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Estimation of High Blood Lead Levels Among Children in Georgia: An Application of Bayesian Analysis

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Abstract

In Georgia, children in high-risk counties are at increased risk for lead exposure. Those children and others in high-risk groups, such as families receiving Medicaid and Peach Care for Kids (i.e., health coverage for children in low-income families), are screened for blood lead levels (BLLs). Such screening, however, might not include all children at high risk for having BLLs above the reference levels (≥5 μg/dL) in the state. In our study, Bayesian methods were used to estimate the predictive density of the number of children <6 years with BLLs of 5–9 μg/dL in a targeted county from each of five selected regions of Georgia. Furthermore, the estimated mean number of children with BLLs of 5–9 μg/dL in each targeted county, along with its 95% credible interval, were calculated. The model revealed likely underreporting of some children <6 years with BLLs of 5–9 μg/dL in counties of Georgia. Further investigation might help reduce underreporting and better protect children who are at risk for lead poisoning.

Introduction

Lead exposure can seriously affect the health of children (World Health Organization, 2022). High levels of lead exposure can harm the brain and central nervous system of children. High levels of lead exposure can also cause coma, convulsions, and death in children. Children who survive severe lead poisoning can suffer from mental deficiencies and behavioral disorders. Lead is known to affect children's brain development and can result in reduced IQ and behavioral changes such as short attention span and reduced educational attainment. Most importantly, these neurological and behavioral effects of lead are irreversible (Centers for Disease Control and Prevention [CDC], 2022; Egan et al., 2021).

Georgia Department of Public Health (n.d.) guidelines for blood lead screening recommend screening children who belong to high-risk groups such as families receiving Medicaid or Peach Care for Kids (i.e., health coverage for children in low-income families). The guidelines also recommend screening in 16 counties in which children are at greater risk for lead exposure. Following these guidelines, the resulting group of children to be tested

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for elevated blood lead levels (BLLs), however, is limited and some children with elevated BLLs might be missed.

In 2012, the Centers for Disease Control and Prevention (CDC, 2021) defined a BLL of 5 μg/dL as a reference value for children <6 years. Note, this reference value was changed to a more stringent level of 3.5 μg/dL but at the time of our study the limit was 5 μg/dL. Bayesian analysis with limited beliefs about a parameter can be helpful in modeling the exposure of lead in children by suitably matching these beliefs with some known distribution.

The primary objective of our study was to estimate and validate the observed number of children with BLLs of 5–9 μg/dL among children <6 years in different counties of Georgia, selected by region. This objective was important to investigate if screening of a limited group of children in Georgia resulted in underreporting of children with elevated BLLs. Although some studies have connected targeted screening and missed children with elevated BLLs (Roberts et al., 2017), no such research work has been found evaluating the impact of targeted screening on the rate of children <6 years with elevated BLLs in a region, especially in Georgia.

Methods

Data Collection

We used data collected by the Healthy Homes and Lead Poisoning Prevention Program of the Georgia Department of Public Health for 2015. Child blood lead surveillance data was used, including the number of children <6 years who were tested and the number of children with BLLs of 5–9 μg/dL, by race and county. Estimates of children <6 years were available from the Georgia Governor's Office of Planning and Budget (2016).

Bayesian Model

The variable z was used to represent the number of children <6 years with BLLs of 5–9 μg/dL in a county in Georgia. Because this event is rare, one can safely assume that z follows a statistical distribution known as Poisson distribution shown by:

$$p(z/\theta) = e^{-(m\,.\,\theta)}(m\,.\,\theta)^{z}/z! \quad (1)$$

Where θ is the rate of children with BLLs of 5–9 μg/dL (i.e., θ = children with BLLs of 5–9 μg/dL/children tested for BLL); m is the number of children <6 years who were tested for BLL; m . θ is the number of children with BLLs of 5–9 μg/dL; and p(z/θ) is the probability that there are z number of children <6 years with BLLs of 5–9 μg/dL under the assumption that θ is the rate of children with BLLs of 5–9 μg/dL.

