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Bayesian Simultaneous Intervals for Small Areas: An Application to Mapping Mortality Rates in U.S. Health Service Areas

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BAYESIAN SIMULTANEOUS INTERVALS FOR SMALL AREAS: AN APPLICATION TO MAPPING MORTALITY RATES IN U.S. HEALTH SERVICE AREAS

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To my family,
who made everything I am possible
(regardless of how improbable).

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ABBREVIATIONS

CI	credible interval (used for equal-tailed case)
HPD	highest posterior density
r.v.	random variable
pdf	probability density function
cdf	cumulative distribution function
MCMC	Markov chain Monte Carlo
NSE	numerical standard error
NCHS	National Center for Health Statistics
WHO	World Health Organization
HSA	health service area
SMR	standardized mortality rate
COPD	chronic obstructive pulmonary disease (includes emphysema, asthma and bronchitis)

ABSTRACT

It is customary when presenting a choropleth map of rates or counts to present only the estimates (mean or mode) of the parameters of interest. While this technique illustrates spatial variation, it ignores the variation inherent in the estimates. We describe an approach to present variability in choropleth maps by constructing $100(1-\alpha)\%$ simultaneous intervals. The result provides three maps (estimate with two bands).

We propose two methods to construct simultaneous intervals from the optimal individual highest posterior density (HPD) intervals to ensure joint simultaneous coverage of $100(1-\alpha)\%$.

Both methods exhibit the main feature of multiplying the lower bound and dividing the upper bound of the individual HPD intervals by parameters $0 < \gamma_1, \gamma_2 < 1$ to "stretch" the interval until the simultaneous probability content is $100(1-\alpha)\%$. We employ the Nelder-Mead minimization algorithm to solve a system of nonlinear equations involving the probability content and an optimality condition. Our Single-γ Method, where $\gamma_1 = \gamma_2$, optimizes over the probability content only, while the Double-γ Method includes an optimality condition. For our example, we found that these methods are comparable, appearing that the optimality condition adds very little information.

For illustrative purposes we apply our methods to chronic obstructive pulmonary disease (COPD) mortality rates from 1988–92, subset White Males age group 65 and older, for the continental United States consisting of 798 Health Service Areas (HSA).

1. INTRODUCTION

Presenting simultaneous estimate variability for a large number of small areas in choropleth maps can be done by constructing $100(1-\alpha)\%$ simultaneous intervals. While it is customary when presenting a choropleth map of rates or counts to present only the estimates (mean or mode) of the parameters of interest, this technique illustrates spatial variation only. It is also important to describe the variation inherent in the estimates. We describe an approach to present variability in choropleth maps by constructing $100(1-\alpha)\%$ simultaneous intervals.

In this chapter we discuss our motivation in conducting this study, describe our application problem of mapping rates of chronic obstructive pulmonary disease (COPD) and its potential risk factors, the recent related research works and their main contributions, and finally, introduce the following chapters of this thesis.

1.1 Choropleth Maps

Choropleth maps are one of the most commonly used means of displaying areal data. The first known choropleth map was constructed in France in 1826 by Charles Dupin, an education reformist not a cartographer, on education rates. But the word "choropleth" had to wait over one hundred years before it was invented in 1938 by Wright, a cartographer from the American Geographical Society in New York city. A choropleth is an areal symbol and the word "choropleth" is derived from Greek words choros (place), and pleth (value). It consists of two components: a base map and attribute data (statistical data). Technically a choropleth is based on a stepped statistical surface identified by colored or shaded areas called chorograms (e.g., statistical or administrative areas). Choropleth maps are divided into parts

corresponding to the physical extents of the enumeration areas and these parts are shaded according to the value of a variable for that area.

One of the most common forms of mapping data today is the choropleth map, in which each area (e.g., state or county) is shaded according to the characteristic (e.g., mortality rate, crime rate, income, rain fall). Areas with higher values of the characteristic are shaded more darkly and vice versa. In the United States of America choropleth maps are used in almost all applications, even in the daily newspapers and on television. Three characteristics of these maps are (a) the value at specific areas, (b) the overall pattern on the map and (c) the pattern on one map as compared with the pattern on other maps. There is an assumption of uniform distribution: the spatial unit used for shaded mapping is the smallest detail that the shaded map can represent. Within this unit the variable being mapped is uniformly distributed. If the areas are too large, this type of mapping can hide important variation in these areas; areas that are too small may, however, introduce visual noise. Aggregating these units to larger ones may better reveal a visual pettern of the data. It is important to choose the right classification method and there are two main considerations: (a) the interpretation skills of an expected user and (b) the best classification method to represent the particular data. Classification of the areas can be done by forming intervals across the range of the data. For example, these intervals can be equal widths, formed from quantiles or using natural breaks. In our work on mortality data we generally use quantiles (e.g., quintiles) and the areas in the higher quantiles get deeper colors or heavier shades in gray scale.

One of the most common types of measurement to map using the choropleth technique is the density value. This gives an average value of the variable per unit area for each enumeration area. A disadvantage of the density values is that often where total population density is greatest the densities of other variables will also be high and mapping these values may reveal little new information. Another type of value often represented using choropleths is a ratio where some value is expressed as

a proportion of a total e.g. as a percentage or a number per thousand. In the maps in this paper, proportions of deaths per total per thousand are used for mapping.

1.2 Mapping Small Area Mortality

Recently, there has been increased interest in estimating mortality rates for small geographical areas. Mapping small area death rates is a valuable public health tool, which may be used to generate etiologic hypotheses and identify high rate areas where intervention or treatment programs may be profitable. Dr. John Snow (1855) was the first researcher to link a disease with "hot-spot" patterns [Snow, 1855]. He used mapping techniques to link the London cholera epidemic to a contaminated water supply by identifing outliers from the overall pattern and investigating their cause. Also, mapping has always been of interest to know how and where to allocate limited resources, especially for local and federal government. For example, if we know a particular disease occurs in some areas more often than in others, we might want to provide better medical facilities and services in these areas. Furthermore, if we can find some potential risk factors which show a statistically significant relation with the occurrence of a disease, we might be able to implement some prevention program much more efficiently.

Before 1975 most of the mapping was limited to state or national level or larger areas, and it was only after the development of high speed computers in the late 1970s that small-area levels were taken into consideration. The National Cancer Institute in the late 1970s, with cutting edge technology, published the first map of the United States cancer death rate at the small-area level. This research helped to discover unnoticed patterns of high death rates of cancer, and this led to numerous field studies in various geographical vicinity. These field studies uncovered several related linkages between geographical conditions and some disease, for example, the link between shipyard asbestos and lung cancer or sniff dipping and oral cancer.

1.3 The 1996 Atlas

The success of mapping small-area death rates and subsequent findings make mapping a valuable public health tool in environmental research, to generate etiologic hypotheses and identify high-rate communities where intervention measures are needed. The 1996 Atlas [Pickle et al., 1996] presents maps of eighteen leading causes of death by sex, age and race in the United States for the period 1988 through 1992. This is the first publication of maps of all leading causes of death in the United States on a small-area scale. [The research underlying this project has lead to improved statistical methods for modeling death rates and innovative presentation formats for maps and graphics based on cognitive research.] In this Atlas, information previously available only in tabular form or summarized on single map is presented on multiple maps and graphs. Broad geographic patterns by age group are highlighted by application of a new smoothing algorithm, and the geographic unit for mapping is defined on the basis of patterns of health care. These new features allow the public health researcher to examine the data at several geographic levels, to discern clusters of similar rate areas, to visualize broad geographic patterns, and to compare regional rates. With these additional tools, important geographic pattern of cause-specific mortality can more easily be identified.

Although many causes of death included in this Atlas have been mapped before, previous efforts focused on limited range of causes or have presented data only at state level. Comparison of map patterns across causes of death, sex, or race can provide clues to disease etiology. For this reason, unlike many earlier Atlases, separate maps by sex and race are included in the same volume, using consistent methods of presentation.

The specific numbers of deaths were modeled for each combination of race, sex, cause and place using mixed effects generalized linear models. Beiefly, logarithm of the age specific rates were modeled as a function of age, allowing each HSA to have a random slope within its particular region. Predicted age specific rates for each

HSA were smoothed using a weighted head banging algorithm, with weights equal to the inverse of the rates of estimated standard errors [Hansen, 1991] [Mungiole et al., 1998] [Mungiole et al., 1999].

1.4 Models and Methods

1.4.1 Rate Estimation

Models and methods of analysis on rates are abundant for inferece about mortality rates for small geographical areas.

[Nandram et al., 1999] developed several Poisson regression models for the analysis of mortality data of *All Cancer* using a spline regression model on age, introduced earlier by [Pickle et al., 1996]. [Pickle et al., 1997] described the random effects model used for the construction of the *Atlas*. In this application the units are Health Service Areas (HSAs), where there are very few deaths relative to the populations. Hence, the death rates are very small, and so small area estimation techniques are appropriate for the analysis of these data. [Nandram, 1998] gave a review of the use of generalized linear models in small area estimation, with an emphasis on Poisson regression models.

[McCullagh and Nelder, 1989] described approaches and models in detail for analyzing over dispersed Poisson rates within the framework of generalized linear models for both nonspatial and spatial phenomena. There are Bayesian approaches ([Albert and Pepple, 1989] and [Lu and Morris, 1994]), empirical Bayes approaches ([Albert, 1988] and [Kass and Steffey, 1989]), methods based on double-exponential families ([Efron, 1996] and [Bernardo et al., 1985]), and there is a method based on the parametric empirical Bayes bootstraps ([Laird and Lewis, 1987]).

[Christiansen and Morris, 1997] proposed a hierarchical Poisson regression model using non-exchangeable Gamma distributions, their technique does not accommodate the simultaneous modeling of mortality data for several age classes. [Clayton and Kaldor, 1997] incorporated spatial dependencies into empirical Bayes model of

standardized mortality rate (SMR). The predicted SMRs were much less dispersed than the original lip cancer data, and the ranks of the geographical areas were remarkably similar. [Tsutakawa, 1985] applied both empirical Bayes and an appoximation of fully Bayes methods to the analysis of cancer mortality data in Missouri cities. Disease incidence and mortality rates were analyzed by [Bernardinelli and Montomoli, 1992] using Bayesian methods facilitated by the Gibbs sampler.

[Waller et al., 1997] extended the spatial models developed by [Besag et al., 1991] to accomodate general temporal effects, as well as space-time interaction. They focused as on accurate estimation of mortality rate incorporating sociodemographic variables across geographic regions and disease incidence (or other outcomes of interest) in small subregions. [Colon and Waller, 1998] described two methods for regionalization using variable weights and weight induced by direct modeling of spatial correlation.

[Nandram et al., 1999] and [Delcroix, 2000] compared alternative models for estimating age specific and age adjusted mortality rates for all cancer for white males. They used Bayesian methods with four hierarchical models. The alternative specifications differ in their assumptions about the variation in $\log(\lambda_{ij})$ over HSAs and age classes. See also [Nandram et al., 2000] for methods used on chronic obstructive pulmonary disease (COPD). They found that the of a spatial model is not much different from a nonspatial model. [Aweh, 1999] studied Bayesian methods on Poisson regression models based on the first model suggested by [Nandram et al., 1999] for breast cancer mortality data. Spatialtemporal mapping was investigated by [Waller et al., 1997]. Both nonspatial and spatial analyses were investigated by [Aweh, 1999].

[Christiansen and Morris, 1997] describe a hierarchical Bayesian model for heterogeneous Poisson counts under the exchangeability assumption, called Poisson regression interactive multilevel modeling (PRIMM). See [Nandram et al., 2000] for a review of this model. This is a Poisson regression model that has been used to study mortality data and other rare events when there are occurrences from several areas. The model utilizes a form in which there are convenient Rao-Blackwellized estimators

of the mortality rates. They have made some analytical approximations which are very accurate, and it is important to note that these approximations avoid the use of sampling based methods such as Markov chain Monte Carlo (MCMC) methods. A sampling based method helps us to find the rates that make the posterior density over the entire ensemble the highest. This is a desirable approach in a Bayesian analysis. [Liu, 2002] constructed posterior modal maps rather than posterior mean maps, as that is the most likely rate estimate. Additionally, he used a latent class model to contruct maps without using quantiles, providing a more natural representation of the colors. Their model was based on the Bayesian hierarchical model recently discussed by [Christiansen and Morris, 1997]. See also [Nandram et al., 2003].

In this paper we continue with the model developed in [Liu, 2002] and use it to investigate simultaneous inference.

1.4.2 Simultaneous Inference

By 1955 three principal investigators, Duncan [Duncan, 1952], Scheffé [Scheffé, 1953] and Tukey [Tukey, 1953], brought the general principles of multiple comparisons into their current structure [Miller, 1981] (p. 2). The basic technique of multiple comparisons divide themselves into two groups: those which can provide confidence intervals or corresponding tests of hypothesies (confidence regions), and those which are essentially only tests of hypotheses because of their multistage structure (significance tests). Our study contributes to the first of these groups.

The purpose of simultaneous statistical inference is to give increased protection against a type I error, rejection of the null hypothesis when it is true, when the null hypothesis involves a family, or group, of parameters. This protection is often at the expense of a type II error, failing to reject the null hypothesis when it is false, increasing the number of errors under the alternative. For confidence regions, to require simultaneous inclusion of all the parameters disregards the size of the region necessary to accomplish this. Because the null hypothesis is not always true,

attention must also be given to error rates under the alternative, or the size of the confidence region. Provided the family probability error rate under the null hypothesis is maintained, as the family size increases, confidence intervals are widened, reducing the power of the test. To increase the power, either family size must be reduced, the error rate increased, or the sample size increased [Miller, 1981] (p. 32, 33).

The simplest and most conservative approach is the Bonferroni correction. The Bonferroni correction is a multiple-comparison correction used when several independent statistical tests are being performed simultaneously (since while a given alpha value α may be appropriate for each individual comparison, it is not for the set of all comparisons). In order to avoid a lot of spurious positives, the alpha value needs to be lowered to account for the number of comparisons being performed [Bonferroni, 1935] [Bonferroni, 1936]. The simplest correction sets the alpha value for the entire set of n comparisons equal to α by taking the alpha value for each comparison equal to α/n. Another correction instead uses $1-(1-\alpha)^{1/n}$; while this choice is applicable for two-sided hypotheses, multivariate normal statistics, and positive orthant dependent statistics, it is not, in general, correct [Shaffer, 1995].

While the well known methods of Bonferroni, Tukey, Scheffé and others are reasonable for simultaneous intervals of a moderate number of parameters, they become overly conservative for a large number of parameters.

The literature lacks many possibilities for calculating simultaneous probability intervals relating to a, potentially large, number of parameters. We mention a few comparable methods here.

[Nandram, 1993] describes a method for constructing simultaneous cuboid intervals (hyper-rectanglar) for the prediction of k new observations. He uses a one-way analysis of variance (ANOVA) model under a normality assumption with a Lindley-Smith [Lindley and Smith, 1972] type prior. This gives intervals based on the multivariate t distribution which are the simple cuboid which engineers use, instead of the optimal ellipse. The bounds on each interval are obtained by solving a pair of

equations simultaneously. The first equation satisfies the highest posterior density (HPD) optimality criterion of equal ordinates by forcing the difference of the values of the probability density function evaluated at the interval bounds to be zero. The second equation satisfies the simultaneous probability content by forcing the difference of the values of the cumulative density function evaluated at the lesser interval bound from the greater interval bound to be $1 - \alpha$. Thus the cuboids are optimized by constructing the smallest such k-dimensional cuboid by using HPD intervals in each dimension.

The method presented in our paper is an extention of the method of [Nandram, 1993]. Two main differences are that we consider a large number of parameters $\ell = 798$, where he considered up to $k = 10$ predictions, and we use a Poisson-gamma hierarchical model instead of an ANOVA model under normality.

[Besag et al., 1995] (p. 30) presents a method to calculate simultaneous credible regions based on order statistics (details in Appendix B.3). The idea is to use samples drawn from the empirical distribution of each parameter of interest. The procedure is analagous to ordering each sample, counting in from the minimum and maximum of each ordered sample a fixed number of ranks and use those order statistics as the simultaneous interval. Because the method is nonparametric, it ignores the properties of the empirical distribution the stored sample was drawn from, but uses an assumption of symmetry. Therefore, the method conservatively makes the intervals wider than necessary.

[Nandram and Choi, 2003] constructs simultaneous concentration bands for quantile-quantile probability plots, accounting for the correlation of order statistics and providing exact coverage probability. Comparisons of pointwise and Bonferroni concentration bands are given.

[Lui and Cumberland, 1987] uses simultaneous interval estimates in small domain estimation under the Bayesian paradigm. They use the Bonferroni method, the multivariate t method and Scheffé's method and make comparisons. [Andrews and Birdsall, 1988] compare three simultaneous confidence interval procedures: ordinary-

χ^2, full-design and Bayesian. They find that for their study, the Bayesian procedure had the best properties in terms of correct coverage with small average interval width having small variation over replications.

[Nandram et al., 2000] described a method to study variation in maps in Section 4 of their paper. They use the 1000 iterates from the 798 λ values by finding the identity of the quantiles of a HSA in the mean map and over each of the 1000 alternative maps. This method addresses directly the issue of how the apparent map patterns change, but it is difficult to present all the available information from 1000 maps. Thus our idea is to construct three maps, the mean map, and the end points of 95% simultaneous intervals (upper and lower maps) for all HSAs.

1.5 Source of Data

The death counts and number at risk for this paper were obtained from records of all United States death certificates in the fifty States and District of Columbia for 1988 through 1992 and population census data for 1990. The number of deaths by age, race, sex, place of residence and cause of death is based on original death certificates reported to the National Center for Health Statistics (NCHS) by the States. Death certificates with age not stated were excluded, 0.025 percent of the total. Race was classified following standard procedures for United States statistics. Hispanics with no racial designation are included in the "White" category [Pickle et al., 1996].

The population counts from the 1990 census, classified by age, race, sex and county, were multiplied by five to create a denominator corresponding to the five years of mortality data. In few instances where the calculated number of person years was less than the reported number of deaths, as when death occurred in a sparsely populated county before census enumeration, the years at risk were inflated to equal the total number of deaths due to any cause. The age classes are classified as 0–4 years, 5–14 years, 15–24 years, 25–34 years, 35–44 years, 45–54 years, 55–64

years, 65–74 years, 75–84 years, 85 years and over, coded as decades 0.25, 1, 2, ..., 9, the midpoints of the decade intervals (class 1 is decade 0.25, class j is decade $j-1$, for $j = 2, \ldots, 10$) [Pickle et al., 1996]. Further details on the method of data collection and processing of death certificates may be found in the Technical Appendix of [National Center for Health Statistics, 1990].

The quality of the data is determined by the accuracy and completeness of the information from medical diagnosis to final coding and processing of the underlying cause of death. Beginning with mortality data for 1968, the underlying cause of death has been determined by the NCHS computerized system that consistently applies the World Health Organization (WHO) coding and selection rule to each death certificate using all conditions reported by the certifier. Automation of these tasks and cross verification of medical conditions coding have reduced errors in assigning underlying cause of death certificate information to less than one percent. However, the completeness and accuracy of the information supplied on the certificate and the decedent's medical diagnosis remain potential sources of error [Pickle et al., 1996].

Deaths were initially assigned to a county (or equivalent administrative unit, such as independent city or parish) according to the residence of the deceased, regardless of the place of death. There were in all 3141 geographical units, which were further aggregated into HSAs [Pickle et al., 1996] by a cluster analysis of where residents aged 65 and over obtained routine short-term hospital care in 1988. A HSA may be thought of as an area that is relatively self-contained with respect to hospital care. The median number of counties per HSA is about 2 with a range of 1 through 20. The median number of HSAs per state is 16 with a range of 1 through 58. With the exception of New York City, the area of each HSA is at least 250 square miles. There are twelve regions and 798 HSA, three of the nine census divisions were split to make a total of twelve regions to achieve greater homogeneity of rates [Pickle et al., 1996].

1.5.1 Chronic Obstructive Pulmonary Disease (COPD)

Chronic obstructive pulmonary disease (COPD) is a term used for two closely related diseases of the respiratory system: chronic bronchitis and emphysema. These diseases often occur together in patients, most of which have a long history of heavy cigarette smoking. The disease worsens over time, beginning with mild shortness of breath and occasional coughing developing into a chronic cough with clear, colorless sputum. As the disease progresses, the cough becomes more frequent and breathing becomes difficult. In later stages of the disease, the heart may be affected. Eventually death occurs when the function of the lungs and heart is no longer adequate to deliver oxygen to the body's organs and tissues [National Institutes of Health, 1995].

Risk for developing COPD is most strongly linked to cigarette smoking; it would probably be a minor health problem if people did not smoke. Other risk factors include age, heredity, exposure to air pollution at work and in the environment, and a history of childhood respiratory infections. Living in low socioeconomic conditions also seems to be a contributing factor [National Institutes of Health, 1995].

More than 13.5 million Americans are thought to have COPD. It is the fifth leading cause of death in the United States. Between 1980 and 1990, the total death rate from COPD increased by 22 percent. In 1990, it was estimated that there were 84,000 deaths due to COPD, approximately 34 per 100,000 people. Although COPD is still much more common in men than women, the greatest increase in the COPD death rate between 1979 and 1989 occurred in females, particularly in black females (117.6 percent for black females vs. 93 percent for white females). These increases reflect the increased number of women who smoke cigarettes [National Institutes of Health, 1995].

COPD attacks people at the height of their productive years, disabling them with constant shortness of breath. It destroys their ability to earn a living, causes frequent use of the health care system, and disrupts the lives of the victims' family

members for as long as 20 years before death occurs [National Institutes of Health, 1995].

In 1990, COPD was the cause of approximately 16.2 million office visits to doctors and 1.9 million hospital days. The economic costs of this disease are enormous. In 1989, an estimated $7 billion was spent for care of persons with COPD and another $8 billion was lost to the economy by lost productivity due to morbidity and mortality from COPD [National Institutes of Health, 1995].

1.6 Bayesian Method

For convenience we denote the number of HSAs by $\ell = 798$. Let $\underset{\sim}{\lambda} = (\lambda_1, \ldots, \lambda_\ell)'$ denote the ensemble of mortality rate parameters, $\underset{\sim}{d} = (d_1, \ldots, d_\ell)'$ denote the deaths and $\underset{\sim}{n} = (n_1, \ldots, n_\ell)'$ the population sizes which are known. We ignore the covariates momentarily. In the Bayesian view, given $\underset{\sim}{\lambda}$, the deaths have a distribution; given hyperparameters, $\underset{\sim}{\lambda}$ have a distribution (hyperparameters are parameters of this distribution), and finally the hyperparameters have a distribution. This is a hierarchical Bayesian model. Note that unlike in non-Bayesian inference, $\underset{\sim}{\lambda}$ is a random vector. Then, using Bayes' theorem and some integration, the joint posterior density of $\underset{\sim}{\lambda}$ is $\pi(\underset{\sim}{\lambda} | \underset{\sim}{d})$. Note that the key idea in Bayesian statistics is that all information about $\underset{\sim}{\lambda}$ resides in $\pi(\underset{\sim}{\lambda} | \underset{\sim}{d})$. Also, it is important to note that the components of $\underset{\sim}{\lambda}$ are correlated a posteriori. The posterior mean map is obtained by drawing the choropleth map for the posterior means of each λ_i, $i = 1, \ldots, \ell$. Clearly, this ignores the inherrent correlation among the components of $\underset{\sim}{\lambda}$, and this is one additional obvious short-comings of presenting the posterior mean map alone. One needs to construct a map simultaneously across the areas (i.e., incorporate the correlation). It is the simultaneous interval map that plots the joint posterior density over the surface $\pi(\underset{\sim}{\lambda} | \underset{\sim}{d})$ providing a region in ℓ-dimensional space that includes this correlation (i.e., the synergism or antagonism over the components of $\underset{\sim}{\lambda}$).

1.7 Thesis Overview

In the current chapter, by way of providing an introduction, we discussed choropleth maps, small area mapping, models and methods, the source of the data and discussed briefly the Bayesian method.

In Chapter 2 we discuss interval estimation, detailing all the intervals we employ, and develop the Single-γ Method and Double-γ Method simultaneous intervals. These two methods are used to construct simultaneous intervals from the optimal individual highest posterior density (HPD) intervals to ensure joint simultaneous coverage of $100(1-\alpha)\%$.

In Chapter 3 we discuss the Poisson-gamma hierarchical regression model and the construction of intervals in this model context. Therefore, in addition to rate parameter estimation, we describe an approach to present variability in choropleth maps by constructing simultaneous intervals from the optimal individual highest posterior density (HPD) intervals to ensure joint simultaneous coverage of $100(1-\alpha)\%$. The result provides three maps (estimate with two bands). Both methods exhibit the main feature of multiplying the lower bound and dividing the upper bound of the individual HPD intervals by parameters $0 < \gamma_1, \gamma_2 < 1$ to "stretch" the interval until the simultaneous probability content is $100(1-\alpha)\%$. In Appendix A we give an overview of the statistical methodology used in this research. In Appendix B we give details and explanations for mathematical results in Chapter 3.

In Chapter 4 we present choropleth maps and the results from the simultaneous interval methods. These include interval maps and difference maps and tables, both novel methods of describing variation in maps.

For illustrative purposes we apply our methods to chronic obstructive pulmonary disease (COPD) mortality rates from 1988–92, subset White Males age group 65 and older, for the continental United States for the 798 Health Service Areas (HSA). In Chapter 5 we make conclusions from this research and provide suggestions for extensions and further work on this topic.

2. SIMULTANEOUS INTERVAL ESTIMATION

The main idea of interval estimation is to take data $X_1, \ldots, X_n \sim f(\underset{\sim}{x}|\,\underset{\sim}{\theta})$ and produce a set $C(\underset{\sim}{X}) \subseteq \underset{\sim}{\theta}$ that is a subset of the support of the parameter(s) of interest, $\underset{\sim}{\theta}$. Ideally, this set will have two properties. First, the set should be more likely to contain the true value of $\underset{\sim}{\theta}$ than its complement. Second, the set should be small in some sense. In many respects, the Bayesian approach to interval estimation is simple and easily interpreted.

The purpose of using an interval estimator, rather than just a point estimator, is to have some guarantee of capturing the parameter of interest. The interval estimator combines both a point estimator and a measure of spread. The interval provides a level of confidence, or assurance, that our assertion about the population parameters is correct.

Common choices for the degree of confidence are 90%, 95% and 99%. The choice of 95% is most common, since it seems to represent a good balance between precision (as reflected in the width of the confidence interval) and reliability (as expressed by the degree of confidence). Levels above 99% are generally unsatisfacotry because of sensitivity to the assumed form of the tails of the distribution.

2.1 Review of Credible Intervals

2.1.1 Credible Intervals (CI)

Let $f(\theta|\,\underset{\sim}{d})$ denote the posterior density of a parameter θ given data $\underset{\sim}{d}$.

Definition 2.1.1 *An interval* (a, b) *is called a* $100(1-\alpha)\%$ *credible interval if its posterior probability content is* $1-\alpha$*, that is,* $\int_a^b f(\theta|\,\underset{\sim}{d})\,\mathrm{d}\theta = 1-\alpha$.

Credible intervals are not unique. Two credible intervals can exist such that

$$\int_{a_1}^{b_1} f(\theta|\,\underset{\sim}{d})\,\mathrm{d}\theta = \int_{a_2}^{b_2} f(\theta|\,\underset{\sim}{d})\,\mathrm{d}\theta \;\; = \;\; 1-\alpha \tag{2.1}$$

or

$$F(b_1) - F(a_1) = F(b_2) - F(a_2) \;\; = \;\; 1-\alpha, \tag{2.2}$$

$a_1 \neq a_2$ and $b_1 \neq b_2$, where $F(\cdot)$ is the cdf. As an example the plot in Figure 2.1 gives three 95% credible intervals for the Gamma(α, β) distribution, that is, $f(x|\,\alpha, \beta) = \frac{1}{\Gamma(\alpha)\beta^\alpha} x^{\alpha-1} e^{-x/\beta}$ where $0 \leq x < \infty$ and $\alpha, \beta > 0$, with $\alpha = 3$ and $\beta = 1$. The first interval $(a_1, b_1) = (0.4360, 6.5989)$ covers from the 0.01 to 0.96 quantile, the second interval $(a_2, b_2) = (0.7462, 8.4059)$ covers from the 0.04 to 0.99 quantile, and the third interval $(a_{\text{cred}}, b_{\text{cred}}) = (0.6187, 7.2247)$ covers from the 0.025 to 0.975 quantile.

Credible intervals are easy to construct. Typically, we construct credible intervals with equal tail probabilities to their left and to their right. For a $100(1-\alpha)\%$ credible interval, there is $100(\frac{\alpha}{2})\%$ probability in each tail. The plot in Figure 2.1 gives such a 95% credible interval where the interval $(a_{\text{cred}}, b_{\text{cred}}) = (0.6187, 7.2247)$ covers from the 0.025 to 0.975 quantile.

Interval Construction

There are two ways to construct credible intervals: numerical and sampling-based.

Method 1 (Numerical) Let $F(\theta|\,\underline{d}) = \int_{-\infty}^{\theta} f(t|\,\underline{d})\,\mathrm{d}t$ be the cumulative distribution function (cdf). Let $F^{-1}(.|\,\underline{d})$ be the inverse cdf. Then $a = F^{-1}(\frac{\alpha}{2}|\,\underline{d})$ and $b = F^{-1}(1-\frac{\alpha}{2}|\,\underline{d})$ give the $100(1-\alpha)\%$ credible interval (a, b).

Method 2 (Sampling-based) Draw a random sample of 1,000 values from $f(\theta|\,\underline{d})$. Place the values in ascending order, $\theta^{(1)} < \theta^{(2)} < \ldots < \theta^{(1000)}$. Then an estimate from these order statistics of the 95% credible interval is $(\theta^{(25)}, \theta^{(976)})$. This method is usually used in complex problems, and is the method used in this paper. This method works well for large samples (i.e., about 1000).

2.1.2 Highest Posterior Density (HPD) Intervals

Not only should we be concerned with the probability content of the interval, but we wish to use the interval with the highest posterior density.

Definition 2.1.2 *A $100(1-\alpha)\%$ credible interval (a, b) is a highest posterior density (HPD) interval if for any $\theta_1 \in (a, b)$ and $\theta_2 \notin (a, b)$, $f(\theta_1|\,\underline{d}) \geq f(\theta_2|\,\underline{d})$. In other words, the height of any point of the density within the HPD interval is greater than for any point outside the interval.*

All candidate intervals must contain the mode. The $100(1-\alpha)\%$ HPD interval is unique for any unimodal posterior density. If the mode is on a boundary of the posterior density, then that boundary is one of the end points in the interval. The $100(1-\alpha)\%$ HPD interval is the shortest interval with $100(1-\alpha)\%$ coverage.

The plots in Figure 2.2 give examples of HPD intervals on densities with a mode on the boundary and not on the boundary.

Theorem 2.1.1 *For a unimodal posterior density the $100(1-\alpha)\%$ HPD interval is obtained by solving the two equations*

$$\int_a^b f(\theta|\,\underline{d})\,\mathrm{d}\theta = 1-\alpha \tag{2.3}$$

$$f(a|\,\underline{d}) = f(b|\,\underline{d}) \tag{2.4}$$

for (a, b).

The first equation (2.3) ensures the probability content. The second equation (2.4) ensures the equal ordinates optimality condition (interval boundaries with equal height).

Proof. The first equation states that the interval is a $100(1-\alpha)\%$ credible interval. The second equation states that the interval has the highest posterior density (probability) among all $100(1-\alpha)\%$ credible intervals. This satisfies the equal ordinates condition (interval boundaries have equal height).

The geometric interpretation of finding the HPD interval is to slide a horizontal line up and down until the area within the interval (a, b) is $1-\alpha$. ■

The plot in Figure 2.3 gives a 95% credible interval where the interval $(a_{\text{hpd}}, b_{\text{hpd}}) = (0.3035, 6.4012)$ covers from the 0.00372 to 0.95372 quantile. This plot also compares the HPD interval with the coresponding CI. The horizontal line on the plot illustrates the equal ordinates condition.

HPD Computation

If $f(\theta|\,\underline{d})$ is a unimodal posterior density with mode on the lower boundary B, the interval is $\int_B^a f(\theta|\,\underline{d})\,\mathrm{d}\theta = 1-\alpha$, or simply $(B, F^{-1}(a|\,\underline{d}))$.

If $f(\theta|\,\underline{d})$ is a unimodal posterior density with mode not on the boundary,

$$f(a|\,\underline{d}) = f(b|\,\underline{d}) \tag{2.5}$$

$$F(a|\,\underline{d}) - F(b|\,\underline{d}) = \int_a^b f(\theta|\,\underline{d})\,\mathrm{d}\theta = 1-\alpha. \tag{2.6}$$

Conditions (2.5) and (2.6) guarentee that the $100(1-\alpha)\%$ CI is the shortest. Condition (2.5) can be expressed by a single term, for example, by solving in terms of a,

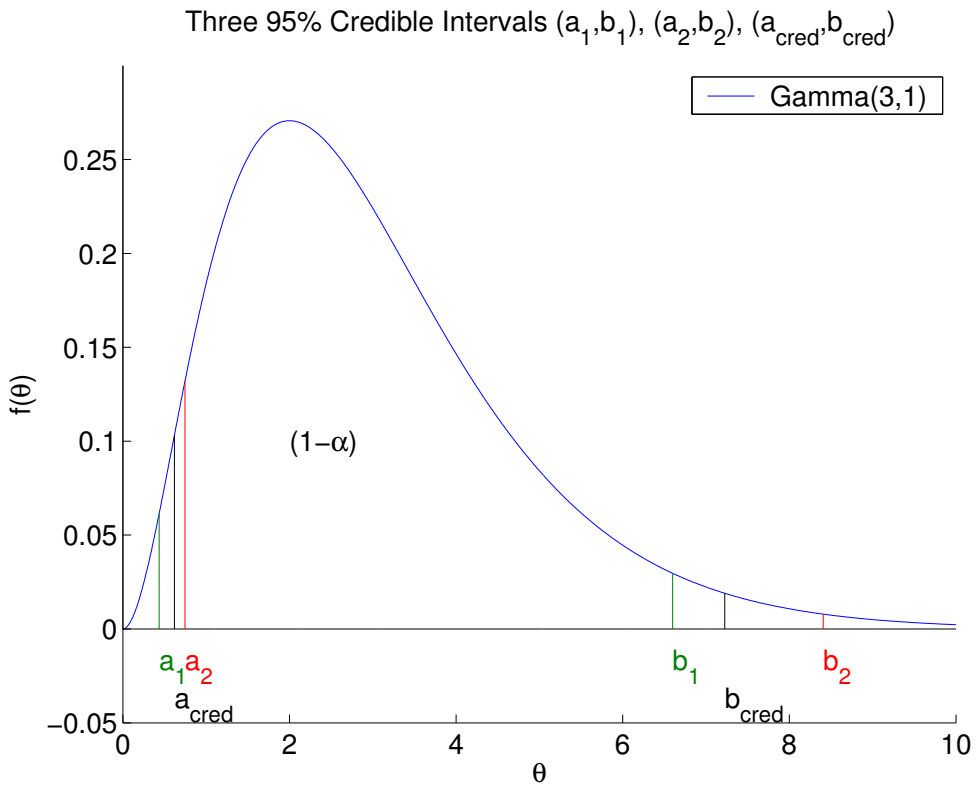
$$f(a|\,\underline{d}) = f(b|\,\underline{d}) \tag{2.7}$$

$$= f(F^{-1}[F(a) + (1-\alpha)]). \tag{2.8}$$

We begin with the credible interval (a, b), then use a numerical routine to find $(a_{\text{hpd}}, b_{\text{hpd}})$, searching for a_{hpd} near a and b_{hpd} near b.

It is worthwhile noting that if m is the mode of a symmetric density then the $100(1-\alpha)\%$ HPD interval is $(m-a, m+a)$ where $\int_m^{m+a} f(\theta|\,\underline{d})\,\mathrm{d}\theta = \frac{1-\alpha}{2}$. Also, for a symmetric density, the equal ordinate condition guarantees equal tails. Therefore the HPD interval is the same as the credible interval with equal tails.

We close with some remarks on HPD intervals. While HPD intervals are desireable they may be difficult to compute. Credible intervals can be easily obtained from the output of a sampling-based method. For multimodal densities, the construction for HPD intervals (set of intervals) seems to be an open problem, but it can be done. HPD regions can be constructed for multi-dimensional parameters. For example, for a d-variate normal posterior density, the HPD region is an ellipsoid.



$(a_1, b_1) = (0.4360, 6.5989)$ covers from the 0.01 to 0.96 quantile,

$(a_2, b_2) = (0.7462, 8.4059)$ covers from the 0.04 to 0.99 quantile, and

$(a_{\text{cred}}, b_{\text{cred}}) = (0.6187, 7.2247)$ covers from the 0.025 to 0.975 quantile.

Figure 2.1. Credible intervals are not unique.

