

# TECHNICAL NOTES

The primary purpose of the 2010-2014 HIV & STD Burden by Health District is to support geographic prioritization of Los Angeles County Department of Public Health (LAC/DPH) Division of HIV and STD Programs (DHSP) resources, placing emphasis on HIV and reduced acquisition and transmission of STDs monitored by DHSP based on the acuteness of symptoms. Accordingly, weighted consideration was given in the following order: HIV, syphilis, gonorrhea and chlamydia.

To get a comprehensive snapshot of the HIV and sexually transmitted disease (STD) burden in Los Angeles County (LAC) from 2010-2014 period, we compiled incident-level surveillance data from three (3) data systems: Enhanced HIV/AIDS Reporting System (eHARS) for HIV cases; the California Reportable Disease Information Exchange (CalRedie) for syphilis, gonorrhea and chlamydia cases in the cities of Long Beach and Pasadena; and STD CaseWatch Millennium for syphilis, gonorrhea and chlamydia cases in all other areas of LAC. Each data system collects incident-related data through passive surveillance (i.e., physicians, laboratories, and other healthcare providers report HIV and STD diagnoses to their jurisdiction's health department). Additional data collection for HIV occurs via active surveillance (i.e., health department staff contact hospitals, laboratories, physicians, jails, and other sentinel sites). Aggregating 5 years of data makes it possible to incorporate data on residents with a history of high risk behavior, minimize the impact of an outbreak, and look at the potential for service delivery at a granular scale with minimal data suppression due to geoprivacy or unstable rates. A minimum dataset consisting of variables across all surveillance systems was used. These records contained demographic information for each reported incident, including age, sex, race/ethnicity, resident address at diagnosis, morbidity date, pregnancy status (if appropriate) and syphilis stage (if appropriate).

All calculations were performed using the SAS statistical software package, version 9.3 (SAS Institute, Cary, North Carolina, USA), and/or ArcMap 10.2.2 (Environmental Systems Research Institute, Redlands, California, USA).

## Data Preparation

### Person-level Match Merges & Incident De-Duplication

Using Link Plus, a probabilistic record linkage program developed at the CDC (<https://www.cdc.gov/cancer/npcr/tools/registryplus/lp>), and the SAS statistical software package, we assessed for co-morbidity with HIV/AIDS among LAC residents with a reported STD in the 2010-2014 period. These record linkages between the Enhanced HIV/AIDS Reporting System (eHARS) and each of the other 3 datasets were matched for all Persons Living with HIV (PLWH) as of August 29, 2016. Manual review of a subset of records were done for quality assurance. The resulting linkage datasets were later employed to re-establish the link with the STD datasets and import in relevant sociodemographic characteristics and select incident-specific characteristics.

Simultaneous analysis of surveillance data from the cities of Long Beach and Pasadena demonstrated a considerable number of residents with records overlapping more than one jurisdiction during the 5-year period and modicum incident duplication within and across data systems. We addressed these data discrepancies by creating a new person-level identifier based on match-merges by person identifiers, such as name, sex, date of birth, social security number and address. Following each match-merge, manual review of 20% or more of records were done for quality assurance. The new person-level identifier and morbidity date were then utilized to de-duplicate any STD incidents within +/- 30 days of

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the morbidity date, in accordance to California's 30-day cut point guidance (<http://www.cdph.ca.gov/programs/std/Documents/STD-CalREDIE-CTGC-30Day-Guidance.pdf>). While the cut point guidance is standard for gonorrhea and chlamydia, the same definition was extended to syphilis since information on titers and symptoms were not readily available.

## All HIV & STD Incidents

To allow for rate comparison with jurisdictions in and outside of LAC, rate information for HIV, syphilis, gonorrhea and chlamydia for the 2010-2014 period in the profiles are reported in persons per year (i.e., person-years) and inclusive of any reported case including those from residents with only chlamydia. Calculations are based on crude rates, meaning the data is not adjusted for sociodemographics or other factors (e.g., by sex or age). We applied the following formula for each disease:

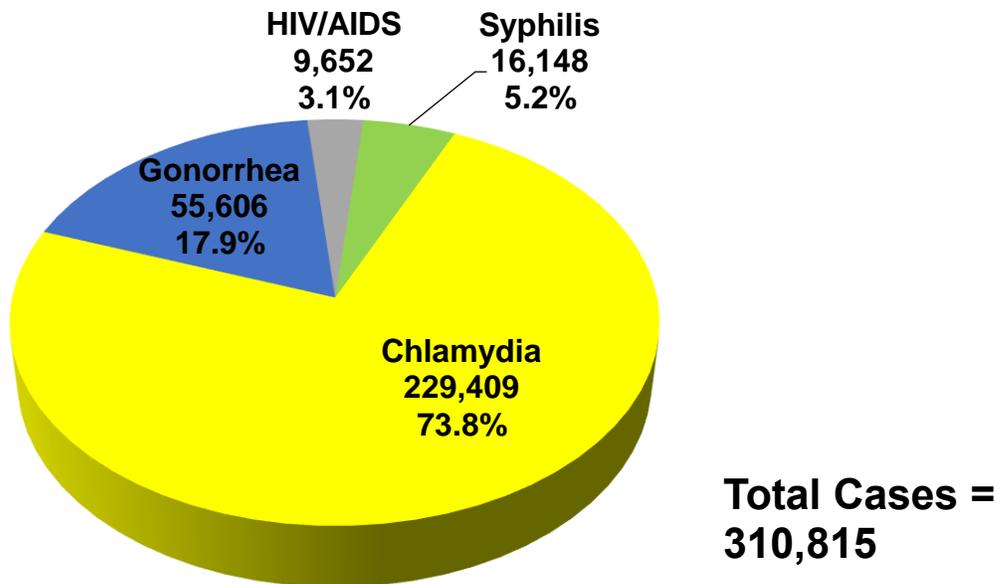
$$\frac{\text{new cases diagnosed in 2010-2014}}{(\text{2010 population} + \text{2011 population} + \text{2012 population} + \text{2013 population} + \text{2014 population}) * 100,000}$$

Population data are sourced to the 2010-2014 population estimates provided by LAC Internal Services Department and contracted through Hedderson Demographic Services.[1] All data are derived from an algorithm based on the 2010 Census Summary File, the American Community Survey Summary File and population estimate as of January 1 each year by the California Department of Finance, Demographic Research Unit.

The most common reportable STD, chlamydia, outpaces the total of HIV, gonorrhea and syphilis cases in any given time period. For the 2010-2014 dataset, chlamydia cases represented 73.8% of all reported HIV and STD incidents [Figure 1]. As such, their addition into analyses intended for general geographic planning mask a great deal of the variation seen among the other diseases. Moreover, the demographic profile of individuals with a chlamydia infection is distinctly different from the demographic profile of individuals with HIV, syphilis or gonorrhea.