Clearly, θ is unknown or a parameter, and under the Bayesian principle, one tries to estimate it based on a reasonable assumption of its statistical distribution, called "prior distribution" or simply "prior." It is reasonable to assume that a parameter coming from a Poisson distribution should follow a statistical distribution called gamma distribution.

Thus, this model assumes that θ follows a gamma (α, β) prior:

$$p(\theta) = e^{-(\beta\,\theta)}\beta^{\alpha}\theta^{\alpha-1}/\Gamma(\alpha) \tag{2}$$

Where θ > 0, and α and β are its unknowns or parameters.

Then, according to Bayesian rule, actual or simply put, posterior distribution, p(θ/z) of θ, will be given by p(θ/z) = p(z/θ) × p(θ)/p(z), which is the distribution of the observed number multiplied by the prior of its parameter divided by the constant p(z). That is:

$$p(\theta/z) = e^{-(m\,.\,\theta)}(m\,.\,\theta)^{z} \times e^{-(\beta\,\theta)}\beta^{\alpha}\theta^{\alpha-1}/z!\;\Gamma(\alpha)p(z) \tag{2a}$$

$$\text{or, } p(\theta/z) = e^{-\theta(\beta+m)}(\theta)^{z+\alpha-1} \times \text{constant} \tag{3}$$

Here, the right-hand side of Equation 2 and that of the posterior distribution in Equation 3 are similar, which indicates that the posterior is also a gamma (α_1, β_1) distribution with parameters α_1 and β_1 where:

$$\alpha_1 = z + \alpha \text{ and } \beta_1 = \beta + m \tag{3a}$$

This equation means that if one assumes that the prior information about parameter θ (the rate of children with BLLs of 5–9 μg/dL) can be obtained from a small group of counties in Georgia, each of which is believed to have the same rate (θ) of 5–9 μg/dL BLLs among children <6 years, then applying Bayesian rule, the posterior for θ can be estimated from a gamma distribution as shown in Equation 3.

Moreover, if one supposes z_j is the number of children <6 years with BLLs of 5–9 μg/dL among x_j children from county j, then, assuming z_j follows a Poisson distribution, one would have, as in Equation 1:

$$p(z_j/\theta) = e^{-(xj\,\theta)}(x_j\theta)^{zj}/z_j! \tag{4}$$

Where θ is the same as defined earlier.

Thus, the likelihood function for n counties with the same parameter θ is given as follows:

$$L\left(\sum z_j/\theta\right) = e^{-(\Sigma xj\,\theta)}\Pi(x_j\theta)^{zj}/z_1!z_2!\ldots z_n! \tag{5}$$

This equation is obtained by multiplying density functions like Equation 4 for n counties. Omitting the constant terms, one has:

$$L\left(\sum z_j/\theta\right) \propto e^{-(\Sigma xj\,\theta)}(\theta)^{\Sigma zj} \tag{6}$$

Where ∝ indicates proportionality.

If for all these n counties, one assumes that θ follows a noninformative prior 1/θ (i.e., p(θ) = 1/θ), then as was done in Equation 2a and from Equation 6, the posterior distribution of θ is given by the following:

$$p(\theta/\Sigma z_i) \propto e^{-(\Sigma xj\theta)}(\theta)^{\Sigma zj}.1/\theta \text{ (i.e., } p(\theta/\Sigma z_j) \propto e^{-(\Sigma xj\theta)}(\theta)^{\Sigma zj-1}) \quad (7)$$

This is a gamma (α_2, β_2), where:

$$\alpha_2 = \sum z_j \text{ and } \beta_2 = \sum x_j \quad (8)$$

Here, $\sum z_j$ is the shape parameter and $\sum x_j$ is the rate parameter of this gamma distribution, where z_j is the number of children <6 years with BLLs of 5–9 μg/dL in county j and x_j is the number of children tested for BLL in county j. The assumption is that the rate of children with BLLs of 5–9 μg/dL among children <6 years in these counties is similar to that in a targeted county where one wants to estimate that rate. One can then use known α and β from Equation 8 in Equations 2 and 3 to evaluate the prior and posterior distributions of the parameter θ in the targeted county.