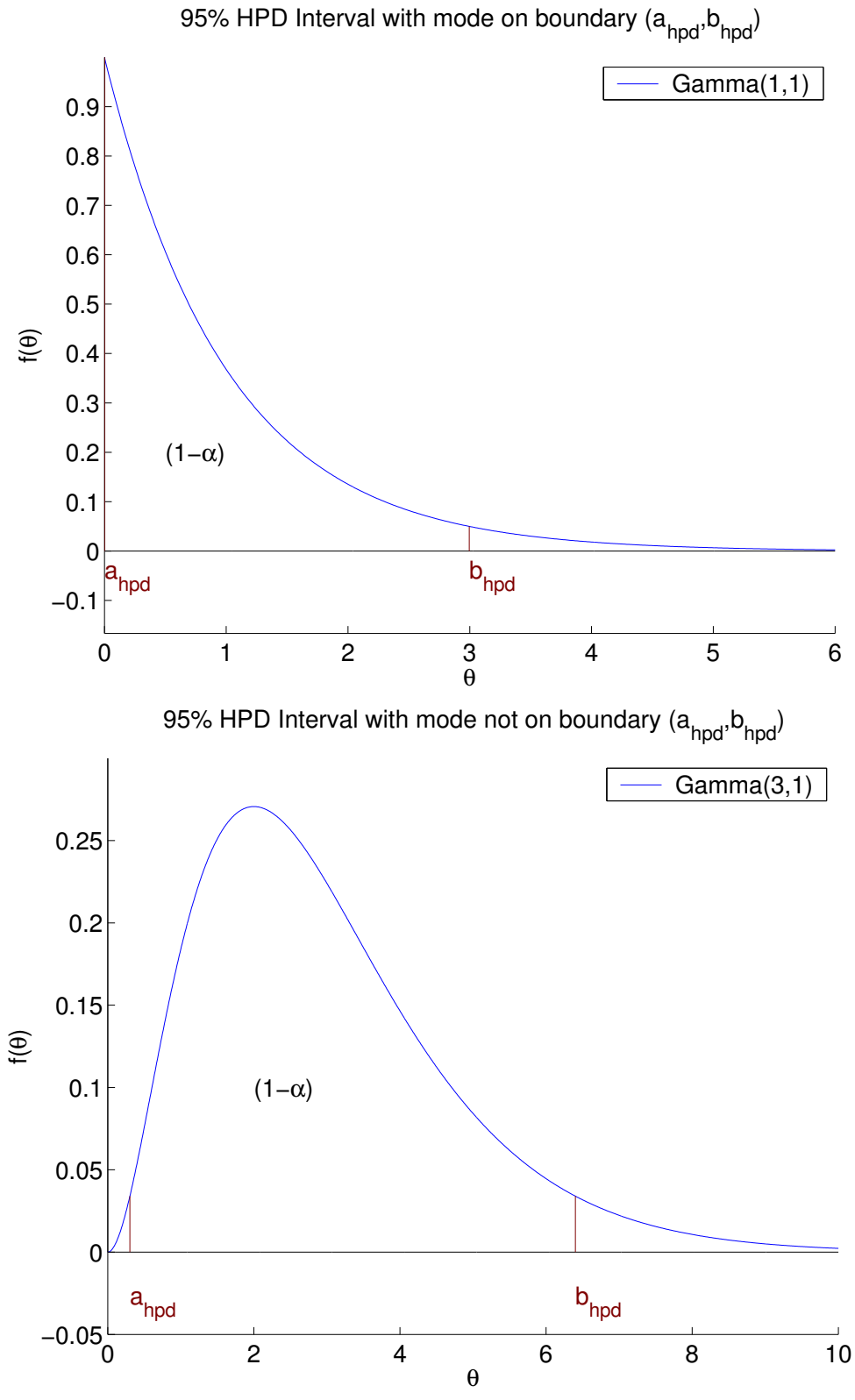
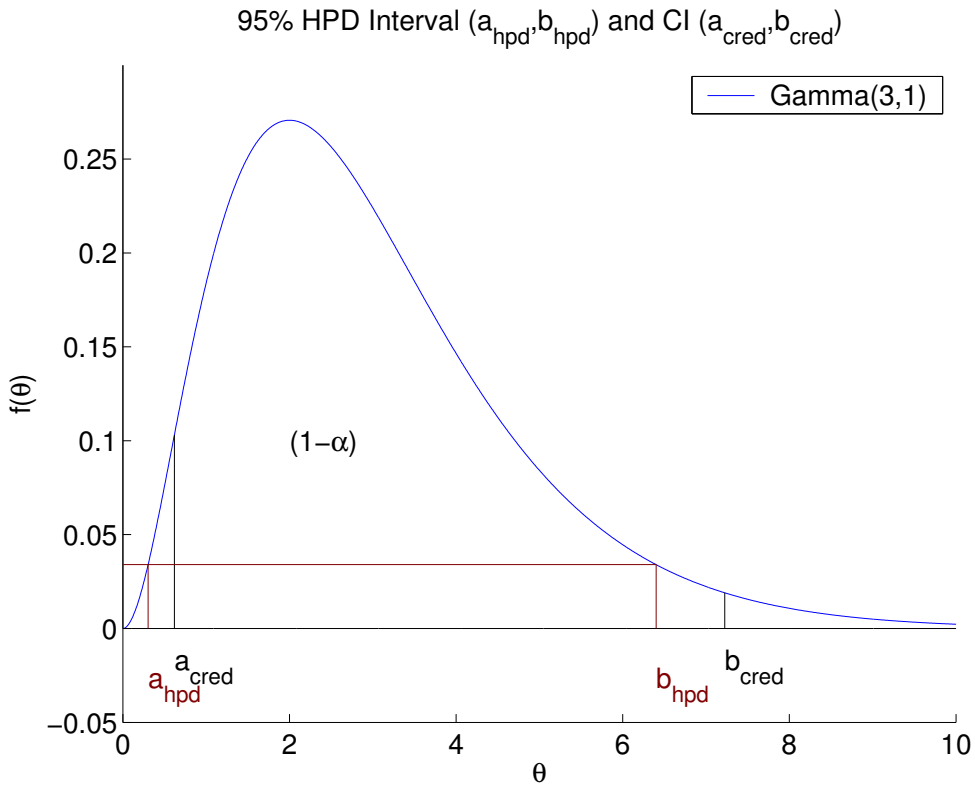


Figure 2.2. 95% HPD Interval with mode on boundary and not on boundary.



$(a_{\text{cred}}, b_{\text{cred}}) = (0.6187, 7.2247)$ covers from the 0.025 to 0.975 quantile and $(a_{\text{hpd}}, b_{\text{hpd}}) = (0.3035, 6.4012)$ covers from the 0.00372 to 0.95372 quantile.

Figure 2.3. 95% HPD Interval $(a_{\text{hpd}}, b_{\text{hpd}})$ and CI $(a_{\text{cred}}, b_{\text{cred}})$.

2.2 Simultaneous Intervals

Why do we need simultaneous intervals? Consider two parameters μ_1 and μ_2. Let a 95% CI for μ_1 be (a_1, b_1) and a 95% CI for μ_2 be (a_2, b_2). Then the intersection $(a_1, b_1) \cap (a_2, b_2)$ does not form a set giving a 95% credible interval (i.e., smaller than 95%). So all we need is to lengthen these individual intervals in an optimal manner.

2.2.1 Boole's inequality

Bonferroni's inequality, $P(A \cap B) \geq P(A) + P(B) - 1$, allows us to bound the probability of a simultaneous event (the intersection) in terms of the probabilities of the individual events [Miller, 1981] (p. 8). Boole's inequality, $P(\cap_{i=1}^{n} A_i) \geq \sum_{i=1}^{n} P(A_i) - (n-1)$, gives a more general form of the Bonferroni inequality, allowing for more than two events. This method gives a meaningful result when the number of events is small and the probabilities of the individual events are sufficiently large.

In our case, we wish to have a simultaneous interval containing 798 individual intervals, an extremely large quantity of events. By Boole's inequality, we wish the intersection of the individual intervals to be at least 0.95. We have $P(\cap_{i=1}^{n} A_i) \geq \sum_{i=1}^{n} P(A_i) - (n-1) = 0.95$, $\sum_{i=1}^{n} P(A_i) = 0.95 + (n-1)$, $798P(A) \leq 0.95 + (798-1)$ (since each area should have the same probability content), $P(A) \leq \frac{0.95+797}{798} = 0.999937343 \doteq 0.99994$. Therefore, the probability content of each individual event's interval is bounded above by 0.99994. The credible interval is $(F^{-1}(0.00003), F^{-1}(0.99997))$ for two-tailed, and $(F^{-1}(0), F^{-1}(0.99994))$ for one-tailed. Computations break down at this strict lower bound limit given by Boole's inequality.

We should not apply Boole's correction directly to our problem since it is strictly an upper bound (a worst-case scenario). As these individual intervals are covering nearly the entire support of the individual densities, they are somewhat meaningless. The true individual probabilities will most likely lie somewhere between 0.95 and the above 0.99994. A more exact method is preferred.

2.3 Methods for constructing simultaneous $100(1-\alpha)\%$ intervals

Three popular simultaneous intervals for a moderate number of parameters, in the form of tests, are the Bonferroni, Tukey and Scheffé Methods. The Bonferroni Method tests, or puts simultaneous confidence intervals around, a pre-selected group of contrasts. Tukey's Method tests all possible pairwise differences of means to determine if at least one difference is significantly different from zero [Tukey, 1953]. Scheffé's Method tests all possible contrasts at the same time, to see if at least one is significantly different from zero [Scheffé, 1953].

The literature lacks many possibilities to calculate simultaneous probability intervals relating to a, potentially large, number of parameters. A notable exception is described in [Besag et al., 1995] (p.30), a method to calculate simultaneous credible regions based on order statistics. Their approach defines such a region as the product of (symmetric) univariate prosterior credible intervals (of the same univaiate level) for each parameter; the simultaneous credible level is then essentially defined as the proportion of samples which fall simultaneously in this region. Being based only on ranks, the method is invariant to monotonic transformations of the variables. Details of this method are given in Appendix B.3.

[Nandram, 1993] describes a method for constructing simultaneous cuboid intervals (hyper-rectanglar) for the prediction of k new observations. He uses a one-way analysis of variance (ANOVA) model under a normality assumption with a Lindley-Smith [Lindley and Smith, 1972] type prior. This gives intervals based on the multivariate t distribution which are the simple cuboid which engineers use, instead of the optimal ellipse. The bounds on each interval are obtained by solving a pair of equations simultaneously. The first equation satisfies the highest posterior density (HPD) optimality criterion of equal ordinates by forcing the difference of the values of the probability density function evaluated at the interval bounds to be zero. The second equation satisfies the simultaneous probability content by forcing the difference of the values of the cumulative density function evaluated at the lesser interval

bound from the greater interval bound to be $1-\alpha$. Thus the cuboids are optimized by constructing the smallest such k-dimensional cuboid by using HPD intervals in each dimension.

The method presented in our paper is an extention of the method of [Nandram, 1993]. Two main differences are that we consider a large number of parameters $\ell = 798$, where he considered up to $k = 10$ predictions, and we use a Poisson-gamma hierarchical model instead of an ANOVA model under normality.

We propose to construct simultaneous $100(1-\alpha)\%$ intervals by "stretching" individual HPD intervals until the desired content is obtained, together with an optimality criterion. The simultaneous intervals are defined as the product of the univariate intervals, which are by construction restricted to be hyper-rectanglar.

Ultimately, we want to solve this system of equations:

$$\begin{aligned} \int_{a_\ell}^{b_\ell} \cdots \int_{a_1}^{b_1} f(\lambda_1, \ldots, \lambda_\ell | \underline{d})\, \mathrm{d}\lambda_1 \cdots \mathrm{d}\lambda_\ell &= 1-\alpha \qquad (2.9) \\ f(a_1 | \underline{d}) &= f(b_1 | \underline{d}) \\ &\vdots \\ f(a_\ell | \underline{d}) &= f(b_\ell | \underline{d}) \qquad (2.10) \end{aligned}$$

The first equation (2.9) ensures the probability content. The set of equations (2.10) ensure the equal ordinates optimality condition (interval boundaries with equal height).

However, because we have nearly twice as many unknowns as we have equations, there is not a unique solution. Even if there were a unique solution, optimizing over such a large set of parameters is, understatedly, computationally demanding.

2.3.1 Simultaneous interval visualization example

In order to help visualize what a simultaneous interval looks like, we present an extremely simple example with two independent Gamma distributions. The two distributions are

$$\lambda_1 | \, d_1 \sim \text{Gamma}(3, 1) \tag{2.11}$$

$$\lambda_2 | \, d_2 \sim \text{Gamma}(10, 0.5). \tag{2.12}$$

First, we want the probability of the simultaneous region of the joint posterior density function (pdf) to equal $1 - \alpha$. That is,

$$1 - \alpha = \int_{a_2}^{b_2} \int_{a_1}^{b_1} f(\lambda_1, \lambda_2 | \, \underline{d}) \, \mathrm{d}\lambda_1 \, \mathrm{d}\lambda_2 \tag{2.13}$$

$$= \int_{a_2}^{b_2} \int_{a_1}^{b_1} f(\lambda_1 | \, d_1) f(\lambda_2 | \, d_2) \, \mathrm{d}\lambda_1 \, \mathrm{d}\lambda_2 \tag{2.14}$$

$$= \prod_{i=1}^{2} \left\{ \int_{a_i}^{b_i} f(\lambda_i | \, d_i) \, \mathrm{d}\lambda_i \right\}. \tag{2.15}$$

It makes sense for both of the distributions to have, what is now, a $100(1-\alpha)^{1/2}\%$ HPD interval. The plots in Figure 2.4 gives these intervals, $(a_1, b_1), (a_2, b_2)$.

The simultaneous interval $\{(a_1, b_1), (a_2, b_2)\}$ that results from the conditions given in equations (2.13) through (2.15) is given in the plot in Figure 2.5. The volume under the colored portion of the plot has probability $1 - \alpha$.

Following this example, it is intuitive that for ℓ independent distributions the individual $100(1-\alpha)^{1/\ell}\%$ HPD intervals will intersect to give the simultaneous interval $\{(a_1, b_1), \ldots, (a_\ell, b_\ell)\}$ with probability content $1 - \alpha$.

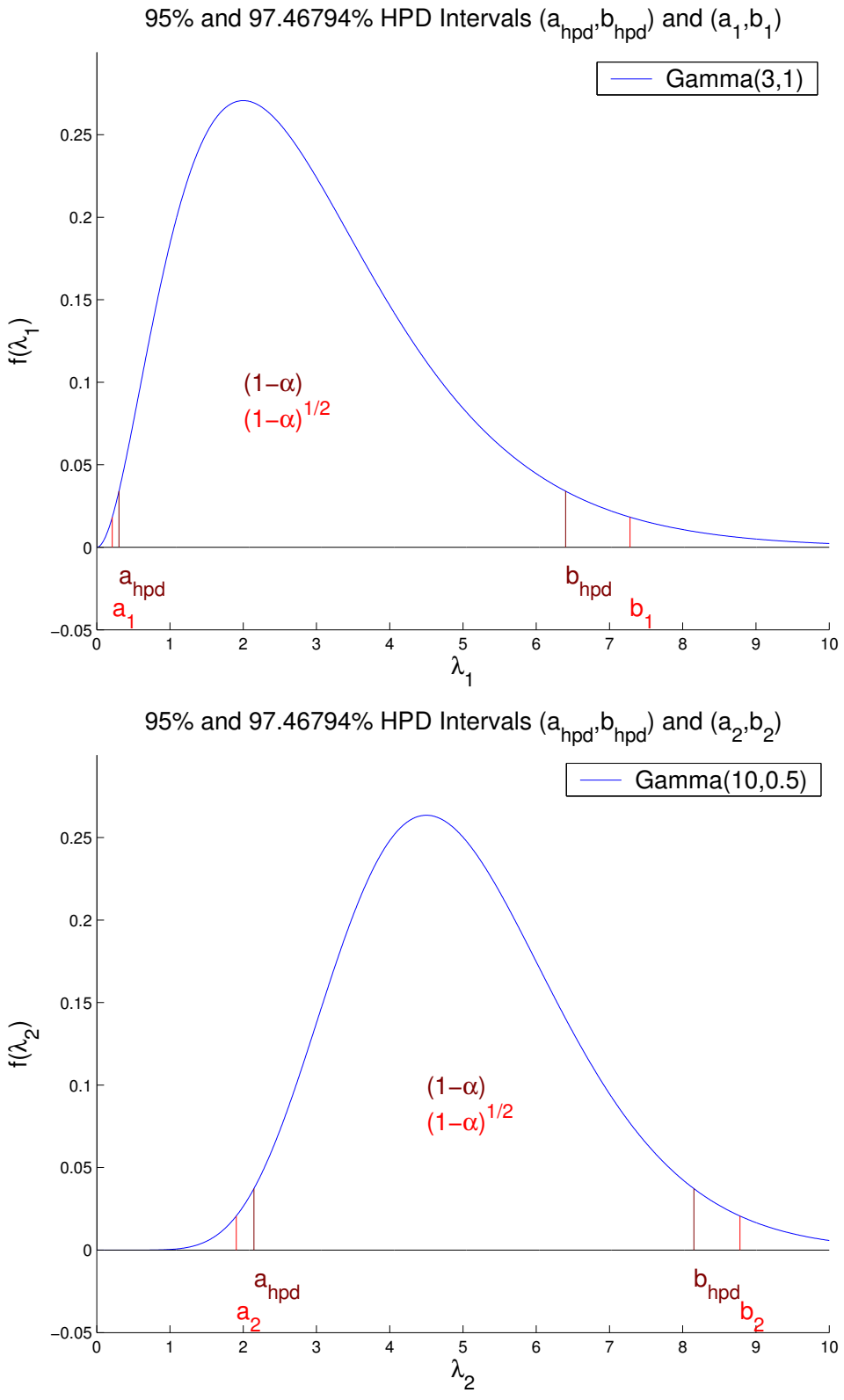


Figure 2.4. $100(1-\alpha)^{1/2}\%$ Individual HPD Intervals $(a_1, b_1), (a_2, b_2)$.

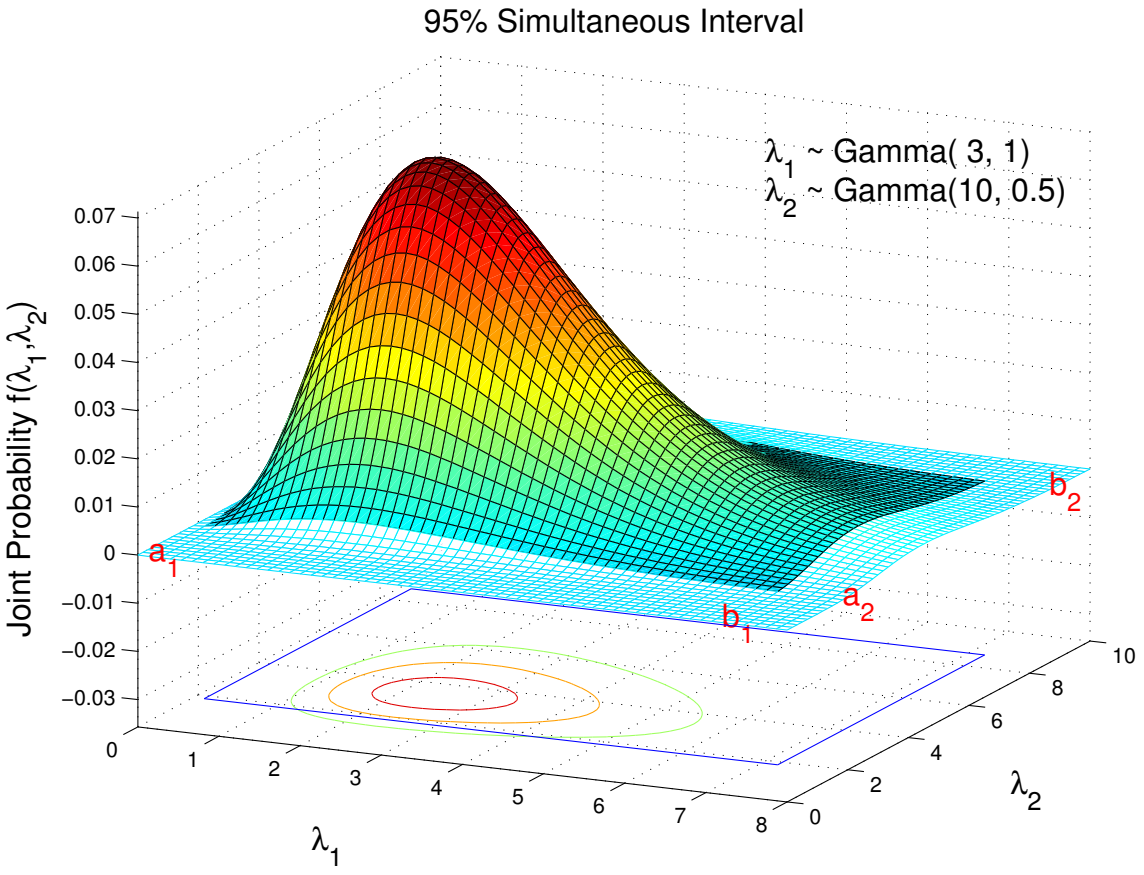


Figure 2.5. $100(1-\alpha)\%$ Simultaneous Interval $\{(a_1, b_1), (a_2, b_2)\}$.

2.4 Single-γ Method Simultaneous $100(1-\alpha)\%$ interval

One method to simplify our goal in equation (2.9) is to provide one parameter to operate on the individual HPD intervals. Let $0 < \gamma < 1$ be a "stretching" factor on the HPD interval (a_i, b_i), giving the stretched interval higher content than the initial interval,

$$\int_{\gamma a_i}^{b_i/\gamma} f(\lambda_i|\, d_i)\, \mathrm{d}\lambda_i \;\; \geq \;\; \int_{a_i}^{b_i} f(\lambda_i|\, d_i)\, \mathrm{d}\lambda_i. \tag{2.16}$$

In this way we can begin with an optimized condition of HPD intervals (a_i, b_i) and stretch them until the desired content is obtained. Thus our goal using the Single-γ Method is to satisfy the equation

$$\int_{\gamma a_\ell}^{b_\ell/\gamma} \cdots \int_{\gamma a_1}^{b_1/\gamma} f(\lambda_1, \ldots, \lambda_\ell|\, \underset{\sim}{d})\, \mathrm{d}\lambda_1 \cdots \mathrm{d}\lambda_\ell \;\; = \;\; 1-\alpha \tag{2.17}$$

for $i = 1, \ldots, \ell$.

2.4.1 Single-γ Method Computations

The goal is to optimize the following equation (2.18) by determining the value for γ such that $\min_\gamma F(\gamma)$ approaches zero.

$$F(\gamma) \;\; = \;\; \left| \int_{\gamma a_\ell}^{b_\ell/\gamma} \cdots \int_{\gamma a_1}^{b_1/\gamma} f(\lambda_1, \ldots, \lambda_\ell|\, \underset{\sim}{d})\, \mathrm{d}\lambda_1 \cdots \mathrm{d}\lambda_\ell - (1-\alpha) \right| \tag{2.18}$$

The following theorem shows that the Single-γ Method has a unique solution with the correct probability content in equation (2.17).

Theorem 2.4.1 *Given a set of HPD credible intervals $A_i' = \{\lambda_i : a_i < \lambda_i < b_i\}$, $i = 1, \ldots, \ell$, defined on a set of densities with positive support and given the transformation $A_i = \{\lambda_i : \gamma a_i < \lambda_i < b_i/\gamma\}$, there is a unique γ satisfying $P(\cap_{i=1}^{\ell} A_i|\, \underset{\sim}{d}) = 1-\alpha$, where $\underset{\sim}{d}$ is the data.*

Proof. Let $A_i' = \{\lambda_i : a_i < \lambda_i < b_i\}$ be the individual $100(1-\alpha)\%$ HPD credible interval defined on a set of densities with positive support, $P(A_i'|\, d_i) = 1-\alpha$, $i =$

$1, \ldots, \ell$. We will use γ as a "stretching" factor for this interval to allow us to find a unique solution for a simultaneous interval.

Let $A_i = \{\lambda_i : \gamma a_i < \lambda_i < b_i/\gamma\}$ be the stretched individual HPD interval with $P(A_i|\, d_i) \geq 1-\alpha$, $i = 1, \ldots, \ell$, and $P(\cap_{i=1}^{\ell} A_i|\, d_i) = 1-\alpha$ be the probability of the intersection. Observe that as γ decreases to 0, each $\{A_i\}$ is a sequence of increasing sets so that $\{\cap_{i=1}^{\ell} A_i|\, d_i\}$ is a sequence of increasing sets. So, by the continuity theorem,

$$\begin{aligned}
\lim_{\gamma \to 0} P(\cap_{i=1}^{\ell} A_i|\, d_i) &= P\Big(\lim_{\gamma \to 0} \cap_{i=1}^{\ell} A_i|\, d_i\Big) \\
&= P(\underset{\sim}{\lambda} \in \Re_+^{\ell}|\, \underset{\sim}{d}), \qquad \underset{\sim}{\lambda} = (\lambda_1, \ldots, \lambda_\ell)' \\
&= 1.
\end{aligned}$$

That is, at the limit, as γ goes to 0, the sequence of increasing sets $\{\cap_{i=1}^{\ell} A_i|\, d_i\}$ encompasses the entire space $\Re_+^{\ell}$, the positive ℓ-dimensional reals. Also, at $\gamma = 1$, $P(\cap_{i=1}^{\ell} A_i|\, d_i) < P(A_i'|\, d_i) = 1-\alpha$. Thus, as $\gamma \to 0$, $P(\cap_{i=1}^{\ell} A_i|\, d_i)$ increases smoothly from a value less than $1-\alpha$ to 1. Therefore, there is a unique solution to $P(\cap_{i=1}^{\ell} A_i|\, d_i) = 1-\alpha$ in terms of γ. ■

2.5 Double-γ Method Simultaneous $100(1-\alpha)\%$ interval

One method to simplify our goal set in equations (2.9) and (2.10) is to provide two parameters to operate on the individual HPD intervals. Let $0 < \gamma_1 < 1$ and $0 < \gamma_2 < 1$ be "stretching" factors on the HPD interval (a_i, b_i), giving the stretched interval higher content than the initial interval,

$$\int_{\gamma_1 a_i}^{b_i/\gamma_2} f(\lambda_i|\,\underline{d})\,\mathrm{d}\lambda_i \;\;\geq\;\; \int_{a_i}^{b_i} f(\lambda_i|\,\underline{d})\,\mathrm{d}\lambda_i. \tag{2.19}$$

In this way we can begin with an optimized condition of HPD intervals (a_i, b_i), and stretch them until the desired content is obtained together with an ordinate optimality criterion. Thus our goal using the Double-γ Method is to satisfy the two equations

$$\int_{\gamma_1 a_\ell}^{b_\ell/\gamma_2} \cdots \int_{\gamma_1 a_1}^{b_1/\gamma_2} f(\lambda_1, \ldots, \lambda_\ell|\,\underline{d})\,\mathrm{d}\lambda_1 \cdots \mathrm{d}\lambda_\ell \;=\; 1-\alpha \tag{2.20}$$

$$f(\gamma_1 a_i|\,d_i) \;=\; f(b_i/\gamma_2|\,d_i) \tag{2.21}$$

for $i = 1, \ldots, \ell$. Note that we have two parameters and have at least two equations, depending on how we wish to formulate our ordinate optimization criterion in equation (2.21). These two equations may lead to different values of $\{\gamma_1, \gamma_2\}$ when optimized. Therefore, when we must choose, the content (2.20) takes precedence.

2.5.1 Double-γ Method Computations

The goal is to optimize the following equation (2.22) by determining values for γ_1, γ_2 such that $\min_{\gamma_1,\gamma_2} F(\gamma_1, \gamma_2)$ approaches zero. The value of the ordinate optimality criterion S_o^* is determined by the methods described in Section 2.6.

$$\begin{aligned} F(\gamma_1, \gamma_2) \;=\; & \left| \int_{\gamma_1 a_\ell}^{b_\ell/\gamma_2} \cdots \int_{\gamma_1 a_1}^{b_1/\gamma_2} f(\lambda_1, \ldots, \lambda_\ell|\,\underline{d})\,\mathrm{d}\lambda_1 \cdots \mathrm{d}\lambda_\ell - (1-\alpha) \right| \\ & + |S_o^*| \end{aligned} \tag{2.22}$$

2.6 Equal Ordinate condition optimization criterion

Our goal is to construct simultaneous HPD intervals for a large number of small areas. To obtain the precise properties of HPD intervals (see definition 2.1.2) in the simultaneous case, equation (2.9) and set of equations (2.10) need to be solved. As stated earlier (Section 2.3), this requires the solution for more unknowns than we have equations.

To make this situation solvable, we introduce approximations to the exact optimality condition from equations (2.10) which will be computed from a function of the ordinates in (2.21).

A number of ordinate optimization criterion have been considered. For each of these criteria, the object during optimization is to bring the value of the expression to zero.

2.6.1 Maximum Relative Difference Criterion

To calculate the Maximum Relative Difference, evaluate the ordinates for each of the ℓ areas, and take the ratio of the larger average over the lesser average to obtain the larger ratio. This ratio will be one when the ordinates are equal. Subtract one from the ratio and take absolute value as a measure of the difference between these ordinates. Finally, find the maximum value over all ℓ areas. Set this equal to S_1^* and use in equation (2.22), where

$$S_1^* = \max_{i\in\{1,\ldots,\ell\}} \left[\left| \max \left\{ \frac{f(\gamma_1 a_i |\, d_i)}{f(b_i/\gamma_2 |\, d_i)}, \frac{f(b_i/\gamma_2 |\, d_i)}{f(\gamma_1 a_i |\, d_i)} \right\} - 1 \right| \right]. \tag{2.23}$$

2.6.2 Average Relative Difference Criterion

To calculate the Average Relative Difference, evaluate the ordinates for each of the ℓ areas, and take the ratio of the absolute difference of the left and right ordinates

over their sum. This ratio will be zero when the ordinates are equal. Average these over all ℓ areas. Set this equal to S_2^* and use in equation (2.22), where

$$S_2^* = \ell^{-1} \sum_{i=1}^{\ell} \frac{|f(\gamma_1 a_i|\, d_i) - f(b_i/\gamma_2|\, d_i)|}{f(\gamma_1 a_i|\, d_i) + f(b_i/\gamma_2|\, d_i)}. \tag{2.24}$$

This method uses the ratio of the difference to the sum to adjust for possibly large differences in ordinate magnitude between areas. This gives each area equal weight in the optimization.

2.6.3 Average Absolute Difference Criterion

To calculate the Average Absolute Difference, evaluate the ordinates for each of the ℓ areas, and take the absolute difference of the left and right ordinates. This difference will be zero when the ordinates are equal. Average these over all ℓ areas. Set this equal to S_3^* and use in equation (2.22), where

$$S_3^* = \ell^{-1} \sum_{i=1}^{\ell} |f(\gamma_1 a_i|\, d_i) - f(b_i/\gamma_2|\, d_i)|\,. \tag{2.25}$$

This method does not adjust for possibly large differences in ordinate magnitude between areas. A few areas are likely to dominate this optimization.

3. SIMULTANEOUS INTERVALS FOR A HIERARCHICAL POISSON MODEL

3.1 The Poisson-Gamma Hierarchical Regression Model

In this chapter we describe the Poisson-gamma hierarchical Bayesian model and how to fit it using the Metropolis-Hastings sampler.

Let λ_i denote the mortality rate for HSA i, $i = 1, \ldots, \ell$, where $\ell = 798$. The observations consist of the number of deaths d_i and the population size n_i for HSA i, $i = 1, \ldots, \ell$. To link the d_i and the n_i to the mortality rate λ_i, we assume

$$d_i | \, \lambda_i \overset{ind}{\sim} \text{Poisson}(n_i \lambda_i), \qquad i = 1, \ldots, \ell. \tag{3.1}$$

Under this model the maximum likelihood estimator (MLE) of λ_i is $r_i = d_i/n_i$, $i = 1, \ldots, \ell$, the observed mortality rate.

It is standard to estimate the λ_i by "borrowing strength" across the 798 HSAs. Four potential risk factors were selected in [Nandram et al., 2000] for COPD. These risk factors, used as covariates, help to explain the spatial patterns of COPD and its constituent diseases (asthma, chronic bronchitis and emphysema). These are recalled in Table 3.1, and maps are given in Figure 3.1. All the 95% credible intervals do not contain zero, meaning they are all significant [Liu, 2002]. (Population sizes and death counts may also be of interest; these are given in Figure 3.2.)

β_1, the coefficient for white male lung cancer mortality rate is positive. This confirms [Morris and Munasinghe, 1994]; those places where more people smoke tend to have a higher COPD mortality rate.

β_2, the coefficient for population density is negative, this confirms [Nandram et al., 2000]. The possible reason might be, those places with a high population

density usually have better medical services, and when there is an emergency people living in a remote area are more likely to be delayed by the long travel to the nearest hospital.

β_3, the coefficient for elevation is positive. This confirms that extreme climatic conditions aggravate existing asthma and bronchitis [Bates, 1989], as is living at high altitudes because of the reduced oxygen supply [Schoene, 1999].

β_4, the coefficient for the annual rainfall level is negative. As claimed before, repeated exposure to particulate matter and other air pollutants, primarily from traffic exhaust and coal-burning power plants, can aggravate existing lung conditions and can even cause death [English et al., 1999] [Sunyer et al., 2000]. In particular, small airborne particles such as SO_2 found in urban air pollution can be deposited deep in the lungs, causing severe pulmonary effects [Sunyer et al., 2000] [Schwartz and Neas, 2000]. Aerosolized toxins and viruses can be inhaled in dusty environments, causing pulmonary effects [National Center for Health Statistics, 1998]. Rainfall, on the contrary, can lower the density of airborne particles and dust in the air, thus lower the chance of catching a pulmonary disease.

We link these covariates to the mortality rate, λ_i. Thus, letting $\underset{\sim}{x}_i = (1, x_{i,1}, \ldots, x_{i,p-1})'$ denote the vector of $(p-1)$ covariates and an intercept, and fitting the covariates in the regression model (with mortality rate λ_i as the response variable) we assume that

$$\lambda_i |\, \alpha, \underset{\sim}{\beta} \overset{ind}{\sim} \text{Gamma}\Big(\alpha, \alpha e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}\Big), \qquad i = 1, \ldots, \ell. \tag{3.2}$$

Observe that in this model $\log(\text{E}(\lambda_i |\, \alpha, \underset{\sim}{\beta})) = \underset{\sim}{x}_i'\underset{\sim}{\beta}$ and $\sqrt{\alpha}$ is the coefficient of variation of the λ_i. (Throughout, by $T \sim \text{Gamma}(a, b)$ we mean $f_T(t) = b^a t^{a-1} e^{-bt}/\Gamma(a), t \geq 0$.)

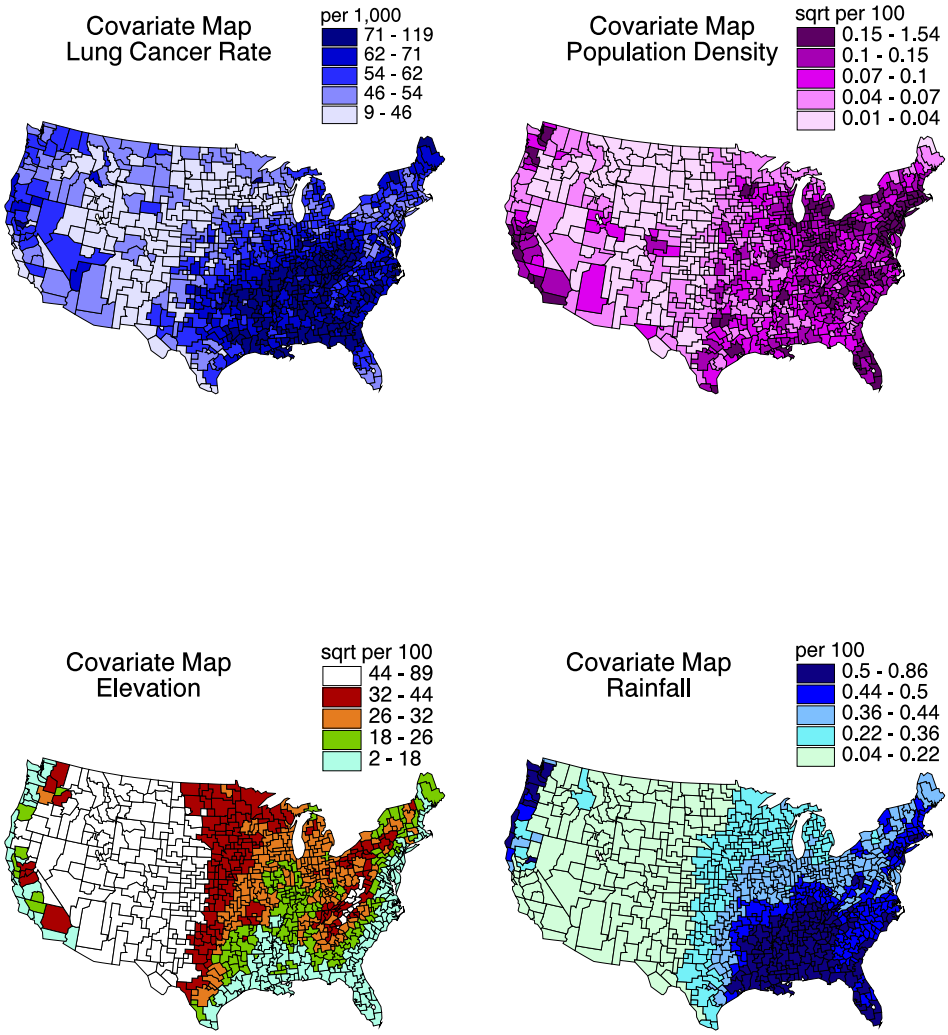


Figure 3.1. Regression Covariate (Risk Factor) Maps.

Table 3.1
Regression Covariates (Risk Factors)

Covariates ($\underset{\sim}{x}$)	Coefficients ($\underset{\sim}{\beta}$)	Risk Factor
x_0 ($\equiv 1$)	β_0	Intercept
x_1	β_1	white male lung cancer rate per 1,000 population
x_2	β_2	square root of (population density/10^4)
x_3	β_3	square root of (elevation/10^4)
x_4	β_4	(annual rainfall/100)

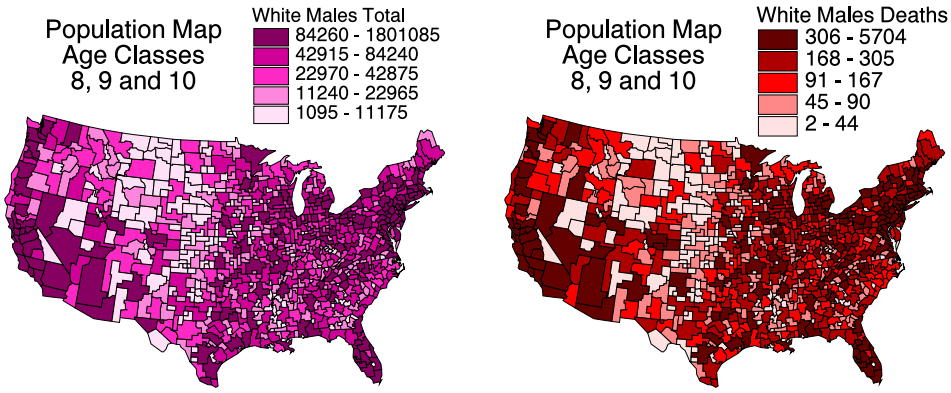


Figure 3.2. Population size and death counts for COPD White Males Age Classes 8, 9 and 10.

Letting $\underset{\sim}{\lambda}$ denote the vector of mortality rates, the joint density for the λ_i, given $\alpha, \underset{\sim}{\beta}$, is

$$\pi(\underset{\sim}{\lambda}|\,\alpha, \underset{\sim}{\beta}) \;=\; \prod_{i=1}^{\ell} \frac{\left(\alpha e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}\right)^{\alpha} \lambda_i^{\alpha-1} \exp\left\{-\left(\alpha e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}\right)\lambda_i\right\}}{\Gamma(\alpha)}. \tag{3.3}$$

(Note that $\underset{\sim}{x}_i'\underset{\sim}{\beta} = \beta_0 + \beta_1 x_1 + \cdots + \beta_{p-1}x_{p-1}$.)

The Poisson-Gamma model is an example of a famous result in Bayesian analysis, namely that the posterior mean is a weighted average of the prior mean and the sample mean. The details for our situation are given in Appendix B.2.

This model is attractive because of the conjugacy in which the conditional posterior density of the λ_i is the simple gamma distribution. This permits us to construct Rao-Blackwellized estimators of the λ_i. Such an estimator has smaller mean square error than its empirical counterpart [Gelfand and Smith, 1990]. This makes it convenient to construct the posterior simultaneous interval maps. In the standard generalized linear model in which the $\log(\lambda_i)$ follow a normal linear model, it is not possible to obtain simple Rao-Blackwellized estimators of the λ_i.

We take the shrinkage prior as the proper prior density for hyper-parameter α,

$$\pi(\alpha) \;=\; \frac{1}{(1+\alpha)^2}, \qquad \alpha \geq 0. \tag{3.4}$$

One might prefer $\pi(\alpha) = \frac{a_0}{(a_0+\alpha)^2}$, $\alpha \geq 0$, where a_0 is the prior median of α, but we have found that inference is nonsensitive to the choice of a_0 (see [Albert, 1988] for the choice of $a_0 = 1$).

We take a multivariate normal density as the proper prior density for hyper-parameters $\underset{\sim}{\beta}$,

$$\underset{\sim}{\beta} \;\sim\; \text{Normal}\Big(\underset{\sim}{\mu_\beta}, \underset{\sim}{\Delta_\beta}\Big) \tag{3.5}$$

where $\underset{\sim}{\mu_\beta}$ and $\underset{\sim}{\Delta_\beta}$ are constants to be specified ($\underset{\sim}{\Delta_\beta}$ includes variance inflation factor, κ_{v}). We show how to specify $\underset{\sim}{\mu_\beta}$ and $\underset{\sim}{\Delta_\beta}$ using a weighted least squares analysis in Appendix B.1.