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Figure 1. Reported STD and HIV/AIDS Cases, Los Angeles County, 2010-2014



When accounting for co-infection and re-infection, chlamydia continues to contribute a large portion of the disease burden (i.e., 66.4%) in LAC and for all health districts except one, the Hollywood-Wilshire health district. This is best illustrated by the smaller pie chart in the profiles, which demarcates the distribution of infections by residents with only chlamydia (*CT Only*) during the 5-year time period and *All Others*. The larger pie explodes the *All Others* portion of the smaller pie to show the breakdown for residents with a HIV, syphilis, gonorrhea or high risk chlamydia incident at any time during the 5-year period. A high risk chlamydia incident is defined as having a diagnosed HIV infection as of 8/29/2016 or being co-infected with syphilis or gonorrhea.

Geographically, chlamydia is evenly distributed across LAC making geographically-targeted interventions less effective than focusing on areas disproportionately burdened with HIV, syphilis and gonorrhea. The STD bivariate maps illustrate the differences well, highlighting characteristics that may indicate higher risk for HIV infection or transmission [Figures 2, 3, 4, 5].

Adding residents with only chlamydia would mask variation in infection and co-infection for the other diseases, skew to a younger and more female population and deviate from DHSP’s current management and investigation of STDs (i.e., no investigations for chlamydia except for high risk cases). Consequently, we chose to exclude persons with only chlamydia incidents in data shown “among infected persons.”

**Infection Characteristics**

The twenty-nine (29) combinations of infection and co-infection are mutually exclusive when enumerated at the infection-level. The larger pie chart provides a snapshot of the more common

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infections and co-infections occurring in LAC and in each health district for residents with a HIV, syphilis or gonorrhea incident. Subsequently, the total incidents represented will always be larger than the total indicated for the combinations of infection and co-infection. Given that the definition for co-infection (within +/- 30 days of the incident's morbidity date) is disease-specific, there were data discrepancies among a handful of residents in the combined dataset. For example, a person had a chlamydia morbidity date of 1/1/2012, another chlamydia morbidity date of 3/1/2012 and a gonorrhea morbidity date of 2/1/2012. In the chlamydia-specific dataset, we would show chlamydia and gonorrhea co-infection for morbidity dates 1/1/2012 and 3/1/2012. But, in the gonorrhea-specific dataset, we would show chlamydia and gonorrhea co-infection for 2/1/2012. When combining person-level records for all diseases, the chlamydia and gonorrhea co-infection will show different numbers despite being legitimate co-infections. To address such discrepancies and populate the profiles, we averaged each combination across the disease-specific datasets.

Data reported as incidents in the profiles represent every case regardless of co-infection and are used to produce all other data points. *Incidents Represented* reflect those from residents with a reported HIV, syphilis, gonorrhea or high risk chlamydia incident during the 2010-2014 period. Case classification for HIV, syphilis, gonorrhea and chlamydia align with the case definitions produced by the CDC and used in LAC/DPH annual surveillance reports [2, 3].

## Resident characteristics

Sociodemographic characteristics and select incident-specific characteristics were retained for each incident record. Inconsistent values across each resident's records for gender and race/ethnicity were managed by selecting according to a hierarchical approach, placing more emphasis on records with a greater likelihood of completeness and accuracy, given DHSP current data systems and public health investigation protocols. For instance, HIV and syphilis surveillance involve detailed follow-up of cases resulting in more thorough reporting of characteristics. Though not all individuals infected with gonorrhea present with symptoms, those who do are likely to seek treatment contributing to increased likelihood for reporting to the health department and more complete confidential morbidity reports (CMR) forms. Furthermore, public health investigation protocols are in place for certain cases of gonorrhea. On the other hand, a majority of individuals with chlamydia have no symptoms and learn of their infection during routine screening, often resulting in missing information for CMRs. Staff capacity hinders follow-up of chlamydia cases for sociodemographic characteristics and incident-specific characteristics, given the large number reported (i.e., around 50,000 annually). These factors contribute to why DHSP no longer investigates chlamydia except for high risk cases.

As such, the hierarchical approach defined each gender and race/ethnicity on reported values in the following order: (1) HIV, (2) syphilis, (3) gonorrhea, (4) chlamydia. Recurrent infections for each were addressed by using the latest morbidity date on file. Any missing values would be skipped to retrieve the next value for the selected characteristic.

All other resident-level characteristics (i.e., MSM/MSMW, Youth (15-19), Youth (15-24), Pregnant, Early Syphilis and Congenital Syphilis) were defined as having 'ever reported' the characteristic during the 5-year period since they are incident-specific. For instance, if a 24-year old female was infected with gonorrhea in 2012 and then infected with primary syphilis while pregnant in 2014, that resident would

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be added into Youth (15-24), Pregnant and Early Syphilis categories. MSM/MSMW and Pregnant deviate from the other four (4) characteristics in that the results from the hierarchical approach used to determine gender restricted the pool from which each can be assessed. Furthermore, we defined MSM/MSMW as having a male sexual partner in the last 12 months and/or a mode of HIV transmission as being a male sexual partner. Residents may self-identify differently, but the datasets involved precluded that level of analysis and MSM/MSMW, as it is defined, allows us to assess for sexual behavior across a 5-year time period. For quality assurance, a 20% sample of potentially problematic MSM/MSMW records were cross-checked for accuracy. Early Syphilis includes all cases staged as primary, secondary, or early latent. Case classification for Early Syphilis and Congenital Syphilis align with the case definitions produced by the CDC and used in LAC/DPH annual surveillance reports [2, 3].

Incident-specific characteristics, such as recurrent infections and co-infections, were also retrieved for each resident included in the profiles. Recurrent infections during the 2010-2014 period were positively skewed across all STDs with roughly 99% residents with 3 or fewer incidents. Breaks at 1 incident, 2 incidents, 3 incidents and 4 or more were indicated to show variation among the majority of infected residents included in the analysis.

Using the morbidity date of each incident, we assessed for co-infection for every incident included in our analysis resulting in twenty-nine (29) combinations among all HIV and STDs. For instance, a resident would be counted four (4) times in the Infections & Co-infections Combination section, if infected with chlamydia in January 2010, had a chlamydia & gonorrhea co-infection in June 2010, been infected with syphilis infection in 2012 and later diagnosed with HIV in 2014. Delineating the re-occurrence and co-occurrence of the HIV and STD burden allows for a better understanding of high risk sexual behaviors that sustain transmission and/or increase susceptibility to acquiring HIV or developing STD complications in the future. To operationalize the analysis, we defined co-infection as another HIV or STD occurring within +/- 30 days of the incident. Match-merging and incident level de-duplication was conducted among the STD datasets on September 26, 2016. We also defined co-morbidity with HIV as having a diagnosis of HIV infection 30 days or more before or after the STD incident and are indicated in the sections “Acquired HIV Infection **Before** STD” and “Acquired HIV Infection **After** STD.” The time point for the record linkage between eHARS and the STD datasets occurred on August 29, 2016 and would reflect residents with HIV as of that date. Consequently, the number of residents who have acquired HIV Infection after STD are far fewer in number. We purposely distinguished between co-infection versus co-morbidity of HIV to emphasize data that reflect residents with acute HIV syndrome at the time of STD infection.