According to the multiplication rule of probability, the joint distribution of data z and the parameter θ are given by the following:

$$p(z, \theta) = p(\theta) \times p(z/\theta), \text{ and also}$$
$$p(z, \theta) = p(z) \times p(\theta/z)$$

Thus, p(z) × p(θ/z) = p(θ) × p(z/θ), giving:

$$p(z) = p(\theta) \times p(z/\theta)/p(\theta/z) \quad (9)$$

Here, p(θ) and p(θ/z) are the known prior and posterior distributions, respectively, of the parameter θ. Thus, p(θ) is a gamma density with the known shape and rate parameters from Equation 8. Similarly, p(θ/z) is a gamma density with known shape and rate parameters from Equations 8 and 3a. Assuming that p(z/θ) is the sampling distribution of data in the targeted county, one can estimate the predictive density p(z) of z in the targeted county from Equation 9 before any data are observed, where p(z/θ) is a Poisson density with known mean (mθ) as shown in Equation 1.

If our model assumptions for sampling distribution of data and prior density are valid, one can check the validity of the observed values of the number of children <6 years with BLLs of 5–9 μg/dL in the targeted county.

Detailed information about this Bayesian model can be found at www.neha.org/jeh/supplemental.

County and Region Selection

The model was applied by dividing Georgia into five different regions: North, South, East, West, and Central. Then 11 neighboring counties were arbitrarily selected in each region, assuming similarity of BLL rates of 5–9 μg/dL among children ages <6 years in these counties. For each region, the county with the lowest observed proportion of children with BLLs 5–9 μg/dL was selected as the targeted county. The remaining 10 counties from each region provided data for estimation of parameters α and β for the prior distribution. The parameter θ, the rate of children with BLLs of 5–9 μg/dL in the targeted county, was estimated from the mean value α/β of the gamma distribution, as the predictive density (Equation 9) is valid for all θ.

Data Analysis

Data were analyzed using statistical software SAS (version 9.4) and R package. For each region, predictive density was calculated for the targeted county from Equation 9 for all children, and separately for White and non-White children. We assumed that the observed value for the number of children with BLLs of 5–9 μg/dL among children <6 years within the three largest predictive probabilities was compatible.

Additionally, the mean number of children with BLLs of 5–9 μg/dL was estimated in the targeted county from Equation 9 by simultaneously simulating 1,000 values from each of the probability densities $p(\theta)$, $p(\theta/z)$, and $p(z/\theta)$. A 95% credible interval for the mean number of children with BLLs of 5–9 μg/dL was estimated from the simulated values. An observed number of children with BLLs of 5–9 μg/dL in the targeted county was considered an acceptable number if within the boundaries of the credible interval for that county. The estimated mean number of children <6 years with BLLs of 5–9 μg/dL in the targeted county was recommended as the true value if the observed value was outside the boundaries of the credible interval.

Results

Tables 1, 2, and 3 show the observed numbers of White, non-White, and total children who had their BLLs tested and those children with BLLs of 5–9 μg/dL in the North, East, and South regions of Georgia. The 11 counties chosen in each of the regions, including West and Central regions (not shown in the tables), were next to each other. For our study, it was assumed that the BLL rates among children <6 years could be similar in each county because of their proximity to each other. County X in the last row of each table represents the targeted county where the proportion of children <6 years with BLLs of 5–9 μg/dL was found to be lowest among the 11 counties and the value of county X was estimated by the model.

Tables 1, 2, and 3 (representing North, East, and South regions of Georgia, respectively) have slightly difierent distributions of proportion of children with BLLs of 5–9 μg/dL between White and non-White children. In the North region (Table 1), a smaller proportion of non-White children were tested for BLL in almost all the counties—and yet a higher percentage of them were found to have BLLs of 5–9 μg/dL. Thus, in county I in the North

region, only 3 (0.07%) out of 415 White children tested had BLLs of 5–9 μg/dL, compared with 7 (2.15%) out of 325 non-White children tested. This finding is similar to that of county C in the North region: 1 (0.06%) out of 157 White children tested had BLLs of 5–9 μg/dL, compared with 2 (5.4%) out of 37 non-White children tested.

