Measuring and Mapping Small Area Racial Disparities in Heart Disease

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Abstract

In light of the increasing interest in documenting and eliminating racial and ethnic disparities in health, a pressing need exists for appropriate methods to measure these disparities at the local level. The authors measured county-level disparity in heart disease mortality between African Americans and whites in South Carolina during 1996–2000, modelled via an extension of a spatial hierarchical Bayesian disease mapping model derived for incidence proportions. County-level maps of median disparity appear with figures displaying associated variability estimates. Race-specific maps of the burden of heart disease enable the reader to evaluate race-specific contributions to the disparity measure for each county. The findings highlight geographic variations across counties in magnitude of excess burden of heart disease mortality borne by African Americans relative to whites and indicate the largest racial disparities in heart disease mortality often occur in counties containing metropolitan or economically developed areas. Other maps and figures illustrate the versatility of the disparity measure. The authors discuss the merits and potential liabilities of the disparity measure and provide suggestions for wider application of such Bayesian techniques to the measurement of small area racial disparities, such as identifying community-level covariates of the racial disparities in heart disease mortality.

Bayesian smoothing; health disparities; hierarchical Bayesian disease mapping; rate standardization; small area analysis; standardized mortality ratio (SMR).

(Word counts: Abstract, 193 words; Text, 3911 words.)

Abbreviations: SMR, Standardized Mortality Ratio; MCMC, Markov chain Monte Carlo.
Measurement of disparities in health-related outcomes between socio-demographic sub-populations is of increasing interest in public health research and setting U.S. public health policy (1). The health disparity literature contains numerous articles documenting disparate incidence and prevalence measures for particular health outcomes. Most measures of disparity use ratios or differences in mortality rates, incidence, or prevalence proportions between groups of interest (2). Recent work also focuses on data necessary to measure and monitor health disparities (3).

There is also concern about geographic disparity in health outcomes and treatment practices, in addition to racial, ethnic, and socioeconomic disparities. Documenting and understanding geographic disparity is gaining attention in atlases of health outcomes and care (4–10) and studies of spatial and neighborhood trends in health-related outcomes (11–13). In this paper we combine purposes and extend hierarchial Bayesian disease mapping models to examine geographic variations in county-level measures of racial disparity in heart disease mortality in South Carolina for the years 1996–2000.

Nationally, excess heart disease mortality burden among African Americans compared to whites has been well documented (14). However, few studies have examined local-level African American–white disparities. Small area maps of heart disease mortality rates by racial or ethnic group highlight similarities and differences in geographic patterns for African Americans and whites across the nation (8, 9, 15). Recent maps cover 1996–2000 and indicate the highest rates for whites are primarily in the Mississippi Delta region, along the southeast coastal plain, and in much of the Appalachian region (16). Among African Americans, the highest rates are also observed primarily in the Mississippi Delta region and other parts of the southeast, but not in the Appalachian region. While map legends and frequency distributions indicate differences in the distributions of mortality rates for African Americans and whites, they do not indicate directly where African American–white disparities are largest and smallest. To our knowledge there are no maps documenting the
A geographic pattern of African American–white disparities in heart disease mortality rates.

A related study examined absolute excess burden of premature coronary heart disease among African Americans compared to whites by urbanicity and region (measured by rate difference) and found excess burden among African Americans varied from 71 to 127 deaths per 100,000 among men and 64 to 82 deaths per 100,000 among women (17). The largest disparities occurred in major metropolitan areas outside the United States’ southern region. In another study the same authors calculated temporal trends in coronary heart disease mortality for labor market areas from 1985 through 1995 (18). The results showed a larger percentage of labor market areas experienced increases for African American women (6 percent) and African American men (13 percent) than for white women (3 percent) and white men (1 percent). These findings are disturbing in light of steady overall declines in coronary heart disease mortality observed nationally during this time period (19).

Because of increasing interest in documenting and eliminating racial and ethnic disparities in health, a pressing need exists for appropriate methods to measure these disparities at the local level (20). This goal presents interesting statistical challenges due to an inherent trade-off between the statistical accuracy of local estimates (of mortality and disparity) and geographic resolution. Simply put, using smaller geographic areas—for example, counties instead of states—reduces local sample sizes, which increases statistical variation in local estimates. In contrast, increasing local sample sizes by aggregating regions loses geographic precision. Some atlases use moving spatial windows to aggregate local values to stabilize rate estimates (8–10), use weighted headbanging algorithms (5), or use no spatial smoothing (7).