Table 1 details the definitions for each resident-level characteristic included in the profiles.

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Table 1. Resident-level characteristic definitions

Characteristic	Definition
Gender <sup>1</sup>	Current Gender OR Biological sex at birth + transgender <sup>2</sup> , recoded to reflect current gender  Male Female Transgender Transgender MF (Male-to-Female) Transgender FM (Female-to-Male)
Race/ethnicity <sup>1</sup>	Detailed race/ethnicity (Hispanic origin + race), recoded to mutually exclusive categories  White African American Latino Asian AI/AN (American Indian/Alaskan Native) NHOPI (Native Hawaiian or Other Pacific Islander)
MSM/MSMW <sup>1</sup>	Biological sex at birth (male) + reported to have had sex with men in the past 12 months OR Biological sex at birth (male) + reported to have had sex with men and women in the past 12 months OR Biological sex at birth (male) + reported to have a HIV transmission category of MSM or MSM/IDU
Youth (15-19 years)	Morbidity date – birth date (15 years old to 19 years old) at the time of a HIV or STD incident
Youth (15-24 years)	Morbidity date – birth date (15 years old to 24 years old) at the time of a HIV or STD incident
Pregnant	Biological sex at birth (female) + Pregnant indicated at the time of the incident
Recurrent STD Infections	Number of incidents by disease
Infection & Co-infection Combinations	Co-infection defined as occurring within +/- 30 days of the HIV or STD incident.

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Characteristic	Definition
	HIV Infection Only HIV incident (No STDs reported in 2010-2014)
	Co-infected with HIV Morbidity date of HIV incident $\leq 30$ days before or after morbidity date of STD incident
	Acquired HIV Infection <b>Before</b> STD Morbidity date of HIV incident is $>30$ days before morbidity date of STD incident
	Acquired HIV Infection <b>After</b> STD Morbidity date of HIV incident is $>30$ days after morbidity date of STD incident
	No HIV Infection STD incident (No HIV diagnosis on record, as of 8/29/2016)

<sup>1</sup> Inconsistent values across a resident’s records were managed based on a hierarchical approach using disease type and/or morbidity date.

<sup>2</sup> Transgender is based on the Centers for Disease Control and Prevention’s algorithm for calculating transgender, which uses values of biological sex and current gender across all CMRs and laboratory reports under one patient.

## Bivariate Maps

In combination, the bivariate maps highlight the differences in spread for HIV, syphilis, gonorrhea and chlamydia relative to risk for HIV infection or transmission [Figures 2, 3, 4, 5].

Like the profiles, the rates are reported in persons per year (i.e., person-years) and applies the same calculations. In map form, additional considerations were incorporated since rates are calculated for smaller geographical areas (i.e., census tracts) in order to show more local variation. To minimize the effect of random variation potentially resulting in unstable rates, we suppressed any census tracts with less than 12 cases as is the standard criterion used by the National Center for Health Statistics. We also suppressed any census tracts with a 2012 population less than 500 to protect against geoprivacy breaches. This is consistent with the standards set at the CDC Division of HIV/AIDS Prevention, AIDSvu and DHSP (at the time of this analysis). Symbology breaks for all maps adhere to quantile-based classification.

To leverage the person-level datasets, we juxtaposed rates with residential characteristics and behavior of our priority populations. Given the types of programs/service delivery contracts at DHSP, we assigned residents to categories according to a hierarchical approach that reflect differences in service delivery.

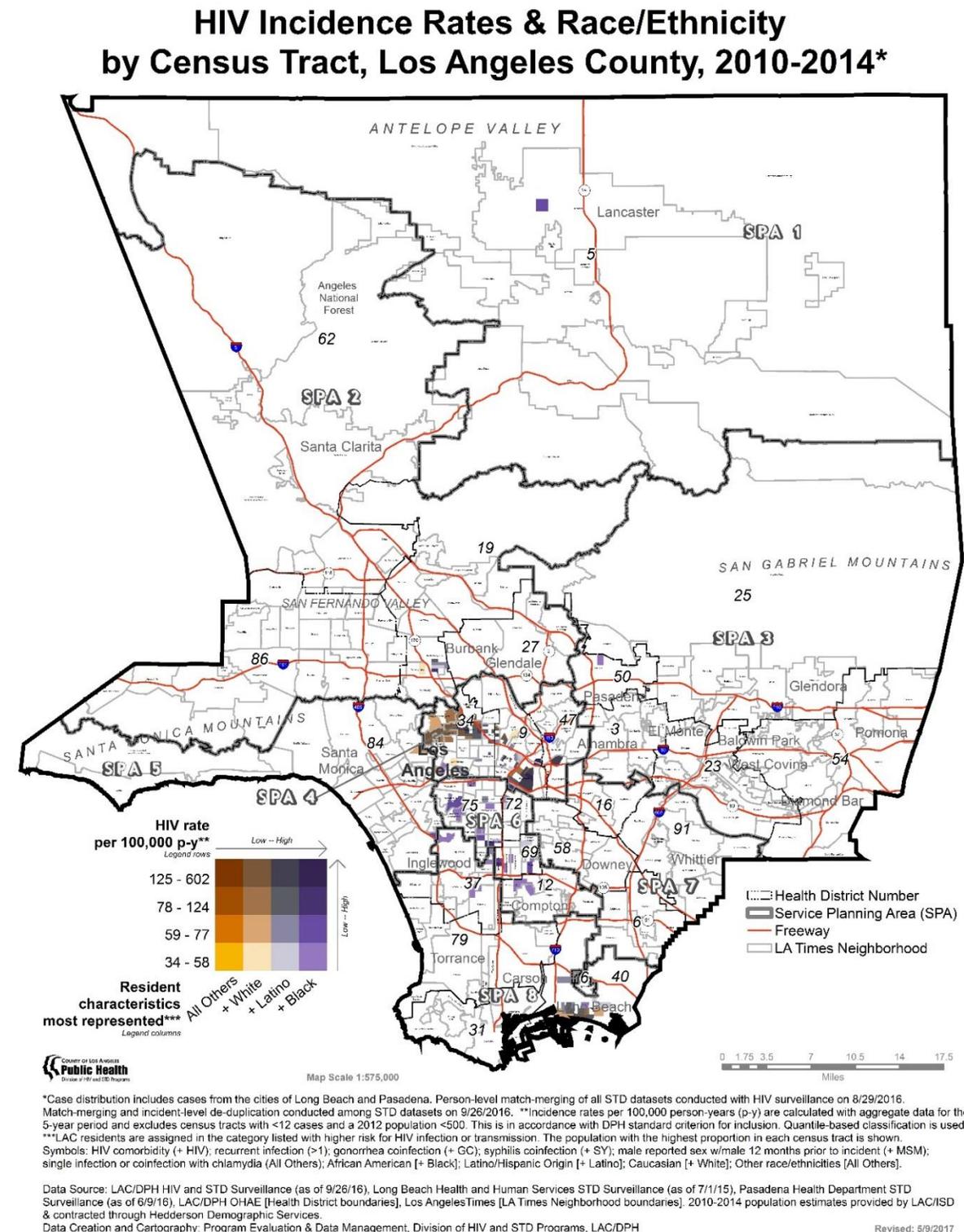
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For STDs, each resident was assigned in the following rank order: (1) residents with an HIV infection, (2) residents who are co-infected w/syphilis or gonorrhea or have recurrent infections, (3) male residents who report sex with a male 12 months prior to the incident (i.e., MSM/MSMW) and (4) all other residents. The category with the highest proportion in each census tract is shown. For HIV, each resident was assigned in the following rank order: (1) African American, (2) Latino/Hispanic Origin, (3) Caucasian and (4) other race/ethnicities.