In the East region (Table 2) and South region (Table 3), however, the situation was found to be completely the opposite. In both these regions, a smaller proportion of White children were tested, with a higher proportion of children with BLLs of 5–9 μg/dL in almost all the counties. Thus, in county A in the East region, 3 (23.08%) out of 13 White children had BLLs of 5–9 μg/dL, compared with 1 (3.84%) out of 26 non-White children. Similarly, in county A in the South region, 5 (8.77%) out of 57 White children tested had BLLs of 5–9 μg/dL, compared with 7 (1.00%) out of 70 non-White children tested.

Tables 4, 5, and 6 show the predictive densities or estimated probabilities for 0–15 children <6 years with BLLs of 5–9 μg/dL in the targeted county for all, White, and non-White children, respectively. Each of these tables show probabilities for the five regions calculated based on Equation 9. According to Table 4, the estimated probabilities were found to be highest (0.190, 0.212, 0.181) at moderately three smaller numbers (2, 3, and 4, respectively) of all children <6 years with BLLs of 5–9 μg/dL in the targeted county in the North region. This finding indicates that the number of all children <6 years with BLLs of 5–9 μg/dL in the targeted county in the North region should be small, which is corroborated by its 95% credible interval [0.0, 9.3] shown in Table 7. Moreover, this finding proves that the “0” observed number of all children with BLLs of 5–9 μg/dL in the targeted county (Table 1) is acceptable according to our model.

The same findings holds true for the Central region, where the probabilities are highest (0.256, 0.270, 0.189) for a relatively smaller number (1, 2, and 3, respectively) of all children <6 years with BLLs of 5–9 μg/dL in the targeted county. The probabilities are, however, highest for a slightly larger number (9, 10, and 11) of all children <6 years with BLLs of 5–9 μg/dL in the targeted county in the East region. For the South and West regions, the highest probabilities are not reached within a number of 15 for all children <6 years with BLLs of 5–9 μg/dL in the targeted county, indicating the number of children should be higher (Table 4). Clearly, an observed number of 14 for all children <6 years with BLLs of 5–9 μg/dL in the targeted county in the West region (Table 7) is not acceptable because its 95% credible interval based on our model is [30.7, 65.3].

The same trend is observed for estimated probabilities for White and non-White children as shown in Tables 5 and 6. Table 7 shows the observed number of children <6 years with BLLs of 5–9 μg/dL in the targeted county, along with their estimated number and their 95% credible interval based on simulation. It is important to note from Table 7 that in only two regions—North and Central—the estimated numbers of children <6 years with BLLs of 5–9 μg/dL in the targeted county concurred with the observed values, which is true for all, White, and non-White children.

Figure 1 shows the estimated probability distribution for all children <6 years with BLLs of 5–9 μg/dL in the targeted county in the West and Central regions. The distribution in the

West region, where the observed value of those children was not acceptable according to the model, is markedly different from the distribution in the Central region, where the model supported the observed value. The estimated probability is shown to be highest around 40 in the West region, indicating that the number of all children ages <6 years with BLLs of 5–9 μg/dL in the targeted county should be much higher than the observed value of 14, which is not acceptable. In the Central region, however, the estimated probability is shown to be highest around 2 or 3, indicating that the number of all children <6 years with BLLs of 5–9 μg/dL is closer to the observed value of 1, which is acceptable.

Discussion

The estimated probabilities for all children <6 years with BLLs of 5–9 μg/dL in the targeted county in the Central region was highest for 1, 2, and 3 children (Table 4). The observed number of all children <6 years with BLLs of 5–9 μg/dL in the targeted county was 1 (Table 7). These results support the observed value. As further corroboration, the estimated number of all children with BLLs of 5–9 μg/dL in the targeted county in the Central region was found to be 2.1 through simulation. Its 95% credible interval was [0.0, 5.9] (Table 7), which included 1.

