_dt;run;


/*create count var to count number of labs for each uid*/
data labdocs3; set labdocs2;
by ehars_uid;
if first.ehars_uid then count=0;
count+1;
run;

/*freq count var to get max # labs*/
proc freq data=labdocs3;
tables count;
run;

/*limit lab dataset and create vars   */
data labdocs4; set labdocs3;
keep ehars_uid sample_dt lab_test_cd result_interpretation result
result_units count sampdt provider_uid facid;
if sample_dt ne ' ';
sampdt=mdy(substr(sample_dt,5,2),'15',substr(sample_dt,1,4));
/*create sas date for calculations*/
if provider_uid ne ' ' then facid=provider_uid;
else facid=facility_uid;
run;


/*transpose data to get one obs for each ehars_uid, including all
lab dates*/
proc transpose data=labdocs4 out=labdates prefix=labdt;
by ehars_uid;
copy count sampdt;
var sampdt;
run;
/*transpose data to get one obs for each ehars_uid, including all
lab codes*/
proc transpose data=labdocs4 out=labcodes prefix=labcd;
by ehars_uid;
copy count lab_test_cd;
var lab_test_cd;
run;
/*transpose data to get one obs for each ehars_uid, including all
lab interpretations*/
proc transpose data=labdocs4 out=labints prefix=labint;
by ehars_uid;
copy count result_interpretation;
var result_interpretation;
```

```
run;
/*transpose data to get one obs for each ehars_uid, including all
lab results*/
proc transpose data=labdocs4 out=labres prefix=labres;
by ehars_uid;
copy count result;
var result;
run;
/*transpose data to get one obs for each ehars_uid, including all
lab result units*/
proc transpose data=labdocs4 out=labresu prefix=labresu;
by ehars_uid;
copy count result_units;
var result_units;
run;
/*transpose data to get one obs for each ehars_uid, including all
lab result units*/
proc transpose data=labdocs4 out=labfac prefix=labfac;
by ehars_uid;
copy count facid;
var facid;
run;
/*pull data together*/
data combtrans; merge labdates labcodes labints labres labresu
labfac;
by ehars_uid count;
if _name_ ne ' ';
keep ehars_uid count labdt1-labdt124 labcd1-labcd124  labint1-
labint124 labres1-labres124 labresu1-labresu124 labfac1-
labfac124;
run;


libname ret 'H:\Share Drive\Brian';

/*combine transposed lab data with case data and save permanent
dataset*/
proc sql;
create table ret.case1011 as
select  *
from rsd_1011 a left join combtrans b
on (a.ehars_uid=b.ehars_uid);
quit;

proc format;
value care .='No care'
           low-29='<30 days'
           30-89='1-3 months'
           90-180='4-6 months'
           181-high='>6 months';
value care3mo .='No care'
           low-89='<3 months'
```

```
           90-high='>3 months';
value $racecalc       '1'="Hispanic"
                      '2'="Other/Unk"
                      '3'="Asian"
                      '4'="Black"
                      '5'="Other/Unk"
                      '6'="White"
                      '7'="Other/Unk"
                      '8'="Multi-race"
                      '9'="Other/Unk"
                      ' '='Other/Unk';
value noyes 0='No'
            1='Yes';
value $sex 'M'="Male"
           'F'="Female";
value $moden '01'="MSM"
             '02'="IDU"
             '03'="Heterosexual"
             '04'="IDU"
             '05'="IDU"
             '06'="MSM"
             '07'="IDU"
             '08'="Other/NIR"
             '09'="Other/NIR"
             '10'="Other/NIR"
             '11'="Other/NIR"
                 ;
value $diag      '1'='HIV (Non-AIDS)'
                 '2'='AIDS'
                 '4'='HIV (Non-AIDS)'
                 '5'='AIDS';