The model specified by (3.1), (3.2) and (3.4) is described by [Christiansen and Morris, 1997] using a prior density of the form $\pi(\alpha) = \frac{a_0}{(a_0+\alpha)^2}$, but their prior specification for $\underset{\sim}{\beta}$ is noninformative (i.e., a flat prior).

Using Bayes' theorem to expand the joint density function gives the joint posterior distribution of all the parameters given $\underset{\sim}{d}$,

$$\begin{aligned}
p(\underset{\sim}{\lambda}, \alpha, \underset{\sim}{\beta} | \underset{\sim}{d}) &= \frac{p(\underset{\sim}{d} | \underset{\sim}{\lambda}, \alpha, \underset{\sim}{\beta}) p(\underset{\sim}{\lambda}, \alpha, \underset{\sim}{\beta})}{p(\underset{\sim}{d})} \\
&= \frac{p(\underset{\sim}{d} | \underset{\sim}{\lambda}, \alpha, \underset{\sim}{\beta}) p(\underset{\sim}{\lambda} | \alpha, \underset{\sim}{\beta}) p(\alpha, \underset{\sim}{\beta})}{p(\underset{\sim}{d})} \\
&\propto \prod_{i=1}^{\ell} \frac{\lambda_i^{d_i} e^{-n_i \lambda_i}}{d_i!} \\
&\quad \times \prod_{i=1}^{\ell} \frac{\left(\alpha e^{-\underset{\sim}{x}_i' \underset{\sim}{\beta}}\right)^{\alpha} \lambda_i^{\alpha-1} \exp\left\{ -\left(\alpha e^{-\underset{\sim}{x}_i' \underset{\sim}{\beta}}\right) \lambda_i \right\}}{\Gamma(\alpha)} \\
&\quad \times \frac{1}{(1+\alpha)^2} \\
&\quad \times \exp\left\{ -\frac{1}{2} (\underset{\sim}{\beta} - \mu_{\underset{\sim}{\beta}})' \Delta_{\underset{\sim}{\beta}}^{-1} (\underset{\sim}{\beta} - \mu_{\underset{\sim}{\beta}}) \right\}. \qquad (3.6)
\end{aligned}$$

In [Christiansen and Morris, 1997] Poisson regression interactive multilevel modeling (PRIMM) is used to evaluate (3.6). Our method for constructing the simultaneous intervals requires a sampling-based method. So we use the Metropolis-Hastings sampler to fit the model; see [Chib and Greenberg, 1995] for a pedagogical discussion. We used the diagnostics reviewed by [Cowles and Carlin, 1996] to study convergence (i.e., we used the trace plots and autocorrelations) and we used the suggestion of [Gelman et al., 1996] to monitor the jumping probability in each Metropolis step. The jumping probability is obtained by counting the number of times the Markov chain moves from one state to another divided by the number of iterations after convergence; [Gelman et al., 1996] suggested that the jumping probability should be between 0.25 and 0.50.

To run the Metropolis-Hastings sampler, we need the conditional posterior density of the λ_i, α and $\underset{\sim}{\beta}$. The conditional posterior density for the λ_i is in the form of a Gamma distribution.

$$\lambda_i|\,\alpha,\underset{\sim}{\beta},d_i \overset{ind}{\sim} \text{Gamma}\Big(d_i+\alpha, n_i+\alpha e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}\Big) \tag{3.7}$$

$$p(\underset{\sim}{\lambda}|\,\alpha,\underset{\sim}{\beta},\underset{\sim}{d}) \propto \prod_{i=1}^{\ell}\lambda_i^{d_i+\alpha-1}\exp\Big\{-\Big(n_i+\alpha e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}\Big)\lambda_i\Big\} \tag{3.8}$$

The conditional posterior density for α and $\underset{\sim}{\beta}$ is a not so simple result.

$$\begin{aligned} p(\alpha,\underset{\sim}{\beta}|\,\underset{\sim}{\lambda},\underset{\sim}{d}) \propto & \prod_{i=1}^{\ell}\frac{\Big(\alpha e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}\Big)^{\alpha}\lambda_i^{\alpha-1}\exp\Big\{-\Big(\alpha e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}\Big)\lambda_i\Big\}}{\Gamma(\alpha)} \\ & \times\frac{1}{(1+\alpha)^2} \\ & \times\exp\Big\{-\frac{1}{2}(\underset{\sim}{\beta}-\mu_{\underset{\sim}{\beta}})'\Delta_{\underset{\sim}{\beta}}^{-1}(\underset{\sim}{\beta}-\mu_{\underset{\sim}{\beta}})\Big\} \end{aligned} \tag{3.9}$$

3.2 Computation using Markov chain Monte Carlo

With the model defined we proceed using Markov chain Monte Carlo (MCMC) to make inference about the parameters of interest in the model, namely the rate parameter $\underset{\sim}{\lambda}$. (Refer to Section A.3 for general information about Bayesian computational methods.) The particular MCMC method (see Section A.3.5) used here is the Metropolis-Hastings sampler (see Section A.3.6). It works by drawing samples from the conditional distributions. After a large number of iterations, the sample converges to the joint posterior distribution.

3.2.1 Metropolis-Hastings sampler

We draw α and $\underset{\sim}{\beta}$ simultaneously from the joint conditional posterior density (3.9) using a Metropolis step with an independence chain.

For computational reasons we perform the transformation of variable $\tau = \log(\alpha)$, $(\alpha = e^{\tau})$. This modifies the conditional posterior from which to draw samples from equation (3.9) to (3.10). Note the Jacobian is e^{τ}. (The subscripted $\alpha = e^{\tau}$ is a reminder of the tranformation of variable.)

$$\begin{aligned} p(\tau, \underset{\sim}{\beta} | \underset{\sim}{\lambda}, \underset{\sim}{d}) \quad \propto \quad & \prod_{i=1}^{\ell} \left\{ \frac{\left(e^{\tau - \underset{\sim}{x}_i' \underset{\sim}{\beta}}\right)^{e^{\tau}} \lambda_i^{e^{\tau}-1} \exp\left\{ - e^{\tau - \underset{\sim}{x}_i' \underset{\sim}{\beta}} \lambda_i \right\}}{\Gamma(e^{\tau})} \right\} \\ & \times \left\{ \frac{1}{(1+\alpha)^2} \right\}_{\alpha = e^{\tau}} \times |e^{\tau}| \\ & \times \exp\left\{ - \frac{1}{2} (\underset{\sim}{\beta} - \underset{\sim}{\mu_\beta})' \Delta_{\underset{\sim}{\beta}}^{-1} (\underset{\sim}{\beta} - \underset{\sim}{\mu_\beta}) \right\} \end{aligned} \tag{3.10}$$

For the remaining discussion we consider the model in the original units (3.9).

We obtain a proposal density for the conditional posterior density of $(\alpha, \underset{\sim}{\beta})'$ using the normal density in which the mean is taken to be the mode and the variance is the negative inverse Hessian matrix.

Taking the logarithm of the conditional posterior density (3.9), we have

$$\Delta(\alpha, \underset{\sim}{\beta}) \quad \propto \quad \sum_{i=1}^{\ell} \left[(d_i + \alpha) \log\left(n_i + \alpha e^{-\underset{\sim}{x}_i' \underset{\sim}{\beta}} \right) + (d_i + \alpha - 1) \log(\lambda_i) \right.$$

$$-\left(n_i + \alpha e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}\right)\lambda_i - \log(\Gamma(d_i+\alpha))\Big]$$
$$-2\log(1+\alpha) - \frac{1}{2}(\underset{\sim}{\beta} - \underset{\sim}{\mu_\beta})'\Delta_{\underset{\sim}{\beta}}^{-1}(\underset{\sim}{\beta} - \underset{\sim}{\mu_\beta}). \tag{3.11}$$

We obtain the modal values, $(\hat{\alpha}, \hat{\underset{\sim}{\beta}})'$, of $(\alpha, \underset{\sim}{\beta})'$ in (3.11) using the Nelder-Mead Method[1] [Nelder and Mead, 1965]. Thus, the mean of the conditional posterior density of $(\alpha, \underset{\sim}{\beta})'$ is $(\hat{\alpha}, \hat{\underset{\sim}{\beta}})'$. We next construct a surrogate for the variance using the Hessian matrix. The Hessian matrix H is the matrix of second derivatives of the multivariate function in (3.9) of $(\alpha, \underset{\sim}{\beta})'$.

$$H = \begin{pmatrix} \frac{\partial^2\Delta}{\partial\alpha^2} & \frac{\partial^2\Delta}{\partial\alpha\partial\beta_0} & \frac{\partial^2\Delta}{\partial\alpha\partial\beta_1} & \cdots & \frac{\partial^2\Delta}{\partial\alpha\partial\beta_{p-1}} \\ \frac{\partial^2\Delta}{\partial\beta_0\partial\alpha} & \frac{\partial^2\Delta}{\partial\beta_0^2} & \frac{\partial^2\Delta}{\partial\beta_0\partial\beta_1} & \cdots & \frac{\partial^2\Delta}{\partial\beta_0\partial\beta_{p-1}} \\ \frac{\partial^2\Delta}{\partial\beta_1\partial\alpha} & \frac{\partial^2\Delta}{\partial\beta_1\partial\beta_0} & \frac{\partial^2\Delta}{\partial\beta_1^2} & \cdots & \frac{\partial^2\Delta}{\partial\beta_1\partial\beta_{p-1}} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \frac{\partial^2\Delta}{\partial\beta_{p-1}\partial\alpha} & \frac{\partial^2\Delta}{\partial\beta_{p-1}\partial\beta_0} & \frac{\partial^2\Delta}{\partial\beta_{p-1}\partial\beta_1} & \cdots & \frac{\partial^2\Delta}{\partial\beta_{p-1}^2} \end{pmatrix} \tag{3.12}$$

Letting $\psi'(\cdot)$ denote the trigamma function, the second derivative of $\Delta(\alpha, \underset{\sim}{\beta})$ with respect to α is

$$d = \frac{\partial^2\Delta}{\partial\alpha^2} = \sum_{i=1}^{\ell}\left\{\frac{1}{\alpha} - \psi'(\alpha)\right\} + \frac{2}{(1+\alpha)^2}, \tag{3.13}$$

the second derivative, $H_{\underset{\sim}{\beta}}$, with respect to $\underset{\sim}{\beta}$ is

$$H_{\underset{\sim}{\beta}} = -\left(\Delta_{\underset{\sim}{\beta}}^{-1} + \alpha\sum_{i=1}^{\ell}\lambda_i e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}\underset{\sim}{x}_i\underset{\sim}{x}_i'\right) \tag{3.14}$$

and the second derivative with respect to both α and $\underset{\sim}{\beta}$ is

$$\underset{\sim}{c} = -\sum_{i=1}^{\ell}\left(1 - \lambda_i e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}\right)\underset{\sim}{x}_i. \tag{3.15}$$

Then, an approximation for the covariance matrix of $(\alpha, \underset{\sim}{\beta})'$ in the conditional posterior density is

$$\Sigma = \begin{bmatrix} \sigma_\alpha^2 & \underset{\sim}{c}' \\ \underset{\sim}{c} & \Delta_{\underset{\sim}{\beta}} \end{bmatrix} = -\kappa_{\mathrm{t}}\begin{bmatrix} d & \underset{\sim}{c}' \\ \underset{\sim}{c} & H_{\underset{\sim}{\beta}} \end{bmatrix}^{-1}, \tag{3.16}$$

[1] The Nelder-Mead Method is a direct search method of optimization that works moderately well for stochastic problems. It is based on evaluating a function at the vertices of a simplex, then iteratively shrinking the simplex as better points are found until some desired bound is obtained.

where κ_t is a tuning constant selected by trial and error in order to ensure a Metropolis jump probability in equation (3.26) between 0.25 and 0.5 as discussed in Section A.4. We complete the process for the approximation by replacing $(\alpha, \underset{\sim}{\beta})'$ in (3.16) by the modal estimates, $(\hat{\alpha}, \underset{\sim}{\hat{\beta}})'$, to obtain $\hat{\Sigma}$ with components $\hat{\sigma}^2_{\hat{\alpha}}$, $\hat{\underset{\sim}{\nu}}$ and $\hat{\Delta}_{\underset{\sim}{\hat{\beta}}}$. These modal values, $(\hat{\alpha}, \underset{\sim}{\hat{\beta}})'$ are given in (3.17) and (3.18) with covariance matrix (3.19).

$$\hat{\alpha} = 19.98417 \tag{3.17}$$

$$\underset{\sim}{\hat{\beta}} = [-5.558162, 0.112785, -0.041747, 0.056042, -0.056112]' \tag{3.18}$$

$$\hat{\Sigma} = \begin{pmatrix} 0.000777 & -0.000003 & -0.000013 & 0.000001 & -0.000007 & 0.000003 \\ -0.000003 & 0.000078 & -0.000003 & -0.000005 & 0.000002 & 0.000001 \\ -0.000013 & -0.000003 & 0.000158 & 0.000023 & 0.000019 & -0.000094 \\ 0.000001 & -0.000005 & 0.000023 & 0.000078 & 0.000038 & -0.000007 \\ -0.000007 & 0.000002 & 0.000019 & 0.000038 & 0.000177 & 0.000101 \\ 0.000003 & 0.000001 & -0.000094 & -0.000007 & 0.000101 & 0.000213 \end{pmatrix} \tag{3.19}$$

Finally, the multivariate proposal density is obtained by taking

$$\alpha|\, \underset{\sim}{\beta} \sim \text{Gamma}(a, b) \tag{3.20}$$

$$\underset{\sim}{\beta} \sim \text{Normal}(\underset{\sim}{\hat{\beta}}, \hat{\Delta}_{\underset{\sim}{\hat{\beta}}}) \tag{3.21}$$

with

$$a = \frac{\tilde{\mu}^2}{\tilde{\sigma}^2} \qquad \text{and} \qquad b = \frac{\tilde{\mu}}{\tilde{\sigma}^2} \tag{3.22}$$

where

$$\tilde{\mu} = \hat{\sigma} + \hat{\underset{\sim}{\nu}}' \hat{\Delta}^{-1}_{\underset{\sim}{\hat{\beta}}} (\underset{\sim}{\beta} - \underset{\sim}{\hat{\beta}}) \qquad \text{and} \qquad \tilde{\sigma}^2 = \hat{\sigma}^2_{\hat{\alpha}} - \hat{\underset{\sim}{\nu}}' \hat{\Delta}^{-1}_{\underset{\sim}{\hat{\beta}}} \hat{\underset{\sim}{\nu}}. \tag{3.23}$$

We obtain a proposal density for the Metropolis step by approximating $p(\alpha, \underset{\sim}{\beta}|\, \underset{\sim}{\lambda}, \underset{\sim}{d})$ in (3.9) by $p_a(\alpha, \underset{\sim}{\beta}|\, \underset{\sim}{\lambda}, \underset{\sim}{d})$ in (3.24). To aid in drawing this vector we note that equation (3.9) can be distilled into the component parts shown in equation (3.24).

$$p_a(\alpha, \underset{\sim}{\beta}|\, \underset{\sim}{\lambda}, \underset{\sim}{d}) = p_a(\alpha|\, \underset{\sim}{\lambda}, \underset{\sim}{\beta}, \underset{\sim}{d}) \times p_a(\underset{\sim}{\beta}|\, \underset{\sim}{\lambda}, \underset{\sim}{d}) \tag{3.24}$$

When we have a distribution we wish to generate, it may be easier, or save computation time, if we break it into pieces. This is called the composition method [Tanner, 1993]. For example, to draw (x, y) from $f(x, y) = f(x|\, y)f(y)$, the composition method draws y first from $f(y)$, and then with this y, x is drawn from $f(x|\, y)$. The first distribution $p_{\mathrm{a}}(\alpha|\, \underset{\sim}{\lambda}, \underset{\sim}{\beta}, \underset{\sim}{d})$ is Gamma while the second distribution $p_{\mathrm{a}}(\underset{\sim}{\beta}|\, \underset{\sim}{\lambda}, \underset{\sim}{d})$ is Multivariate Normal given by realizations of (3.20) and (3.21).

First, a vector of $\underset{\sim}{\beta}$ deviates is drawn from the Multivariate Normal distribution in equation (3.21). Next, a deviate of α is drawn from the Gamma distribution in equation (3.20).

The Metropolis acception/rejection criterion is described in Section A.3.6. The Metropolis ratio is defined as $\psi(\alpha, \underset{\sim}{\beta})$ in equation (3.25) which is the ratio of equation (3.9) by equation (3.24). The probability of accepting the current proposal density j and transitioning from the previous density i, or the jumping probability, is given by equation (3.26).

$$\psi(\alpha, \underset{\sim}{\beta}) = \frac{p(\alpha, \underset{\sim}{\beta}|\, \underset{\sim}{\lambda}, \underset{\sim}{d})}{p_{\mathrm{a}}(\alpha, \underset{\sim}{\beta}|\, \underset{\sim}{\lambda}, \underset{\sim}{d})} \tag{3.25}$$

$$\alpha_j^i = \min\left\{\frac{\psi(\alpha^{(j)}, \underset{\sim}{\beta}^{(j)})}{\psi(\alpha^{(i)}, \underset{\sim}{\beta}^{(i)})}, 1\right\} \tag{3.26}$$

3.2.2 Sampling

To compute our maps, we first need a random sample from the joint posterior density of $\Omega = (\alpha, \underset{\sim}{\beta})$. We obtain a random sample $\Omega^{(h)}$, $h = 1, \ldots, M$ $(M = 10000)$, from the Metropolis-Hastings sampler. We ran the Metropolis-Hastings sampler for 101000 interations, using the first 1000 iterations as a "burn-in". Then, we picked every tenth interation from the remaining 100000 to make the autocorrelations among the iterates negligible. A further check on the jumping rate of the Metropolis-Hastings sampler shows the jumping probability is around 0.40 for all our activities. Also, all the autocorrelations and numerical standard errors are small. Tuning of

the Metropolis step is obtained by varying the parameter κ_{t} in equation (3.16). We found that $\kappa_{\mathrm{t}} = 1.3333$ worked well.

3.2.3 Sampling Assessment

An assessment of the autocorrelations of the α and $\underset{\sim}{\beta}$ parameters show no significant correlation between iterations. This indicates they are from a random process.

Numerical standard error (NSE), or Monte Carlo error, using the batch means method indicated high repeatibility because of the small standard error. As an illustration of the batch means method, consider the NSE for the iterations of α. Frist, average groups of iterates of a reasonable size (this paper uses groups of size 25 for 10,000 iterates), then take a grand average of the group averages.

$$\begin{aligned}
\bar{x}_1 &= \frac{1}{25}\sum_{i=1}^{25}\alpha^{(i)} \\
\bar{x}_2 &= \frac{1}{25}\sum_{i=26}^{50}\alpha^{(i)} \\
&\vdots \\
\bar{x}_{400} &= \frac{1}{25}\sum_{i=9976}^{10000}\alpha^{(i)} \\
\bar{\bar{x}} &= \frac{1}{400}\sum_{j=1}^{400}\bar{x}_j \\
\mathrm{NSE} &= \sqrt{\sum_{i=1}^{400}(\bar{x}_i - \bar{\bar{x}})^2/399}
\end{aligned}$$

Also the acceptance rate in the Metropolis step was approximately 0.40, well within the recommended range of 0.25 to 0.5.

We have specified the values of $\mu_{\underset{\sim}{\beta}}$ and $\Delta_{\underset{\sim}{\beta}}$ in our analysis, and therefore a sensitivity analysis is relevant which has been studied through the variance inflation factor κ_{v} by [Liu, 2002]. For various large values of κ_{v} [Liu, 2002] computed the averages of the posterior mean and posterior standard deviation for the ℓ mortality rates. For six values of κ_{v} from 10 to 100000, there were virtually no changes, indicating that our method is robust to misspecification of these parameters and we can use almost

noninformative priors (see [Christiansen and Morris, 1997]) for a condition about propriety of the posterior density, which is automatic in our model. In our empirical work we set $\kappa_{\mathrm{v}} = 100000$, which is almost a noninformative prior.

[Liu, 2002] also considered a measure, based on standardized cross-validation residuals, to assess the fit of the model. Diagnositics described in [Nandram et al., 1999] indicated the Poisson-gamma regression model provides a good fit to the COPD mortality data for white males 65+.

Additionally, Table 3.2 gives the quantile values and 95% equal-tailed credible interval from the 10,000 iterates of the α and $\underset{\sim}{\beta}$ parameters, and Table 3.3 gives the means, standard deviations and confidence intervals for the mean.

Table 3.2
Quantile values from 10,000 iterates of the α and β_0 through β_4 model parameters.

Parameter	Min	2.5%	Q_1	Q_2 (Med)	Q_3	97.5%	Max
α	18.8431	19.4798	19.7405	20.2008	21.1155	36.7517	74.2015
β_0	-5.59958	-5.58038	-5.56819	-5.56290	-5.55684	-5.54356	-5.52273
β_1	0.04480	0.08612	0.11136	0.12193	0.12961	0.14590	0.17974
β_2	-0.08694	-0.06414	-0.05004	-0.04346	-0.03782	-0.02547	-0.00242
β_3	0.00597	0.03446	0.05974	0.06774	0.07380	0.09504	0.13300
β_4	-0.14360	-0.08792	-0.06798	-0.06144	-0.05161	-0.02537	0.02253

Table 3.3
Sample summary for model parameters α and β_0 through β_4 from 10,000 iterates.

Parameter	Mean	Std. Dev.	95% Confidence Interval
α	21.4771396	4.3199729	(21.3924595, 21.5618198)
β_0	-5.5624099	0.0090993	(-5.5625883, -5.5622315)
β_1	0.1197570	0.0147994	(0.1194669, 0.1200471)
β_2	-0.0439811	0.0096623	(-0.0441705, -0.0437917)
β_3	0.0666663	0.0138813	(0.0663942, 0.0669384)
β_4	-0.0594216	0.0150388	(-0.0597164, -0.0591268)

3.3 Construction of the posterior interval maps

Our objective in this section is to show how to construct the maps of the posterior mean and intervals described in Chapter 2 from the model described in Sections 3.1 and 3.2.

Note that the posterior density of $\underset{\sim}{\lambda}$ is

$$p(\underset{\sim}{\lambda}|\,\underline{d}) \;=\; \int_{\Omega} p(\underset{\sim}{\lambda}|\,\underline{d},\Omega)\pi(\Omega|\,\underline{d})\,\mathrm{d}\Omega \tag{3.27}$$

where $\Omega = (\alpha, \underset{\sim}{\beta})$ and the conditional posterior density of $p(\underset{\sim}{\lambda}|\,\underline{d},\Omega)$ is given by equations (3.7) and (3.8). Equation (3.27) shows how we average over nuisance parameters Ω to obtain the conditional posterior density of the parameter of interest $\underset{\sim}{\lambda}$, given the observed data.

Here, Ω is a small $p{+}1$ dimensional vector, while $\underset{\sim}{\lambda}$ is the large $\ell = 798$ dimensional vector. As described in Section 3.2.1 we have a random sample $\underset{\sim}{\lambda}^{(1)}, \ldots, \underset{\sim}{\lambda}^{(M)}$ from $p(\underset{\sim}{\lambda}|\,\underline{d})$.

To determine the bounds of our intervals, we need to find two points $(a_i, b_i)_{\lambda_i}$ that return the correct probability content, and satisfy a possible optimality criterion. Note that it is impossible to obtain this result directly from $p(\underset{\sim}{\lambda}|\,\underline{d})$ because we need to integrate over the posterior density of Ω, $\pi(\Omega|\,\underline{d})$, which does not exist in closed form. Therefore, we can not use standard analytical techniques such as calculus, but use a numerical technique.

Below we first show how to construct the mean map, then resume discussing interval maps.

3.3.1 Constructing the Mean Map

We construct the posterior mean map using Rao-Blackwellized estimators for the λ_i. As in Section 3.1, letting $r_i = d_i/n_i$, $i = 1, \ldots, \ell$, denote the observed mortality rate and letting $\Lambda_i = n_i/(n_i + \alpha e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}})$, from (3.7) the expectation of the conditional posterior mean of λ_i is

$$\mathrm{E}(\lambda_i |\, \alpha, \underset{\sim}{\beta}, d_i) \;=\; \Lambda_i r_i + (1 - \Lambda_i) e^{\underset{\sim}{x}_i'\underset{\sim}{\beta}}. \tag{3.28}$$

As expected, this is a weighted average of the observed mortality rate and the prior mortality rate (see Appendix B.2). It follows that the posterior mean (unconditional) of λ_i is

$$\begin{aligned} \mu_i &= \mathrm{E}(\lambda_i |\, \underset{\sim}{d}) \\ &= \mathrm{E}_{\Omega |\, \underset{\sim}{d}_i} \left\{ \Lambda_i r_i + (1 - \Lambda_i) e^{\underset{\sim}{x}_i'\underset{\sim}{\beta}} \right\}. \end{aligned} \tag{3.29}$$

Note that because of the conditioning (posterior) on the data, μ_i is a function of the data. The Rao-Blackwellized estimator of μ_i is

$$\hat{\mu}_i \;=\; M^{-1} \sum_{h=1}^{M} \left\{ \Lambda_i^{(h)} r_i + (1 - \Lambda_i^{(h)}) e^{\underset{\sim}{x}_i'\underset{\sim}{\beta}^{(h)}} \right\} \tag{3.30}$$

where $\Lambda_i^{(h)} = n_i/(n_i + \alpha^{(h)} e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}^{(h)}})$ and $\Omega^{(h)} = (\alpha^{(h)}, \underset{\sim}{\beta}^{(h)})$, $h = 1, \ldots, M$, are the M iterates obtained from the Metropolis-Hastings sampler. Therefore, the iterates of λ_i are $\lambda_i^{(h)} = \Lambda_i^{(h)} r_i + (1 - \Lambda_i^{(h)}) e^{\underset{\sim}{x}_i'\underset{\sim}{\beta}^{(h)}}$. The posterior mean map is obtained by mapping the $\hat{\mu}_i$ in (3.30) for all $\ell = 798$ HSAs. See Section 4.1.1 for the resulting map from this process.

3.3.2 Constructing the Credible Interval Map

The method for constructing the posterior credible interval map follows automatically from the output of the Metropolis-Hastings sampler already described. First, perform a sort on each set $\lambda_i^{(1)}, \ldots, \lambda_i^{(M)}$, $i = 1, \ldots, \ell$, giving $\lambda_i^{(1^*)}, \ldots, \lambda_i^{(M^*)}$. Next, choose from these the $\frac{\alpha}{2}$ and $1 - \frac{\alpha}{2}$ quantiles (see Section 2.1.1); for $\alpha = 0.05$ and $M = 10000$, we choose the 2.5 and 97.5 quantiles, or $\lambda_i^{(250^*)}$ and $\lambda_i^{(9751^*)}$. Thus the problem simply reduces to sorting and extracting the desired quantiles for each HSA. See Section 4.1.2 for the resulting map from this process.

3.3.3 Constructing the HPD Interval Map

The method for constructing the posterior HPD interval Map is computationally intensive, but it follows easily from the output of the Metropolis-Hastings sampler already described. Our procedure calculates ordinates $p(\lambda_i|\, d_i)$ at each of the points $\lambda_i^{(1)}, \ldots, \lambda_i^{(M)}$, $i = 1, \ldots, \ell$. Therefore, we need to find lower and upper bounds a_i and b_i, on the support of λ_i, such that both conditions in equations (3.31), content, and (3.32), equal ordinates, are satisified (see Section 2.1.2).

$$\int_{a_i}^{b_i} p(\lambda_i|\, d_i)\, \mathrm{d}\lambda_i = 1 - \alpha \tag{3.31}$$

$$p(a_i|\, d_i) = p(b_i|\, d_i) \tag{3.32}$$

Using the output of the Metropolis-Hastings sampler, we approximate the content in equation (3.31) by

$$\begin{aligned} 1 - \alpha &= \int_\Omega \int_{a_i}^{b_i} p(\lambda_i|\, d_i, \Omega)\pi(\Omega|\, d_i)\, \mathrm{d}\lambda_i\, \mathrm{d}\Omega \\ &= \int_\Omega \left\{F(b_i|\, d_i, \Omega) - F(a_i|\, d_i, \Omega)\right\} \pi(\Omega|\, d_i)\, \mathrm{d}\Omega \\ &\approx M^{-1} \sum_{h=1}^{M} \left\{F(b_i|\, d_i, \Omega^{(h)}) - F(a_i|\, d_i, \Omega^{(h)})\right\} \end{aligned} \tag{3.33}$$

where $F(\cdot)$ is the cdf and we approximate the ordinates in equation (3.32) for a_i by

$$\begin{aligned} p(a_i|\, d_i, \Omega) &= \int_\Omega p(a_i|\, d_i, \Omega)\pi(\Omega|\, d_i)\, \mathrm{d}\Omega \\ &\approx M^{-1} \sum_{h=1}^{M} p(a_i|\, d_i, \Omega^{(h)}) \end{aligned} \tag{3.34}$$

and for b_i by

$$\begin{aligned} p(b_i|\, d_i, \Omega) &= \int_\Omega p(b_i|\, d_i, \Omega)\pi(\Omega|\, d_i)\, \mathrm{d}\Omega \\ &\approx M^{-1} \sum_{h=1}^{M} p(b_i|\, d_i, \Omega^{(h)}). \end{aligned} \tag{3.35}$$

For the simultaneous solution to both these non-linear equations we use the Nelder-Mead Method to minimize a function composed from (3.33), (3.34) and (3.35). We use the results from the credible interval in Section 3.3.2 as starts for a_i and b_i

in the minimization routine. Function $f(a_i, b_i)$ in equation (3.36) is minimized over parameters a_i and b_i. The minimum value of the fuction $f(a_i, b_i)$ occurs at the same point where $f(a_i, b_i) = 0$ (i.e., each term in equation (3.36) is 0).

$$\begin{aligned} f(a_i, b_i) &= \left| M^{-1} \sum_{h=1}^{M} \left\{ F(b_i |\, d_i, \Omega^{(h)}) - F(a_i |\, d_i, \Omega^{(h)}) \right\} - (1 - \alpha) \right| \\ &\quad + \left| M^{-1} \sum_{h=1}^{M} p(a_i |\, d_i, \Omega^{(h)}) - M^{-1} \sum_{h=1}^{M} p(b_i |\, d_i, \Omega^{(h)}) \right| \end{aligned} \tag{3.36}$$

3.3.4 Constructing the Simultaneous Interval Map

The method for constructing the posterior simultaneous interval map is computationally intensive, but it follows easily from the output of the HPD Interval routine. As described in Sections 2.4 and 2.5 we use parameter γ as a "stretching" factor on the HPD intervals (a_i, b_i), $i = 1, \ldots, \ell$, to produce the desired simultaneous probability content. For the Single-γ Method, $0 < \gamma < 1$ is used to obtain the content; for the Double-γ Method, $0 < \gamma_1 < 1$ and $0 < \gamma_2 < 1$ are used to obtain the content and satisfy an equal ordinates optimality criterion.

3.3.5 Single-γ Method

We need to find the value of γ in the lower and upper bounds γa_i and b_i/γ such that the probability content in equation (3.37) is satisified. Using the output of the Metropolis-Hastings sampler, we approximate the integral in equation (3.37) by (3.39).

$$\begin{aligned} 1-\alpha &= \int_\Omega \int_{\gamma a_\ell}^{b_\ell/\gamma} \cdots \int_{\gamma a_1}^{b_1/\gamma} \\ &\qquad p(\lambda_1|\, d_1, \Omega) \cdots p(\lambda_\ell|\, d_\ell, \Omega) \pi(\Omega|\, \underline{d}) \\ &\qquad \mathrm{d}\lambda_1 \cdots \mathrm{d}\lambda_\ell \, \mathrm{d}\Omega \qquad (3.37) \\ &= \int_\Omega \prod_{i=1}^{\ell} \left\{ F(b_i/\gamma|\, d_i, \Omega) - F(\gamma a_i|\, d_i, \Omega) \right\} \pi(\Omega|\, d_i) \, \mathrm{d}\Omega \qquad (3.38) \\ &\approx M^{-1} \sum_{h=1}^{M} \left[\prod_{i=1}^{\ell} \left\{ F(b_i/\gamma|\, d_i, \Omega^{(h)}) - F(\gamma a_i|\, d_i, \Omega^{(h)}) \right\} \right]. \qquad (3.39) \end{aligned}$$

For the solution to this non-linear equation we use the Nelder-Mead Method to minimize a function composed from (3.39). Function $f(\gamma)$ in equation (3.40) is minimized over parameter γ. The minimum value of this function is clearly zero.

$$f(\gamma) = \left| M^{-1} \sum_{h=1}^{M} \left[\prod_{i=1}^{\ell} \left\{ F(b_i/\gamma|\, d_i, \Omega^{(h)}) - F(\gamma a_i|\, d_i, \Omega^{(h)}) \right\} \right] - (1-\alpha) \right| \qquad (3.40)$$

3.3.6 Double-γ Method

We need to find the values of γ_1 and γ_2 in the lower and upper bounds $\gamma_1 a_i$ and b_i/γ_2 such that both conditions of content, in equation (3.41), and equal ordinates, S_o^* (see Section 2.6), are satisified. Using the output of the Metropolis-Hastings sampler, we approximate the integral in equation (3.41) by (3.43).

$$\begin{aligned} 1-\alpha &= \int_\Omega \int_{\gamma_1 a_\ell}^{b_\ell/\gamma_2} \cdots \int_{\gamma_1 a_1}^{b_1/\gamma_2} \\ &\qquad p(\lambda_1|\, d_1, \Omega) \cdots p(\lambda_\ell|\, d_\ell, \Omega) \pi(\Omega|\, \underset{\sim}{d}) \\ &\qquad \mathrm{d}\lambda_1 \cdots \mathrm{d}\lambda_\ell \, \mathrm{d}\Omega \qquad (3.41) \\ &= \int_\Omega \prod_{i=1}^{\ell} \left\{ F(b_i/\gamma_2|\, d_i, \Omega) - F(\gamma_1 a_i|\, d_i, \Omega) \right\} \pi(\Omega|\, d_i)\, \mathrm{d}\Omega \qquad (3.42) \\ &\approx M^{-1} \sum_{h=1}^{M} \left[\prod_{i=1}^{\ell} \left\{ F(b_i/\gamma_2|\, d_i, \Omega^{(h)}) - F(\gamma_1 a_i|\, d_i, \Omega^{(h)}) \right\} \right]. \qquad (3.43) \end{aligned}$$

For the solution to this non-linear equation we use the Nelder-Mead Method to minimize a function composed from (3.43) and optimality criterion S_o^*. Function $f(\gamma_1, \gamma_2)$ in equation (3.44) is minimized over parameters γ_1 and γ_2. The minimum value of this function is clearly zero.

$$\begin{aligned} f(\gamma_1, \gamma_2) &= \left| M^{-1} \sum_{h=1}^{M} \left[\prod_{i=1}^{\ell} \left\{ F(b_i/\gamma_2|\, d_i, \Omega^{(h)}) - F(\gamma_1 a_i|\, d_i, \Omega^{(h)}) \right\} \right] - (1-\alpha) \right| \\ &\quad + |S_o^*| \qquad (3.44) \end{aligned}$$

3.3.7 Equal Ordinate condition optimization criterion

The computational aspects of those methods described in Section 2.6 are provided below. Because these are calculated numerically, they are dependent upon M samples from a MCMC simulation.

3.3.8 Maximum Relative Difference Criterion

To calculate the Maximum Relative Difference, evaluate the ordinates over the M iterates for each of the ℓ areas. Individually average the left and right ordinates

for each area and take the ratio of the larger average over the lesser average to obtain the larger ratio. This ratio will be one when the ordinates are equal. Subtract one from the ratio and take absolute value as a measure of the difference between these ordinates. Finally, find the maximum value over all ℓ areas. Set this equal to S_1^* and use in equation (3.44), where

$$S_1^* = \max_{i\in\{1,\ldots,\ell\}} \left[\left| \max \left\{ \frac{M^{-1}\sum_{h=1}^{M} p(\gamma_1 a_i |\, d_i, \Omega^{(h)})}{M^{-1}\sum_{h=1}^{M} p(b_i/\gamma_2 |\, d_i, \Omega^{(h)})}, \frac{M^{-1}\sum_{h=1}^{M} p(b_i/\gamma_2 |\, d_i, \Omega^{(h)})}{M^{-1}\sum_{h=1}^{M} p(\gamma_1 a_i |\, d_i, \Omega^{(h)})} \right\} - 1 \right| \right]. \quad (3.45)$$

3.3.9 Average Relative Difference Criterion

To calculate the Average Relative Difference, evaluate the ordinates for each of the ℓ areas over the M iterates. Take the ratio of the absolute difference of the left and right ordinates over their sum. This ratio will be zero when the ordinates are equal. Average these over all ℓ areas. Finally, average over the M iterates. Set this equal to S_2^* and use in equation (3.44), where

$$S_2^* = \left\{ \ell^{-1} \sum_{i=1}^{\ell} \frac{\left| M^{-1}\sum_{h=1}^{M} p(\gamma_1 a_i |\, d_i, \Omega^{(h)}) - M^{-1}\sum_{h=1}^{M} p(b_i/\gamma_2 |\, d_i, \Omega^{(h)}) \right|}{M^{-1}\sum_{h=1}^{M} p(\gamma_1 a_i |\, d_i, \Omega^{(h)}) + M^{-1}\sum_{h=1}^{M} p(b_i/\gamma_2 |\, d_i, \Omega^{(h)})} \right\}. \quad (3.46)$$

This method uses the ratio of the difference to the sum to adjust for possibly large differences in ordinate magnitude between areas. This gives each area equal weight in the optimization.

3.3.10 Average Absolute Difference Criterion

To calculate the Average Absolute Difference, evaluate the ordinates for each of the ℓ areas over the M iterates. Take the absolute difference of the left and right ordinates. This difference will be zero when the ordinates are equal. Average these

over all ℓ areas. Finally, average over the M iterates. Set this equal to S_3^* and use in equation (3.44), where

$$S_3^* = \left\{ \ell^{-1} \sum_{i=1}^{\ell} \left| M^{-1} \sum_{h=1}^{M} p(\gamma_1 a_i |\, d_i, \Omega^{(h)}) - M^{-1} \sum_{h=1}^{M} p(b_i/\gamma_2 |\, d_i, \Omega^{(h)}) \right| \right\}. \quad (3.47)$$

This method does not adjust for possibly large differences in ordinate magnitude between areas. A few areas are likely to dominate this optimization.

4. MAPS AND ASSESSMENT

The following are the results from the individual and simultaneous interval methods discussed in previous chapters. A variety of methods are used to present the results. We present two types of choropleth map: interval maps and difference maps. Two types of interval maps are used. The first are *mean legend* maps, where the interval maps use the common legend of the mean map. The second are *individual legend* maps, where the interval maps use their own legend. These interval maps are given for credible intervals (CI), highest posterior density intervals (HPD), and simultaneous intervals. Simultaneous interval maps are given for regions considered together (all) and seperately (regions 1 through 12). To accompany each of these interval maps, difference maps are given in an attempt to capture the variation observed between the lower and upper interval maps in terms of legend color difference. Difference tables are provided as a further summary.

We first present the mean map, which is the map of the parameter estimates. The mean map is then banded by a set of interval maps, an upper and a lower. The first set of interval maps are mean legend maps: CI, HPD and simultaneous intervals. Values for γ are given for the Single-γ Method and the simultaneous probability content of the CI, HPD, Single-γ Method, and Besag intervals. The Single-γ Method is the only method providing the correct probability content. Mean legend difference maps and tables are then presented to help summarize the variation observed.