Similar results were found for all, White, and non-White children for the North and Central regions. For the East region, however, the observed number of all children with BLLs of 5–9 μg/dL in the targeted county was 2 (Table 2) and the highest estimated probabilities were for 9, 10, and 11 children (Table 4). Similarly, the number of all children with BLLs of 5–9 μg/dL in the targeted county in the East region was estimated to be 11.9 by simulation and its 95% credible interval was [5.1, 20.2] (Table 7), which did not include 2. This finding shows discrepancies between the observed and estimated values of children with BLLs of 5–9 μg/dL in the targeted county. Similar results were found in the East region for White and non-White children. Discrepancies between observed and estimated numbers of children <6 years with BLLs of 5–9 μg/dL were also found for the targeted county in the South and West regions (Table 7).

Our model shows the possibility of checking the validity of observed numbers of children with BLLs of 5–9 μg/dL and, if necessary, replacing those numbers with estimates that better reflect the actual probable numbers in the targeted counties. The model could reveal incorrect reporting of elevated BLLs in children <6 years, which might be the case if many of the targeted counties in different regions of a state show discrepancies between the observed and estimated numbers of children with BLLs of 5–9 μg/dL. Therefore, this finding might also point to inadequacies in the screening process used in the state, and thus lead to modifications to improve the process.

Some studies have observed this inadequacy in the screening process of BLL surveillance data. Based on estimates of elevated BLL (≥10 μg/dL) data for children 1–5 years from 1999–2010 for 39 states (including Washington, DC) that were reported to CDC, Roberts et al. (2017) found that approximately 1.2 million children had elevated BLLs. Among these, 337,405 (approximately 28%) were not reported because of incomplete case ascertainment and far fewer cases were ascertained in the South and West regions.

In Georgia, the case ascertainment ratio (i.e., the number reported/number of cases) was only 0.10. This finding points to undertesting of children with elevated BLL in many states, including Georgia. Similar results have been observed from other studies. According to data from the California Department of Health Care Services during 2009–2010 through 2017–2018, fewer than 27% of eligible children in California received all the required blood tests they should have, although many of these children lived in areas of the state with occurrences of elevated BLLs (Auditor of the State of California, 2020).

Although these studies point to the inadequacy of the screening process for children, no study showed how inadequacy can affect actual BLLs among children <6 years. Our study fills the gap in that research and detects the discrepancy between estimated and observed numbers of children with higher (i.e., 5–9 μg/dL) BLLs—a discrepancy that resulted, most likely, from an undertesting of children with elevated BLLs. Most importantly, we find the corrected number of children with higher (i.e., 5–9 μg/dL) BLLs.

Limitations

Our study is subject to several limitations. For example, we assumed that the neighboring counties have similar BLL rates to what was found in the targeted county, which might not be true. If the neighboring counties do not have similar BLL rates, then the prior and posterior distributions of the parameter θ in the targeted county (Equation 9) will be distorted. The equation might still provide a reasonably reliable estimate, however, of the number of children with BLLs of 5–9 μg/dL in the targeted county, which is possible because prior $p(\theta)$ and posterior $p(\theta/z)$ occur in the numerator and denominator, respectively, of Equation 9 and might, to some extent, nullify each other's distorting effect. If the risk factors for elevated BLLs in the targeted county, however, vastly differ from those in the neighboring counties, then this approach might not give a good estimate. We also assumed that the number of children with BLLs of 5–9 μg/dL followed a Poisson distribution and the BLL rate was distributed as gamma. The results might change if these model assumptions were modified.

Conclusion

We observed underreporting of children <6 years with BLLs of 5–9 μg/dL in some counties of Georgia. This finding is based on the application of a Bayesian model on county data. More research is needed to investigate BLLs among children to ensure they are adequately protected from lead poisoning. Our study has the appeal of being applied in any situation where surveillance data are collected to obtain vital information in institutions or communities, such as hospital-acquired infection in a specific hospital. For example, assuming that the rate of infection is similar to other hospitals in the vicinity, one can check the validity of the rates in this specific hospital and possibly correct it, if necessary, as we did in our study. Similar situations can arise in estimating heart transplant mortality in a hospital, or, as another example, estimating crime rate in a community from self-reported statistics. Our study, then, highlights a general approach to verify useful information and details an opportunity to estimate an actual value or index from observed data.