We consider an alternative approach based on models originally developed for small area estimation (21, 22) and disease mapping (23). In both areas, Bayesian hierarchical models provide a more formal statistical approach for “borrowing strength” from neighboring areas to improve local estimates. Briefly, the models provide local estimates based on a statistical
compromise between local and neighboring data. The benefit of added statistical formality in model set-up is a richer set of inferential outcomes, including local estimates of mortality and disparity, and associated probabilistic summaries (e.g., probability local disparity exceeds 20 percent excess deaths.) Extending the methodology from local mortality estimation to local disparity estimation also raises interesting issues of interpretation regarding indirectly standardized rates.

The goal of this paper is two-fold: introduce an innovative approach for measuring local disparity levels and use the approach to document African American–white disparities in heart disease morality at the county level in South Carolina during 1996–2000.

**MATERIALS AND METHODS**

**Data**

We abstracted county-level numbers of heart disease deaths in South Carolina for 1996–2000 from the National Vital Statistics System’s public-use tapes, maintained by the National Center for Health Statistics. We define deaths from heart disease as those for which the underlying cause of death listed on the death certificate was coded according to International Classification of Disease–9th Revision (24) as 390-398, 402, or 404-429 for 1996–1998 or according to International Classification of Disease–10th Revision (25) as I00-I09, I11, I13, I20-I51 for 1999–2000. These codes compose the category “diseases of heart” developed by the National Center for Health Statistics (26). Because the estimated comparability ratio for diseases of heart is 0.9858 and is not race-specific, we do not adjust the data or results for the switch from International Classification of Disease–9th Revision to International Classification of Disease–10th Revision. (27). Person-years at risk for heart disease death derive from population estimates for 1996–2000 for all South Carolina counties, provided by the U.S. Census Bureau, which calculates postcensal estimates by projecting changes in the
decennial census due to births, deaths, and migrations.

We label the 46 counties of South Carolina with index $i$, $i = 1, 2, \ldots, 46$, and use index $j$ to label the two groups in our study, white men ($j = 1$) and African American men ($j = 2$). (For clarity, we develop our small area disparity model for only two groups, white men and African American men; we also present results for two additional groups, comparing heart disease mortality in white women versus African American women.) We note racial categories reflect socially distinct groups of people, not biological differences (28, 29), and measurement and classification of race are complex issues. Finally, we use index $k$ for six age strata, where $k = 1$ represents age stratum 35-44 years, $k = 2$ represents 45-54 years, and so on, through $k = 6$ represents 85 years or older. State-wide, age strata-specific mortality rates (over the entire study period) by gender and race appear in figure 1. We note the crossover (30, 31) in mortality rates for African Americans compared to whites between the age strata 75-84 years and 85 years and older, for both men and women.

**Modelling**

Disease maps of raw, local mortality estimates possess well-known deficiencies. Frequently, geographically large but sparsely populated counties visually dominate the map but provide the least reliable estimates, especially for rare diseases. Researchers can attempt to overcome these deficiencies by employing methods that smooth, spatially or otherwise, raw estimates by “borrowing strength” across small areas. Bayesian methods for disease mapping formally combine information on observed events in a small area with information on local and overall disease rates in estimating area-specific disease rates. Such models were introduced by Clayton and Kaldor (32) and placed in a fully Bayesian setting by Besag, York, and Mollié (33). Mollié (34) and Wakefield, Best, and Waller (23) give reviews of Bayesian approaches, while Lawson et al. (35) and Lawson and Williams (36) provide overviews of disease mapping. Recently Kleinschmidt et al. employed Bayesian spatial models to study South Africa’s rising
Figure 1:
malaria incidence rates (37).

Our approach to measuring local disparities begins with a hierarchical, fully Bayesian spatial disease mapping model for each of two racial groups under study, white men ($j = 1$) and African American men ($j = 2$). To measure county-level racial disparity in heart disease mortality we extend the usual methodology by linking the two race-specific models and by modifying the calculations of expected number of heart disease deaths.