The second set of interval maps are individual legend maps: CI, HPD and simultaneous intervals. Individual legend difference maps and tables are then presented to help summarize the variation observed.

Finally, values for γ_1, γ_2 are given for the Double-γ Method. In our case, the Single-γ Method and Double-γ Method provide indistinguishable results, so no maps are given for the Double-γ Method. Instead, tables to compare values for γ from

the Single-γ Method and γ_1 and γ_2 from the Double-γ Method are given. Also, to compare the sensitivity of the simultaneous intervals on the prerequisite of HPD intervals, we obtain the simultaneous intervals based on the credible intervals.

4.1 Mean Legend Choropleth Maps

The maps in this section are visualizations of the rate parameter, λ, for mortality of White Males age classes 8, 9 and 10 (65 years and older) for each HSA given by the fitted model in Section 3.1.

In the production and presentation of these maps several standards are adhered to. All maps are colored with the same five-color monochromatic color scheme with light representing a low rate and dark representing a high rate, allowing for gray-scale transition (for non-color printing). The cutpoints of the legend colors are based on the quintiles of the Mean map. All intervals maps are 95% intervals. In the interval maps the map representing the upper bound is the upper map, and the map representing the lower bound is the lower map. The mean map is always presented between the upper and lower maps as a basis of reference. The legend bounds are adjusted to reflect the maximum upper bound and minimum lower bound, but the cutpoints remain the same for comparison. In the simultaneous interval maps by region, only the region of interest is displayed in the upper and lower maps and they differ only in the legend bounds. All the legend bounds are the maximum of all the maximum bounds and the minimum of all the minimum bounds. These similar legends saved hours of legend editing, and the individual bounds can be referenced in Table 4.2.

To illustrate how one might use the interval maps presented, select an HSA from the mean map. Find the corresponding HSA on both the upper and lower maps. The variation of the particular HSA selected based on the quintiles of the mean map can be interpreted from the colors and number of color differences from the lower to the upper map. An HSA that changes one color or not at all can be said to have

little variation, except in the extreme colors, while an HSA that changes four colors can be said to have great variation.

4.1.1 Mean Map

The plot in Figure 4.1 gives the mean map. These means are computed from the model but also correspond with the observed rates.

Mean map minimum, maximum and quintile cutpoints are presented together with the minimum of the lower and maximum of the upper maps for the credible interval (Section 4.1.2) and HPD intervals maps (Section 4.1.3) in Table 4.1. Notice that the HPD extremes are less than the CI extremes.

Table 4.1
Mean map minimum, maximum and quintiles and CI and HPD map minimum lower and maximum upper values

Map	min	Q1	Q2	Q3	Q4	max
Mean	0.001922	0.003279	0.003691	0.004034	0.004409	0.007268
CI	0.001806					0.009326
HPD	0.001788					0.009204

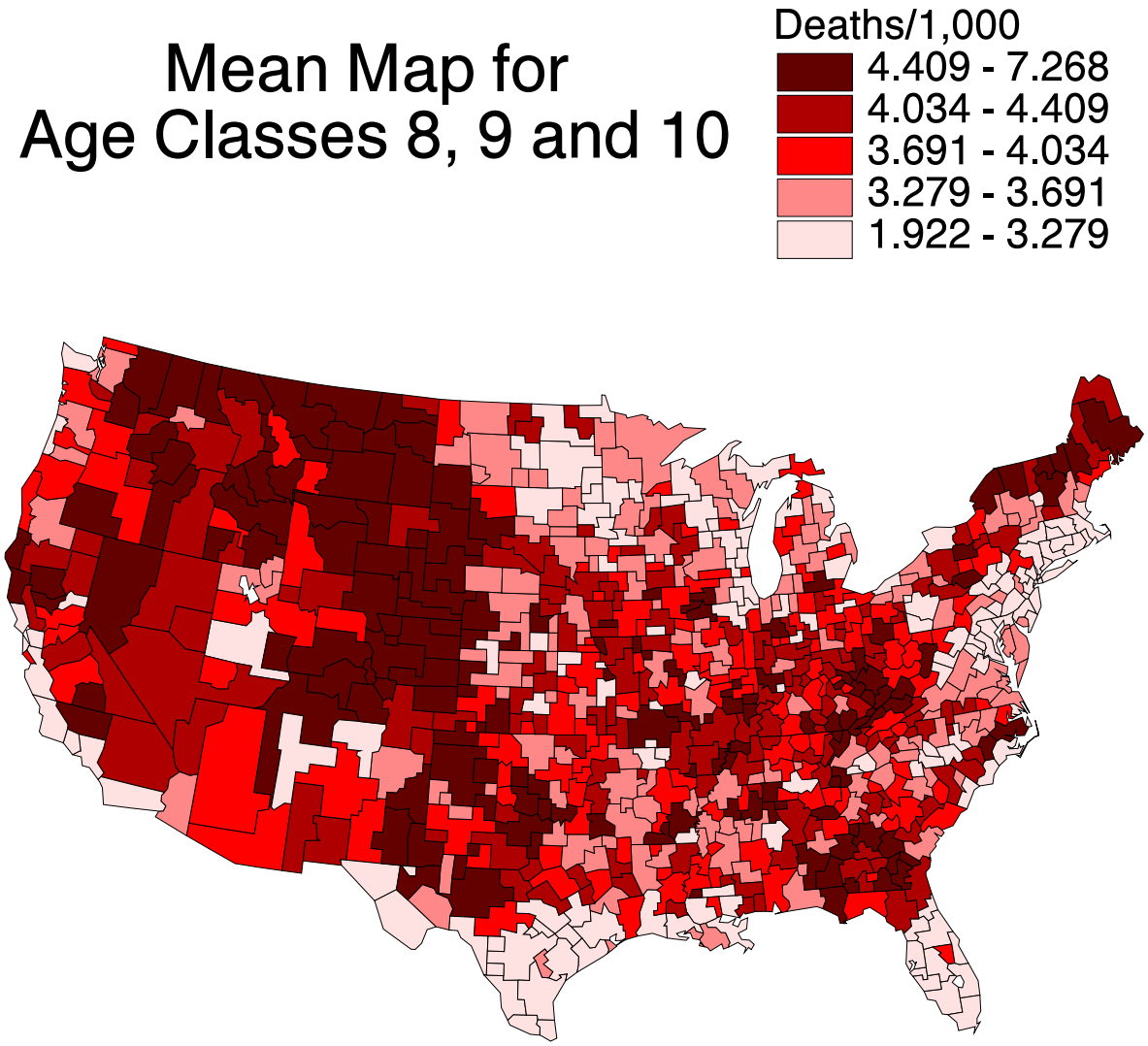


Figure 4.1. Mean Map.

4.1.2 Individual HSA Credible Interval Map

The plot in Figure 4.2 gives the individual HSA credible interval map. The upper and lower maps are based on the equal tail credible intervals described in Section 2.1.1.

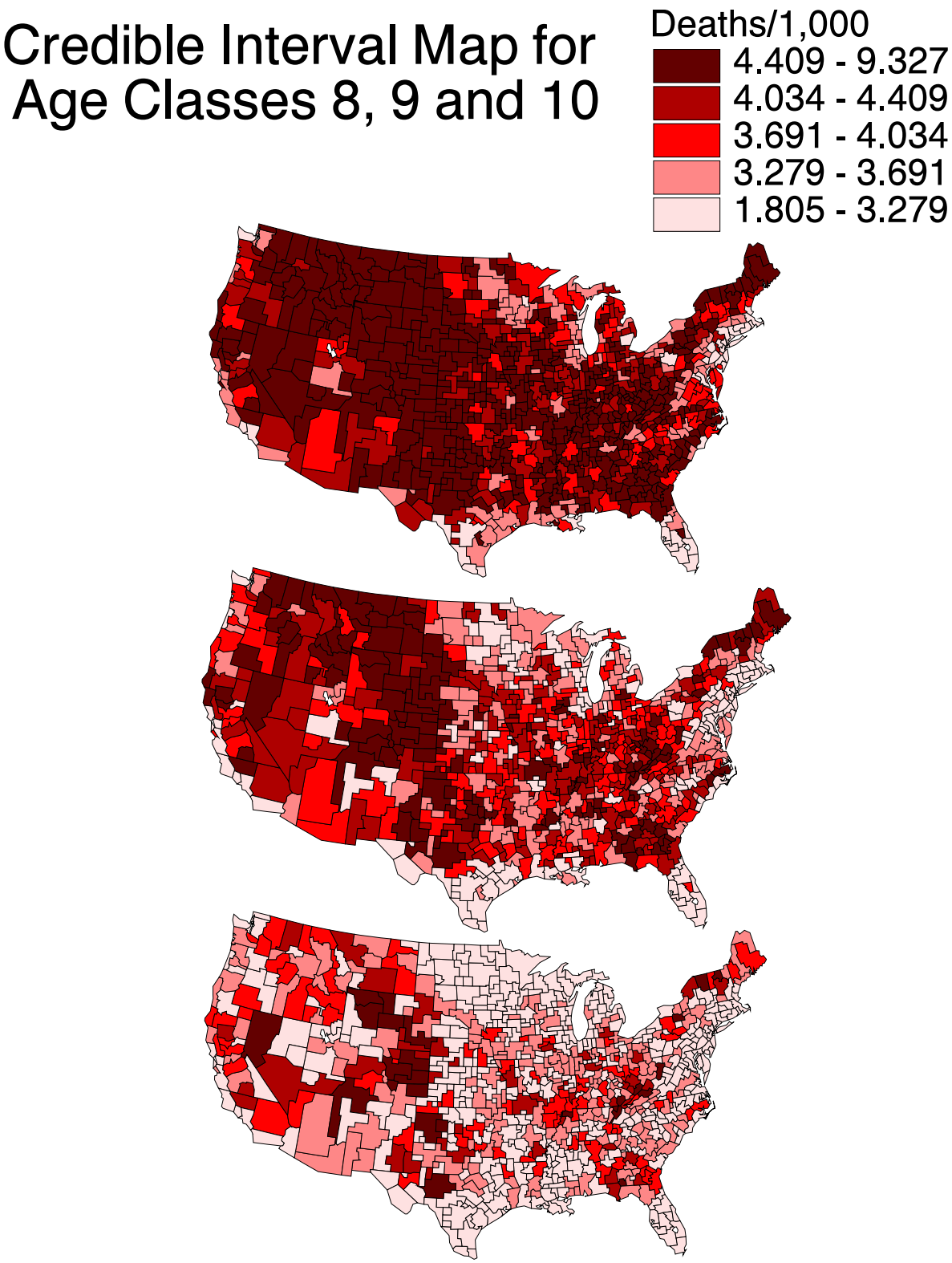


Figure 4.2. Mean Legend Individual HSA Credible Interval Map.

4.1.3 Individual HSA HPD Interval Map

The plot in Figure 4.3 gives the individual HSA HPD interval map. The upper and lower maps are based on the HPD intervals described in Section 2.1.2.

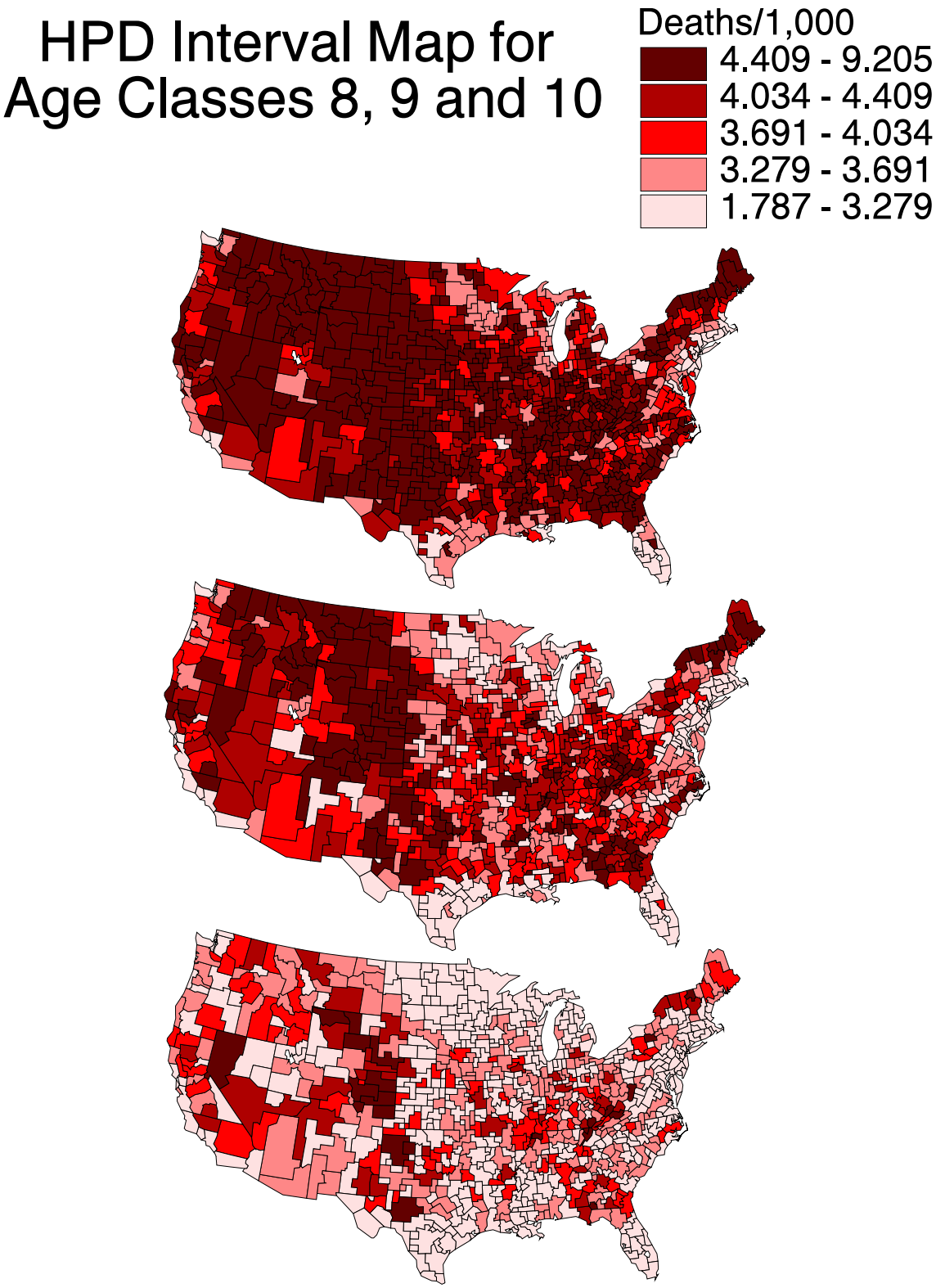


Figure 4.3. Mean Legend Individual HSA HPD Interval Map.

4.1.4 Single-γ Method Simultaneous Interval Map

The plot in Figure 4.4 gives the Single-γ Method simultaneous interval map. The upper and lower maps are based on the Single-γ Method intervals described in Section 2.4.

The value of γ for the various simultaneous maps in Sections 4.1.4 and 4.1.5 are given in Table 4.2. The value for γ is obtained by optimizing equation (2.17). Column headers are Region and the corresponding region number, the number of HSAs in the region (ℓ), the optimum value for γ, and the map legend bounds as the minimum of the lower map and the maximum of the upper map for the HSA rates in the region. As expected, the value for γ is the smallest for when all regions are considered with the general trend that it is larger when fewer HSAs are considered simultaneously.

The simultaneous probability content is given in Table 4.3 (by taking the product of the individual contents, or, for computational reasons, by exponentiating the sum of the logs). The intervals are the Credible Interval (CI) from Section 3.3.2, Highest Posterior Density Interval (HPD) from Section 3.3.3, Single-γ Method simultaneous interval (SINT) from Section 3.3.4 each using 10000 iterates, and the NonParametric Interval described by [Besag et al., 1995] from Appendix B.3 using 10000 iterates (BESAG10) and 25000 iterates (BESAG25). The BESAG intervals are evaluated against the Poisson-Gamma Hierarchical Regression Model for comparison. Obvious details to note are the approximately zero simultaneous content for the CI and HPD intervals for All regions, and the less than 0.15 simultaneous content for each region. The Single-γ Method (SINT) is the only method that consistently obtains the 95% simultaneous coverage for all cases. BESAG10 underestimates and BESAG25 overestimates for All regions showing sensitivity to needing a large number of iterates; 10000 was too few for the correct content and 25000 shows the conservativity of the method. For individual regions, BESAG25 is comparable to SINT.

Table 4.2

Single-γ Method values for γ.

Region		ℓ	γ	min(Lower)	max(Upper)
All	All	798	0.7711593	0.001379	0.011935
New England	1	23	0.9356322	0.002206	0.006979
Middle Atlantic	2	49	0.9192618	0.001713	0.006132
S. Atlantic-North	3	38	0.9109113	0.001852	0.007940
S. Atlantic-South	4	88	0.8659650	0.001568	0.008893
E. S. Central	5	88	0.8959517	0.002458	0.008035
E. N. Central	6	121	0.8849109	0.002182	0.006640
W. N. Central-North	7	45	0.8949770	0.002249	0.006502
W. N. Central-South	8	105	0.8395072	0.001970	0.007899
W. S. Central	9	115	0.8682747	0.001715	0.007171
Mountain-South	10	40	0.8657598	0.001768	0.009689
Mountain-North	11	38	0.8992667	0.003469	0.006927
Pacific	12	48	0.9094602	0.002098	0.005930

Table 4.3

Simultaneous Probability Content by Region for different methods.

Region	ℓ	CI	HPD	SINT	BESAG10	BESAG25
All	798	$\approx 10^{-18}$	$\approx 10^{-18}$	0.9500000559	0.8775405884	0.9867491722
1	23	0.3005571365	0.3073555529	0.9499999767	0.9450204968	0.9489023685
2	49	0.0811103284	0.0809937790	0.9500000607	0.9357133508	0.9422778487
3	38	0.1401147693	0.1423923075	0.9499999308	0.9497816563	0.9472977519
4	88	0.0109376954	0.0109569216	0.9500000762	0.9513514042	0.9564304948
5	88	0.0109985834	0.0109567912	0.9499999677	0.9328913093	0.9498614669
6	121	0.0019661339	0.0020162773	0.9500000947	0.9269511700	0.9537326694
7	45	0.0987905562	0.0994571149	0.9499999487	0.9302505851	0.9332543612
8	105	0.0045152325	0.0045811655	0.9499999014	0.9362568855	0.9520460367
9	115	0.0027406779	0.0027430130	0.9500000387	0.9310526848	0.9593409300
10	40	0.1266464740	0.1285093576	0.9500000617	0.9450564981	0.9487276673
11	38	0.1449352354	0.1424171031	0.9499999458	0.9326382875	0.9342766404
12	48	0.0858865231	0.0852592215	0.9500000411	0.9434457421	0.9476035237

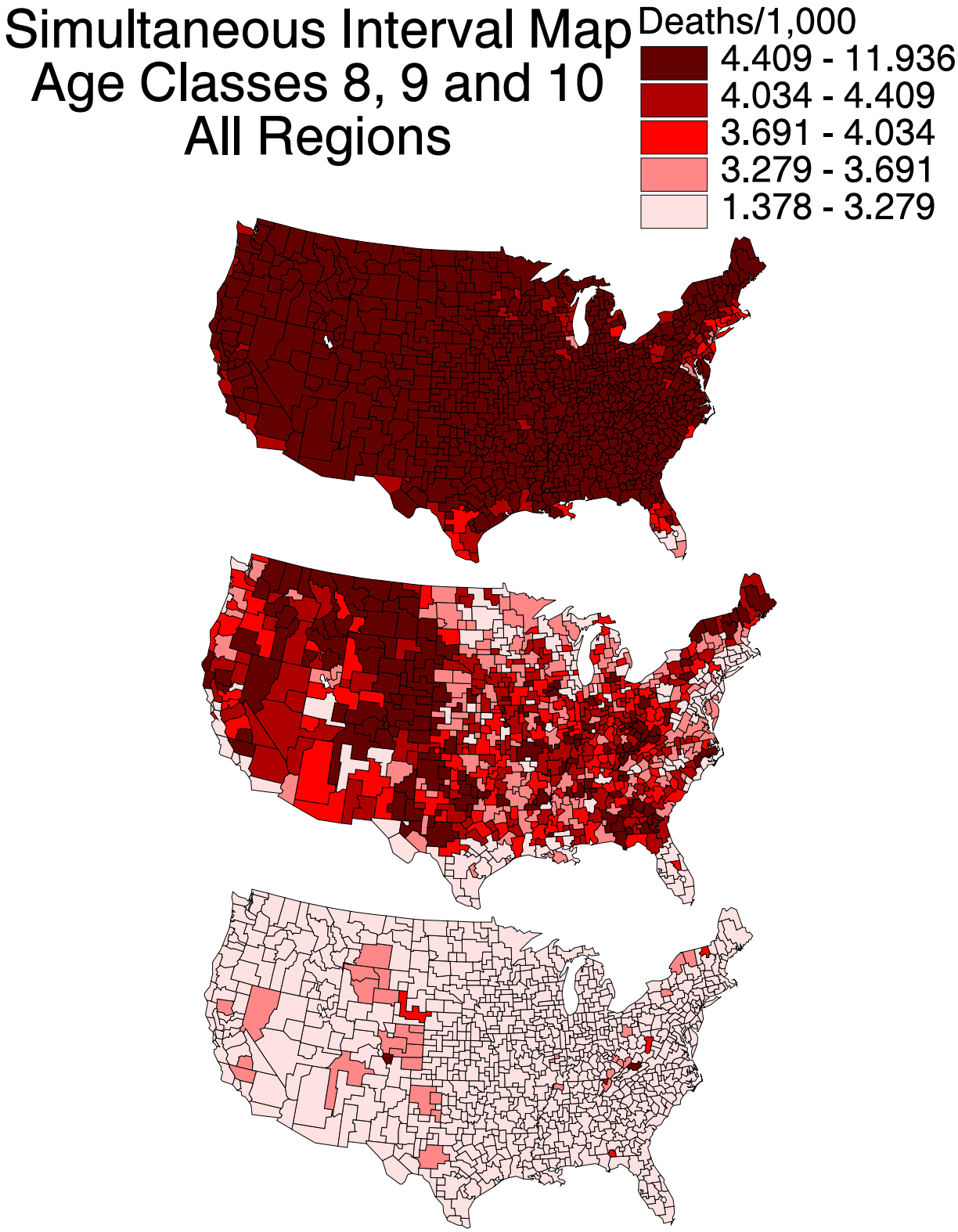


Figure 4.4. Mean Legend Single-γ Method Simultaneous Interval Map.

4.1.5 Single-γ Method Simultaneous Interval by Region Maps

The plots in Figures 4.5 through 4.16 gives the Single-γ Method simultaneous interval by region maps.

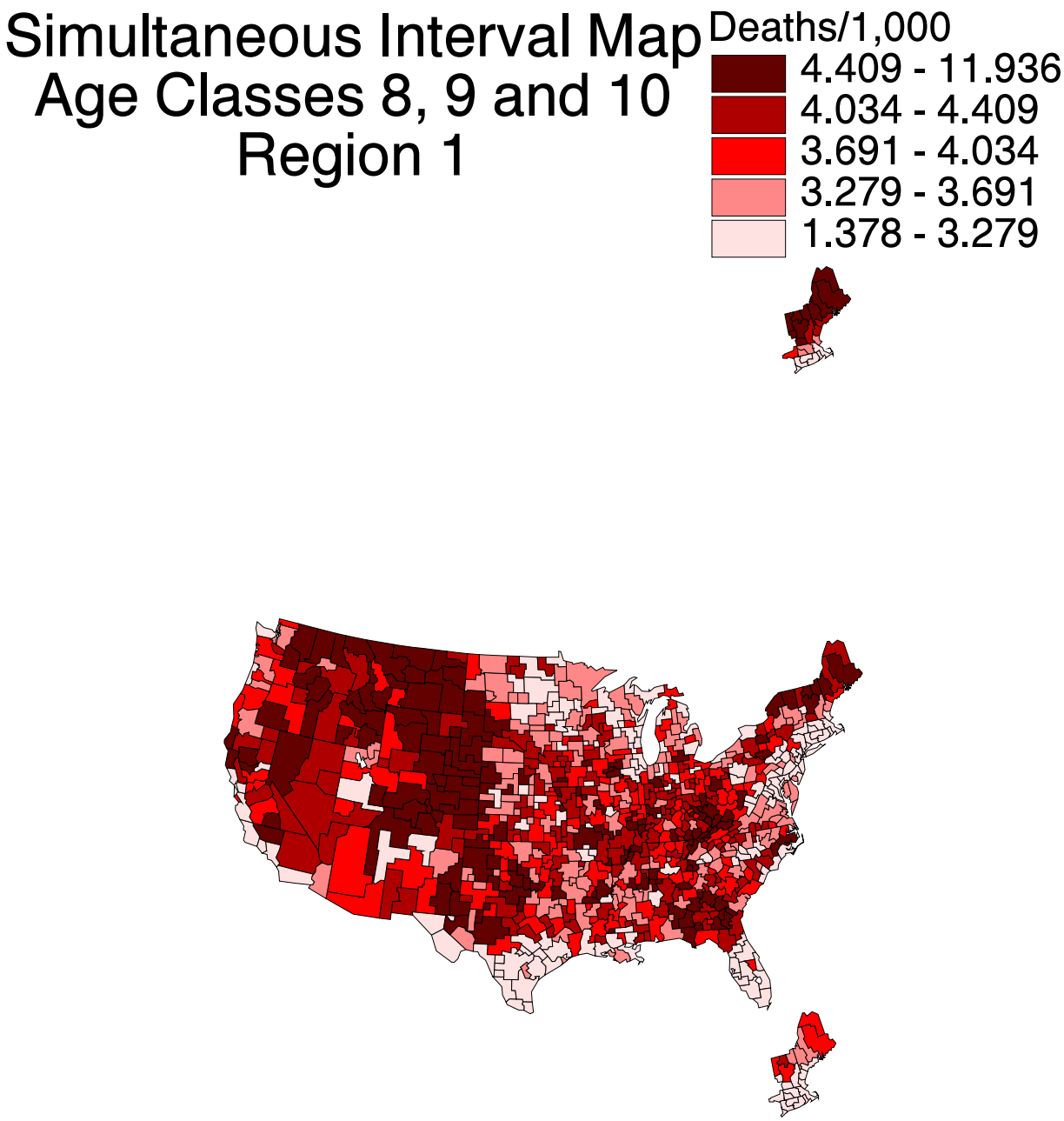


Figure 4.5. Mean Legend Single-γ Method Simultaneous Interval Map – Region 1.

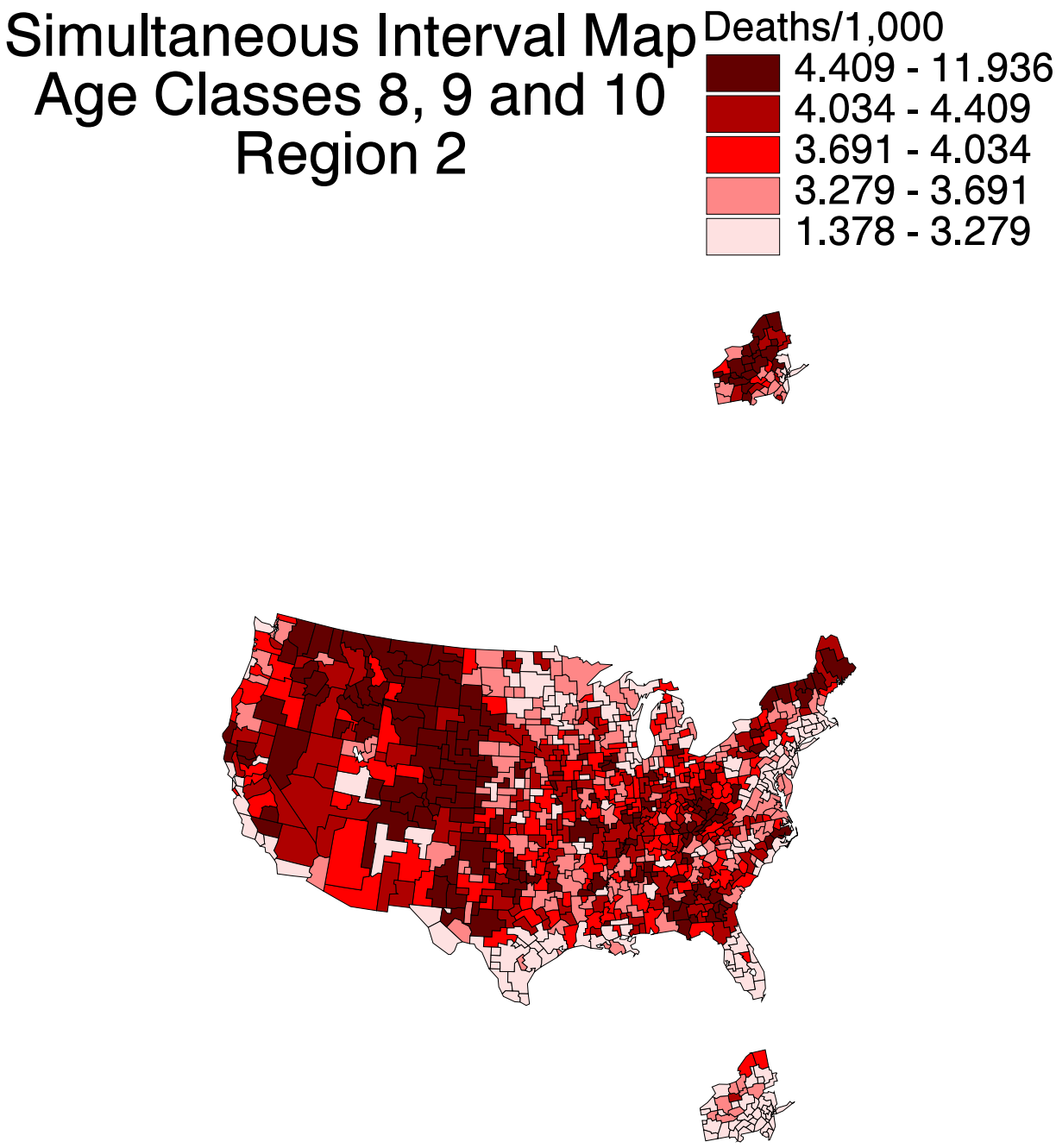


Figure 4.6. Mean Legend Single-γ Method Simultaneous Interval Map – Region 2.

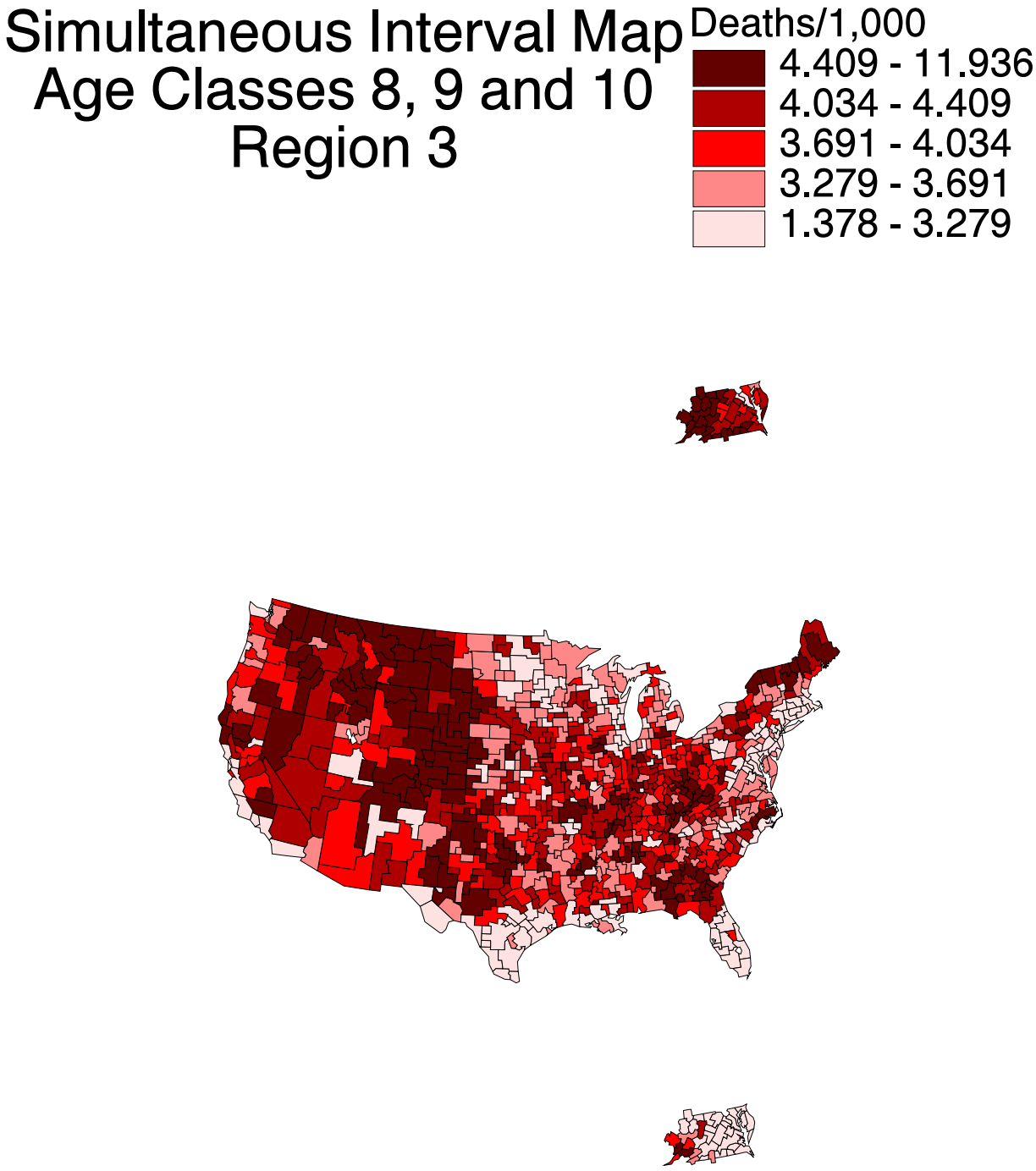


Figure 4.7. Mean Legend Single-γ Method Simultaneous Interval Map – Region 3.

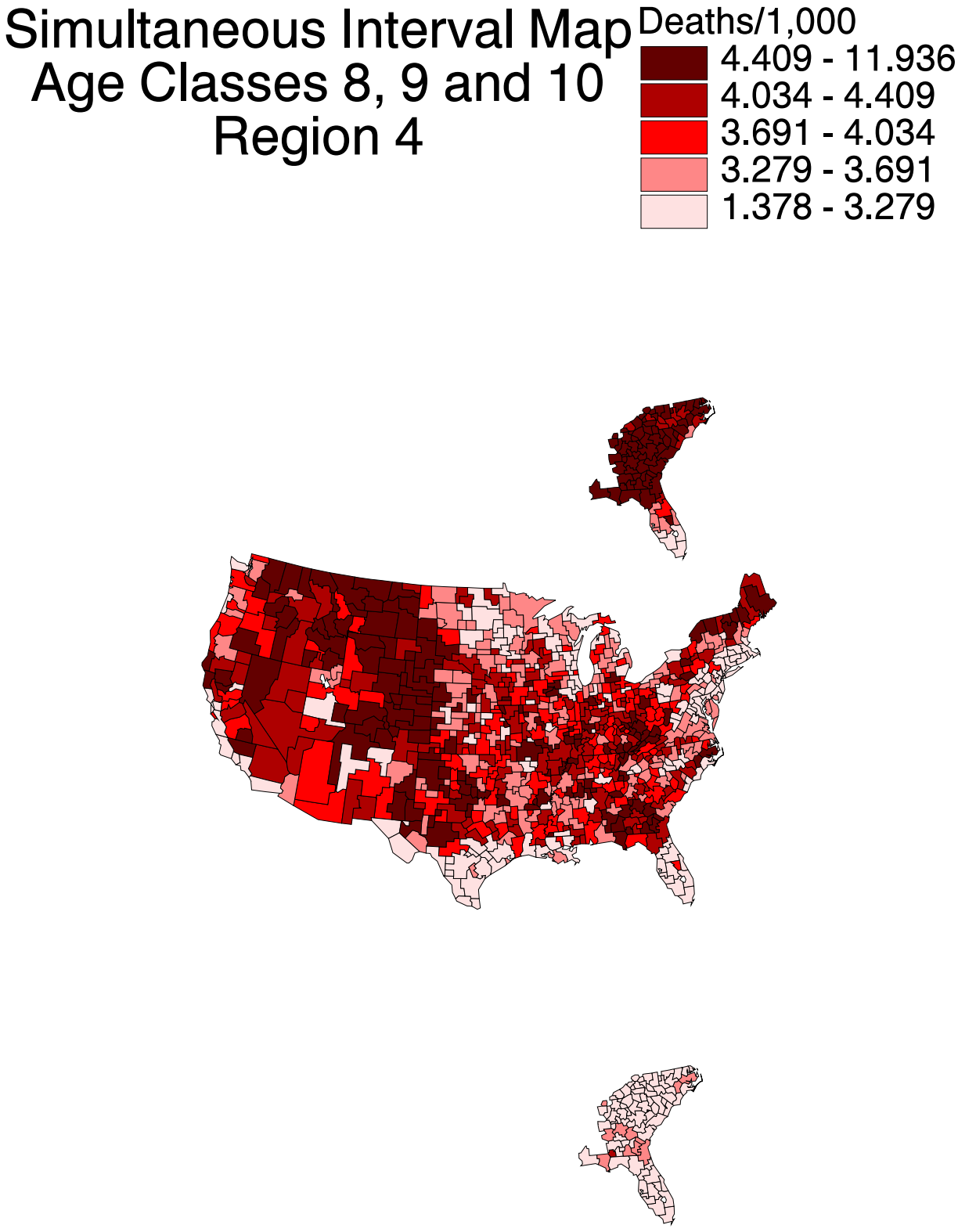


Figure 4.8. Mean Legend Single-γ Method Simultaneous Interval Map – Region 4.