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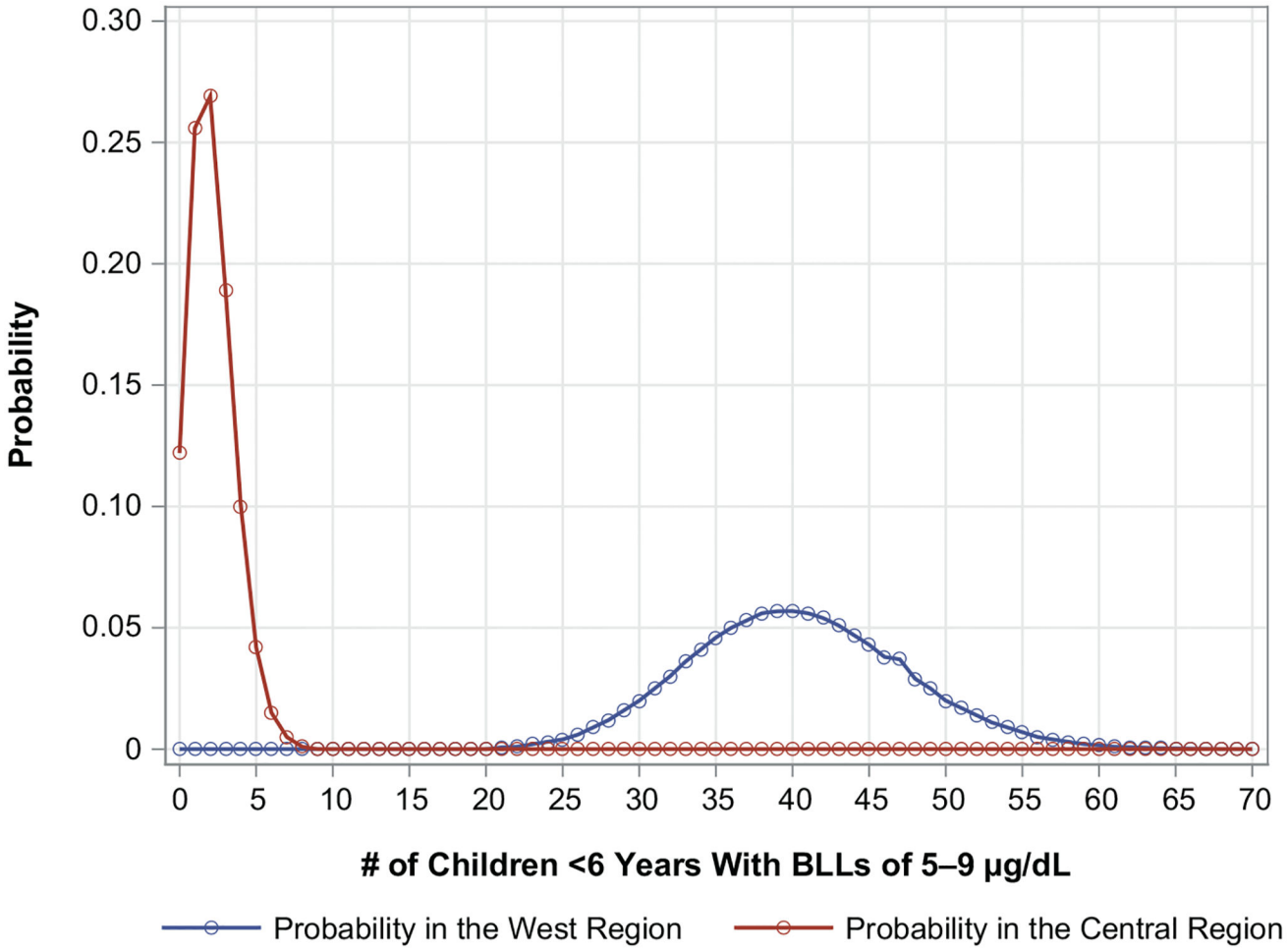

FIGURE 1.