Showing how our higher burdened areas can be more effectively served can be difficult in map form. In the bivariate maps, it becomes increasingly clear how each STD relates to the populations we serve through programs we support or enhance to reduce new HIV and STD infections.

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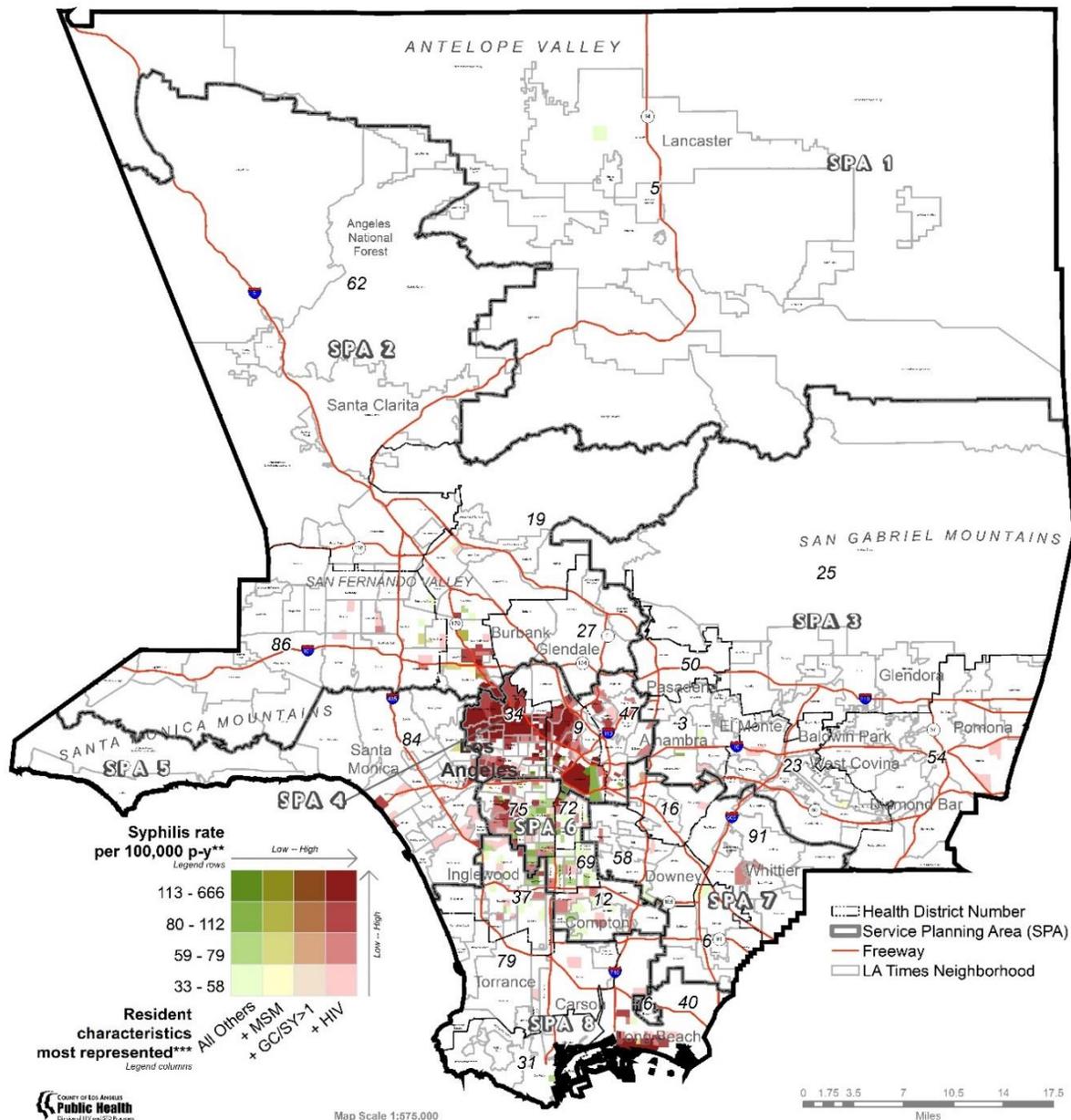
Figure 2. HIV Incidence Rate & Race/Ethnicity by Census Tract, Los Angeles County, 2010-2014



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Figure 3. Syphilis Incidence Rate & Resident Characteristics by Census Tract, Los Angeles County, 2010-2014

**Syphilis Incidence Rates & Resident Characteristics by Census Tract, Los Angeles County, 2010-2014\***



\*Case distribution includes cases from the cities of Long Beach and Pasadena. Person-level match-merging of all STD datasets conducted with HIV surveillance on 8/29/2016. Match-merging and incident-level de-duplication conducted among STD datasets on 9/26/2016. \*\*Incidence rates per 100,000 person-years (p-y) are calculated with aggregate data for the 5-year period and excludes census tracts with <12 cases and a 2012 population <500. This is in accordance with DPH standard criterion for inclusion. Quantile-based classification is used. \*\*\*LAC residents are assigned in the category listed with higher risk for HIV infection or transmission. The population with the highest proportion in each census tract is shown. Symbols: HIV comorbidity (+ HIV); recurrent infection (>1); gonorrhea coinfection (+ GC); syphilis coinfection (+ SY); male reported sex w/male 12 months prior to incident (+ MSM); single infection or coinfection with chlamydia (All Others); African American [+ Black]; Latino/Hispanic Origin [+ Latino]; Caucasian [+ White]; Other race/ethnicities (All Others).