**Poisson Model.** Let $Y_{ijk}$ be the total number of heart disease deaths and $N_{ijk}$ be the total number of person-years at risk of heart disease death in county $i$ for group $j$ in age stratum $k$ during the study period. We model heart disease deaths in county $i$ for group $j$ (i.e., summed over age strata, with $k$ suppressed) as:

$$Y_{ij} \mid \theta_{ij} \sim^\text{ind} \text{Poisson}(E_{ij} \times \theta_{ij}),$$

where $E_{ij}$ is expected number of heart disease deaths in county $i$ for group $j$, and $\theta_{ij}$ is relative risk of heart disease death in county $i$ for group $j$ compared to the reference risk defining the $E_{ij}$’s, here the combined overall heart disease mortality rate across both racial categories, all age groups, and all counties in South Carolina. The maximum likelihood estimate of $\theta_{ij}$ is the standardized mortality ratio (SMR) for group $j$ in county $i$: $\hat{\theta}_{ij} = \frac{Y_{ij}}{E_{ij}}$. The $E_{ij}$’s are regarded as fixed and known, while the $Y_{ij}$’s are regarded as random and conditionally independent of one another given the $\theta_{ij}$’s.

**Calculation of Expected Number of Heart Disease Deaths.** Calculation of the $E_{ij}$’s is rarely discussed in detail in the disease mapping literature but merits clarification in our analysis, as the $E_{ij}$’s play an important role in our disparity measure. Specifically, we use the $E_{ij}$’s to formally model the study population’s racial heterogeneity, which allows measurement of county-level disparity. Following custom, we calculate the $E_{ij}$’s in two steps by indirect, internal standardization (38, chap. 19), which incorporates the population age structure.
of each small area. Such standardization reduces the possibility of confounding by creating age-adjusted expected counts. A critical review of indirect standardization appears in Pickle and White (39), which is discussed below. For a different implementation of indirect standardization see Xia and Carlin (40).

The first step of our standardization computes state-wide age strata-specific death rates based on the union of the two groups \((j = 1 \text{ and } j = 2)\) under study:

\[
\pi_k = \frac{\sum_{i=1}^{I} \sum_{j=1}^{2} Y_{ijk}}{\sum_{i=1}^{I} \sum_{j=1}^{2} N_{ijk}} = \frac{\sum_{i=1}^{I} (Y_{i1k} + Y_{i2k})}{\sum_{i=1}^{I} (N_{i1k} + N_{i2k})}. \tag{2}
\]

Combining racial groups \(j = 1\) and \(j = 2\) when calculating the \(\{\pi_k\}\) treats the two groups in a like manner so that differences in their smoothed SMRs can be considered disparities. Calculating the \(\{\pi_k\}\) this way pools the comparison groups, which occurs in typical Bayesian disease mapping models when, as is customary, the population’s racial heterogeneity is not modeled. Further, according to Fleiss, Levin, and Paik (38, p. 635), using such a composite population as the standard population upon which the \(\{\pi_k\}\) are based avoids possible distortion with indirect standardization.

The second and final step of our standardization uses the \(\{\pi_k\}\) to compute expected heart disease death counts for group \(j\) in county \(i\) as \(E_{ij} = \sum_{k=1}^{K} N_{ijk} \pi_k\).

**Log-linear Model.** We model the log relative risks of equation 1 as:

\[
\log(\theta_{ij}) = \alpha + \gamma_j + U_{ij}, \tag{3}
\]

where the \(\gamma_j\)'s represent group effects and we constrain \(\gamma_1 = 0\) for identifiability. The \(U_{ij}\)’s represent spatially-structured, county-specific random effects. Note that \(\alpha\) does not depend on county and measures a state-wide level of mortality (for group \(j = 1\) since \(\gamma_1 = 0\)), relative to the reference risk defining the \(E_{ij}\)’s, while \(U_{ij}\) measures county \(i\)’s departure from the
overall level for group \( j \). Also, we assume the \( \{U_{i1}\} \) are independent of the \( \{U_{i2}\} \). Equation 3 could incorporate additional covariates via a design matrix and associated parameters but we do not include such terms in this analysis.