value $newage ' '='Unknown'
            '0'-'12', '2', '3', '4', '5','6', '7', '8', '9'='< 13'
            '13'-'19'='13-19'
            '20'-'29'='20-29'
            '30'-'39'='30-39'
            '40'-'49'='40-49'
            '50'-'59'='50+'
            '60'-'69'='50+'
            '70'-'79'='50+'
            '80'-'89'='50+'
            '90'-'99'='50+';

value $aidscat  '7'= 'AIDS (HIV, stage 3) case defined by
immunologic (CD4 count or percent) criteria'
                'A'=  'AIDS (HIV, stage 3) case defined by
clinical disease (OI) criteria'
                '9'= 'Not an AIDS (HIV, stage 3) case';

run;
```

```
/*calculate time between lab dates and create result vars*/
/*we considered several measures for retention before settling on
one visit in each 6 month period for 2 years after dx.  I include
other measures here (2 visits in 12 mos, 2 visits in 24 mos)*/
data labeval; set ret.case1011;
length faclist $512;
dxyear=substr(hiv_aids_dx_dt,1,4);
dxmon=substr(hiv_aids_dx_dt,5,2);
dxday=substr(hiv_aids_dx_dt,7,2);
      if dxday eq '..' then dxday='15';
dxdate=mdy(dxmon,dxday,dxyear);
if dxdate eq . then delete; /*Delete cases with insufficient
diagnosis date info*/
facnum=0;
care10=0;
care11=0;
care12=0;
care13=0;
array lab {124} labdt1-labdt124;
array ldiff {124} diff1-diff124;
array diff {124} t1-t124;
array cd {124} labcd1-labcd124;
array und {124} labres1-labres124;
array resu {124} labresu1-labresu124;
array cdc {124} labcd4c1-labcd4c124;
array cdp {124} labcd4p1-labcd4p124;
array int {124} labint1-labint124;
array vl {124} labvl1-labvl124;
array fac {124} labfac1-labfac124;
array supp {124} vlres1-vlres124;
do i = 1 to 124;
      if lab[i] gt dxdate then do;
      ldiff[i]=lab[i]-dxdate;
      if care10 eq 0 then do;
            if year(lab[i])=2010 then care08=1;
            end;
      if care11 eq 0 then do;
            if year(lab[i])=2011 then care09=1;
            end;
      if care12 eq 0 then do;
            if year(lab[i])=2012 then care10=1;
            end;
      if care13 eq 0 then do;
            if year(lab[i])=2013 then care11=1;
            end;
      end;
end;
careint=min(of diff1-diff124);/*interval (in days) between dx and
first lab*/
do i = 1 to 124; /*establish date linked to care as start point
for retention*/
```

```
      if ldiff[i] eq careint then do;
      caredt=lab[i];
      end;
end;
first=.;
second=.;
      do i=1 to 124;/*evaluate difference (in days) of lab dates
for 12 months post care entry*/
            if (lab[i] gt caredt) and  (lab[i]-caredt le 365) then
do;
                  if first=. then do;
                  first=lab[i];
                  end;
                  else do;
                  if second=. then do;
                  if lab[i]-first ge 90 then do;
                  second=lab[i];
                  end;
                  end;
                  end;
            end;
            end;
if first ne . and second ne . then care12mo=1;else care12mo=0;

first=.;
second=.;
do i=1 to 124;/*evaluate difference (in days) of lab dates for 24
months post care entry*/
            if (lab[i] gt caredt) and  (lab[i]-caredt le 730) then
do;
                  if first=. then do;
                  first=lab[i];
                  end;
                  else do;
                  if second=. then do;
                  if lab[i]-first ge 90 then do;
                  second=lab[i];
                  end;
                  end;
                  end;
            end;
            end;
if first ne . and second ne . then care24mo=1;else care24mo=0;

      do i=1 to 124;
            if lab[i] ge dxdate then do;
                  if faclist=' ' then do;/*first iteration -
facility is 'new' by default*/
                  faclist=fac[i];             /*add to list*/
                  facnum=1;end;            /*and set counter to 1*/
                  else if index(faclist,fac[i]) then do; /*Compare
facility to list*/
```