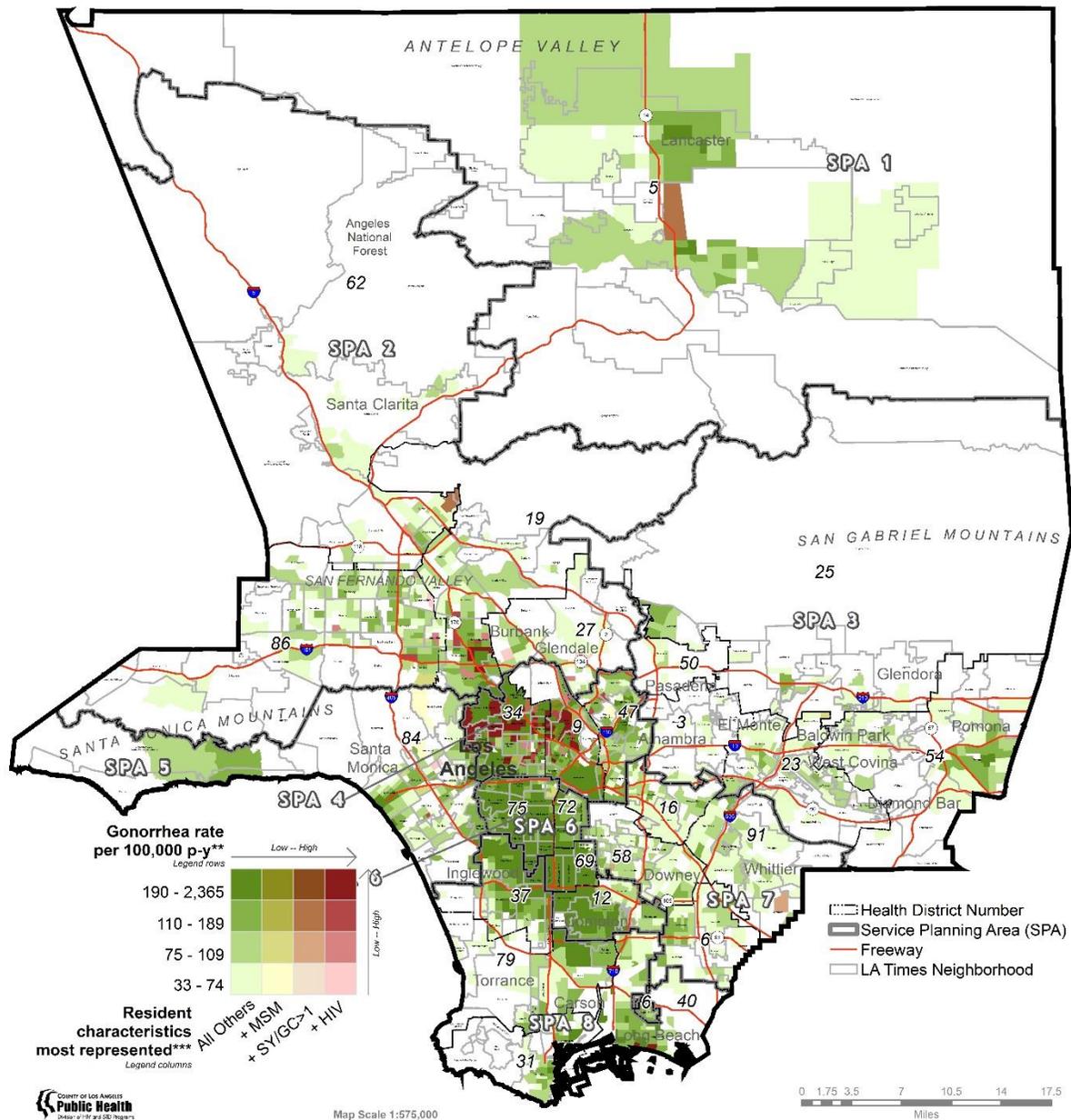
Data Source: LAC/DPH HIV and STD Surveillance (as of 9/26/16), Long Beach Health and Human Services STD Surveillance (as of 7/1/15), Pasadena Health Department STD Surveillance (as of 6/9/16), LAC/DPH OHAE [Health District boundaries], Los Angeles Times [LA Times Neighborhood boundaries], 2010-2014 population estimates provided by LAC/ISD & contracted through Hedderson Demographic Services. Data Creation and Cartography: Program Evaluation & Data Management, Division of HIV and STD Programs, LAC/DPH

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Figure 4. Gonorrhea Incidence Rate & Resident Characteristics by Census Tract, Los Angeles County, 2010-2014

**Gonorrhea Incidence Rates & Resident Characteristics by Census Tract, Los Angeles County, 2010-2014\***



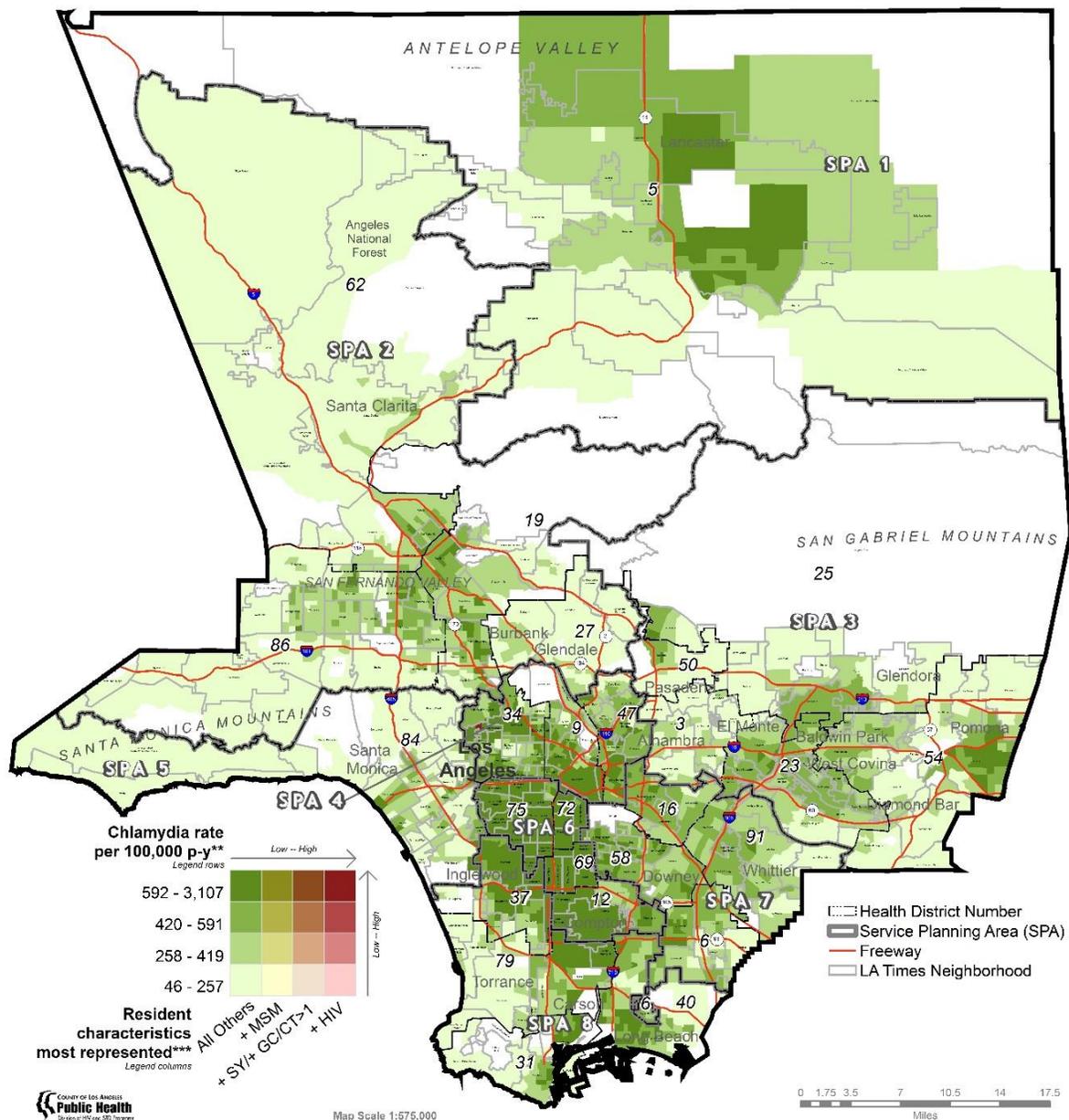
\*Case distribution includes cases from the cities of Long Beach and Pasadena. Person-level match-merging of all STD datasets conducted with HIV surveillance on 8/29/2016. Match-merging and incident-level de-duplication conducted among STD datasets on 9/28/2016. \*\*Incidence rates per 100,000 person-years (p-y) are calculated with aggregate data for the 5-year period and excludes census tracts with <12 cases and a 2012 population <500. This is in accordance with DPH standard criterion for inclusion. Quantile-based classification is used. \*\*\*LAC residents are assigned in the category listed with higher risk for HIV infection or transmission. The population with the highest proportion in each census tract is shown. Symbols: HIV comorbidity (+ HIV); recurrent infection (>1); gonorrhea coinfection (+ GC); syphilis coinfection (+ SY); male reported sex w/male 12 months prior to incident (+ MSM); single infection or coinfection with chlamydia (All Others); African American [+ Black]; Latino/Hispanic Origin [+ Latino]; Caucasian [+ White]; Other race/ethnicities [All Others].