**Choice of Prior Distributions.** We define the prior distribution of \( \alpha \) as an (improper) uniform distribution, the prior distribution of \( \gamma_2 \) as a vague \( \text{Normal}(0, 10,000) \) distribution, and the prior distribution of the \( U_{ij} \)'s as:

\[
U_{mj} \mid U_{nj} (n \neq m) \sim N \left( \frac{\sum_{n \neq m} w_{mn} U_{nj}}{\sum_{n \neq m} w_{mn}}, \frac{1}{\tau_j \sum_{n \neq m} w_{mn}} \right).
\] (4)

This prior for the \( U_{ij} \)'s is an intrinsic Gaussian autoregressive prior distribution (33). The \( w_{mn} \) are a set of weights defined by the neighborhood adjacency structure of South Carolina’s counties. We let \( w_{mn} = 1 \) when county \( n \) is adjacent to county \( m \), with \( w_{mn} = 0 \) otherwise and \( w_{mm} = 0 \) by convention. Consequently, \( \sum_{n \neq m} w_{mn} \) gives the number of adjacent neighbors of county \( m \). The set of conditional priors in equation 4 jointly defines a Markov random field model (41), which induces spatial similarity between adjacent regions and results in spatial smoothing of local estimates. Because equation 3 contains an intercept term, we constrain \( \sum_{i=1}^{I} U_{ij} = 0 \) for identifiability of the \( U_{ij} \)'s (23). To complete the model we specify hyperparameters for the prior distribution of the \( \tau_j \)'s. We follow Wakefield, Best, and Waller (23) and choose \( \text{Gamma}(0.5, 0.0005) \) as priors for the \( \tau_j \)'s.

**Implementation.** We implemented our fully Bayesian model using Markov chain Monte Carlo (MCMC) methods. Such iterative MCMC methods, detailed in Gilks, Richardson, and Spiegelhalter (42), allowed generation of post-convergence samples from the (approximate) posterior distribution of disparity (and other parameters) and overcome potentially intractable integration. From these samples we calculated and mapped standard properties, such as the median and 95 percent credible intervals and other quantities of interest (43).
We used WinBugs 1.4 software to run our model, which ran on a 2.8-GHz Pentium IV processor using Windows XP. Maps were created with ArcView 3.3 software and graphs and many calculations with R-1.9.1 software. In all implementations we ran three overdispersed, random, parallel chains of 15,000 MCMC simulations, discarding the first 5,000 samples as a burn-in period. Convergence was adequate based on Gelman and Rubin diagnostics (44) and visual inspection of the mixing of the multiple chains.

After implementation we obtain a measure of age-adjusted, smoothed SMR for each county and both groups at every MCMC iteration, indexed \((s)\). Specifically, we have at iteration \((s)\):

\[
\text{SMR}_{ij(s)} = \theta_{ij(s)} = e^{\alpha(s) + \gamma_j(s) + U_{ij(s)}} = e^{\alpha(s)} \times e^{\gamma_j(s)} \times e^{U_{ij(s)}} .
\]

We use these age-adjusted, smoothed SMRs to form our disparity measure.

**Measuring disparity**

Our approach calculates disparity for a county as the ratio of the age-adjusted, smoothed SMR for group \(j = 2\) in the county to the age-adjusted, smoothed SMR for group \(j = 1\) in the same county. The disparity measure for county \(i\) is:

\[
\rho_i \equiv \frac{\text{SMR}_{i2}}{\text{SMR}_{i1}} = \frac{\theta_{i2}}{\theta_{i1}} = \frac{e^{\alpha} \times e^{\gamma_2} \times e^{U_{i2}}}{e^{\alpha} \times e^{\gamma_1} \times e^{U_{i1}}} = e^{\gamma_2} \times e^{U_{i2} - U_{i1}} ,
\]

since we constrain \(\gamma_1 = 0\).

A value of \(\rho_i\) exceeding one indicates a greater age-adjusted heart disease mortality rate in county \(i\) for African American men \((j = 2)\) than for white men \((j = 1)\). Also, equation 6 reveals disparity in county \(i\) to be a product involving two terms: a term not depending on county, \(\exp(\gamma_2)\), and a term depending on county, \(\exp(U_{i2} - U_{i1})\). The former term may be interpreted as a state-wide disparity measure for group \(j = 2\) versus group \(j = 1\) and the latter term as county \(i\)'s (multiplicative) departure from the state-wide disparity measure.
Population | Heart Disease Deaths | Person-Years at Risk
--- | --- | ---
All | 49,230 | 9,542,203
Men | 24,903 | 4,422,983
  African-American Men | 6,317 | 1,072,606
  White Men | 18,586 | 3,350,377
Women | 24,327 | 5,119,220
  African-American Women | 6,835 | 1,380,111
  White Women | 17,492 | 3,739,109