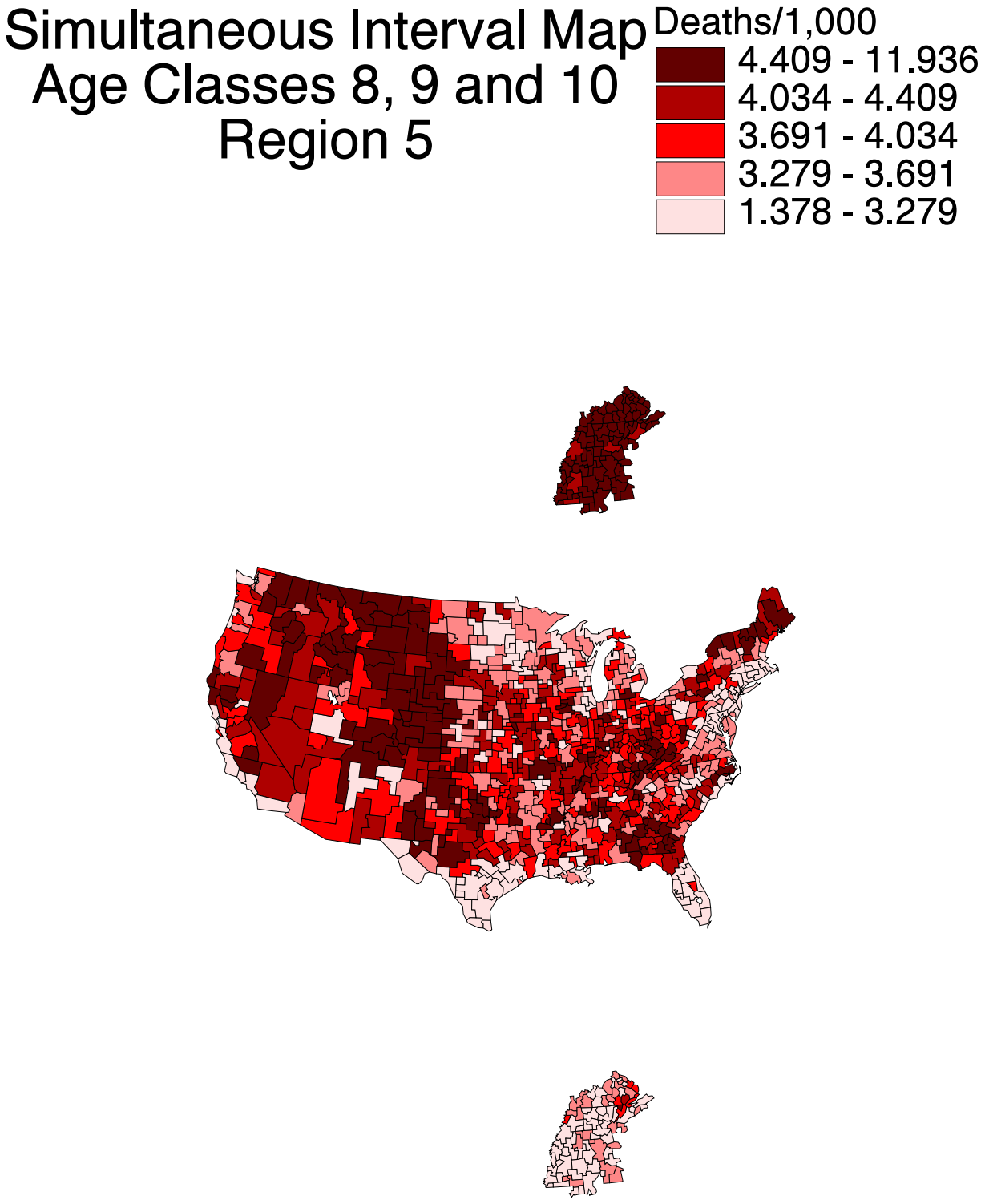


Figure 4.9. Mean Legend Single-γ Method Simultaneous Interval Map – Region 5.

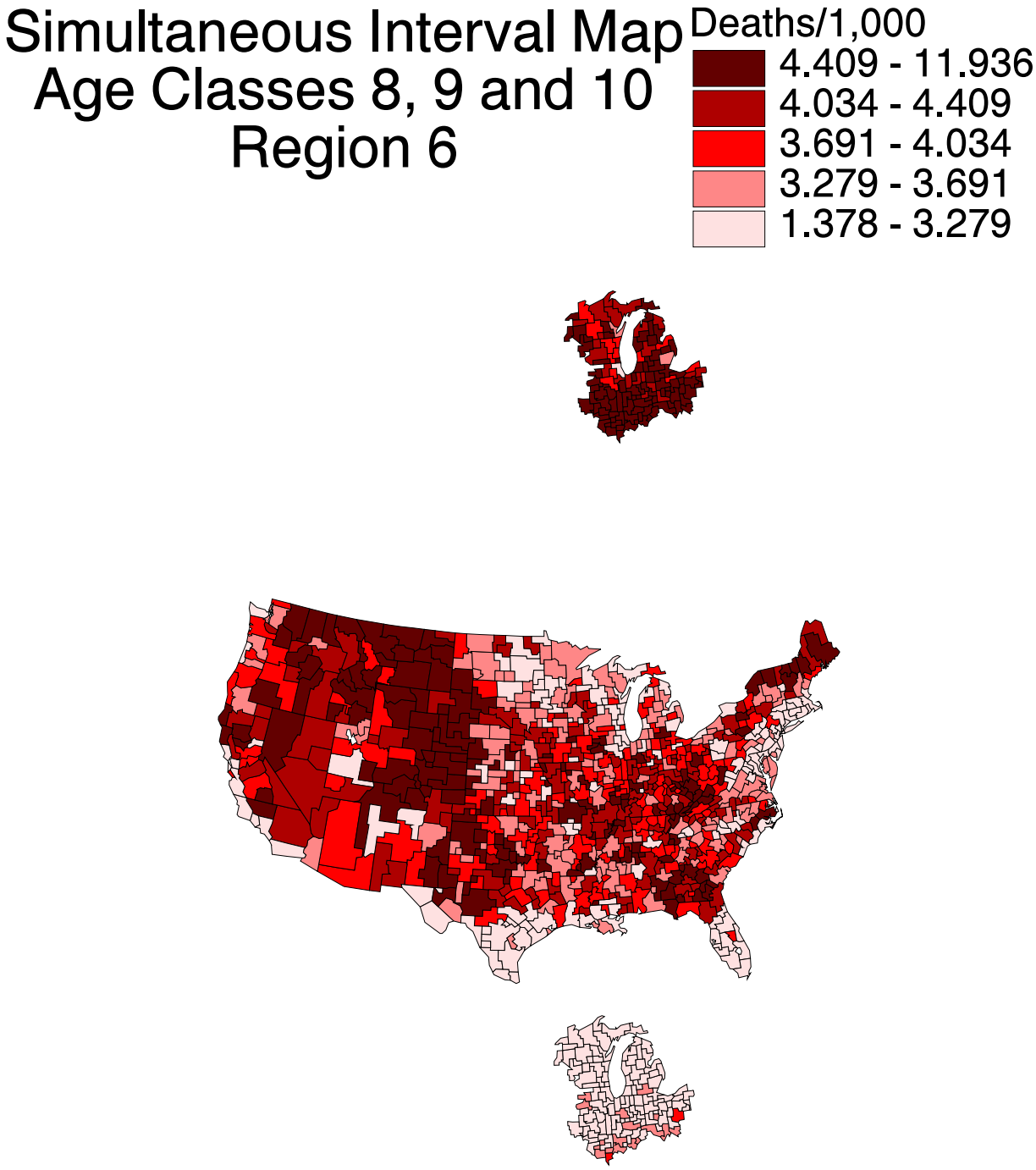


Figure 4.10. Mean Legend Single-γ Method Simultaneous Interval Map – Region 6.

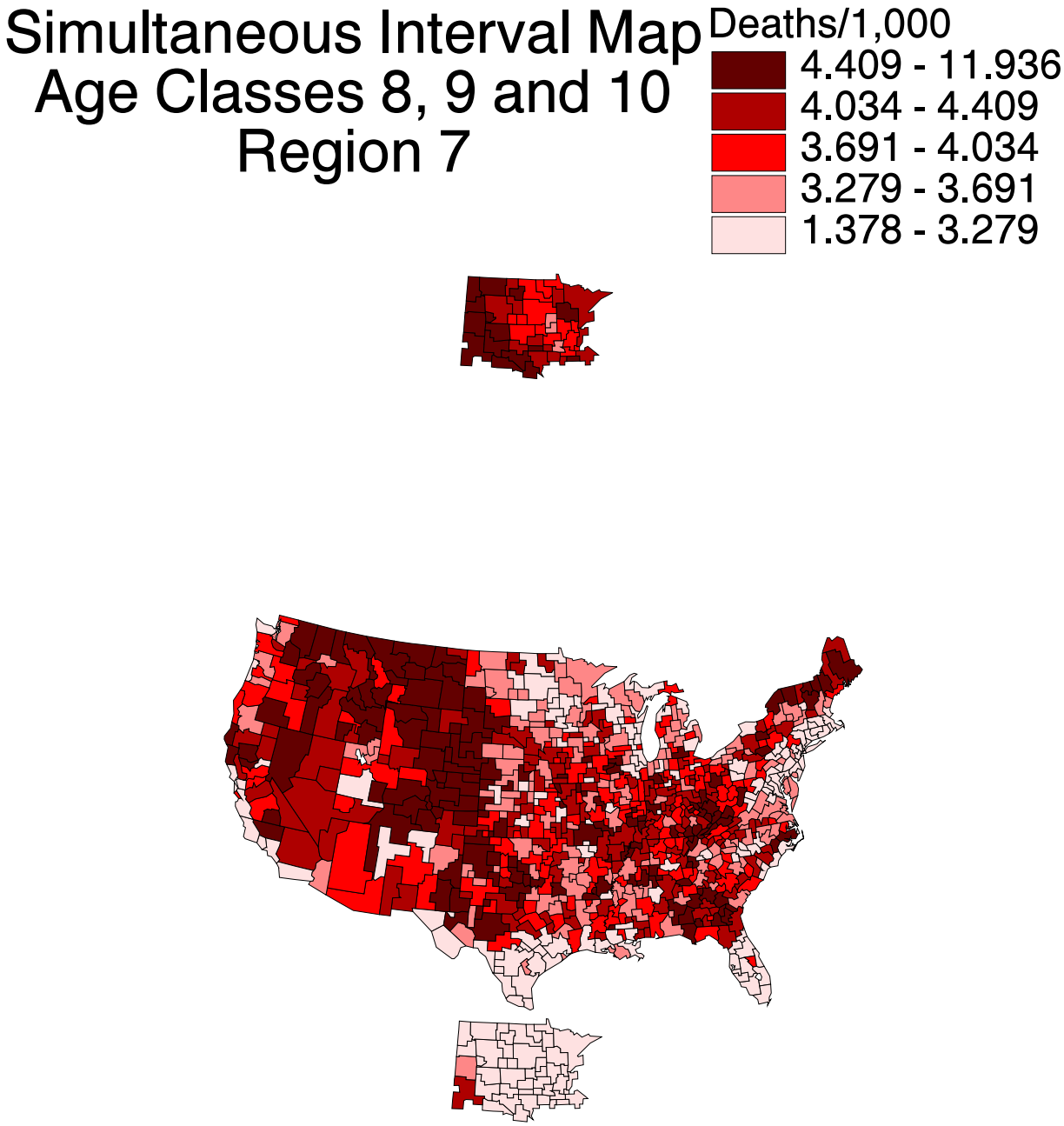


Figure 4.11. Mean Legend Single-γ Method Simultaneous Interval Map – Region 7.

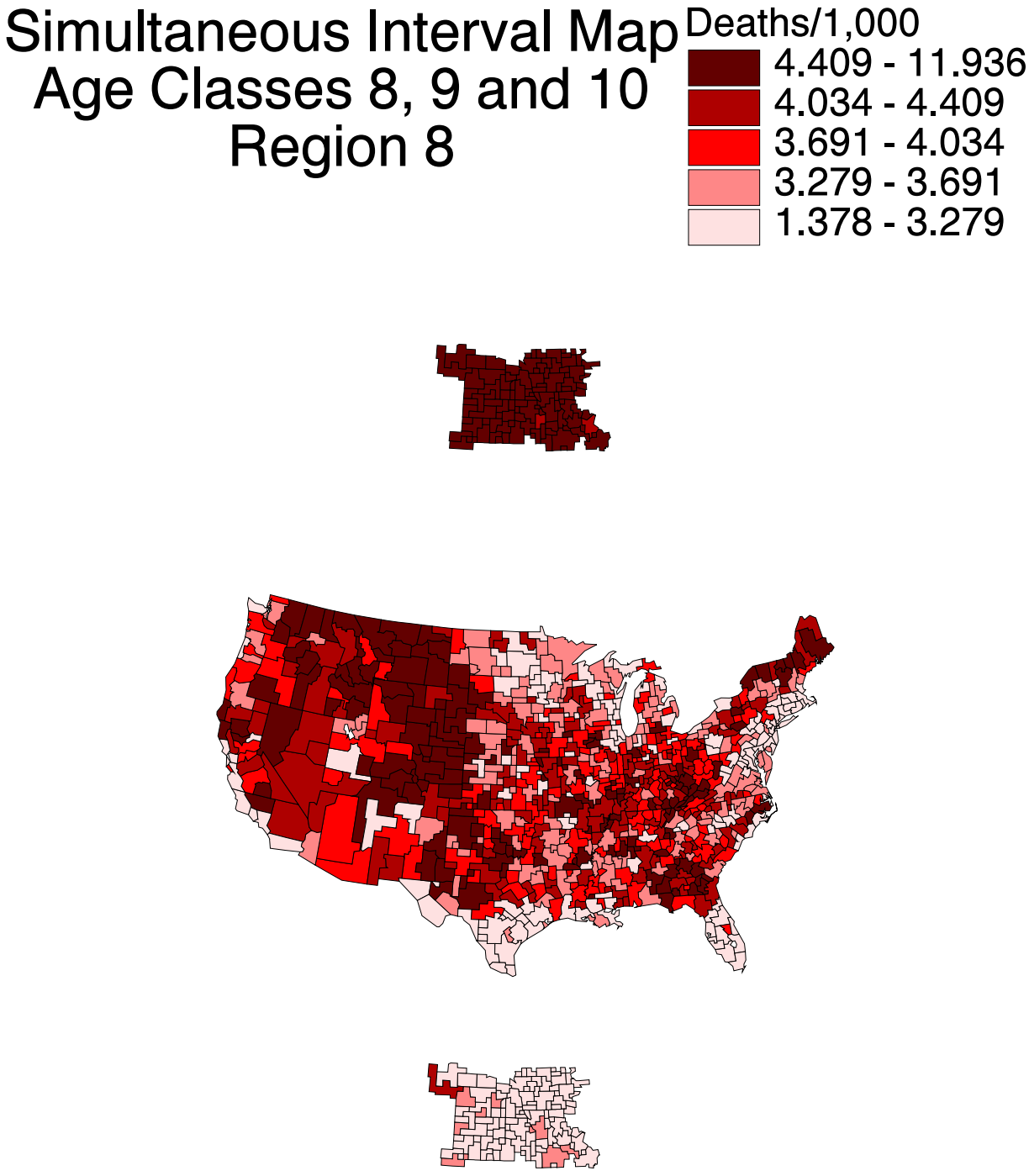


Figure 4.12. Mean Legend Single-γ Method Simultaneous Interval Map – Region 8.

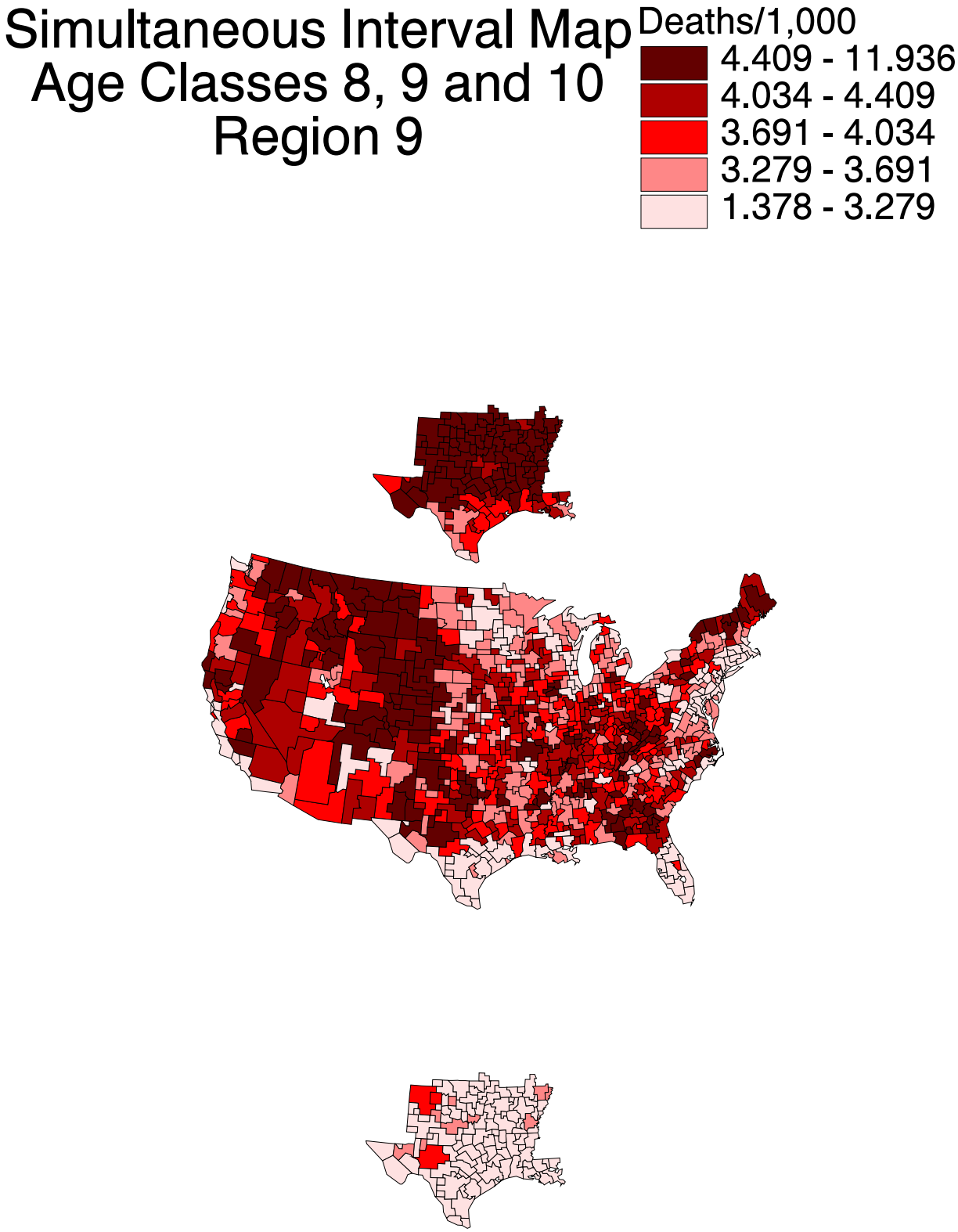


Figure 4.13. Mean Legend Single-γ Method Simultaneous Interval Map – Region 9.

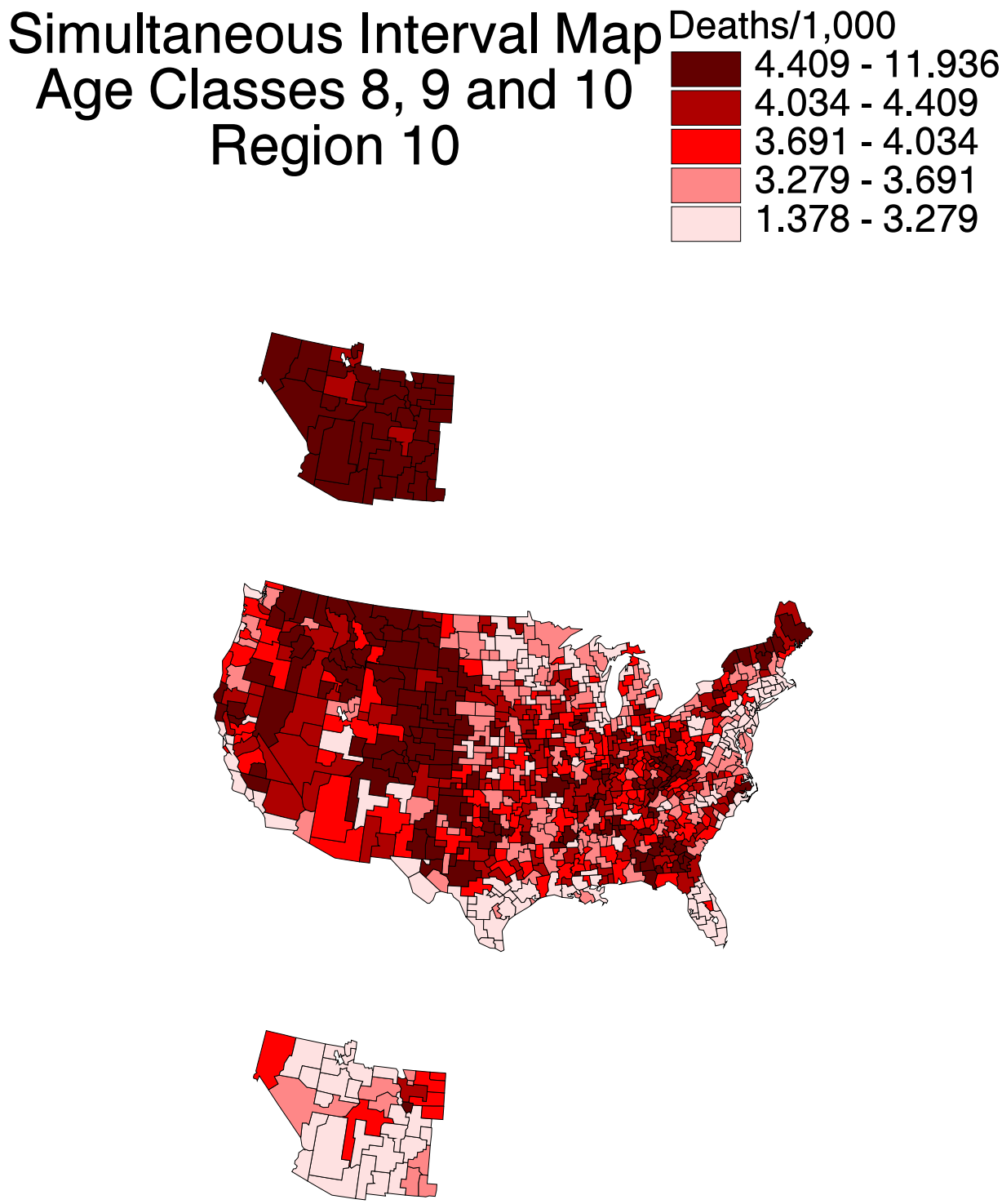


Figure 4.14. Mean Legend Single-γ Method Simultaneous Interval Map – Region 10.

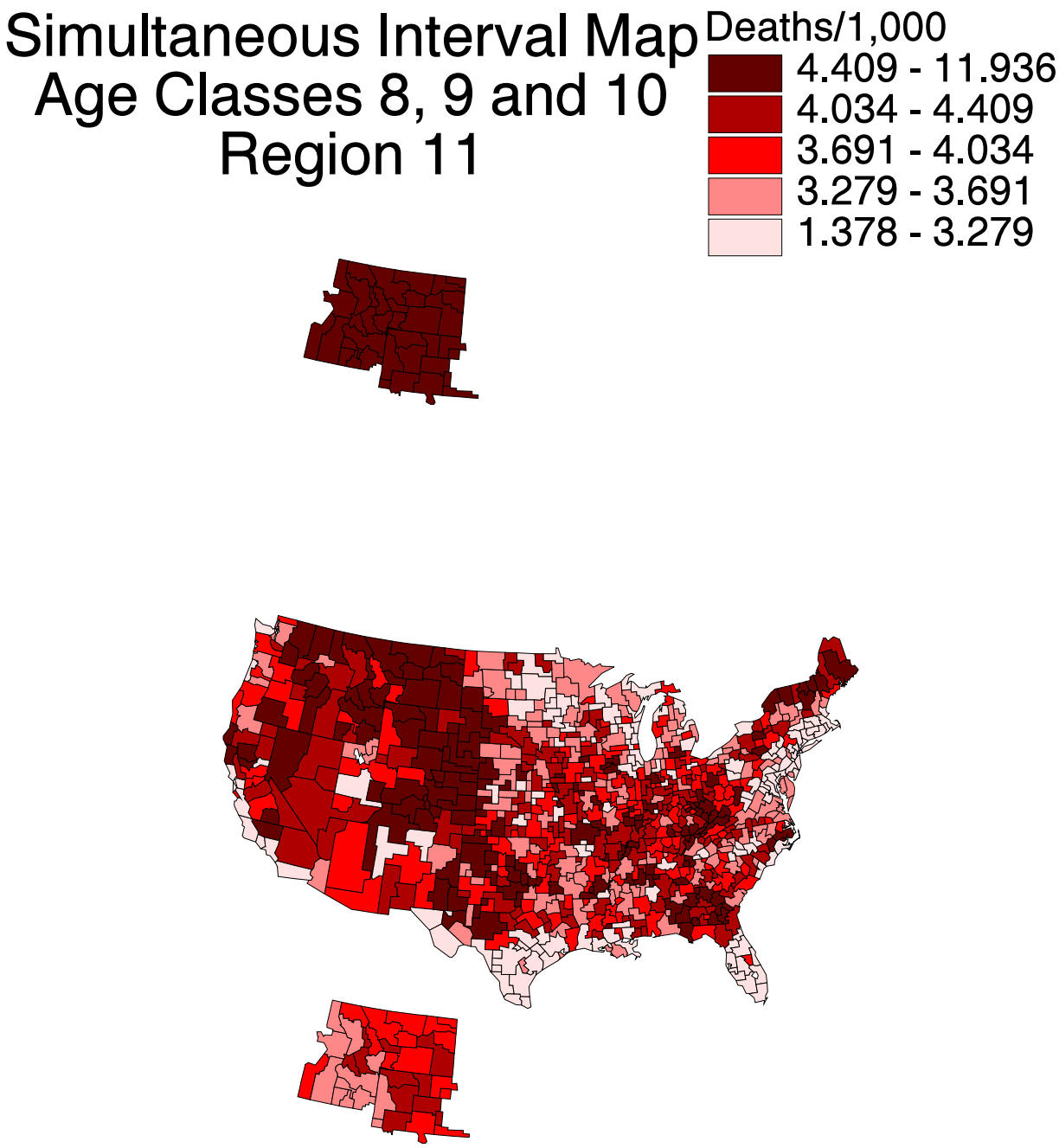


Figure 4.15. Mean Legend Single-γ Method Simultaneous Interval Map – Region 11.

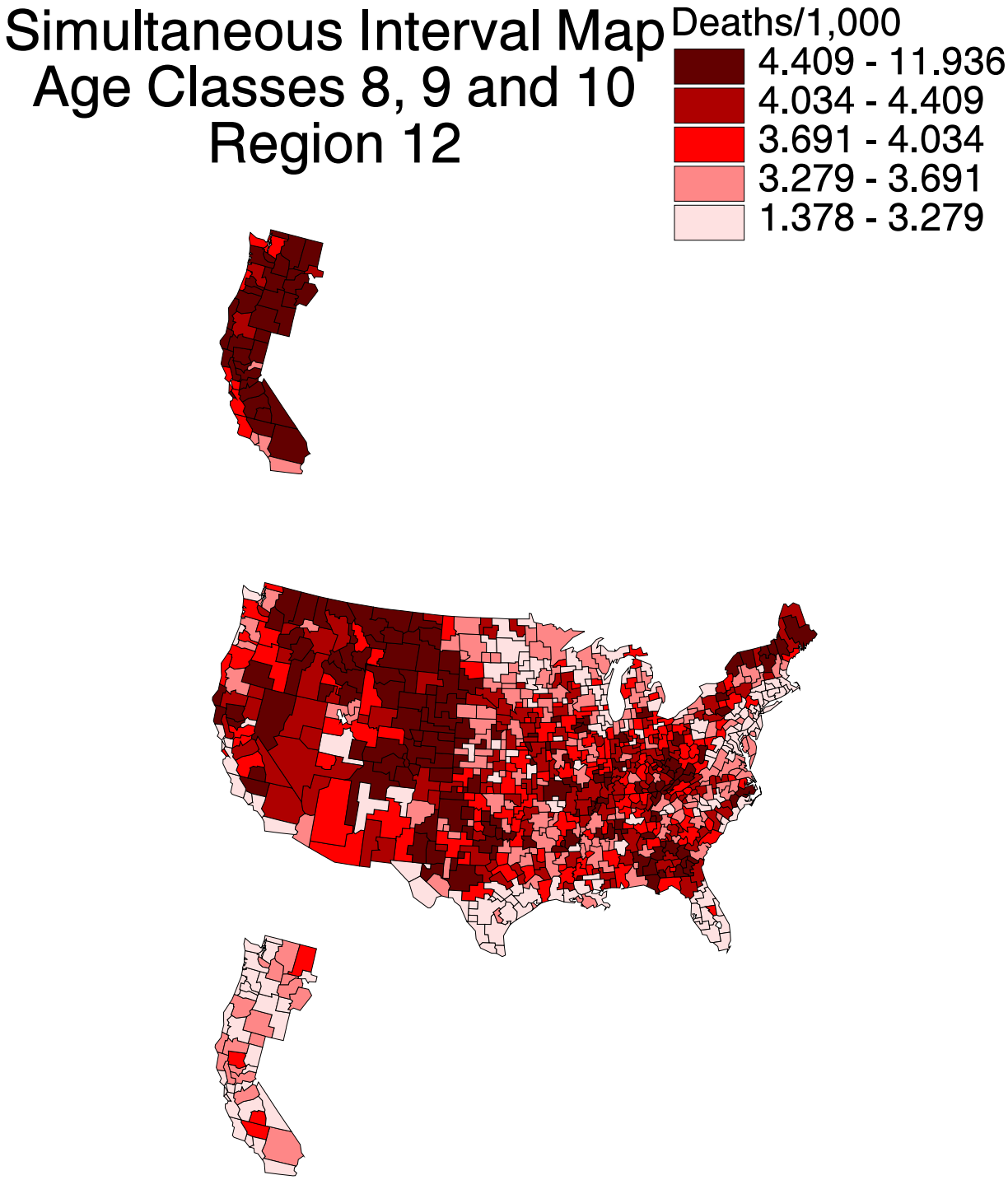


Figure 4.16. Mean Legend Single-γ Method Simultaneous Interval Map – Region 12.

4.2 Mean Legend Difference Maps and Tables

A summary of the amount of variation observed in the maps can be described in terms of the color difference from the low map to the high map based on the quintiles of the Mean map. This comparison is in terms of only what is visible on the map, namely, the color. The lightest color on the map representing the least rate is indicated as 1 and the darkest color on the map representing the greatest rate is indicated as 5. Difference maps and tables are presented below.

The plot in Figure 4.17 gives the Color Difference Maps for CI, HPD and All Regions Simultaneous Maps. The colors given represent the change of color between the low map and the high map. In our example the CI and HPD intervals are not very different. However, because the HPD intervals are the narrowest intervals it is expected that the color change map be slightly lighter in color than the CI maps. Because of the fixed quintiles of the Mean Map, as the interval ends are adjusted from the CI map to the HPD map, it is possible that one bound crosses a quintile cut point so that the interval actually appears wider in terms of the colors. Because our distributions are right skewed, the HPD intervals shift to lower values. Both the left shift and the general trend of narrowing in the HPD can be seen in the tables below.

Tables summarizing the difference maps are given in Table 4.4 for CI maps, Table 4.5 for HPD maps and Table 4.6 for All Regions Simultaneous maps. As an example of how to read these tables, consider cell $(1, 1)$ in Table 4.4; 47 HSAs are color 1 on the low map and color 1 on the high map, possibly indicating little variation. Consider cell $(3, 4)$; 5 HSAs are color 3 on the low map and color 4 on the high map, also indicating little variation. Consider cell $(1, 5)$; 160 HSAs are color 1 on the low map and color 5 on the high map, indicating the largest measurable variation in terms of color.

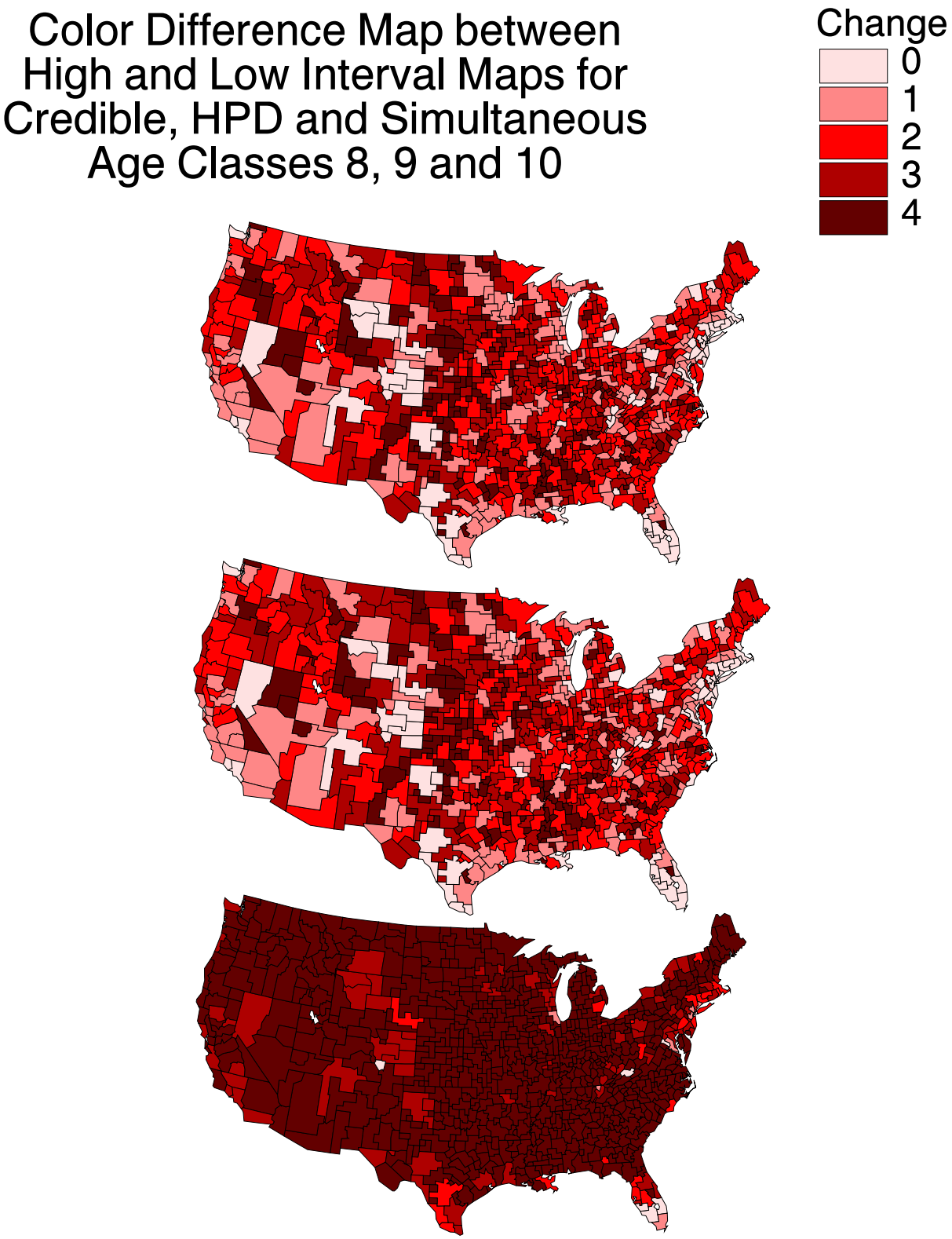


Figure 4.17. Mean Legend Color Difference Maps for CI, HPD and All Regions Simultaneous Maps.

Table 4.4
Mean Legend Credible Interval difference between lower and upper bound maps.

Lower Quintile	Upper Quintile					
	1	2	3	4	5	
1	47	87	73	68	160	435
2	0	0	10	44	144	198
3	0	0	0	5	86	91
4	0	0	0	0	48	48
5	0	0	0	0	26	26
	47	87	83	117	464	798

Table 4.5
Mean Legend HPD Interval difference between lower and upper bound maps.

Lower Quintile	Upper Quintile					
	1	2	3	4	5	
1	48	88	74	77	155	442
2	0	0	10	41	148	199
3	0	0	0	5	82	87
4	0	0	0	0	45	45
5	0	0	0	0	25	25
	48	88	84	123	455	798

Table 4.6
Mean Legend Simultaneous Interval difference between lower and upper bound maps.

Lower Quintile	Upper Quintile					
	1	2	3	4	5	
1	5	6	18	49	683	761
2	0	0	0	0	30	30
3	0	0	0	0	4	4
4	0	0	0	0	1	1
5	0	0	0	0	2	2
	5	6	18	49	720	798

4.3 Individual Legend Choropleth Maps

The maps presented in this section are the same as in Section 4.1, with one difference; the cutpoints of each legend colors are based on the quintiles of each the Upper, the Mean, and the Lower map. Therefore, each of the three maps has its own legend based on the quintiles of that map.

To illustrate how one might use the interval maps presented, select an HSA from the mean map. Find the corresponding HSA on both the upper and lower maps. The variation of the particular HSA selected can be interpreted from the colors and number of color differences from the lower to the upper map. An HSA that changes from a dark color (in the lower) to a light color (in the upper) can be said to have relatively little variation, while an HSA that changes from a light color (in the lower) to a dark color (in the upper) can be said to have relatively great variation.

4.3.1 Individual Legend Individual HSA Credible Interval Map

The plot in Figure 4.18 gives the individual legend individual HSA credible interval map. The upper and lower maps are based on the equal tail credible intervals described in Section 2.1.1.

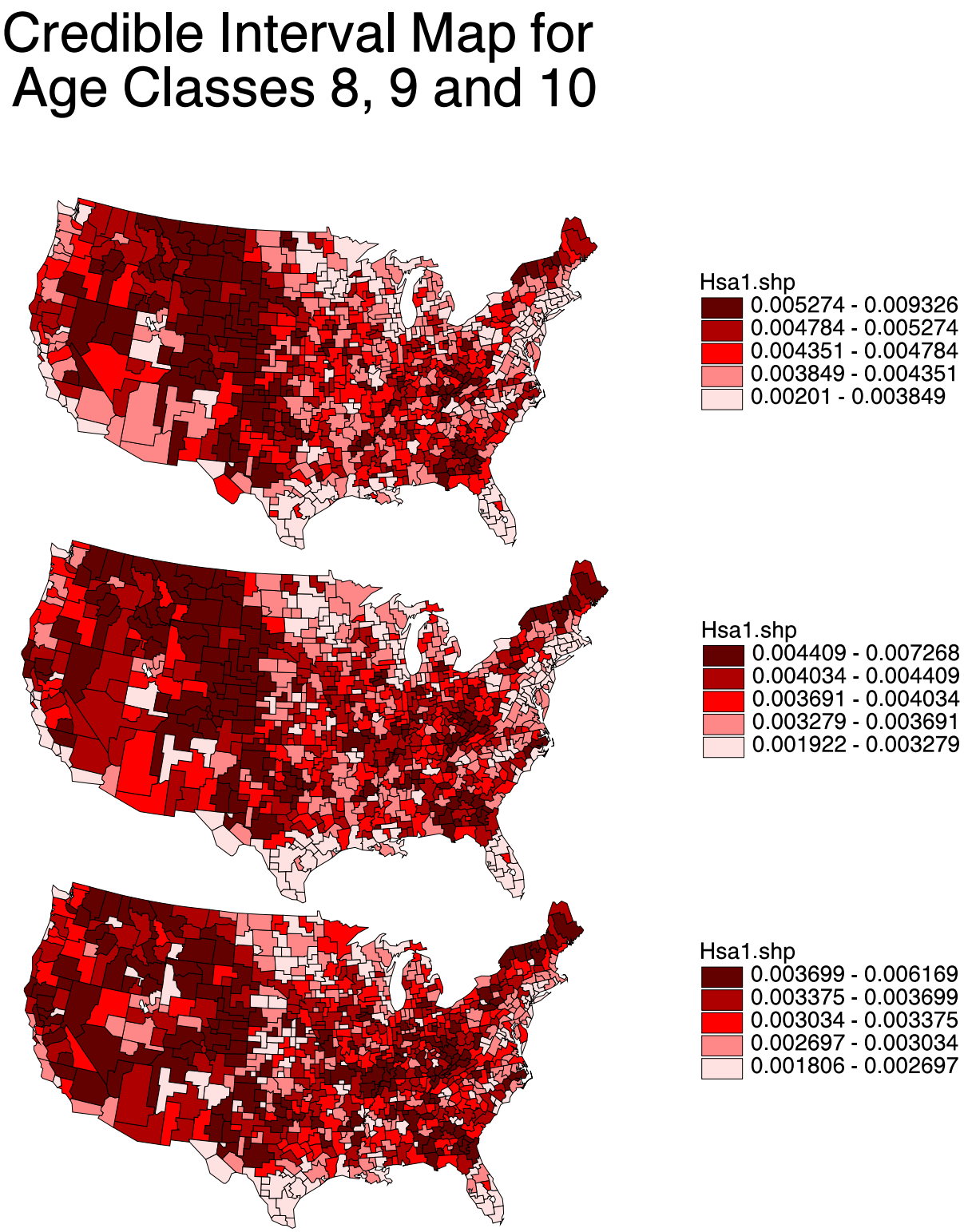


Figure 4.18. Individual Legend Individual HSA Credible Interval Map.