Data Source: LAC/DPH HIV and STD Surveillance (as of 9/26/16), Long Beach Health and Human Services STD Surveillance (as of 7/1/15), Pasadena Health Department STD Surveillance (as of 6/9/16), LAC/DPH OHAe [Health District boundaries], Los AngelesTimes [LA Times Neighborhood boundaries], 2010-2014 population estimates provided by LAC/ISD & contracted through Hedderson Demographic Services. Data Creation and Cartography: Program Evaluation & Data Management, Division of HIV and STD Programs, LAC/DPH. Revised: 5/10/2017

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Figure 5. Chlamydia Incidence Rate & Resident Characteristics by Census Tract, Los Angeles County, 2010-2014

**Chlamydia Incidence Rates & Resident Characteristics by Census Tract, Los Angeles County, 2010-2014\***



\*Case distribution includes cases from the cities of Long Beach and Pasadena. Person-level match-merging of all STD datasets conducted with HIV surveillance on 8/29/2016. Match-merging and incident-level de-duplication conducted among STD datasets on 9/26/2016. \*\*Incidence rates per 100,000 person-years (p-y) are calculated with aggregate data for the 5-year period and excludes census tracts with <12 cases and a 2012 population <500. This is in accordance with DPH standard criterion for inclusion. Quantile-based classification is used. \*\*\*LAC residents are assigned in the category listed with higher risk for HIV infection or transmission. The population with the highest proportion in each census tract is shown. Symbols: HIV comorbidity (+ HIV), recurrent infection (>1), gonorrhea coinfection (+ GC), syphilis coinfection (+ SY), male reported sex w/male 12 months prior to incident (+ MSM), single infection or coinfection with chlamydia (All Others), African American [+ Black], Latino/Hispanic Origin [+ Latino], Caucasian [+ White], Other race/ethnicities [All Others].

Data Source: LAC/DPH HIV and STD Surveillance (as of 9/26/16), Long Beach Health and Human Services STD Surveillance (as of 7/1/15), Pasadena Health Department STD Surveillance (as of 6/9/16), LAC/DPH OHAE [Health District boundaries], Los AngelesTimes [LA Times Neighborhood boundaries], 2010-2014 population estimates provided by LAC/ISD & contracted through Hedderson Demographic Services. Data Creation and Cartography: Program Evaluation & Data Management, Division of HIV and STD Programs, LAC/DPH  
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## Syndemic Analysis of the HIV, Syphilis and Gonorrhea Disease Burden Using Statistical Analysis

Chloropleth maps such as the bivariate maps showcase the spread of the disease burden across LAC, and at first glance, the patterns suggest certain areas to be more highly burdened than others. However, these patterns often disregard key factors that can influence the display of disease burden, such as the area of administrative boundaries used or population data. Statistical analysis allows us to identify key clusters that have higher counts of each HIV or STD than what you might expect from random chance. To assess for these statistically significant “hot spots”, we used the Getis-Ord  $G_i^*$  tool in ArcMap 10.2.2.

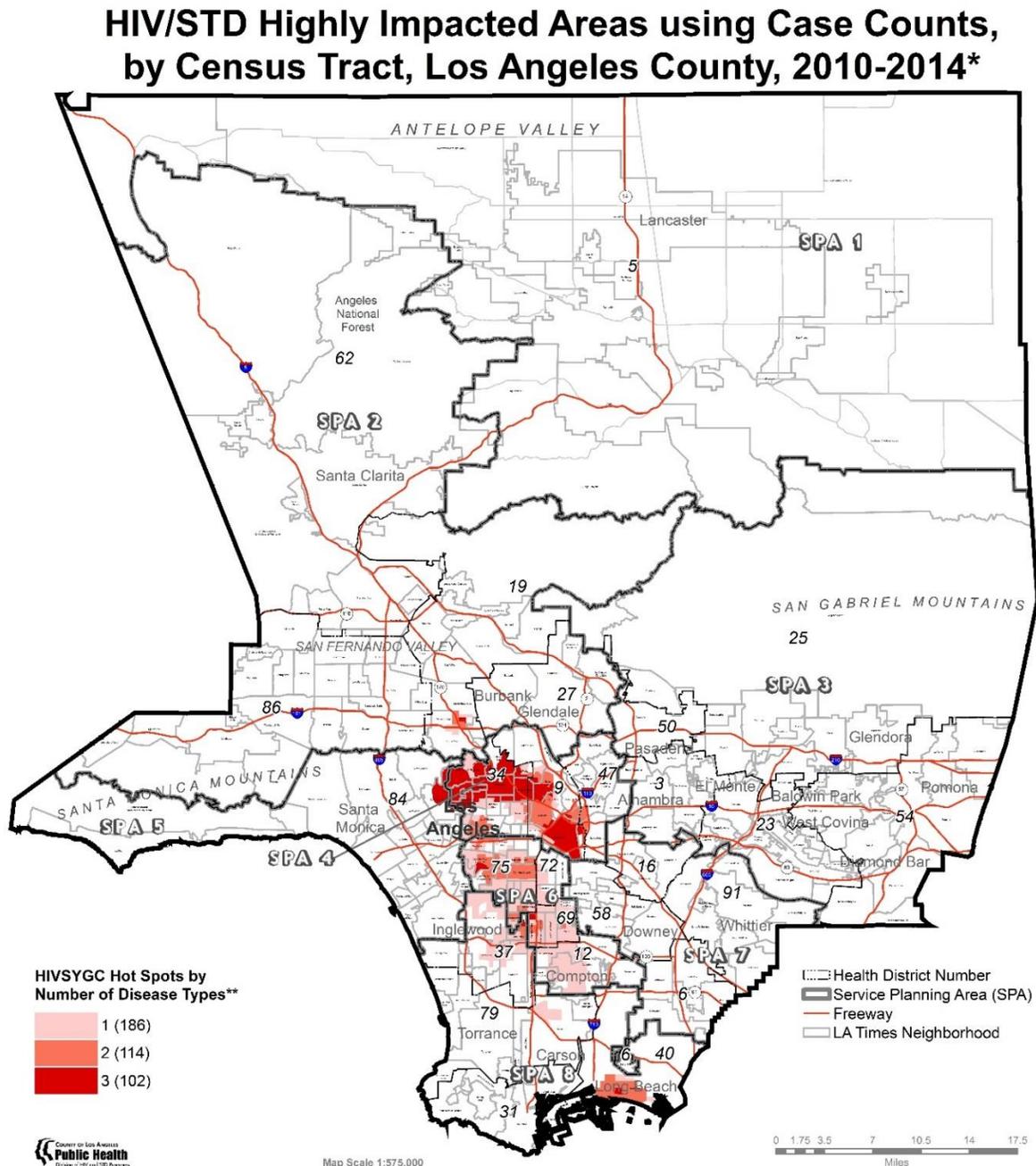
We conducted the analysis on both case counts and rates of HIV, syphilis and gonorrhea aggregated to census tracts during the 2010-2014 time period [Figures 6, 7].