Table 1:

**RESULTS**

During the 1996–2000 study period, 49,230 heart disease deaths occurred among residents in South Carolina in the study population and 9,542,203 person-years at risk for heart disease death accrued. African Americans accounted for 26.7 percent of heart disease deaths and 25.7 percent of person-years. Stratified by gender, values were: African American men, 25.4 percent of heart disease deaths and 24.3 percent of person-years; African American women, 28.1 percent of heart disease deaths and 27.0 percent of person-years. Further details of the data appear in table 1.

Among South Carolina counties, median disparity ($\rho_i$) in heart disease mortality for African American men versus white men ranged from 0.930 to 1.515, and for women from 0.995 to 1.567. State-wide disparity ($\exp(\gamma_2)$) for men was 1.208 (95 percent credible interval: 1.167, 1.250) and for women, 1.236 (95 percent credible interval: 1.196, 1.277).

Maps of county-level posterior median disparity, $\rho_i$, for South Carolina men and women are shown in figure 2. Ancillary maps of county-level posterior median SMRs for African Americans and whites are displayed in figure 3. These maps of median SMRs may be thought of as race-specific components of the disparity maps. Figure 2 shows counties with large disparity (say, greater than 1.200, or equivalently 20 percent excess heart disease mortality for African Americans compared to whites) tend to be in the northern part and southern tip of the state. The map also suggests counties with the greatest disparities often, but not
Figure 2:

Disparity
African Americans compared to whites

Disparity

- Less than 1.000
- 1.000 to 1.100
- 1.100 to 1.200
- 1.200 to 1.300
- 1.300 and up

100 0 100 200 Kilometers
Figure 3:

SMRs for African Americans

SMRs for Whites

SMR, age-adjusted and spatially smooothed

Less than 1.000
1.000 to 1.100
1.100 to 1.200
1.200 to 1.300
1.300 and up

100 0 100 200 Kilometers
always, contain metropolitan or economically developed areas (e.g., Greenville in Greenville County, Spartanburg in Spartanburg County, Columbia in Richland County, and Hilton Head and Beaufort in Beaufort County.) The ancillary maps of age-adjusted and spatially smoothed SMRs in figure 3 indicate, for both African American men and white men, counties with highest SMRs are located primarily in northern counties. However, SMRs for African American men are consistently higher than SMRs for white men.

For women, figure 2 shows counties with largest racial disparities in heart disease mortality are located primarily in the central region, scattered in the northwest region, and along the eastern coast. Similar to men, many counties with disparities greater than 1.200 contain metropolitan or economically developed areas. Several high disparity counties containing metropolitan or economically developed areas overlap with such counties for men (e.g., Columbia in Richland County, Greenville in Greenville County); however, others do not (Myrtle Beach in Horry County, Sumter in Sumter County and Charleston in Charleston County.) Ancillary race-specific SMR maps (figure 3) highlight pervasiveness of larger SMRs among African American women compared to white women.

Because we use Bayesian methods, after convergence MCMC iterations represent samples from approximate posterior distributions of model parameters. An advantage of this approach is that we may use these post-convergence posterior samples of model parameters to create post-convergence posterior samples of any function of the parameters, including $\rho_i$. We use this richness of the Bayesian approach to analyze quantities of interest, such as median SMR and disparity, and to report other maps and plots. For example, ordered values of median disparity along with 95 percent credible intervals appear in figure 4. For men, median disparity is greater than 1.000 in 44 of 46 counties and the 95 percent credible intervals for disparity exclude 1.000 in 19 of 46 counties. For women, 45 counties have median disparity greater than 1.000 and 24 counties have 95 percent credible intervals that exclude 1.000. These results highlight pervasiveness of elevated heart disease mortality rates
Figure 4:
for African Americans compared to whites among South Carolina counties.