```
            facnum=facnum;end;          /*if already in list,
retain counter*/
            else do;
            facnum=facnum+1;      /*If not, increment counter by
1*/
            faclist=compress(faclist||','||fac[i]); /*add facility
to list*/
            end;
            end;
      end;
      do i=1 to 124;/*create numeric values for test results*/
      if lab[i] gt dxdate then do;
      if cd[i] in ('EC-014' 'EC-015') then do; /*Viral Load*/
      if int[i]='<' then do; /*less than values = 1/2 of lower
limit*/
            if und[i] ne ' ' then do;
            vl[i]=(input(und[i],3.))/2;
            end;
            else do;
            vl[i]=100;
            end;
            end;
      else do;/*other values = value (or upper limit)*/
            vl[i]=input(und[i],best.);
            end;
      end;
      if cd[i] in ('EC-016','EC-017') then do; /*CD4*/
            if resu[i]='PCT' then do;/*percent*/
            cdp[i]=input(und[i],best.);
            end;
            if resu[i]='CNT' then do;/*count*/
            cdc[i]=input(und[i],best.);
            end;
      end;
      end;
      end;
do i=1 to 124;
      if caredt ne . then do;
      if (caredt)+640 le lab[i] le (caredt)+824 then do;/*Labs in
window at end of observation period for each case*/
            if cd[i] in ('EC-014' 'EC-015') then do; /*VL tests
only*/
            supp[i]=vl[i];/*Capture result*/
            end;
            end;
            end;
            end;
lowvl=min(of vlres1-vlres124);
if lowvl ne . and lowvl le 200 then suppress=1;else suppress=0;

c1=.;
c2=.;
```

```
c3=.;
c4=.;
do i=1 to 124;/*evaluate lab dates for evidence of care in each 6
month period of 24 months post care entry*/
           if caredt lt lab[i] le (caredt)+182 then do;
                c1=lab[i];
                end;
                else if (caredt)+183 le lab[i] le (caredt)+365
then do;
                c2=lab[i];
                end;
                else if (caredt)+366 le lab[i] le (caredt)+550
then do;
                c3=lab[i];
                end;
                else if (caredt)+551 le lab[i] le (caredt)+730
then do;
                c4=lab[i];
                end;
           end;
if c1 ne . and c2 ne . and c3 ne . and c4 ne . then retcare=1;
else retcare=0;
run;

proc freq data=labeval;
tables retcare careint suppress / missing;
format careint care3mo.;
run;

/*Export data for geocoding*/

data ret.analyticsample;
set labeval
               (keep=ehars_uid
                     stateno
                     dob
                     expo_categ
                     hiv_categ
                     hiv_aids_dx_dt
                     dx_status
                     status_flag
                     aids_categ
                     birth_sex
                     dod
                     hiv_aids_age_yrs
                     hiv_aids_age_mos
                     race
                     vital_status
                     aids_dx_dt
                     hf_name1
                     af_name1
                     hiv_dx_dt
```

```
                        retcare
                        careint
                        suppress
                        prisno
                        cur_street_address1
                        cur_street_address2
                        cur_city_name
                        cur_county_name
                        cur_state_cd
                        cur_zip_cd
                        rsd_street_address1
                        rsd_street_address2
                        rsd_city_name
                        rsd_zip_cd
                        rsd_county_name
                        rsd_county_fips
                        rsd_city_fips
                        );
format      careint care3mo.
            expo_categ moden.
            race racecalc.
            birth_sex sex.
            aids_categ aidscat.
;
run;
```

Appendix B. SAS Code for Multivariable Logistic Regression Models.