The distance band is based on a spatial weights matrix using a Fixed Distance Conceptualization of Spatial Relationships and Euclidean distance method set at a 1 mile threshold distance with at least 1 neighbor to identify clusters. We opted for a spatial matrix based on distance to minimize the modifiable areal unit problem (MAUP), extend spatial contiguity beyond that captured through rook’s criterion or queen’s criterion, and minimize “edge effects” on the analysis.[4,5] This produced a matrix with an average of 7.38 neighbors and a spatial connectivity of 0.32%, which are consistent with best practice for doing a hot spot analysis.[3] Any census tracts with a zero population were excluded. Preliminary hot spot analyses on case counts aggregated to fishnet grids of varying scales and aggregated using the Integrate/Collect Events tool show similarly significant areas, with few exceptions. More local variation was apparent with smaller fishnet cells (e.g., 200 square feet) than larger cells. The varying sizes and shapes of census tracts have not had as much of an impact on the result of the analysis as we had expected given the modifiable areal unit problem (MAUP).[5] Consequently, we opted for census tracts. Furthermore, using census tracts allows for identification of recognizable boundaries and comparisons between the results from the hot spot analyses for counts and rates and eases interpretation and calculation.

The results from the count map answer a different question from those from the rate map. The count map shows where higher counts of each disease cluster spatially. The rate map shows where there are unexpectedly higher counts of each disease, given the population in each census tract. Because we are less interested in statistically significant areas specific for each disease, we overlaid the results from HIV, syphilis and gonorrhea to visualize the results. Two versions of the analysis on the counts were produced: one which indicate how many of the three diseases were statistically significant and another that presents no distinction. The rate map indicates whether the census tract was a hot spot. While we conducted the analysis on all data, we suppressed any statistically significant census tracts in the rates map that were outside the result boundaries indicated in the count maps for geoprivacy reasons. A z-score  $\leq 1.96$  defined statistical significance.

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Figure 6. HIV/STD Highly Impacted Areas using Case Counts, by Census Tract, Los Angeles County, 2010-2014



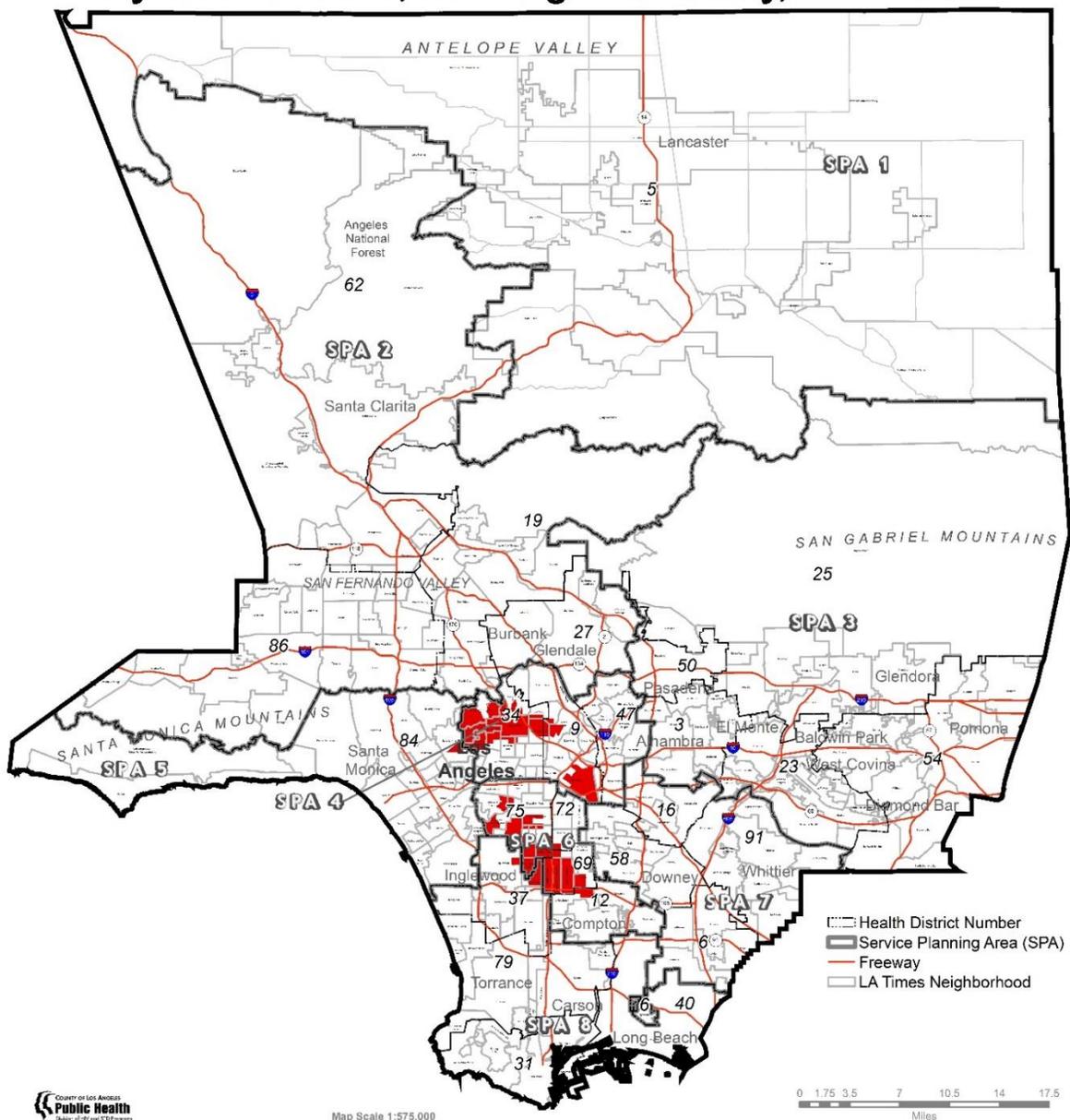
\*2010-2014 incidents for HIV, Syphilis and Gonorrhoea (HIVSYGC) are included. The highly impacted areas are developed using the Getis-Ord  $G_i^*$  Statistic (Hot Spot Analysis) on incident case counts and reflect census tracts with a  $G_i^*$  Z score  $\geq 1.96$  for each disease. A spatial weights matrix with a Fixed Distance Band Conceptualization of Spatial Relationship and Euclidean Distance Method was used for the hot spot analysis. Case distribution includes cases from the cities of Long Beach and Pasadena. Person-level match-merging of all STD datasets conducted with HIV surveillance on 8/29/2016. Match-merging and incident-level de-duplication conducted among STD datasets on 9/26/2016. \*\*Number of disease types include all 7 combinations of statistically significant areas for HIV, syphilis and gonorrhoea (e.g., HIV and SY; SY and GC). Number of census tracts are indicated by ( ).