Again using the richness of the Bayesian approach, figure 5 provides a sequence of maps showing the probability a county exceeds a threshold value of disparity. For both men and women, in almost all counties there is at least a 75 percent probability racial disparity exceeds 1.000. For men, the five counties with greatest probability (i.e., probability greater than 95 percent) disparity exceeds 1.200 are scattered along the northern border, in the center, and in the southern tip of South Carolina. Counties with at least 75 percent probability of exceeding 1.200 are scattered along the northern part and southern tip of the state. For women, the five counties with at least 95 percent probability of exceeding 1.200 are located in the central and west-central regions and along the southeast coast. Counties with at least 75 percent probability of exceeding 1.200 are located primarily in the central and southeastern regions. This pattern differs from the pattern for men. Further, the number of counties with more than 50 percent probability of exceeding 1.200 is greater for women \( n = 25 \) than men \( n = 21 \).

**DISCUSSION**

County-level maps of racial disparity and SMRs (figures 2 and 3) produced by our extended Bayesian hierarchical model illustrate pervasiveness and geographic variation in excess burden of heart disease mortality among African Americans compared to whites in South Carolina. These and other results above raise important questions regarding conditions that give rise to excess burden of heart disease mortality among African Americans compared to whites, and how those conditions vary geographically. Figure 2 shows the largest racial disparities often occur in counties containing metropolitan or economically developed areas. This pattern occurs for women and men, although specific counties differ somewhat. The literature suggests community-level factors such as residential segregation and other
Figure 5:

MEN

Probability disparity exceeds 1.000

WOMEN

Probability disparity exceeds 1.100

Probability disparity exceeds 1.200

Probability disparity exceeds threshold

- 0% to 50%
- 50% to 75%
- 75% to 95%
- 95% to 100%

100 0 100 200 Kilometers

N
forms of institutionalized racism (45–55), urbanization (17, 45, 49, 56), occupational structure (57, 58), and poverty levels (47, 59) could play a role in the observed disparities. The pervasiveness and geographic variation of racial disparities in heart disease mortality signals differential access to heart-healthy living and working conditions for African Americans compared to whites. Additional analyses are needed to identify covariates of observed county-level disparities in heart disease mortality and elucidate pathways that result in higher levels of heart disease mortality for African Americans.

Our approach to measuring local-level racial disparities possesses several advantages. As noted earlier, the Bayesian model offers a more formal statistical approach for borrowing strength from neighboring counties to improve local estimates than many of the methods used in recent atlases. Further, the Bayesian model can produce probability statements for any model parameters of interest, such as county-level estimates of racial disparity. The combination of the disparity measure and the probability statements provides policy makers with critical information in guiding distribution of scarce resources, as in figure 5.

Another advantage is the provision of model-based inferences regarding key components of disparity, namely the race-specific, age-adjusted, and spatially-smoothed SMRs. An obvious type of disparity occurs when one group has high SMR and the other group low SMR. However, inspection of figures 2 and 3 shows disparities can also exist where both groups have low (but different) SMRs or where both groups have high (but different) SMRs. The nature of the disparity can have important implications for designing policies and programs to eliminate racial disparities in heart disease mortality, as well as for identifying determinants of these disparities.

Our approach to measuring small area racial disparities also raises important issues regarding comparison of two SMRs since our disparity measure for county \( i \) is the ratio of the African American SMR for county \( i \) to the white SMR for county \( i \). For instance, Rothman (60, p.262) states, “Except in special situations, two or more SMR estimates will
not be comparable with one another because they are standardized to different exposure
groups.” (For additional criticism of comparing two SMRs, see, for example, Hennekens and
Buring (61, pp. 84–5).)

Breslow and Day (62) provide a thorough discussion of potential problems with comparing
two SMRs. These authors trace such problems to Simpson’s paradox (63) (e.g., differing
aggregate versus age stratum-specific patterns of SMRs) and write, “The SMRs for two
cohorts may be compared safely provided that the ratios of cohort to standard rates are
approximately constant so that there is little or no confounding by age” (62, p. 62). They
cite Gail (64) (which cites Breslow and Day (65)) for a formal test that SMRs represent
good summary measures across comparison groups, referring to the underlying condition
that would permit comparison of SMRs as the “proportionality assumption.”

Pickle and White (39) extend the findings of Breslow and Day (62) to look at the impact
of failure of the proportionality assumption (with respect to age and location effects) on rates
mapped as percentiles and conclude with a warning against using indirect standardization
as typically used in Bayesian disease mapping models. However, Pickle and White note that
when the population structures of the populations being compared are similar, the ratio of
indirectly standardized rates (and consequently the ratio of SMRs) will be “approximately
correct,” meaning the underlying relationship between age-specific rates is preserved.