```
/*Logistic Models*/
/*written by Brian Huylebroeck for use in "Spatial Analysis of
Attrition Along the HIV Care Continuum
in the Atlanta Metropolitan Area"*/

LIBNAME hiv "H:\Share Drive\Brian";

option nofmterr;

 /*import data with hot spot distances from ArcGIS 10.2*/

DATA nl_2339model;
SET hiv.Not_linked_2339;
IF 0 <= hiv_aids_age_yrs < 25 THEN age = "<25";
ELSE IF 25 <= hiv_aids_age_yrs < 45 THEN age = "25-45";
ELSE IF 45 <= hiv_aids_age_yrs THEN age = ">45";
IF birth_sex = "F" then sex = "F";
IF birth_sex = "M" then sex = "M";
IF NEAR_DIST = 0 then Hotspot_in =  "yes";
IF NEAR_DIST ne 0 then Hotspot_in =  "no";
IF expo_categ = 1 then risk="MSM";
IF expo_categ = 2 then risk="IDU";
IF expo_categ = 3 then risk="Het";
IF expo_categ = 4 then risk="IDU";
IF expo_categ = 5 then risk="IDU";
IF expo_categ = 6 then risk="MSM";
IF expo_categ = 7 then risk="IDU";
IF expo_categ = 8 then risk="Other";
IF expo_categ = 9 then risk="Other";
IF expo_categ = 10 then risk="Other";
IF expo_categ = 11 then risk="Other";
IF race = 1 then race2 = "Hispanic";
IF race = 2 then race2 = "Other";
IF race = 3 then race2 = "Other";
IF race = 4 then race2 = "Black";
IF race = 5 then race2 = "Other";
IF race = 6 then race2 = "White";
IF race = 7 then race2 = "Other";
IF race = 8 then race2 = "Other";
IF race = 9 then race2 = "Other";
RUN;


DATA nl90_2067model;
SET hiv.Not_linked_in_90_days_2067;
IF 0 <= hiv_aids_age_yrs < 25 THEN age = "<25";
ELSE IF 25 <= hiv_aids_age_yrs < 45 THEN age = "25-45";
ELSE IF 45 <= hiv_aids_age_yrs THEN age = ">45";
IF birth_sex = "F" then sex = "F";
```

```
IF birth_sex = "M" then sex = "M";
IF NEAR_DIST = 0 then Hotspot_in =  "yes";
IF NEAR_DIST ne 0 then Hotspot_in =  "no";
IF expo_categ = 1 then risk="MSM";
IF expo_categ = 2 then risk="IDU";
IF expo_categ = 3 then risk="Het";
IF expo_categ = 4 then risk="IDU";
IF expo_categ = 5 then risk="IDU";
IF expo_categ = 6 then risk="MSM";
IF expo_categ = 7 then risk="IDU";
IF expo_categ = 8 then risk="Other";
IF expo_categ = 9 then risk="Other";
IF expo_categ = 10 then risk="Other";
IF expo_categ = 11 then risk="Other";
IF race = 1 then race2 = "Hispanic";
IF race = 2 then race2 = "Other";
IF race = 3 then race2 = "Other";
IF race = 4 then race2 = "Black";
IF race = 5 then race2 = "Other";
IF race = 6 then race2 = "White";
IF race = 7 then race2 = "Other";
IF race = 8 then race2 = "Other";
IF race = 9 then race2 = "Other";
RUN;