4.3.2 Individual Legend Individual HSA HPD Interval Map

The plot in Figure 4.19 gives the individual legend individual HSA HPD interval map. The upper and lower maps are based on the HPD intervals described in Section 2.1.2.

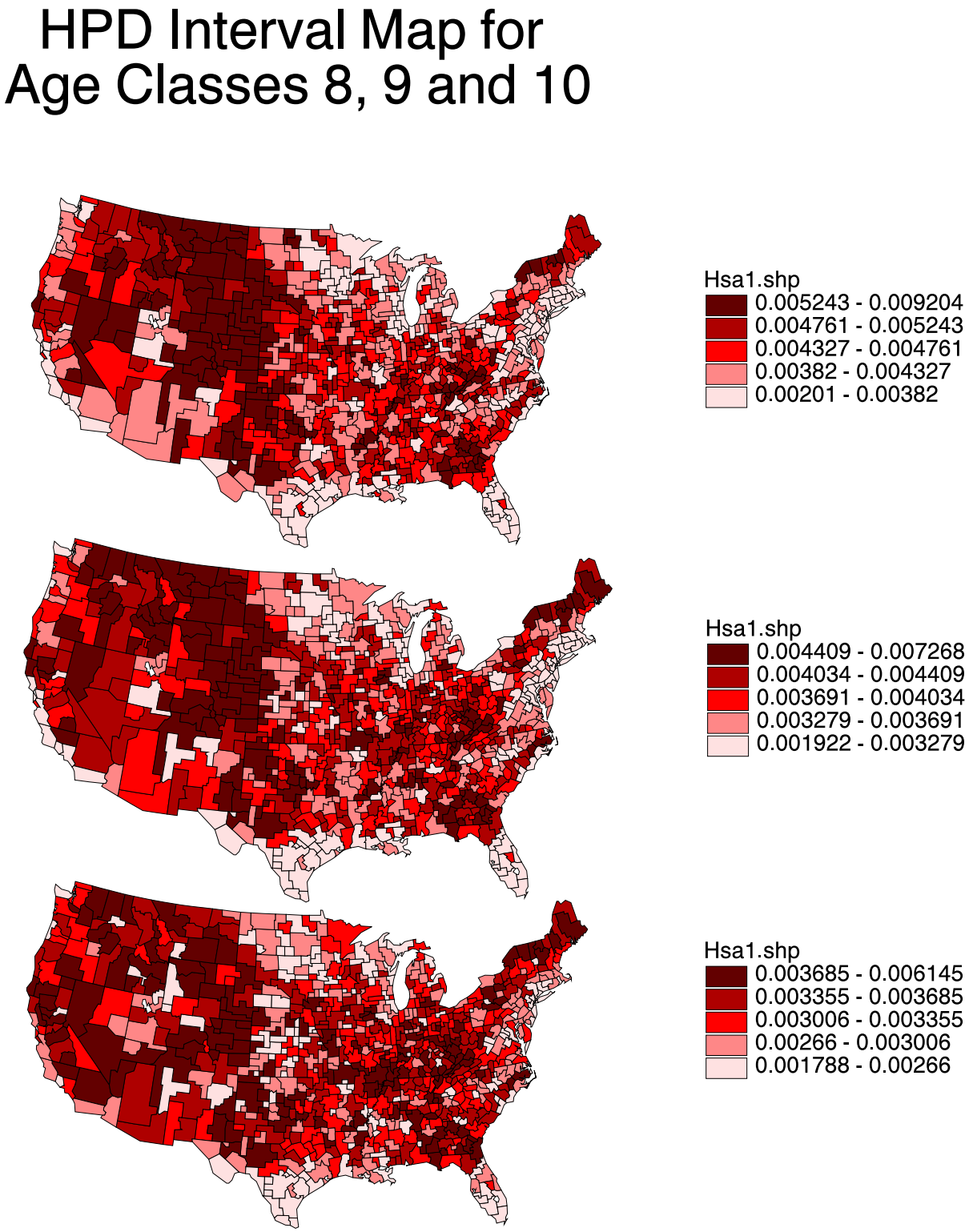


Figure 4.19. Individual Legend Individual HSA HPD Interval Map.

4.3.3 Individual Legend Single-γ Method Simultaneous Interval Map

The plot in Figure 4.20 gives the individual legend Single-γ Method simultaneous interval map. The upper and lower maps are based on the Single-γ Method intervals described in Section 2.4.

The value of γ for the various simultaneous maps in Sections 4.1.4 and 4.1.5 are given in Table 4.2.

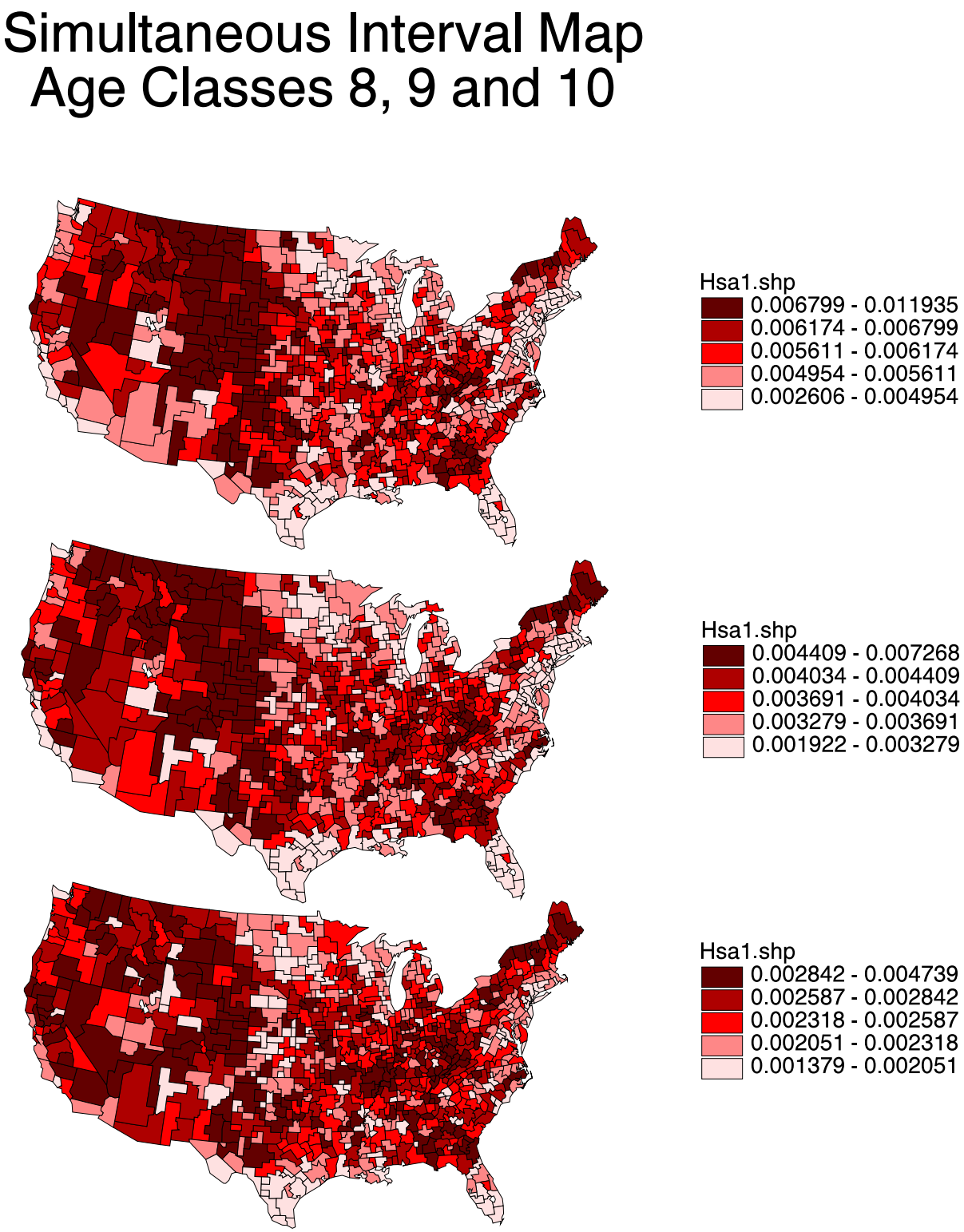


Figure 4.20. Individual Legend Single-γ Method Simultaneous Interval Map.

4.3.4 Individual Legend Single-γ Method Simultaneous Interval by Region Maps

The plots in Figures 4.21 through 4.32 gives the Single-γ Method simultaneous interval by region maps.

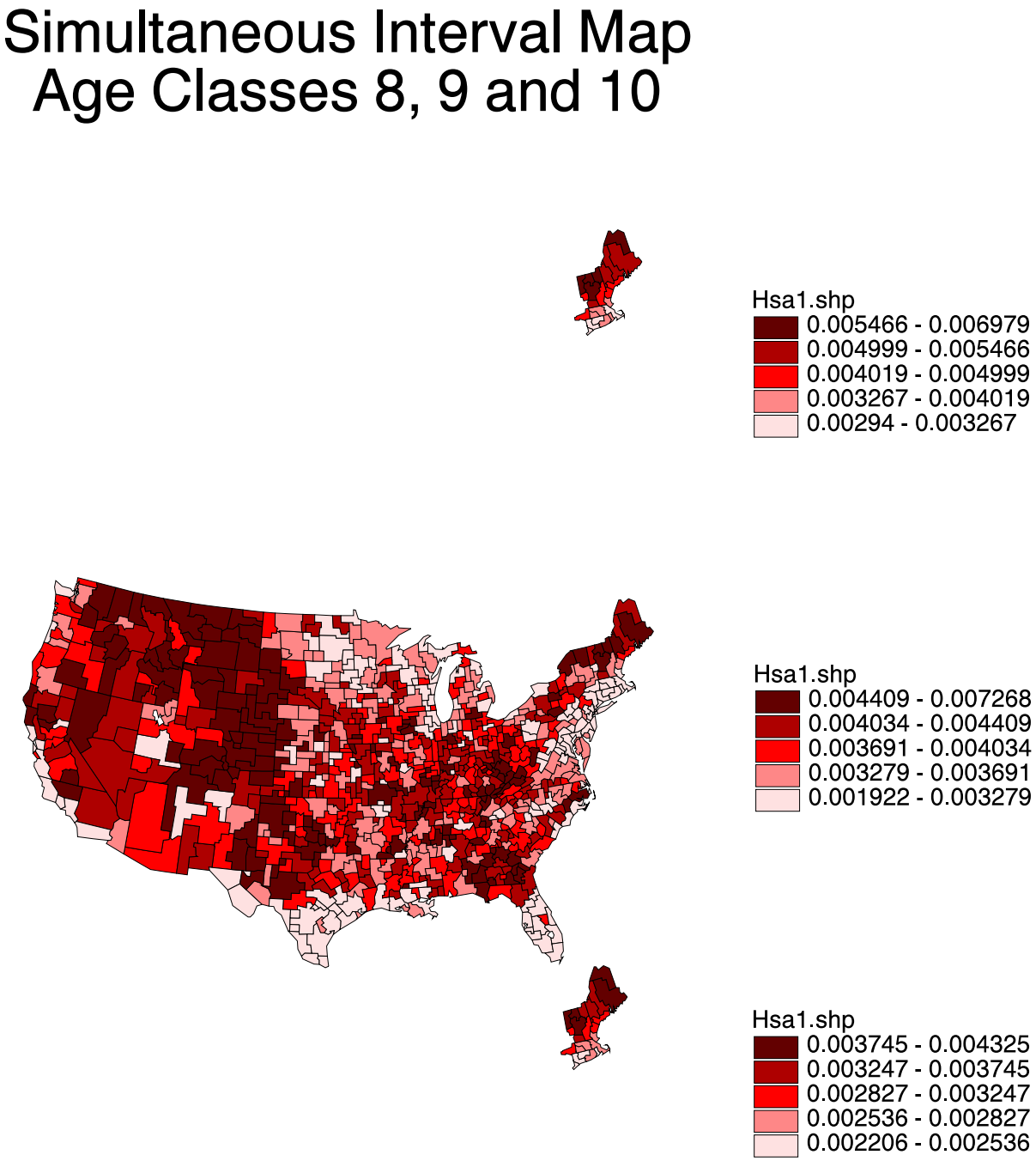


Figure 4.21. Individual Legend Single-γ Method Simultaneous Interval Map – Region 1.

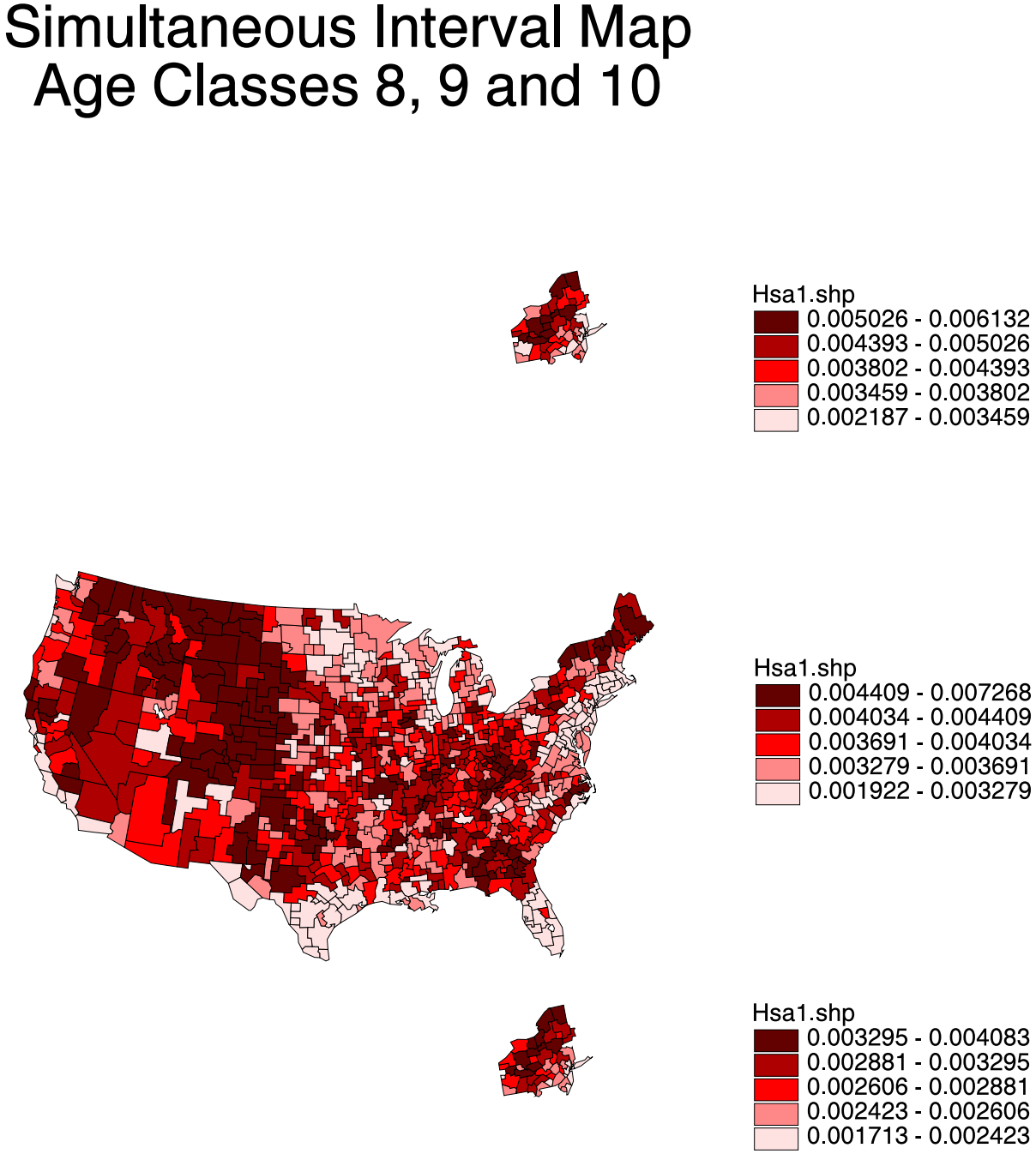


Figure 4.22. Individual Legend Single-γ Method Simultaneous Interval Map – Region 2.

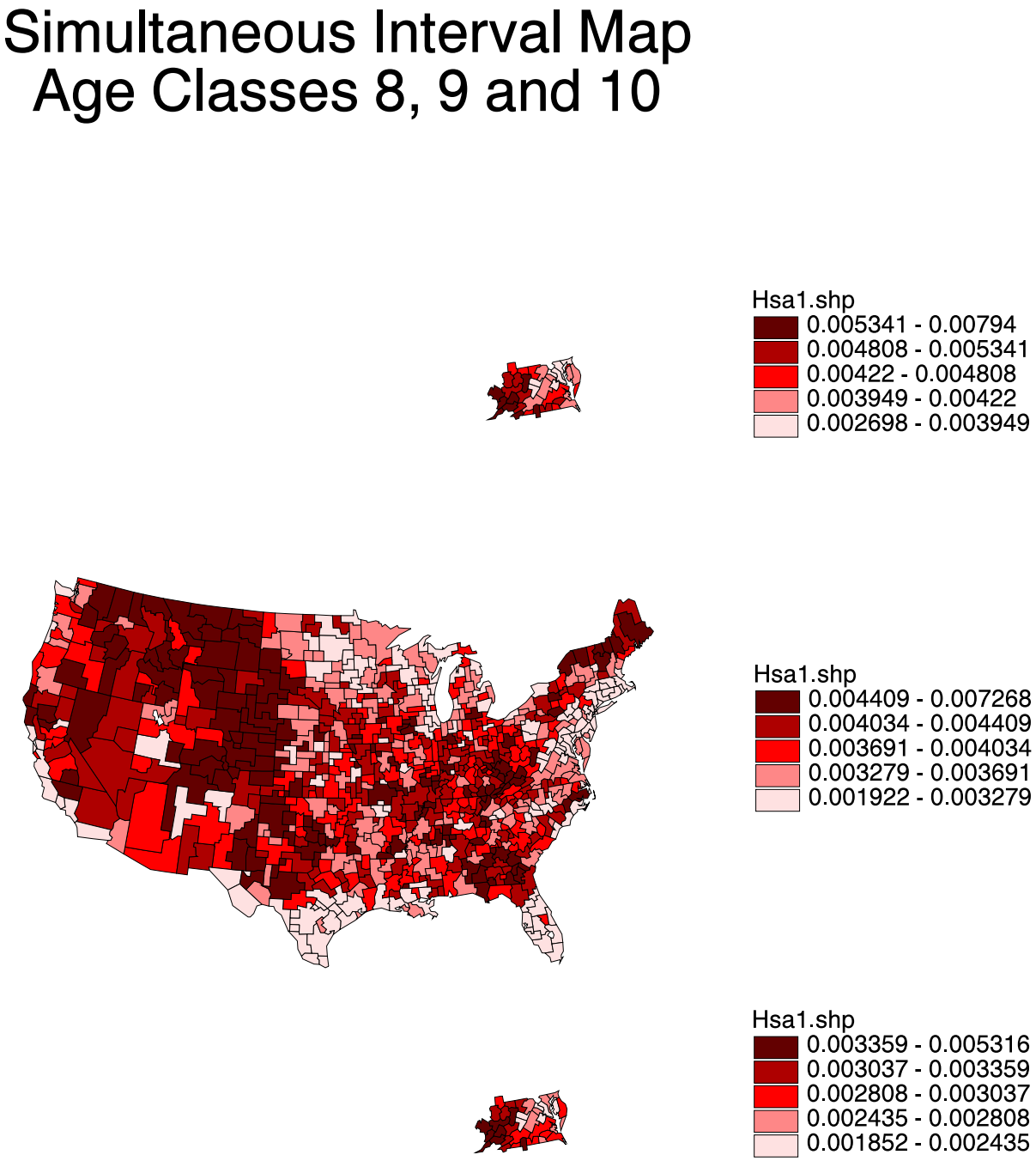


Figure 4.23. Individual Legend Single-γ Method Simultaneous Interval Map – Region 3.

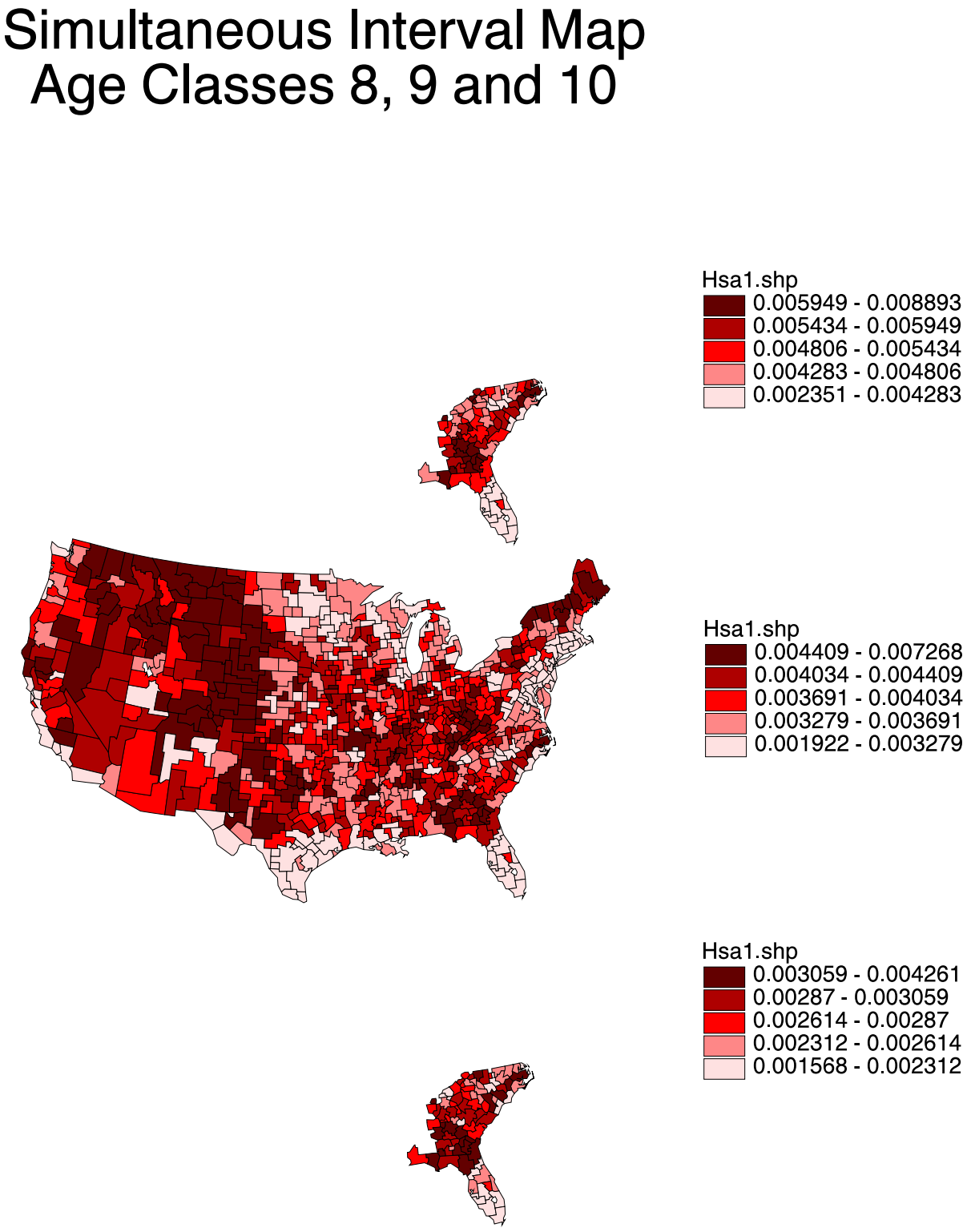


Figure 4.24. Individual Legend Single-γ Method Simultaneous Interval Map – Region 4.

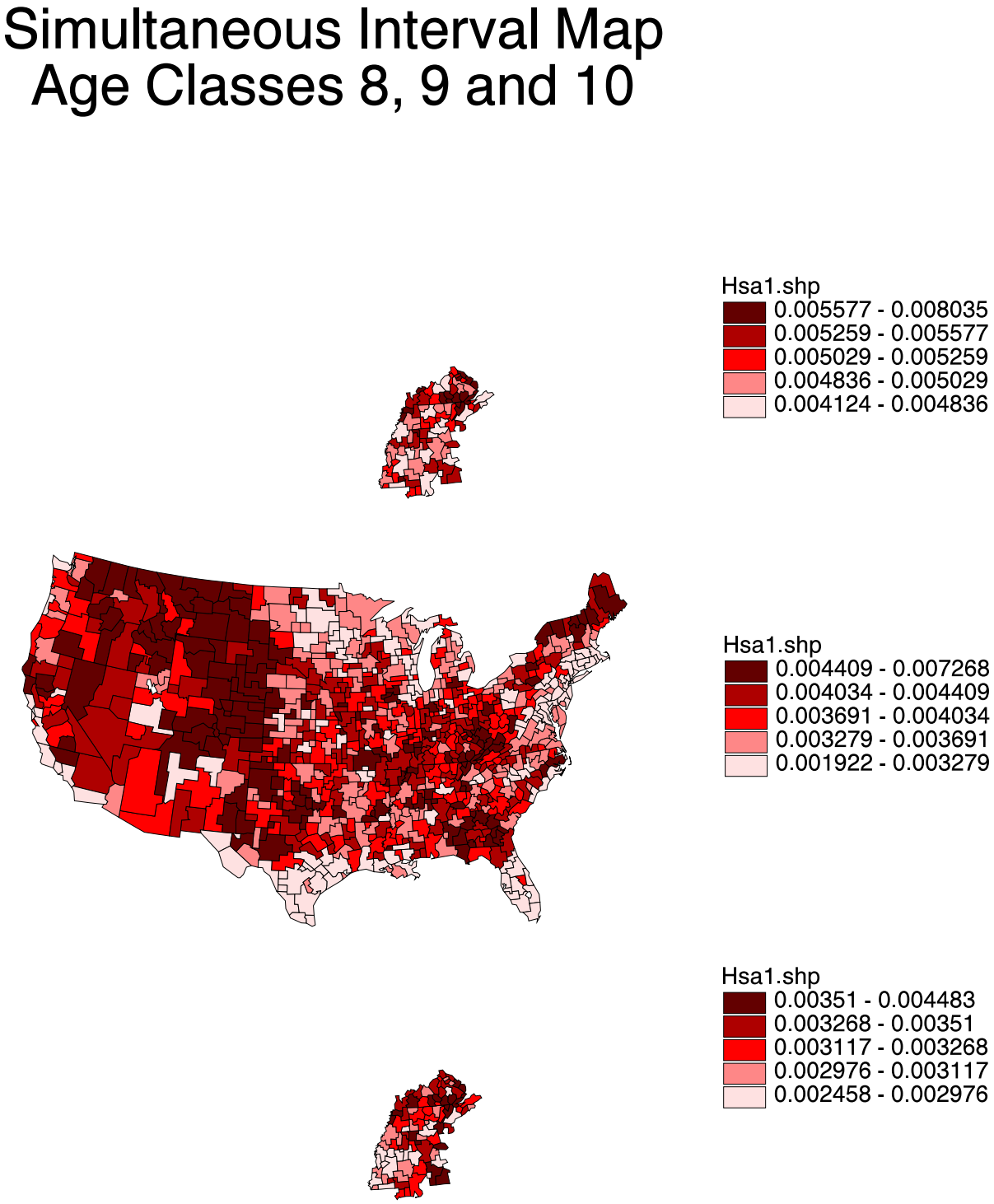


Figure 4.25. Individual Legend Single-γ Method Simultaneous Interval Map – Region 5.

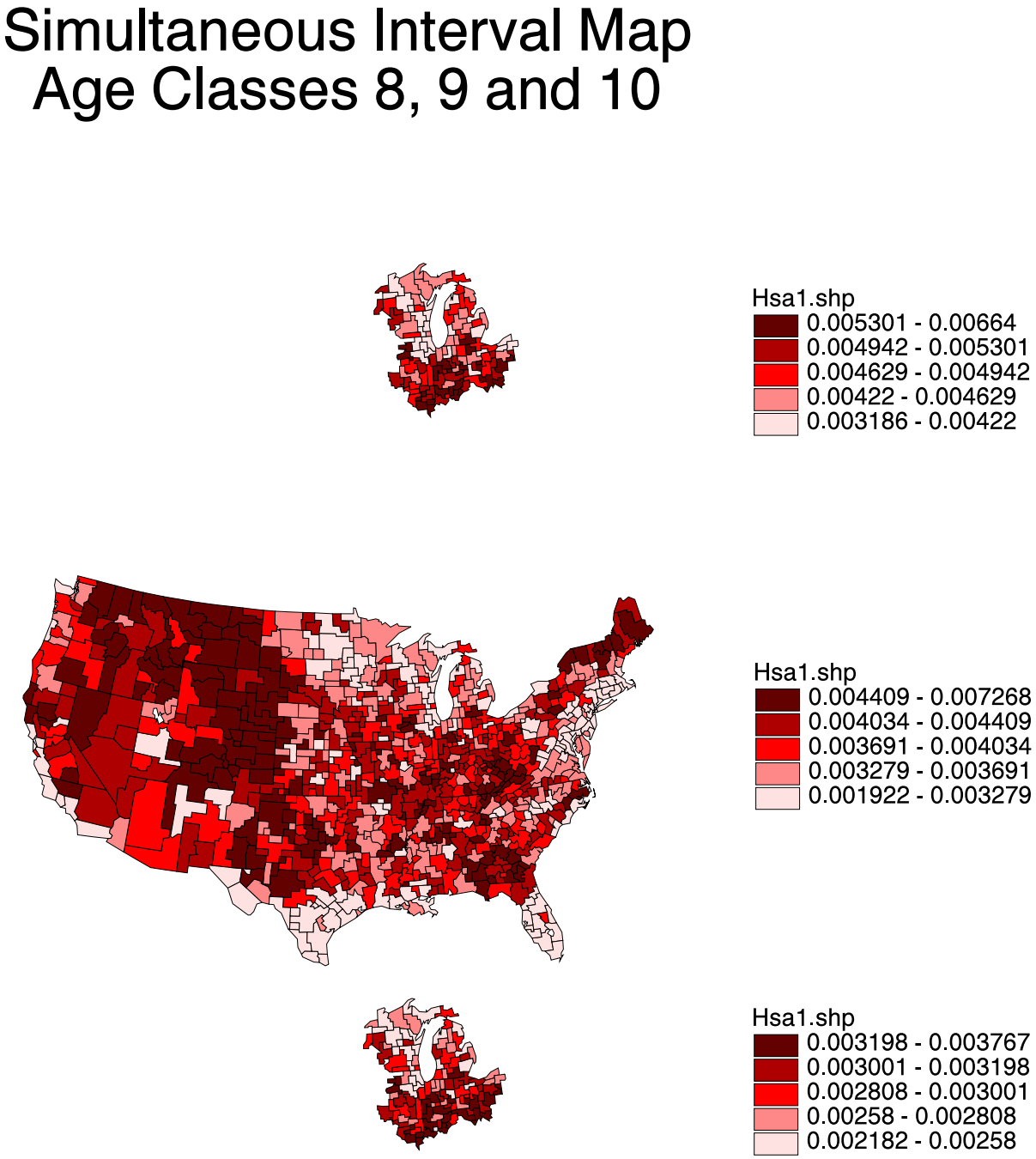


Figure 4.26. Individual Legend Single-γ Method Simultaneous Interval Map – Region 6.

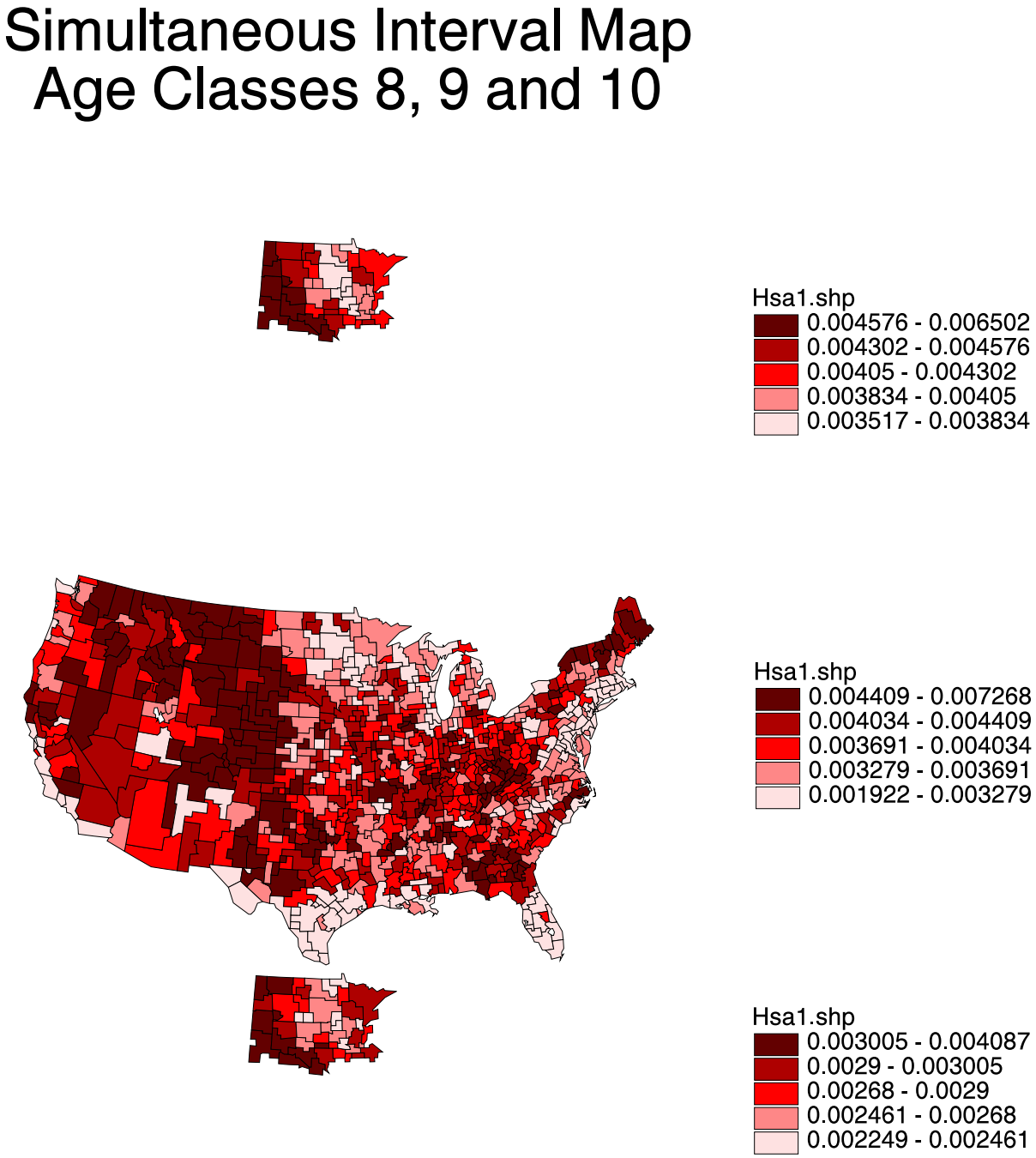


Figure 4.27. Individual Legend Single-γ Method Simultaneous Interval Map – Region 7.

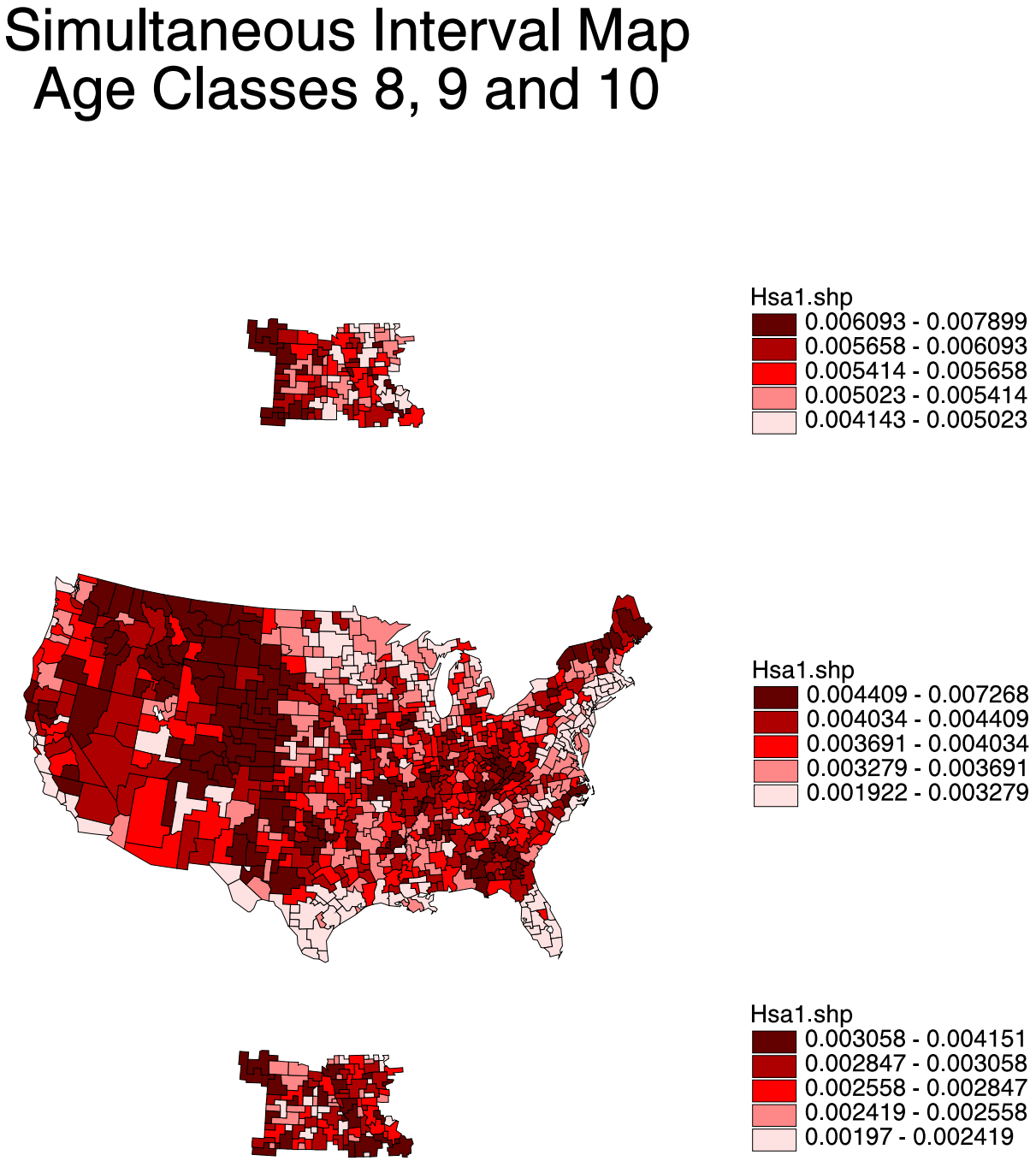


Figure 4.28. Individual Legend Single-γ Method Simultaneous Interval Map – Region 8.