We used the approach of Pickle and White (39) to evaluate the appropriateness of using
indirect standardization in our model. First, we observed the county-level population
structures for African Americans compared to whites are similar for both men and women,
as in figure 6, so that the ratio of indirect rates (and hence ratio of SMRs) should be ap-
proximately correct. Second, we plotted rankings of county heart disease death rates using
indirect versus direct methods of standardization for each race-gender group (figure 7) and
calculated nonparametric correlation coefficients of 0.9962, 0.9847, 0.9922, and 0.9830 for
white men, African American men, white women, African American women, respectively.
Figure 6:

White Men

White Women

African American Men

African American Women
Based on these correlations and figure 7, and on the similarity of population structures in figure 6, we conclude there is little benefit in favoring direct over indirect standardization and are confident indirect standardization is appropriate for our data.

Our approach is amenable to many future research projects. Our approach can easily accommodate small area covariates. Future analyses will examine the role of local socioeconomic conditions on racial disparities in heart disease and stroke mortality. Another possible enhancement of our approach involves its independent treatment of the groups under comparison. This aspect results in no intergroup smoothing. Kim, Sun, and Tsutakawa (66) and Carlin and Banerjee (67) present Bayesian methods based on multivariate conditional autoregressive models, suggesting the possibility of a model that treats groups differently yet allows intergroup smoothing. Such methods may not be appropriate for assessing disparity, which would seem to compel some type of independent treatment of the comparison groups, but are a possible future direction for small area disparity research.

In conclusion, our approach provides model-based small area estimates of racial disparity in heart disease mortality by extending and modifying existing Bayesian disease mapping and SMR methodology. Close examination of our data indicated conditions that could jeopardize the appropriateness of our model did not exist, thereby enabling this study to benefit from the many advantages of the Bayesian approach. Our observation of variation among counties in magnitude of excess burden for heart disease mortality borne by African Americans relative to whites in South Carolina raises important questions about determinants of these disparities and provides new information for public health workers committed to eliminating geographic, racial, and ethnic disparities in heart disease mortality.
Figure 7:

White Men

Spearman correlation = 0.9962

White Women

Spearman correlation = 0.9922

African American Men

Spearman correlation = 0.9847

African American Women

Spearman correlation = 0.9830
References


TABLE 1. Heart Disease Deaths and Person-Years at Risk. This table provides counts of heart disease deaths and person-years at risk for the study population of South Carolina during the 1996–2000 study period and for various subgroups, including men, women, African American men, African American women, white men, and white women.
Figure Titles and Legends

FIGURE 1. Heart Disease Mortality Rates by Age Stratum. The graphs show African American (- - -) and white (—) heart disease mortality rates per 100,000 people on a logarithmic scale over the entire 1996–2000 study period by age stratum, for South Carolina men and women.

FIGURE 2. Disparity. The maps depict median county-level racial disparities in heart disease mortality between African Americans and whites in South Carolina.

FIGURE 3. Race-Specific Standardized Mortality Ratios (SMRs). The maps depict median county-level SMRs for heart disease mortality for African Americans (top row) and whites (bottom row) in South Carolina. These maps may be thought of as the components of the disparity maps in figure 2.

FIGURE 4. Ordered Disparity with 95 percent Credible Intervals. The graphs show ordered values of median disparity (o) in heart disease mortality between African Americans and whites in South Carolina and 95 percent credible intervals (vertical bars) for these values.

FIGURE 5. Probability Disparity Exceeds Specified Values. These maps depict the probability that a county’s heart disease mortality racial disparity value exceeds a specified value. The specified values shown in the maps are, from top to bottom, 1.0, 1.1, and 1.2. These maps are possible because our Bayesian model affords us (approximate) samples from the posterior distribution of disparity conditional on the data.

FIGURE 6. Population Distributions by County. These plots show the population distribution for the counties of South Carolina for the four race-gender groups in this study. The heavy lines denote the group-specific state-wide average, while the dotted (...) lines represent
counties.

FIGURE 7. Heart Disease Mortality Rates Under Direct and Indirect Standardization. These plots compare ranked county heart disease mortality rates under indirect versus direct standardization. The solid line denotes equal ranking.