Plot for the Predictive Density of All Children <6 Years With Blood Lead Levels (BLLs) of 5–9 µg/dL in the Targeted Counties in the West and Central Regions of Georgia, 2015

Note. The observed value of children with BLLs of 5–9 µg/dL in the targeted county in the West region was 14 among 1,587 children tested. The observed value of children with BLLs of 5–9 µg/dL in the targeted county of the Central region was 1 among 170 children tested.

TABLE 1

Observed Blood Lead Levels (BLLs) for Children <6 Years From 11 Neighboring Counties in the North Region of Georgia, 2015

County[a]	# of Children <6 Years	# of Children <6 Years With BLLs of 5–9 µg/dL			Total # of Children <6 Years Tested		
		All	White	Non-White	All	White	Non-White
A	2,401	5	2	3	319	169	150
B	1,067	6	4	2	323	213	110
C	834	3	1	2	194	157	37
D	400	0	0	0	113	91	22
E	3,552	1	1	0	193	142	51
F	1,581	9	3	6	651	330	321
G	1,423	4	3	1	219	130	89
H	1,387	4	3	1	368	208	160
I	2,571	10	3	7	740	415	325
J	1,625	9	7	2	529	365	164
X [b]	743	0	0	0	246	148	98

[a] These 11 counties were chosen arbitrarily because they are contiguous. The assumption was that because they are contiguous, these counties will have similar BLL rates of 5–9 µg/dL among children <6 years.

[b] X indicates the targeted county. A targeted county is one with the lowest observed proportion of tested children with BLLs of 5–9 µg/dL among children <6 years.

TABLE 2

Observed Blood Lead Levels (BLLs) for Children <6 Years From 11 Neighboring Counties in the East Region of Georgia, 2015

County [a]	# of Children <6 Years	# of Children <6 Years With BLLs of 5–9 µg/dL			Total # of Children <6 Years Tested		
		All	White	Non-White	All	White	Non-White
A	400	4	3	1	39	13	26
B	13,956	49	10	39	1,817	303	1,514
C	1,595	8	1	7	393	104	289
D	829	2	0	2	205	57	148
E	535	2	0	2	62	16	46
F	1,467	11	1	10	177	47	130
G	985	3	2	1	162	38	124
H	494	3	2	1	123	50	73
I	4,196	20	9	11	1,203	255	948
J	1,132	16	5	11	722	228	494
X [b]	9,328	2	1	1	458	233	225

[a] These 11 counties were chosen arbitrarily because they are contiguous. The assumption was that because they are contiguous, these counties will have similar BLL rates of 5–9 µg/dL among children <6 years.

[b] X indicates the targeted county. A targeted county is one with the lowest observed proportion of tested children with BLLs of 5–9 µg/dL among children <6 years.

TABLE 3

Observed Blood Lead Levels (BLLs) for Children <6 Years From 11 Neighboring Counties in the South Region of Georgia, 2015

County [a]	# of Children <6 Years	# of Children <6 Years With BLLs of 5–9 µg/dL			Total # of Children <6 Years Tested		
		All	White	Non-White	All	White	Non-White
A	473	12	5	7	127	57	70
B	1,757	9	2	7	109	39	70
C	1,686	11	5	6	554	212	342
D	968	6	2	4	151	54	97
E	7,952	27	9	18	1,206	643	563
F	347	8	3	5	79	41	38
G	1,326	6	2	4	371	124	247
H	3,235	18	7	11	776	366	410
I	1,154	13	6	7	215	112	103
J	769	4	3	1	102	65	37
X [b]	2,910	15	4	11	990	519	471

[a] These 11 counties were chosen arbitrarily because they are contiguous. The assumption was that because they are contiguous, these counties will have similar BLL rates of 5–9 µg/dL among children <6 years.

[b] X indicates the targeted county. A targeted county is one with the lowest observed proportion of tested children with BLLs of 5–9 µg/dL among children <6 years.