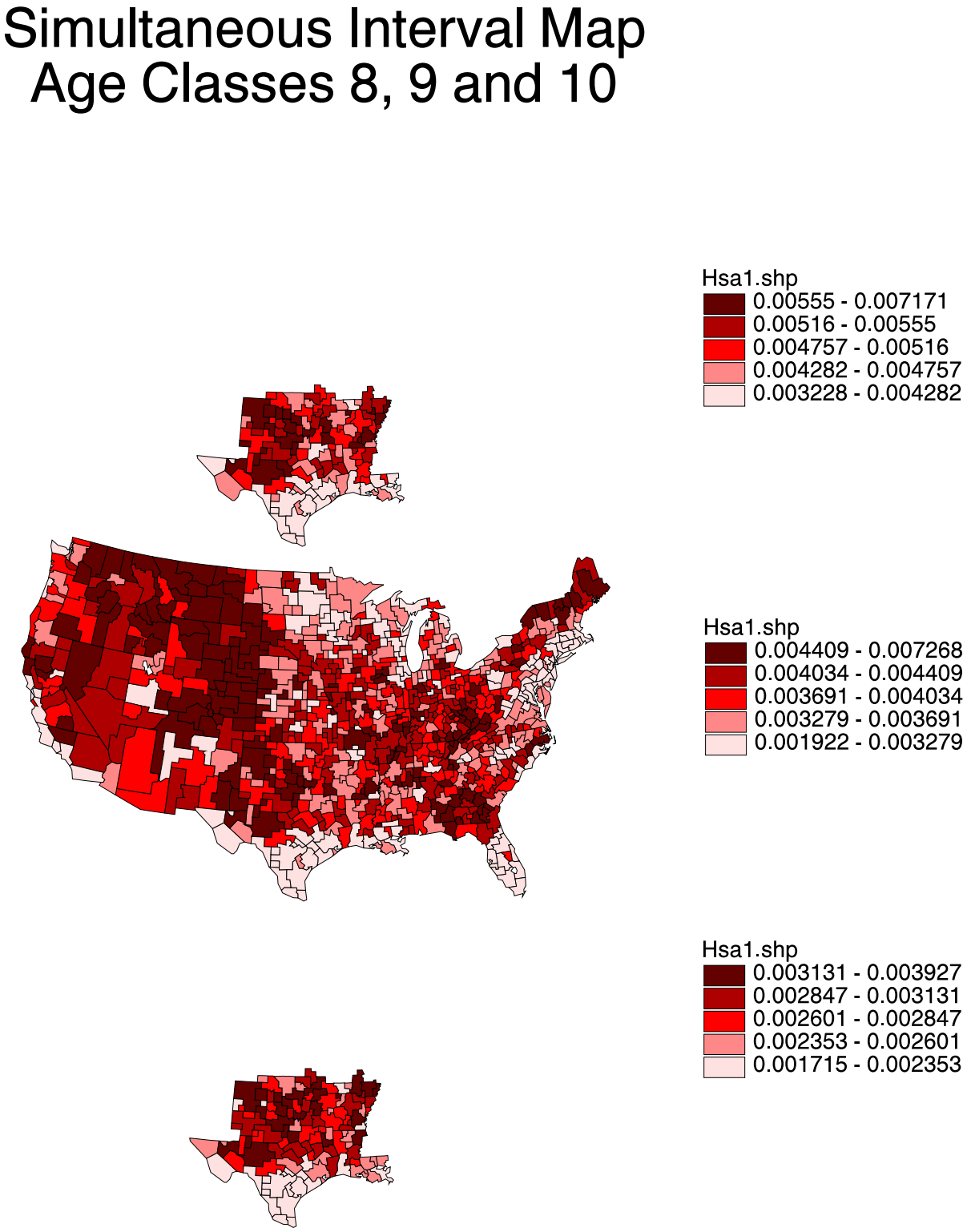


Figure 4.29. Individual Legend Single-γ Method Simultaneous Interval Map – Region 9.

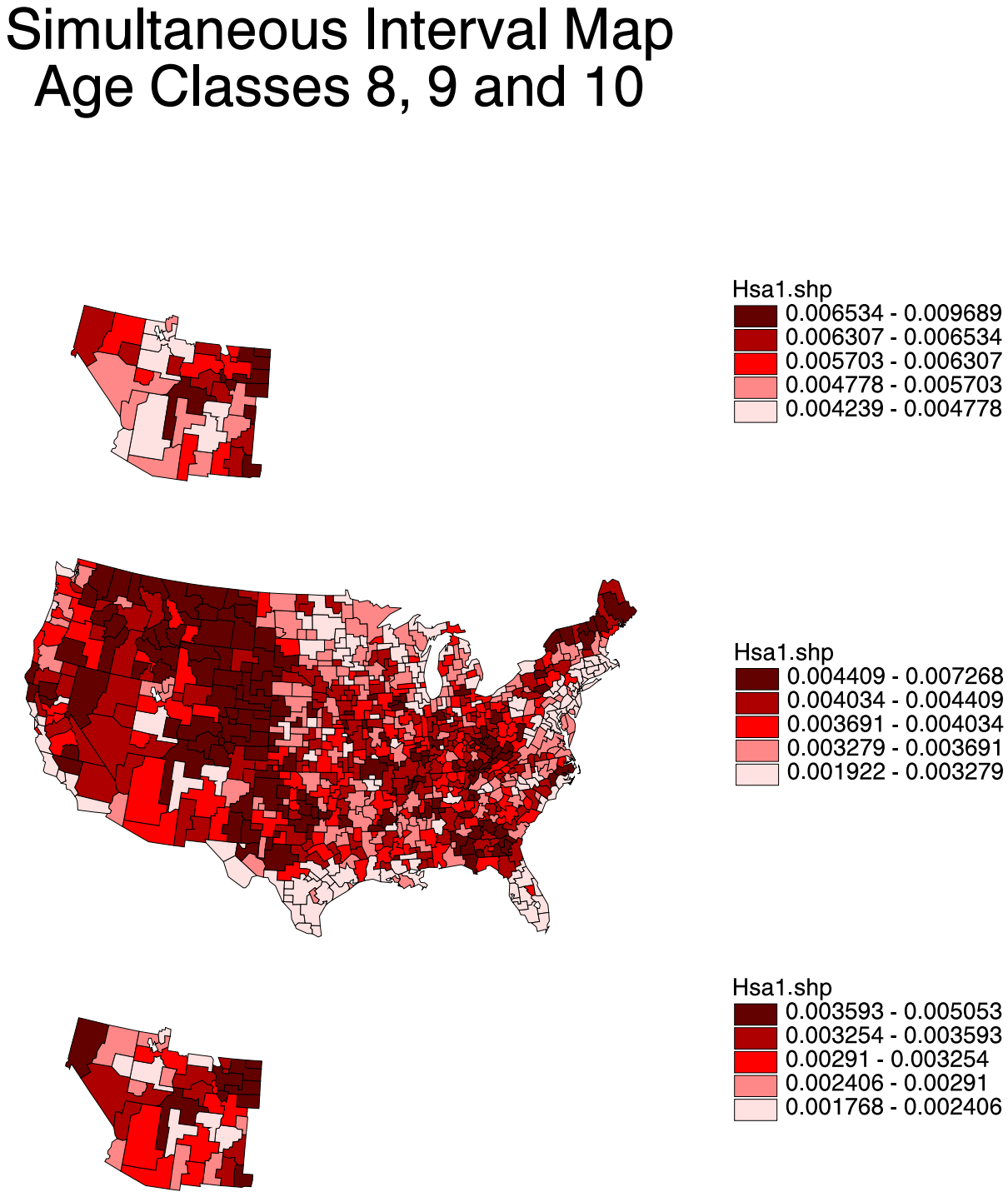


Figure 4.30. Individual Legend Single-γ Method Simultaneous Interval Map – Region 10.

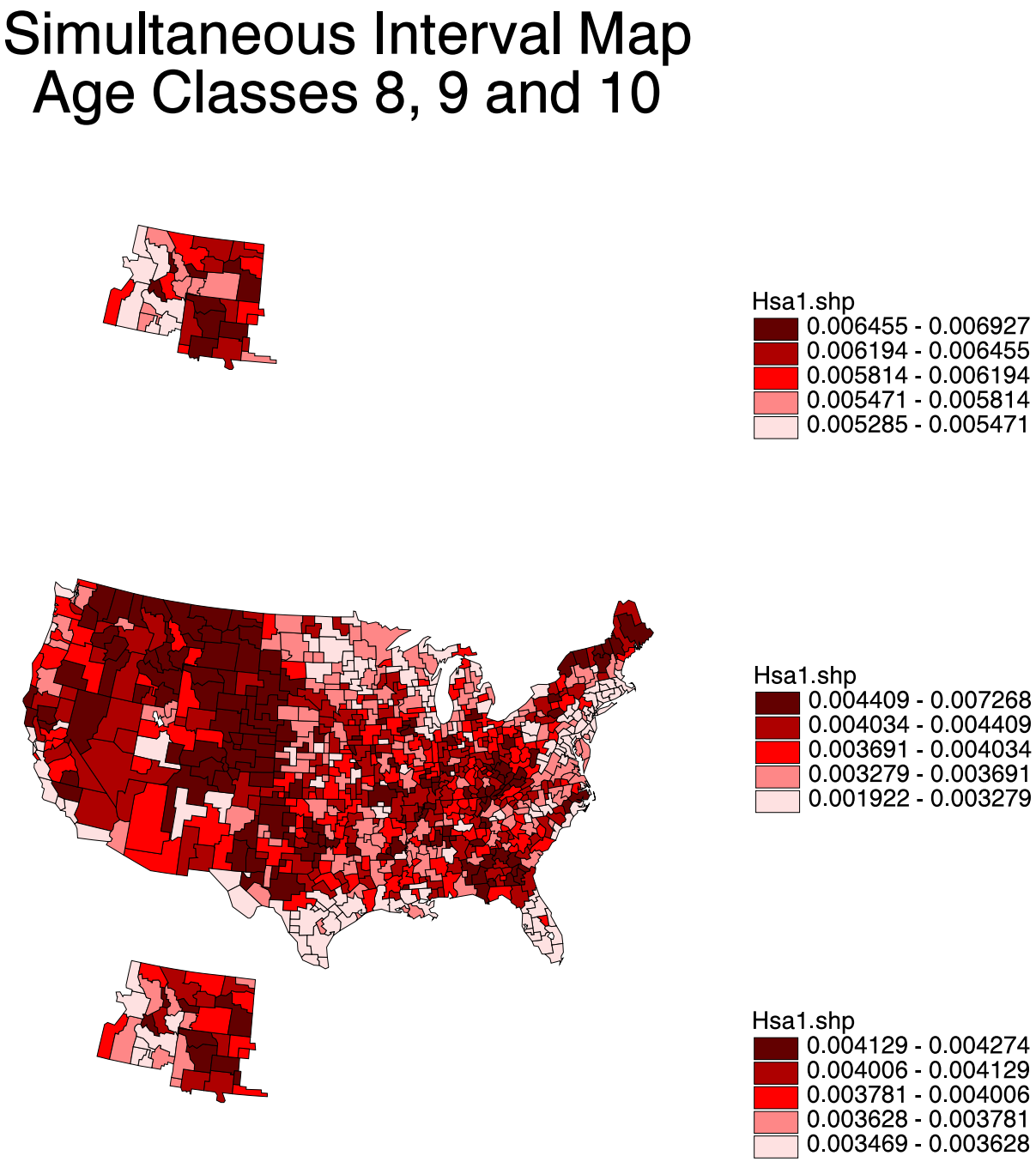


Figure 4.31. Individual Legend Single-γ Method Simultaneous Interval Map – Region 11.

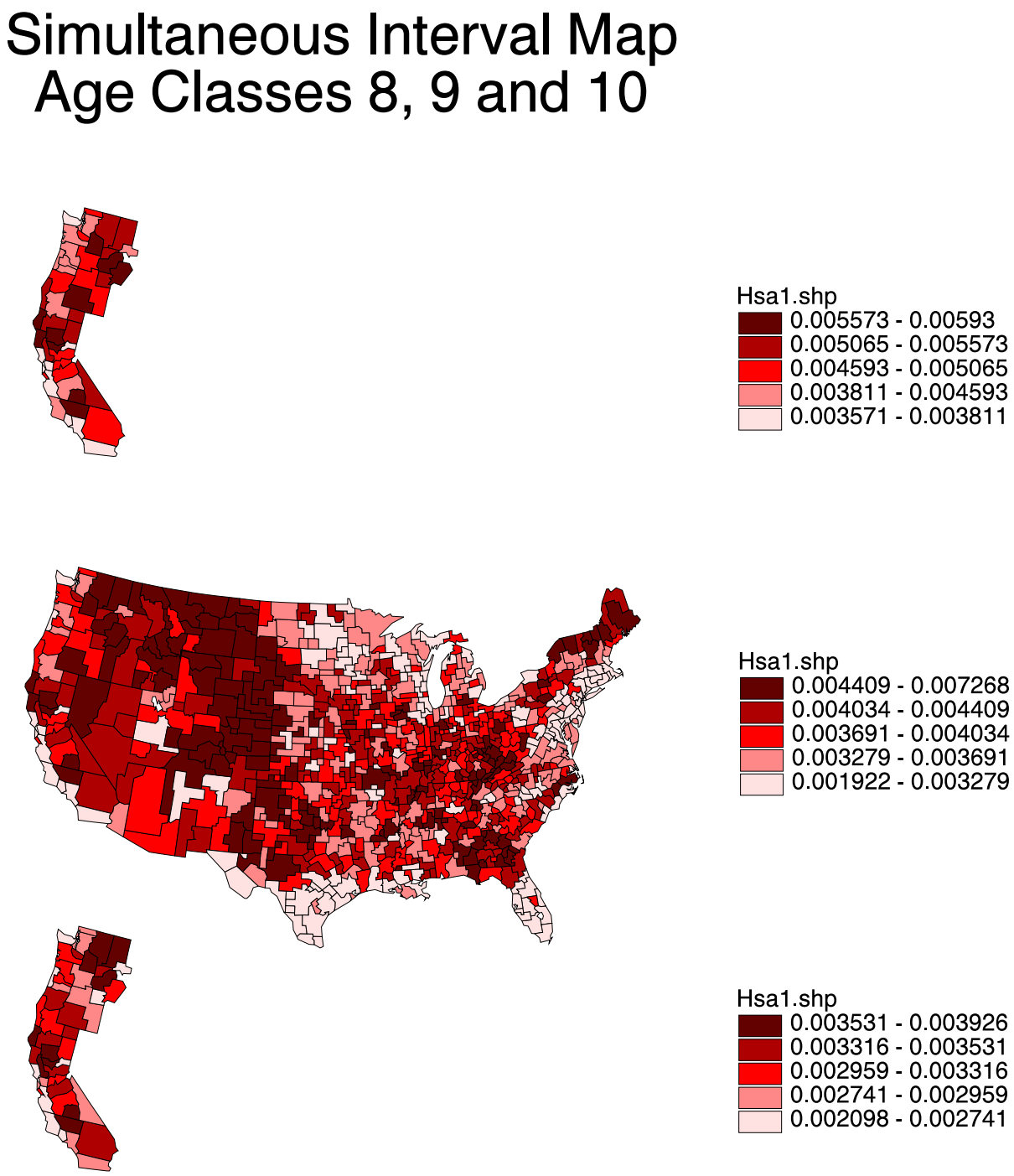


Figure 4.32. Individual Legend Single-γ Method Simultaneous Interval Map – Region 12.

4.4 Individual Legend Difference Maps and Tables

A summary of the amount of variation observed in the maps can be described in terms of the color difference from the low map to the high map. This comparison is in terms of only what is visible on the map, namely, the color. The lightest color on the map representing the least rate is indicated as 1 and the darkest color on the map representing the greatest rate is indicated as 5. The difference presented is the Lower map's color number subtracted from the Upper map's color number. Difference maps and tables are presented below.

The plot in Figure 4.33 gives the Individual Legend Color Difference Maps for CI, HPD and All Regions Simultaneous Maps. The colors given represent the change of color between the low map and the high map.

Tables summarizing the difference maps are given in Table 4.7 for CI maps, Table 4.8 for HPD maps and Table 4.9 for All Regions Simultaneous maps. As an example of how to read these tables, consider cell $(1, 1)$ in Table 4.7; 85 HSAs are color 1 on the low map and color 1 on the high map, indicating moderate variation. Consider cell $(1, 4)$; 15 HSAs are color 1 on the low map and color 4 on the high map, indicating high variation. Consider cell $(5, 2)$; 29 HSAs are color 5 on the low map and color 2 on the high map, indicating very little variation.

Tables summarizing the difference maps are given in Table 4.10 for All maps. As an example of how to read these tables, consider row CI. There were 287 HSAs that remained the same color between the lower and upper maps, 215 that were a shade lighter in the upper map and 70 that were two shades darker in the upper map.

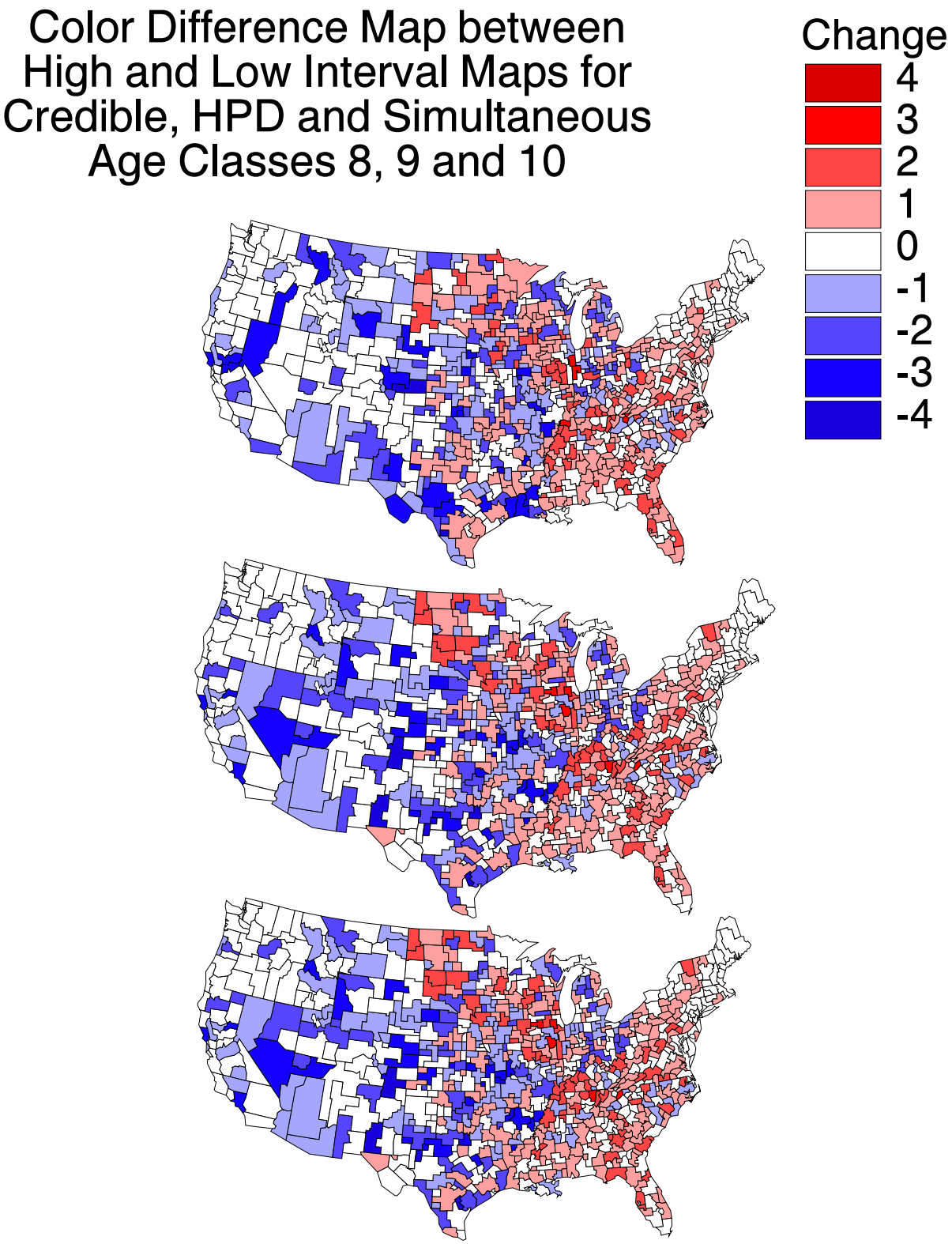


Figure 4.33. Individual Legend Color Difference Maps for CI, HPD and All Regions Simultaneous Maps.

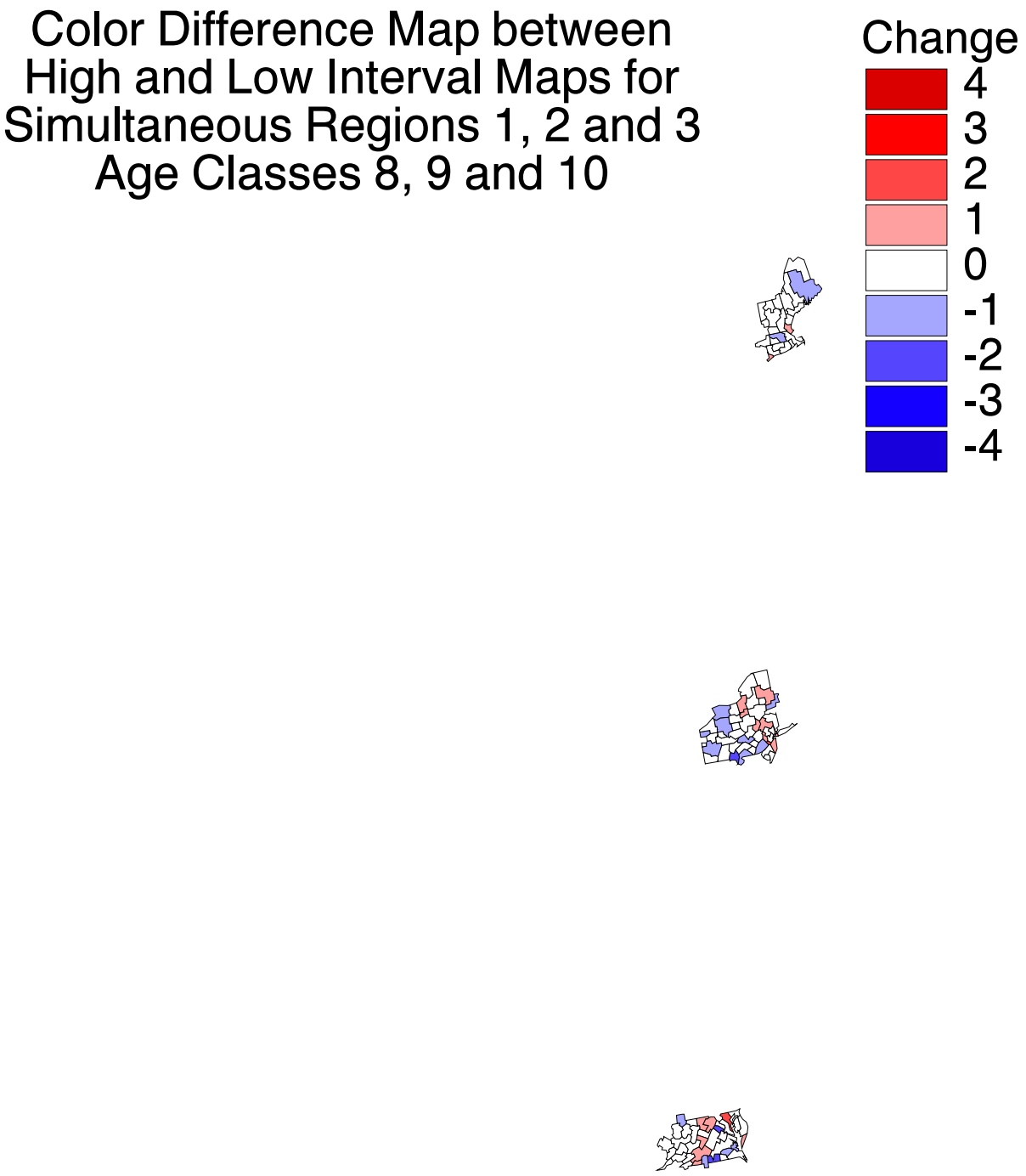


Figure 4.34. Individual Legend Color Difference Maps for Simultaneous Maps Regions 1, 2 and 3.

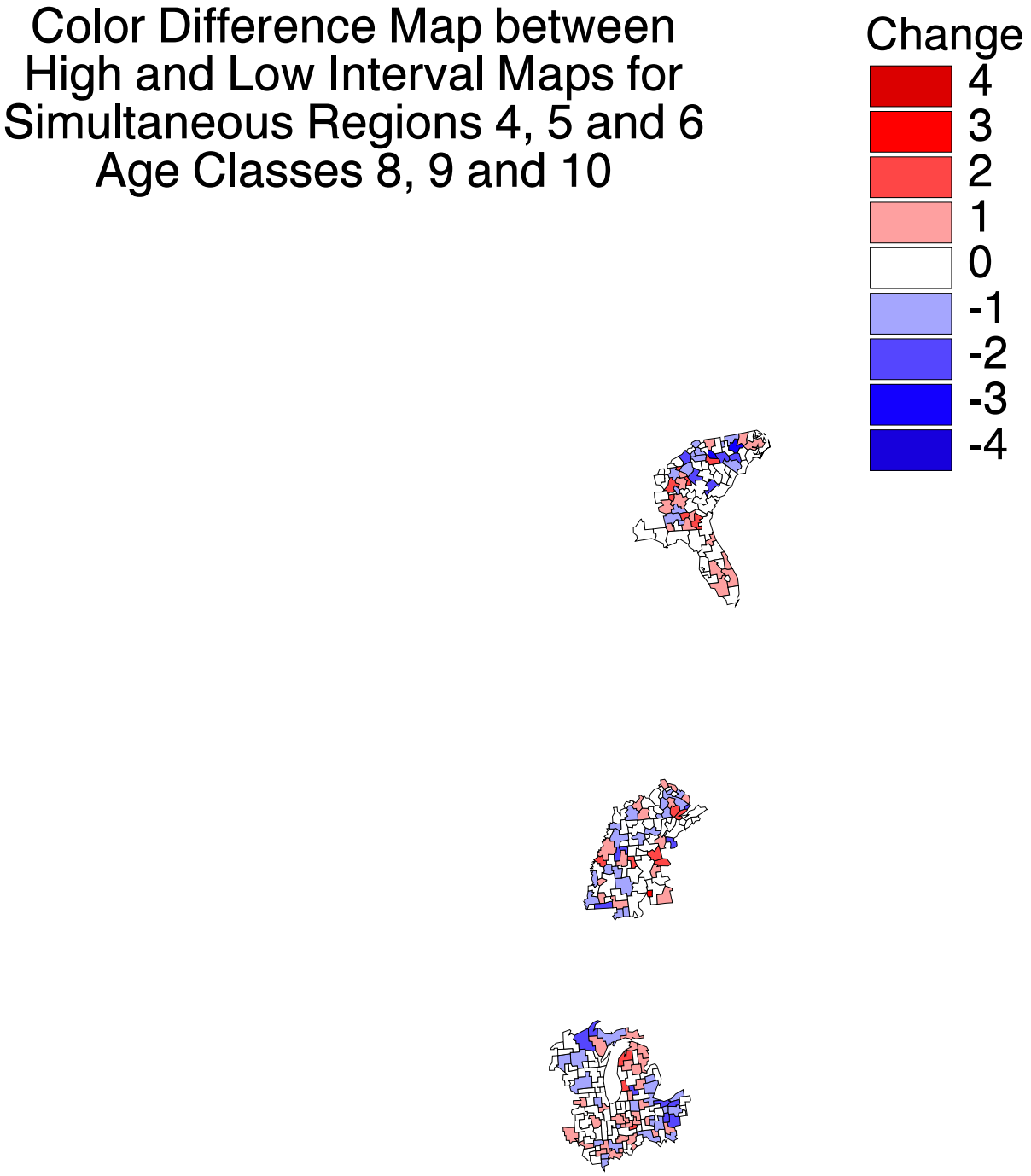


Figure 4.35. Individual Legend Color Difference Maps for Simultaneous Maps Regions 4, 5 and 6.

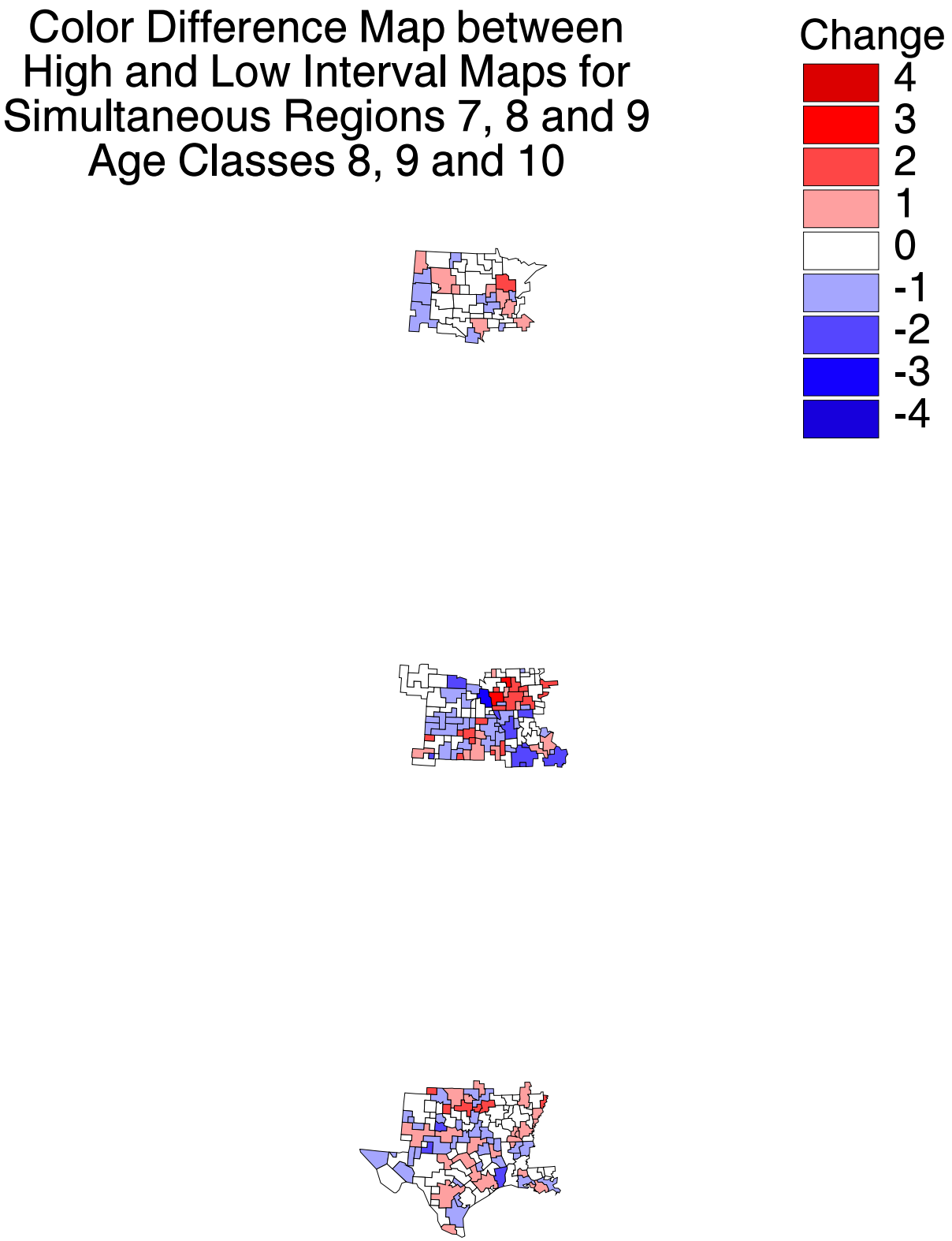


Figure 4.36. Individual Legend Color Difference Maps for Simultaneous Maps Regions 7, 8 and 9.

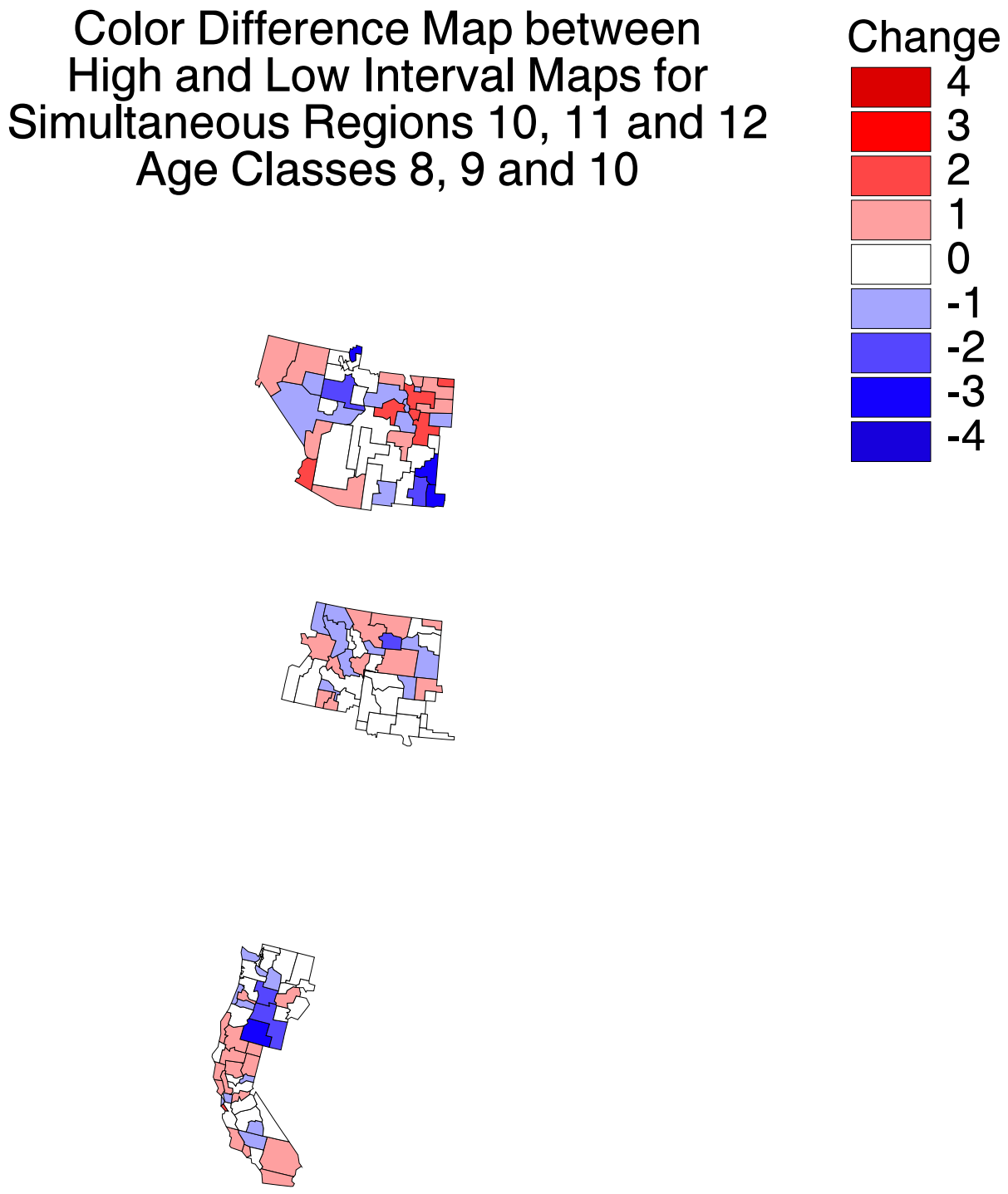


Figure 4.37. Individual Legend Color Difference Maps for Simultaneous Maps Regions 10, 11 and 12.

Table 4.7
Individual Legend Credible Interval difference between lower and upper bound maps.

Lower Quintile	Upper Quintile					
	1	2	3	4	5	
1	89	49	19	4	0	161
2	37	40	53	29	0	159
3	19	33	32	58	19	161
4	13	22	27	41	55	158
5	3	15	29	27	85	159
	161	159	160	159	159	798

Table 4.8
Individual Legend HPD Interval difference between lower and upper bound maps.

Lower Quintile	Upper Quintile					
	1	2	3	4	5	
1	93	46	17	5	0	161
2	34	43	55	27	0	159
3	18	31	34	57	21	161
4	12	22	28	40	56	158
5	5	16	26	30	82	159
	162	158	160	159	159	798

Table 4.9
Individual Legend Simultaneous Interval difference between lower and upper bound maps.

Lower Quintile	Upper Quintile					
	1	2	3	4	5	
1	93	46	17	5	0	161
2	34	43	55	27	0	159
3	18	31	34	57	21	161
4	13	22	28	40	56	159
5	4	16	26	30	82	158
	162	158	160	159	159	798

Table 4.10
Difference between individual legend lower and upper bound maps.

Method	Reg	-4	-3	-2	-1	0	1	2	3	4
CI		3	28	70	124	287	215	67	4	0
HPD		5	28	66	123	292	214	65	5	0
SγM	All	4	29	66	123	292	214	65	5	0
SγM	1	0	0	0	2	19	2	0	0	0
SγM	2	0	0	1	8	31	8	1	0	0
SγM	3	0	0	2	4	25	6	1	0	0
SγM	4	0	2	5	13	46	15	7	0	0
SγM	5	0	0	5	18	44	14	6	1	0
SγM	6	0	0	7	22	59	30	3	0	0
SγM	7	0	0	0	10	26	8	1	0	0
SγM	8	0	1	9	28	38	11	16	2	0
SγM	9	0	0	3	29	54	23	6	0	0
SγM	10	0	3	2	8	12	9	6	0	0
SγM	11	0	0	1	8	19	10	0	0	0
SγM	12	0	1	2	10	19	15	1	0	0

Note: SγM denotes Single-γ Method and Reg the region. The difference presented is the Lower map's color number subtracted from the Upper map's color number.

4.5 Double-γ Method Simultaneous Interval

Because Double-γ Method maps are virtually indistinguishable from Single-γ Method maps, additional maps are not presented. Instead, we compare the value of γ from the Single-γ Method with γ_1 and γ_2 from the Double-γ Method in Table 4.11. As we expect, the value of γ (and γ_1 and γ_2) is generally smaller when more areas are simultaneously considered.

To compare the sensitivity of the simultaneous intervals on the prerequisite of HPD intervals, we obtain the simultaneous intervals based on the credible intervals. The γ and γ_1 and γ_2 values based on CIs are given in Table 4.12. To ease comparison, the difference of these values HPD $-$ CI are given in Table 4.13.