DATA nr_2067model;
SET hiv.Not_retained_2067;
IF 0 <= hiv_aids_age_yrs < 25 THEN age = "<25";
ELSE IF 25 <= hiv_aids_age_yrs < 45 THEN age = "25-45";
ELSE IF 45 <= hiv_aids_age_yrs THEN age = ">45";
IF birth_sex = "F" then sex = "F";
IF birth_sex = "M" then sex = "M";
IF NEAR_DIST = 0 then Hotspot_in =  "yes";
IF NEAR_DIST ne 0 then Hotspot_in =  "no";
IF expo_categ = 1 then risk="MSM";
IF expo_categ = 2 then risk="IDU";
IF expo_categ = 3 then risk="Het";
IF expo_categ = 4 then risk="IDU";
IF expo_categ = 5 then risk="IDU";
IF expo_categ = 6 then risk="MSM";
IF expo_categ = 7 then risk="IDU";
IF expo_categ = 8 then risk="Other";
IF expo_categ = 9 then risk="Other";
IF expo_categ = 10 then risk="Other";
IF expo_categ = 11 then risk="Other";
IF race = 1 then race2 = "Hispanic";
IF race = 2 then race2 = "Other";
IF race = 3 then race2 = "Other";
IF race = 4 then race2 = "Black";
IF race = 5 then race2 = "Other";
IF race = 6 then race2 = "White";
```

```
IF race = 7 then race2 = "Other";
IF race = 8 then race2 = "Other";
IF race = 9 then race2 = "Other";
RUN;

DATA ns_663model;
SET hiv.Not_suppressed_663;
IF 0 <= hiv_aids_age_yrs < 25 THEN age = "<25";
ELSE IF 25 <= hiv_aids_age_yrs < 45 THEN age = "25-45";
ELSE IF 45 <= hiv_aids_age_yrs THEN age = ">45";
IF birth_sex = "F" then sex = "F";
IF birth_sex = "M" then sex = "M";
IF NEAR_DIST = 0 then Hotspot_in =  "yes";
IF NEAR_DIST ne 0 then Hotspot_in =  "no";
IF expo_categ = 1 then risk="MSM";
IF expo_categ = 2 then risk="IDU";
IF expo_categ = 3 then risk="Het";
IF expo_categ = 4 then risk="IDU";
IF expo_categ = 5 then risk="IDU";
IF expo_categ = 6 then risk="MSM";
IF expo_categ = 7 then risk="IDU";
IF expo_categ = 8 then risk="Other";
IF expo_categ = 9 then risk="Other";
IF expo_categ = 10 then risk="Other";
IF expo_categ = 11 then risk="Other";
IF race = 1 then race2 = "Hispanic";
IF race = 2 then race2 = "Other";
IF race = 3 then race2 = "Other";
IF race = 4 then race2 = "Black";
IF race = 5 then race2 = "Other";
IF race = 6 then race2 = "White";
IF race = 7 then race2 = "Other";
IF race = 8 then race2 = "Other";
IF race = 9 then race2 = "Other";
RUN;


/*Model 1 - Not linked to care*/

PROC LOGISTIC DATA=nl_2339model descending;
          CLASS hotspot_in (ref="no") age (ref=">45") sex
(ref="F") race2 (ref="White") risk (ref="Het") / param=ref;
          MODEL nocare (event='1')= age sex race2 risk
hotspot_in
          ;
RUN;


/*Model 2 - Not linked to care within 90 days*/

PROC LOGISTIC DATA=nl90_2067model descending;
```

```
          CLASS hotspot_in (ref="no") age (ref=">45") sex
(ref="F") race2 (ref="White") risk (ref="Het") / param=ref;
          MODEL nocare90 (event='1')= age sex race2 risk
hotspot_in
          ;
RUN;


/*Model 3 - Not retained in care*/
PROC LOGISTIC DATA=nr_2067model descending;
          CLASS hotspot_in (ref="no") age (ref=">45") sex
(ref="F") race2 (ref="White") risk (ref="Het") / param=ref;
          MODEL notretain (event='1')= age sex race2 risk
hotspot_in
          ;
RUN;


/*Model 4 - Not virally suppressed*/
PROC LOGISTIC DATA=ns_663model descending;
          CLASS hotspot_in (ref="no") age (ref=">45") sex
(ref="F") race2 (ref="White") risk (ref="Het") / param=ref;
          MODEL notsupp (event='1') = age sex race2 risk
hotspot_in
         ;
run;
```