TABLE 4

Predictive Density for All Children <6 Years With Blood Lead Levels of 5–9 μg/dL in the Targeted County by Region in Georgia, 2015

# of Children	Probability by Region				
	North	East	South	West	Central
0	0.036	0	0	0	0.121
1	0.116	0	0	0	0.256
2	0.190	0.001	0	0	0.270
3	0.212	0.005	0	0	0.189
4	0.181	0.012	0	0	0.100
5	0.125	0.025	0	0	0.042
6	0.074	0.044	0	0	0.015
7	0.038	0.066	0	0	0.005
8	0.017	0.088	0	0	0.001
9	0.007	0.106	0	0	0
10	0.003	0.115	0	0	0
11	0.001	0.114	0	0	0
12	0	0.105	0	0	0
13	0	0.090	0	0	0
14	0	0.072	0.001	0	0
15	0	0.054	0.002	0	0

TABLE 5

Predictive Density for White Children <6 Years With Blood Lead Levels of 5–9 μg/dL in the Targeted County by Region in Georgia, 2015

# of Children	Probability by Region				
	North	East	South	West	Central
0	0.175	0.002	0	0	0.436
1	0.295	0.011	0	0.001	0.361
2	0.259	0.031	0	0.004	0.150
3	0.156	0.064	0.002	0.011	0.042
4	0.073	0.010	0.005	0.025	0.009
5	0.028	0.128	0.010	0.045	0.002
6	0.009	0.140	0.019	0.069	0
7	0.003	0.135	0.032	0.092	0
8	0.001	0.117	0.048	0.109	0
9	0	0.093	0.064	0.118	0
10	0	0.067	0.079	0.115	0
11	0	0.045	0.090	0.105	0
12	0	0.029	0.096	0.088	0
13	0	0.017	0.096	0.070	0
14	0	0.010	0.091	0.052	0
15	0	0.005	0.082	0.036	0

TABLE 6

Predictive Density for Non-White Children <6 Years With Blood Lead Levels of 5–9 μg/dL in the Targeted County by Region in Georgia, 2015

# of Children	Probability by Region				
	North	East	South	West	Central
0	0.204	0.007	0	0	0.265
1	0.313	0.035	0	0	0.352
2	0.251	0.085	0	0	0.233
3	0.140	0.139	0	0	0.104
4	0.061	0.171	0	0	0.035
5	0.022	0.170	0.001	0	0.009
6	0.007	0.143	0.003	0	0.002
7	0.002	0.104	0.007	0	0
8	0	0.067	0.013	0	0
9	0	0.039	0.021	0	0
10	0	0.020	0.032	0	0
11	0	0.010	0.045	0	0
12	0	0.004	0.058	0	0
13	0	0.002	0.070	0	0
14	0	0.001	0.080	0.001	0
15	0	0	0.087	0.002	0

TABLE 7

Observed and Estimated Mean Number of Children <6 Years With Blood Lead Levels (BLLs) of 5–9 μg/dL and 95% Credible Interval in the Targeted County by Region in Georgia, 2015

Region		Mean # of Children <6 Years With BLLs of 5–9 μg/dL		
		All	White	Non-White
North	Observed	0	0	0
	Estimated	3.8	2.0	1.9
	95% credible interval	[0, 9.3]	[0, 5.9]	[0, 5.6]
East	Observed	2	1	1
	Estimated	11.9	8.4	5.3
	95% credible interval	[5.1, 20.2]	[2.5, 17.1]	[1.1, 11.1]
South	Observed	15	4	11
	Estimated	34.6	16.2	17.9
	95% credible interval	[21.5, 50.8]	[7.8, 28.7]	[8.8, 30.0]
West	Observed	14	1	13
	Estimated	46.0	11.8	35.0
	95% credible interval	[30.7, 65.3]	[4.5, 22.4]	[21.9, 51.6]
Central	Observed	1	0	1
	Estimated	2.1	0.8	1.3
	95% credible interval	[0, 5.9]	[0, 3.3]	[0, 4.1]