Data Source: LAC/DPH HIV and STD Surveillance (as of 9/26/16), Long Beach Health and Human Services STD Surveillance (as of 7/1/15), Pasadena Health Department STD Surveillance (as of 6/9/16), LAC/DPH OHAE [Health District boundaries], Los AngelesTimes [LA Times Neighborhood boundaries], 2010-2014 population estimates provided by LAC/ISD & contracted through Hedderson Demographic Services.  
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Figure 7. HIV/STD Highly Impacted Areas using Incidence Rates by Census Tract, Los Angeles County, 2010-2014

**HIV/STD Highly Impacted Areas using Incidence Rates,  
 by Census Tract, Los Angeles County, 2010-2014\***



Map Scale 1:575,000

0 1.75 3.5 7 10.5 14 17.5  
Miles

\*2010-2014 incidence rates for HIV, Syphilis and Gonorrhea are included. This analysis determines unexpectedly high numbers of cases, given the population in each census tract. Incidence rates per 100,000 person-years (p-y) are calculated with aggregate data for the 5-year period and excludes census tracts with <12 cases and a 2012 population <500. This is in accordance with DPH standard criterion for inclusion. The highly impacted areas are developed using the Getis-Ord  $G_i^*$  Statistic (Hot Spot Analysis) and reflect census tracts with a  $G_i^*$  Z score  $\geq 1.96$  for each disease. A spatial weights matrix with a Fixed Distance Band Conceptualization of Spatial Relationship and Euclidean Distance Method was used for the hot spot analysis. Case distribution includes cases from the cities of Long Beach and Pasadena. Person-level match-merging of all STD datasets conducted with HIV surveillance on 8/29/2016. Match-merging and incident-level de-duplication conducted among STD datasets on 9/26/2016.

Data Source: LAC/DPH HIV and STD Surveillance (as of 9/26/16), Long Beach Health and Human Services STD Surveillance (as of 7/1/15), Pasadena Health Department STD Surveillance (as of 6/9/16), LAC/DPH OHAE [Health District boundaries], Los AngelesTimes [LA Times Neighborhood boundaries], 2010-2014 population estimates provided by LAC/ISD & contracted through Hedderson Demographic Services.  
 Data Creation and Cartography: Program Evaluation & Data Management, Division of HIV and STD Programs, LAC/DPH  
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## Health District Profiles

The Los Angeles County profile and twenty-six (26) health district profiles describe the HIV and STD burden across LAC, highlighting data on sociodemographic groups. Each profile includes a map containing the LA Times Neighborhood boundaries for reference purposes. Please reference the Data Preparation section for detailed information on each of the data points included in the charts. For confidentiality purposes, we masked gender or race/ethnicity counts and percentages if the category has less than five (5) persons and/or a 2014 population less than five hundred (500) people.

As an aid, we produced summary measures of the data points included in the charts and/or produced from the statistical analysis. These measures allow for a quick view of the disease burden in each area. Most important of these measure is the rank relative to the other health districts. Rank is a summary measure of important driving factors for the geographical burden of HIV and STD incidents:

(Infected residents count ÷ HD population) +

(Infection or co-infection count ÷ Area in square miles) +

((Area of census tracts w/z-score ≥ 1.96 for hot spot analysis on rates within each HD ÷ Area of HD \* weight [HIV=300; SY=200; GC=100])) +

((Area of census tracts w/z-score ≥ 1.96 for hot spot analysis on counts within each HD ÷ Area of HD) \* weight [3 diseases=300; 2 diseases=200; 1 disease=100]).

While initially we considered basing the summary measure on merely the number of infections and number of people with a HIV, syphilis, gonorrhea or high risk chlamydia incident during the 2010-2014 period, the analysis produced results that were inconsistent with results from statistical analysis and anecdotal evidence. We took into account other means of combining existing data points and concluded the final calculation reflected important driving factors. To that end, person counts were adjusted by population since the rate hot spot analysis reinforced the link between HIV/STD burden and population. Infection/Co-infection (as a proxy for sexual behavior) was adjusted by geography, under the assumption that HIV/STD transmission and geography are linked (e.g., potential partners tend to live closer than farther apart). The hot spot analysis on rates were incorporated in and weighted by disease type because the working assumption is to place emphasis on HIV and reduced acquisition and transmission of STDs we monitor based on acuteness of symptoms. The other summary measures highlight other aspects of the data that can be difficult to tease out from the charts. We included “Average infections per infected person” to reinforce the existence of core groups or repeatedly infected persons (i.e., the subgroup with high rates of infection, who when removed would bring the average number of infections per person at or below 1). The “Average infections per year per square mile” was included to elucidate the MAUP issues w/sharing data geographically and highlight disproportionately burdened geographical areas.

# TECHNICAL NOTES

## References

1. 2014 Population estimates provided by Los Angeles County Internal Services Department and contracted through Hedderson Demographic Services.
2. CDC. Revised Surveillance Case Definition for HIV Infection – United States, 2014. *MMWR* 2014; 63(No. RR03):1-10.
3. CDC. STD Surveillance Case Definitions. <http://www.cdc.gov/std/stats/casedefinitions-2014.pdf>. Published December 2013. Accessed 2/25/15.
4. ESRI. (2009). Modeling spatial relationships. [http://resources.esri.com/help/9.3/arcgisdesktop/com/gp\\_toolref/spatial\\_statistics\\_toolbox/modeling\\_spatial\\_relationships.htm](http://resources.esri.com/help/9.3/arcgisdesktop/com/gp_toolref/spatial_statistics_toolbox/modeling_spatial_relationships.htm). Accessed 9/30/15.
5. Openshaw, S. (1984). The modifiable areal unit problem. CAT-MOG 38, GeoBooks.

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