We notice that there are differences between values of γ, γ_1 and γ_2 when starting with credible intervals versus using HPD intervals. The difference is not large for the Single-γ Method where no ordinate optimality criterion is specified. However, there is a much larger difference for the Double-γ Method where the method compensates when starting with the credible intervals of nonsymmetric densities to obtain equal ordinates. This small difference is attributed to the symmetry of our individual distributions. If the indiviual distributions are highly skewed, this difference will be even greater.

Table 4.11
Gamma Values from Single-γ Method and Double-γ Method (S^*) under a variety of optimization criteria using HPD Intervals.

		Single-γ Method
Reg	nc	γ
All	798	0.7711593
1	23	0.9356322
2	49	0.9192618
3	38	0.9109113
4	88	0.8659650
5	88	0.8959517
6	121	0.8849109
7	45	0.8949770
8	105	0.8395072
9	115	0.8682747
10	40	0.8657598
11	38	0.8992667
12	48	0.9094602

		S_1^*	S_2^*	S_3^*
Reg	nc	γ_1, γ_2	γ_1, γ_2	γ_1, γ_2
All	798	0.7711571, 0.7711635	0.7711563, 0.7711650	0.7711563, 0.7711650
1	23	0.9356288, 0.9356354	0.9356285, 0.9356356	0.9356285, 0.9356356
2	49	0.9192618, 0.9192618	0.9192618, 0.9192618	0.9192618, 0.9192618
3	38	0.9108956, 0.9109269	0.9108953, 0.9109272	0.9108953, 0.9109272
4	88	0.8658489, 0.8660824	0.8658468, 0.8660845	0.8658468, 0.8660845
5	88	0.8959587, 0.8959435	0.8959575, 0.8959448	0.8959575, 0.8959448
6	121	0.8848981, 0.8849294	0.8848980, 0.8849296	0.8848979, 0.8849298
7	45	0.8949656, 0.8949870	0.8949655, 0.8949870	0.8949655, 0.8949870
8	105	0.8393821, 0.8396899	0.8393824, 0.8396894	0.8393824, 0.8396894
9	115	0.8682786, 0.8682702	0.8682784, 0.8682703	0.8682784, 0.8682703
10	40	0.8657574, 0.8657622	0.8657570, 0.8657627	0.8657570, 0.8657627
11	38	0.8992640, 0.8992702	0.8992674, 0.8992660	0.8992648, 0.8992692
12	48	0.9094743, 0.9094476	0.9094726, 0.9094492	0.9094728, 0.9094489

Table 4.12
Gamma Values from Single-γ Method and Double-γ Method (S^*) under a variety of optimization criteria using Credible Intervals.

		Single-γ Method
Reg	nc	γ
All	798	0.7624622
1	23	0.9374245
2	49	0.9189441
3	38	0.9099173
4	88	0.8640358
5	88	0.8955278
6	121	0.8839585
7	45	0.8998193
8	105	0.8372418
9	115	0.8665459
10	40	0.8625022
11	38	0.9019496
12	48	0.9087083

		S_1^*		S_2^*		S_3^*	
Reg	nc	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2
All	798	0.7586456,	0.7753012	0.7586455,	0.7753015	0.7586455,	0.7753015
1	23	0.9380754,	0.9366143	0.9380755,	0.9366142	0.9380755,	0.9366142
2	49	0.9176296,	0.9205334	0.9176297,	0.9205332	0.9176296,	0.9205334
3	38	0.9084255,	0.9118374	0.9084250,	0.9118379	0.9084249,	0.9118380
4	88	0.8621256,	0.8670360	0.8621253,	0.8670365	0.8621253,	0.8670365
5	88	0.8949273,	0.8964061	0.8949273,	0.8964061	0.8949273,	0.8964061
6	121	0.8827366,	0.8861299	0.8827363,	0.8861304	0.8827363,	0.8861304
7	45	0.9022754,	0.8968298	0.9022771,	0.8968276	0.9022754,	0.8968298
8	105	0.8360214,	0.8398151	0.8360210,	0.8398157	0.8360210,	0.8398157
9	115	0.8652675,	0.8687062	0.8652675,	0.8687062	0.8652674,	0.8687063
10	40	0.8581181,	0.8683229	0.8581180,	0.8683230	0.8581181,	0.8683229
11	38	0.9032226,	0.9002534	0.9033201,	0.9001145	0.9032235,	0.9002520
12	48	0.9076361,	0.9100729	0.9076402,	0.9100680	0.9076403,	0.9100678

Table 4.13
Difference in Gamma Values from Single-γ Method and Double-γ Method (S^*) under a variety of optimization criteria between using HPD − CI Intervals.

		Single-γ Method
Reg	nc	γ
All	798	−0.0086971
1	23	0.0017923
2	49	−0.0003177
3	38	−0.0009940
4	88	−0.0019292
5	88	−0.0004239
6	121	−0.0009524
7	45	0.0048423
8	105	−0.0022654
9	115	−0.0017288
10	40	−0.0032576
11	38	0.0026829
12	48	−0.0007519

		S_1^*		S_2^*		S_3^*	
Reg	nc	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2
All	798	−0.0125115,	0.0041377	−0.0125108,	0.0041365	−0.0125108,	0.0041365
1	23	0.0024466,	0.0009789	0.0024470,	0.0009786	0.0024470,	0.0009786
2	49	−0.0016322,	0.0012716	−0.0016321,	0.0012714	−0.0016322,	0.0012716
3	38	−0.0024701,	0.0009105	−0.0024703,	0.0009107	−0.0024704,	0.0009108
4	88	−0.0037233,	0.0009536	−0.0037215,	0.0009520	−0.0037215,	0.0009520
5	88	−0.0010314,	0.0004626	−0.0010302,	0.0004613	−0.0010302,	0.0004613
6	121	−0.0021615,	0.0012005	−0.0021617,	0.0012008	−0.0021616,	0.0012006
7	45	0.0073098,	0.0018428	0.0073116,	0.0018406	0.0073099,	0.0018428
8	105	−0.0033607,	0.0001252	−0.0033614,	0.0001263	−0.0033614,	0.0001263
9	115	−0.0030111,	0.0004360	−0.0030109,	0.0004359	−0.0030110,	0.0004360
10	40	−0.0076393,	0.0025607	−0.0076390,	0.0025603	−0.0076389,	0.0025602
11	38	0.0039586,	0.0009832	0.0040527,	0.0008485	0.0039587,	0.0009828
12	48	−0.0018382,	0.0006253	−0.0018324,	0.0006188	−0.0018325,	0.0006189

5. CONCLUSION

In Chapter 1 we discussed choropleth maps and motivated the need for simultaneous intervals in mapping applications. In Chapter 2 we discussed interval estimation, and developed the Single-γ Method and Double-γ Method simultaneous intervals. We have shown how to (a) find an exact content $100(1-\alpha)\%$ simultaneous interval having a unique solution with a small number of parameters (one or two), and how to (b) incorporate a variety of possible optimality criteria. In Chapter 3 we have shown how to (c) fit the Poisson-gamma hierarchical regression model and how to (d) construct intervals in this model context. Using an output analysis from the Metropolis-Hastings sampler, we have shown how to (e) perform rate parameter estimation to construct the mean map, and how to (f) construct simultaneous intervals to ensure joint simultaneous coverage of $100(1-\alpha)\%$. In Chapter 4 we presented results from the simultaneous interval methods.

5.1 Accounting for map variation, epidemiological discussion

The model in Chapter 3 included a multiple linear regression to account for COPD rate variation due to the four covariates in Table 3.1. Since the observed variation is already adjusted for the covariates, what remains is unexplained variation. Areas where relationship to covariates is not clear will have large variation.

We can examine the estimate variation unaccounted for by the covariates using difference map in the third map in Figure 4.33 detailing the difference in quintile between the lower and upper maps (upper$-$lower). The plot in Figure 5.1 (originally from Section 4.3.3) gives the individual legend Single-γ Method simultaneous interval map. Areas exhibiting the most variation are (3 color difference, there were none that had 4) HSA 215 (Putnam, TN – Overton, TN), HSA 252 (Greene, TN – Cocke,

TN), HSA 338 (McLean (Bloomington), IL – De Witt, IL), HSA 361 (Clinton, IA – Whiteside, IL) and HSA 373 (Kane (Aurora), IL – De Kalb, IL). Areas exhibiting average variation include (0 color difference) HSA 3 (Sussex, DE – Wicomico, MD), HSA 294 (Emmet, MI – Cheboygan, MI), HSA 565 (Ellis, KS – Graham, KS) and HSA 816 (Inyo, CA – Mono, CA). Areas exhibiting the least variation are (-4 color difference) HSA 513 (Bee, TX – Karnes, TX), HSA 518 (Howard, TX – Glasscock, TX), HSA 704 (Pueblo (Pueblo), CO – Colfax, NM) and HSA 769 (Otero, NM – Lincoln, NM).

5.2 Looking ahead

Another obvious factor effecting parameter variation is the size of the sample (number of deaths in our case), a larger sample size contributing to a smaller variation. HSAs that exhibit variation either contrary or in excess of the sample size effect are worth closer inspection. Accounting for this effect might be done within the model itself, or as part of the output analysis.

Other interval "stretching" techniques can be considered to most preserve the equal ordinate condition. Our Single-γ Method, $(\gamma a, b/\gamma)$, sends the left interval bound a to zero at roughly the same rate as it sends the right interval bound b to infinity while γ is close to one. However, the more the interval needs to be widened to accommodate the desired probability content (γ close to zero), the further the right bound is modified relative to the left bound. In our example we found similar results for the Double-γ Method, $(\gamma_1 a, b/\gamma_2)$, which includes an ordinate optimization criterion in order to maintain the equal ordinate condition.

Another equal ordinate condition optimization criterion to consider optimizes over values of the pdf evaluated at the joint individual interval bounds. That is, for ℓ sets of interval bounds $(a_i, b_i), i = 1, \ldots, \ell$, construct the 2^ℓ sets of joint interval bounds with the objective of making the joint ordinates equal. These would be the prefered ordinates to optimize rather than the individual ordinates.

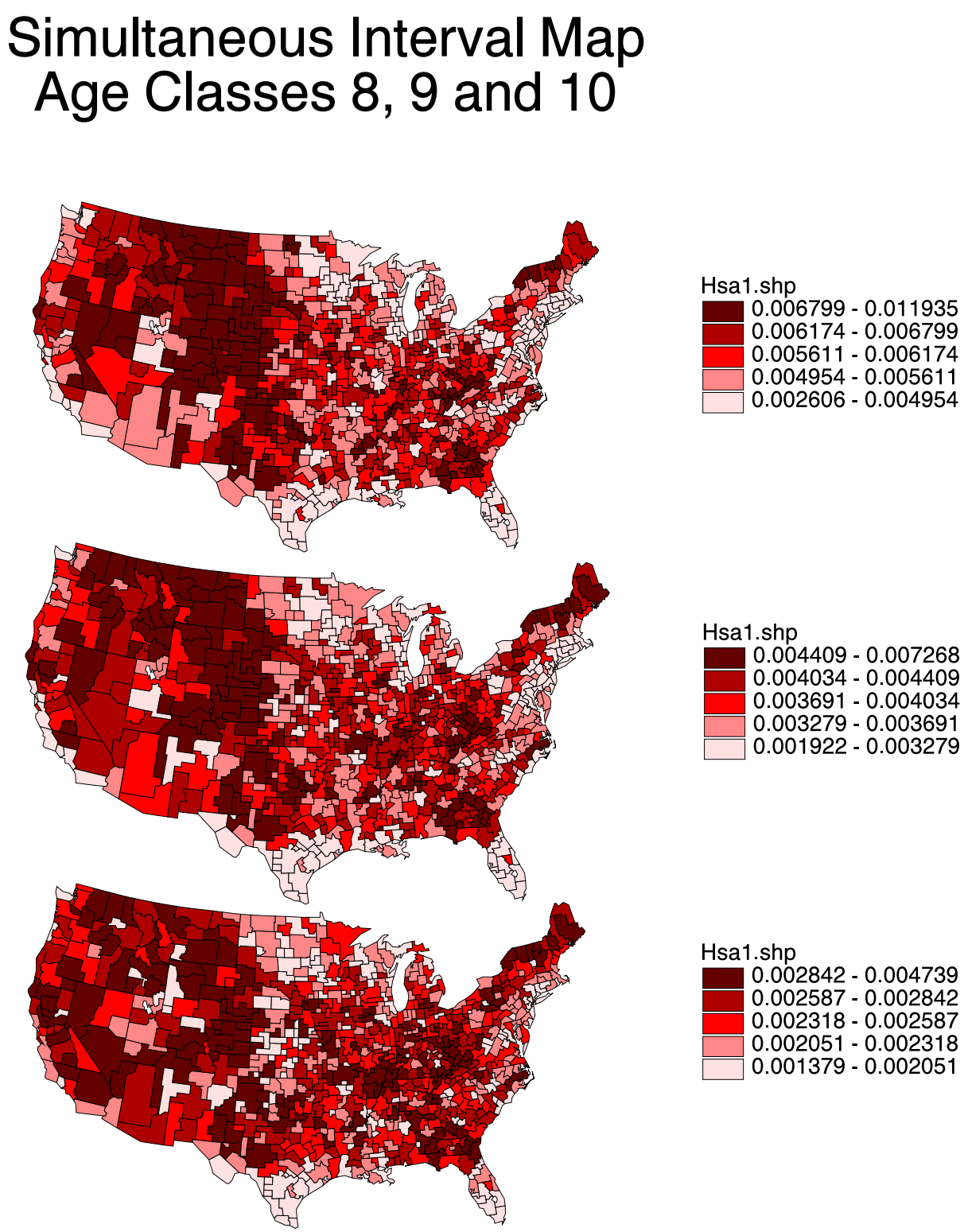


Figure 5.1. Individual Legend Single-γ Method Simultaneous Interval Map, recapitulation.

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A. STATISTICAL METHODOLOGY

The methods used in analyzing data and drawing inferences are termed the statistical methodology. Underlying the model discussed in detail in this paper, there is a significant amount of statistical methodology. The main focus of this chapter is the Metropolis-Hastings sampler, which is used extensively to support model fitting. The material in this chapter is summarized from a number of sources. Principal among them are [Bernardo and Smith, 1994], [Lee, 1997], [O'Hagan, 1994] and [Tierney, 1994], with much of the material available in most texts on stochastic models.

A.1 Statistics

It is mentioned in an introductory text [Connor and Morell, 1964], that the term statistics refers to a collection of numerical facts and estimates, the purpose of statistics being to enable correct decisions to be taken. Elsewhere [Mood et al., 1963], it is noted that one of the functions of statistics is the provision of techniques for making inductive inferences based upon data. It is also important to have an estimate of the uncertainty inherent in those inferences.

In real life situations, information can often be usefully summarised numerically. For example, percentage unemployment, mortality rate for males aged 65 or older, or grade point averages. Statistics have long been used to estimate such quantities based on observed data. For example a random survey of four-year public college students in a particular country, may show that, say, 30 out of 100 students drop out before their second year. From this it may be inferred that the proportion of students in the country attending four-year public college who will drop out before their second year is in the region of 30%. Of course, there is some uncertainty attached to this estimate, and if another sample of 100 four-year public students

were surveyed then a different answer may have been obtained, and there are ways of estimating the uncertainty. In classical statistical inference what one is doing is making an estimate of the true (but unknown) proportion, based on data. The assumption is that the proportion of the total population of students who drop out before their second year is a fixed unknown, and that data is being used to estimate it.

In the context of this research, statistics may be defined to be concerned with the analysis of data collected under uncertainty. Specifically, the aim is to develop suitable models, in order to make reliability predictions based upon recorded actual data. Classical, or frequentist, methodology in statistics concentrates on making inferences about the true situation having observed certain data, whereas the Bayesian approach is concerned with updating subjective knowledge in the light of data.

A.2 Bayesian Approach

Bayesian inference is different from classical inference, in that one is concerned with answering the following question, "What should a rational person believe after collecting the data, given what was believed before the data was collected?"

Essentially, this question differs from what a classical statistician asks in a number of different ways;

- The question is unapologetically subjective.
- Previous information is important.
- The focus is rational belief based on current knowledge, rather than on obtaining an estimate of any "true" value.

The Bayesian framework has attractions for a number of reasons [Bernardo and Smith, 1994]. Bayesian statistics has a strong axiomatic foundation, it incorporates prior information directly into the analysis, and it has a naturally formulated decision structure. Bayesian inference has not been as commonly used as frequentist methods in the past, in part due to computational complexities [Lee, 1997]. Since about 1960

there has been a revival of interest [O'Hagan, 1994] to the extent that it is now well established as an alternative to classical methods.

As to the question of why one might choose to undertake a Bayesian analysis of a situation, rather than an appropriate classical analysis, the answer is simple. Apart from the philosophical reasons, for a number of real problems the answer is that the methodology works [RSSC, 1997] .

A.2.1 Formal Bayesian Methodology

More formally, the following is the method employed. As mentioned above, statistics is concerned with the estimation of numerical quantities. In the Bayesian context, the quantities of interest will be random variables, and could, for example, be the proportion of students who drop out as referred to in Section A.1. Before an experiment or survey, the prior knowledge about the quantities of interest are summarised in the form of a probability statement.

Denote the parameter or parameters of interest as ϑ or $\underset{\sim}{\vartheta}$ and the state of current experiences to date as H. Such experience might be to do with knowledge of the SAT scores of high school students, the state of the economy, generosity of government grants, and indeed knowledge of previous studies. The probability statement about initial beliefs is denoted $p(\vartheta|\, H)$ (read, "the probability of (parameter) theta given (experienced state) H") and is termed the prior belief. Since this is a probability statement it takes the form of a probability distribution and is often referred to as the prior distribution, or more simply the prior.

Prior Knowledge

There are a number of philosophical issues raised in any discussion on prior probabilities. For further information on such discussion see [O'Hagan, 1994], [Lee, 1997], [Bernardo and Smith, 1994]. It is essential, when considering ϑ as a random variable, to assign prior probabilities, simply because such must exist. In the case

where prior knowledge shows that no particular value or values of ϑ are more likely than any others, then ϑ will be uniformly distributed. That is to say, $p(\vartheta|\, H) \propto 1$, on the support, or domain, of the parameters. It is important to note that such a statement of initial belief is saying that at the outset, it is believed that, for example, 100% of students dropping out is as equally likely to be prevalent as 0%, or indeed any other intermediate value.

A more reasonable situation would be one where students are being surveyed in the light of previous work and with some knowledge of the situation involved. Then the prior might take the form of a normal distribution with some mean and (perhaps large, indicating uncertainty) variance.

For notational simplicity the prior $\pi(\vartheta)$ is written and taken to mean $p(\vartheta|\, H)$ from here onwards.

Model or Likelihood

The idea of likelihood is common to all statistical inference, and is well understood by frequentist and Bayesian statisticians alike.

The relationship between the parameters of a model and the observables is fundamental to the process of updating knowledge of parameters based upon the data. The likelihood is sometimes termed the model, and takes the form of a probability statement $p(X|\, \vartheta)$, where X are the observable data in the system.

Note that the likelihood is a conditional probability statement as to how likely it is for X to be observed if the parameters take the value ϑ. In a statistical analysis, it is the knowledge of ϑ which is of interest, that is to say, the distribution of ϑ given that X is observed. This is termed the posterior, and is dealt with below.

Other methods of inference concentrate on the likelihood in their analysis, in which case the focus is $p(X|\, \vartheta)$ as a function of ϑ for fixed X. Of course while $\int_X p(X|\, \vartheta)\, \mathrm{d}X = 1$ the same is not true of the integral with respect to ϑ. For this reason, and to avoid confusion, the likelihood is sometimes written $l(\vartheta|\, X)$.

An Example

O'Hagan [O'Hagan, 1994] gives a somewhat contrived example of why it is important to consider the prior as well as the likelihood. Let G be the event of seeing a big green structure, with blob like attachments outside a window. Let T be the hypothesis that a tree is outside the window, and let C be the hypothesis that a cardboard model is outside the window. Since C and T are equally consistent with the observation, G, one shouldn't have any reason for believing one over the other. That is $l(C|\,G) = l(T|\,G)$. However, the probability that C is in fact outside the window, conditional on the observation, is $p(C|\,G)$, which depends on $p(C)$, the prior probability of cardboard structures being outside windows, and is likely to be much less than $p(T|\,G)$. Incorporation of prior knowledge is an essential part of the inference.

Posterior Distribution

Of interest to the modeller, then, is the conditional distribution of the parameters, given the data, that is $p(\vartheta|\,X)$. Bayes Theorem for random variables [Lee, 1997] yields

$$\begin{aligned} p(\vartheta|\,X) &= \frac{p(X|\,\vartheta)\pi(\vartheta)}{p(X)} \\ &\propto p(X|\,\vartheta)\pi(\vartheta). \end{aligned}$$

The distribution $p(\vartheta|\,X)$ is termed the posterior distribution and describes the current state of knowledge about ϑ, given the initial knowledge of ϑ, together with the model, such knowledge having been updated by information. The constant of proportionality in the above is just $\frac{1}{p(X)}$ where $p(X)$ can be obtained from $p(X) = \int p(X|\,\vartheta)\pi(\vartheta)\,\mathrm{d}\vartheta$.

The Bayesian method, is then, quite straightforward [French and Smith, 1997]:

1. construct a model, obtaining a likelihood $p(X|\,\vartheta)$;
2. elicit a prior distribution $\pi(\vartheta)$;

3. derive the posterior density $p(\vartheta|\, X)$ as above.

In practice these tasks can be difficult to implement.

A.2.2 Predictive Distribution

In the case where one is interested in making a probability statement about the distribution of the random variable of interest, given that one has observed realizations, or data, $\mathcal{D} = \{x_1, \ldots, x_n\}$ one can use the marginal distribution

$$f(X|\,\mathcal{D}) \;=\; \int_\Theta f(X|\,\mathcal{D},\Theta) f(\Theta|\,\mathcal{D})\,\mathrm{d}\Theta$$

which is termed the predictive distribution, and $f(\Theta|\,\mathcal{D})$ is proper. In practice, this integral can not generally be calculated, since the analytical form of $f(\Theta|\,\mathcal{D})$ is not known. However, samples may be drawn from $f(\Theta|\,\mathcal{D})$, in which case the predictive distribution, together with any other distributions may be estimated using the kernel density estimate.

A.2.3 Kernel Density Estimation

Kernel density estimation consists of estimating a posterior density for a function of interest, using samples from the posterior, often drawn using one of the many numerical techniques. Let $\vartheta_1, \ldots, \vartheta_n$ be samples from the posterior distribution $f(\Theta|\,\mathcal{D})$. If one is interested in the properties of the posterior density function $g(X|\,\mathcal{D})$, where conditional on Θ, X is independent of $\mathcal{D}$, that is $g(X|\,\mathcal{D},\Theta) = g(X|\,\Theta)$, the following result is useful;

$$\begin{aligned} g(X|\,\mathcal{D}) &= \int_\Theta g(X|\,\mathcal{D},\Theta) f(\Theta|\,\mathcal{D})\,\mathrm{d}\Theta \\ &= \int_\Theta g(X|\,\Theta) f(\Theta|\,\mathcal{D})\,\mathrm{d}\Theta \\ &= E_{\Theta|\,\mathcal{D}}[g(X|\,\Theta)]. \end{aligned}$$

This expected value may be approximated in the usual fashion, as a simple numerical average of the values of the function at each of the sample points. That is, using $\hat{g}$ given by

$$\hat{g}(X|\,\mathcal{D}) \;=\; \frac{1}{n}\sum_{i=1}^{n} g(X|\,\vartheta_i).$$

The fact that $\hat{g}$ is a density function follows from the fact that each of the $g(X|\,\vartheta_i)$ is a density function. Kernel density estimation is a standard method of examining posterior distributions and properties of functions of the parameters.

A.2.4 A Simple Example - $N(\mu, \frac{1}{\tau})$

Consider the case of drawing from a population of unknown mean, μ, but known variance $\frac{1}{\tau}$. (τ is termed precision, and is just the reciprocal of variance.)

The model is that the data, X, will be normally distributed with unknown mean but given variance. Thus, in terms of a single observation, x, we can write down the likelihood;

$$p(x|\,\mu) \;=\; \sqrt{\frac{\tau}{2\pi}} \times \exp\Big\{ -\frac{\tau}{2}(x-\mu)^2 \Big\}.$$

The next step is to elicit a prior for μ. It may be reasonable to assume that the prior beliefs about μ can be expressed as a normal distribution, that is

$$\mu \;\sim\; N\left(\nu_{\text{prior}}, \frac{1}{\rho_{\text{prior}}}\right)$$

where both ν_{prior} and ρ_{prior} are specified. Typically ν_{prior} is the expected location of μ, and ρ_{prior} is an expression of how precise that estimate is. In general, ρ_{prior} will be small.

Thus, having collected data, it is possible to derive the posterior for μ according to Bayes theorem for random variables;

$$\begin{aligned} p(\mu|\,x) \;&\propto\; p(x|\,\mu)\pi(\mu) \\ &=\; \sqrt{\frac{\tau}{2\pi}} \times \exp\Big\{ -\frac{\tau}{2}(x-\mu)^2 \Big\} \times \sqrt{\frac{\rho_{\text{prior}}}{2\pi}} \times \exp\Big\{ -\frac{\rho_{\text{prior}}}{2}(x-\nu_{\text{prior}})^2 \Big\} \\ &\propto\; h(\nu_{\text{prior}}, \rho_{\text{prior}}, x) \times \exp\Big\{ -\frac{\mu^2}{2}(\rho_{\text{prior}}+\tau) + \mu(\nu_{\text{prior}}\rho_{\text{prior}} + x\tau) \Big\} \end{aligned}$$

where $h(\cdot)$ is independent of μ. Defining

$$\rho_{\text{post}} = \rho_{\text{prior}} + \tau \quad \text{and} \quad \nu_{\text{post}} = \frac{\tau}{\rho_{\text{post}}} x + \frac{\rho_{\text{prior}}}{\rho_{\text{post}}} \nu_{\text{prior}}$$

and multiplying by $\exp\left\{ -\frac{1}{2}\rho_{\text{post}}\nu_{\text{post}}^2 \right\}$ which is independent of μ, the above is

$$\begin{aligned} & \exp\left\{ -\frac{\mu^2}{2}(\rho_{\text{prior}} + \tau) + \mu(\nu_{\text{prior}}\rho_{\text{prior}} + x\tau) \right\} \\ & \qquad = \exp\left\{ -\frac{1}{2}(\mu^2\rho_{\text{post}} - 2\mu(\nu_{\text{post}}\rho_{\text{post}}) + \rho_{\text{post}}\nu_{\text{post}}^2) \right\} \\ \text{which reduces to} \quad & = \exp\left\{ -\frac{\rho_{\text{post}}}{2}(\mu - \nu_{\text{post}})^2 \right\} \end{aligned}$$

which is the form of the normal density with mean ν_{post} and precision ρ_{post}. Thus, in the case of inference for the unknown mean, with normal prior, the posterior is normal. This simple form of the posterior depends on the choice of the prior, given the likelihood. The choice of prior that leads to the simple posterior, is called a conjugate prior; more formally, given a likelihood, $l(\vartheta|\, X)$, then a prior chosen from a family of densities, such that the posterior is also from that family, is said to be conjugate.

As can be seen from the above, in the case of conjugate densities, the problem of obtaining a posterior is simplified [Bernardo and Smith, 1994]. However, this is only appropriate where the chosen prior distribution, with suitable parameters can accurately represent the prior knowledge. The alternative is to use numerical techniques to obtain the properties of interest from the posterior distribution.

The question of prior elicitation is one that needs mentioning also. Apart from the philosophical difficulties that many have with prior probabilities, there are practical problems which need addressing.

A.2.5 Prior Elicitation and Non-informative Prior

Difficulties have arisen with specifying a prior in the situation where there is, in fact, no actual prior information. While it was possible to specify a uniform prior for

the example of determination of the proportion of college dropouts (i.e. $\pi(\vartheta) = 1$) this is not possible where the possible range for ϑ is infinite and the prior being a proper distribution. A prior $\propto 1$ for the range $(0, \infty)$ is a solution, as an improper prior, but even then issues arise as to transformations of the parameters of interest. Clearly, if $\pi(\vartheta) = 1$ then all values of ϑ in the range [0,1] are equally likely. This is not prior ignorance as maintained in [O'Hagan, 1994] but is in fact a concrete and active statement of prior belief that all values of ϑ are as likely as each other, and that belief will quite properly correspond with a non-uniform prior for transformations of ϑ. For example, if we have N competitors each running in a race, with 1 from country A and $N - 1$ from country B, and prior information tells us that each is equally likely to win the race, then this does not correspond to prior information that country A and country B are equally likely to have winners. It is important, therefore to ensure that it is clear as to what prior information is being elicited.

Prior elicitation is the process of specifying, in the form of a probability distribution, prior information about the parameters of interest. The practical issues detailing methods of obtaining an informative prior are dealt with in [O'Hagan, 1998]. Examples in practice are mentioned in [RSSC, 1997] and [van Noortwijk et al., 1997]. It is the assertion of some authors that all priors are informative and that for this reason, due consideration should be given in every circumstance to the elicitation process.

In including an informative prior, the statistical analysis is not objective. It has been mentioned in Section A.2 that the Bayesian framework is unapologetically subjective, and this is emphasised once again here.

In the past there have been attempts to "objectify" Bayesian techniques. Notably we have work by Jeffreys [Jeffrey, 1961], but this depends on the form of the data. Subjective scientific inquiry seems a contradiction in terms, but is quite acceptable, provided that we realise that we have subjective inputs, and are careful about such things. For this reason, Bayesian statisticians are interested in concepts of sensitivity and robustness [Berger, 1990].

A.3 Sampling from the Posterior Distribution

In any Bayesian analysis, the aim is to obtain posterior estimates for some parameters, or functions of parameters. In a limited number of cases, such estimates may be directly obtained, for example, in the case of conjugate priors. However, in general, this is not the case, and one has to resort to more indirect methods.

Before the advent of modern numerical techniques, and computing power, the necessary calculations were in practical terms impossible. However, because of the advances of technology, and due to the development of powerful numerical methods in a range of disciplines, infeasible problems of the past have become tractable.

The most important of these techniques in Bayesian statistics has been Markov chain Monte Carlo and in particular Gibbs and Metropolis-Hastings sampling.

A.3.1 Stratified Sampling

Consider a set of N types of job within an organisation, which has a total of M employees. Let J_j, where $1 \leq j \leq N$, be the number of people who have a job of type j with all people doing the same type of job getting paid the same salary. Then, clearly

$$\sum_{j=1}^{N} J_j = M.$$

If interested in the average salary paid and if M is very large the average may be approximated as

$$\mu_X \approx \bar{X} = \frac{1}{m} \sum_{j=1}^{m} X_i,$$

where we sample a total of m people from the organisation and X_i is the salary paid to the i^{th} person we sampled. Ordinary random sampling would involve picking the m people uniformly from the total population of M people in the organisation. However, another method would be to ensure that the probability of choosing a person from job type j is the number of people doing job type j divided by the total

number of people, M. This latter idea is just stratified sampling and is an important and well known sampling technique.

A.3.2 Importance Sampling

Importance sampling is a technique for numerically approximating an integral. It is mentioned here as a basis for the numerical concepts which follow. It is similar to stratified sampling in that the fundamental idea is that the sampling process is distorted, to take into account the weighting of the underlying distribution.

An example of importance sampling in a Monte-Carlo context, is detailed in Section A.3.3, but the basic principle follows. In wanting to estimate the integral

$$I = \int_{-\infty}^{\infty} g(x)f(x)\,\mathrm{d}x,$$

where $f(x)$ is a density function, one could sample n values of x from $f(x)$ and then approximate with

$$\hat{I} = \frac{1}{n}\sum_{i=1}^{n} g(x_i).$$

Alternatively, m values of x could be sampled from another density $h(x)$ and then I could be estimated using

$$\hat{I} = \frac{1}{m}\sum_{i=1}^{m} \frac{g(x_i)f(x_i)}{h(x_i)}.$$

Consideration can then be made as to how $h(x)$ may be chosen so that the estimator is most efficient. It turns out that the most efficient form for $h(x)$ samples from areas where $g(x)$ is large, provided that $f(x)$ is not small, [Kleijnen, 1974]. Such ideas are important in any method when simulating from the posterior.

A.3.3 Monte Carlo Method

Markov chain Monte Carlo (MCMC) is an important technique used by Bayesian practitioners to sample from the posterior distribution. The Monte Carlo method is,

in general terms, any technique used for obtaining solutions to deterministic problems using random numbers. The term Monte Carlo was coined by von Neumann and Ulam in the 1940's in the context of such problems [Morgenthal, 1961].

By way of general example consider the integral

$$I = \int_{x_1}^{x_2} f(x)\,\mathrm{d}x.$$

There are many quadrature methods, with varying degrees of accuracy, which can be used to evaluate this integral. The trapezium rule and Simpson's method (see "Numerical Recipes", [Press et al., 1986]) are both quadrature methods which involve evaluating $f(x)$ at evenly spaced points, x_i, on a grid. A weighted average of these values $f(x_i)$ gives an estimate of the integral

$$\hat{I} = (x_2 - x_1)\frac{\sum_i w_i f(x_i)}{\sum_i w_i}$$

where the w_i are the weights. The weights and the sampling points are different for different methods of quadrature but all the methods sample the function $f(x)$ using pre-determined weights and sampling points.

Monte Carlo methods do not use specific sampling points but instead we choose points at random. The Monte Carlo estimate of the integral is then,

$$\begin{aligned}\hat{I} &= (x_2 - x_1)\frac{1}{N}\sum_{i=1}^{N} f(x_i) \\ &= (x_2 - x_1)\bar{f}\end{aligned}$$

where the x_i are randomly sampled points and $\bar{f}$ is the arithmetic mean of the values of the function $f(x)$ at the sampling points. The standard deviation of the mean is given by

$$\sigma_m = \frac{\sigma}{\sqrt{N}}$$

where

$$\sigma^2 = \frac{\sum_i [f(x_i) - \bar{f}]^2}{N - 1}$$

gives an estimate of the statistical error in the Monte Carlo estimate of the integral. Note that the error goes as $\frac{1}{\sqrt{N}}$, independent of the dimensionality of the integral.

A specific simple example of this [Kleijnen, 1974] is the evaluation of the following integral;

$$I \;=\; \int_y^\infty \frac{1}{x}\lambda e^{-\lambda x}\,\mathrm{d}x.$$

Analytical solution of the above is difficult, but Monte Carlo simulation proposes the following;

1. Let $i = 1$; Let N be some large number.
2. Sample x_i from the exponential so $f(x) = \lambda e^{-\lambda x}$.
3. Let $g(x_i) = \frac{1}{x_i}$ if $x_i > y$ and 0 otherwise,
4. Let $i = i + 1$. If $i < N$ return to step 2.
5. Then I is estimated by $\hat{I} = \frac{1}{N}\sum_{i=1}^{N} g(x_i)$.

Observe that the above is the standard estimator for $E\left(\frac{1}{x}|\, x < y\right)$. In practice, many of the values of interest are expected values. To obtain posterior expectations of a function of our parameter, $f(\vartheta)$, we need to calculate integrals of the type

$$E(f(\vartheta)|\, X) \;=\; \frac{\int f(\vartheta)p(X|\,\vartheta)p(\vartheta)\,\mathrm{d}\vartheta}{p(X)}.$$

It is possible to use the above idea of Monte Carlo methods, importance sampling, together with some Markov chain theory, to efficiently approximate such expressions. Some theory is outlined below.

A.3.4 Markov Chain

Here some definitions are introduced leading to a theorem.

Definition A.3.1 (Stochastic process) *A stochastic process is a collection of random variables, X_i where $i \in I$ for some indexing set I, with each X_i taking values in a state space, S.*

Definition A.3.2 (Markov Chain) *A Markov chain is a stochastic process with a discrete indexing set, I, such that the conditional distribution of X_{t+1} is independent of all other previous states given X_t, that is $p(X_{t+1}|\, X_1, X_2, \ldots, X_t) = p(X_{t+1}|\, X_t)$.*

For simplicity, theory and details are given for a discrete state space, S.

Definition A.3.3 (Stationary (in time)) *A Markov Chain is said to be stationary if and only if for all $j, k \in S$, and for all $i \in \{1, 2, 3, \ldots\}$,*

$$P(X_i = j|\, X_{i-1} = k) \;\; = \;\; P(X_1 = j|\, X_0 = k).$$

A stationary Markov chain is sometimes referred to as *homogeneous in time*, since, by definition, the probability of moving between two states remains constant in time.

Definition A.3.4 (Markov Matrix) *For a stationary Markov chain, the matrix of probabilities,*

$$\mathcal{M}_j^k \;\; = \;\; P(X_n = j|\, X_{n-1} = k)$$

is called the Markov Matrix.

Note that this definition is independent of n (stationarity), that the entries in the Matrix are $\in [0, 1]$ (probabilities) and that $\sum_j \mathcal{M}_j^k = 1$, since the chain must move to some state, j. This is sometimes called a transition matrix, and the associated probabilities called transition probabilities. It is also worth noting that the matrix $[\mathcal{M}]_k^j$ (from j to k) is the matrix of probabilities $P(X_{n+m} = k|\, X_n = j)$.

Definition A.3.5 (Connected) *A Markov chain is said to be connected or irreducible, if for all $j, k \in S$, there exists a sequence $i_1, \ldots, i_n$ such that*

$$\mathcal{M}_j^{i_n} \mathcal{M}_{i_n}^{i_{n-1}} \cdots \mathcal{M}_{i_1}^k \neq 0.$$

That is, there is a non-zero probability of going from state k to state j in n steps, for some n.

Definition A.3.6 (Recurrent) *A state j is said to be recurrent if and only if $\sum_{n=1}^{\infty}[\mathcal{M}^n]_j^j = \infty$, else it is said to be transient.*

Definition A.3.7 (Aperiodic) *The period $d(j)$ of a state j is that integer such that $[\mathcal{M}^n]_j^j \neq 0$, for all n such that d divides n. A state with $d(j) = 1$ is said to be aperiodic.*

Definition A.3.8 (Limiting Distribution) *If*

$$l_j \;=\; \lim_{n\to\infty}[\mathcal{M}^n]_j^i$$

exists for all j (independent of i), then this is called the limiting distribution of the Markov chain.

Definition A.3.9 (Stationary distribution) *A stationary distribution for a Markov chain is a distribution π such that $\pi_j \geq 0$, for all j, $\sum_j \pi_j = 1$ and*

$$\pi \;=\; \mathcal{M}\pi.$$

The stationary distribution is also referred to as the *invariant distribution* or *equilibrium distribution* of a Markov chain.

Theorem A.3.1 (Ergodic) *For an irreducible, aperiodic, positively recurrent Markov chain, a unique limiting distribution exists, which is the invariant distribution for the chain.*

Recall the discussion above regarding stratified and importance sampling. If it were possible to construct a Markov chain that would visit each category the 'correct' number of times, then this method could be used to sample from the distribution of interest. In practice, what 'correct' means here, is that the equilibrium distribution of the Markov chain is the same as the distribution of interest. In a sense this is the reverse of the theory above, since the distribution of interest is known, and the Markov chain needs to be constructed.

It is possible to do this, under certain conditions, and there are a number of ways of doing it. Of primary interest will be the approach of Metropolis-Hastings.

A.3.5 Markov chain Monte Carlo

Let ϕ_j be the distribution of interest. Let $\mathcal{M}_j^i$ be the Markov matrix to be constructed. Now, what is needed is a method of constructing $\mathcal{M}_j^i$ so that it is indeed a Markov Matrix, and that the stationary distribution of this Matrix is ϕ_j, the distribution of interest.

Definition A.3.10 (Detailed Balance) *If ϕ is some probability distribution, then $(\mathcal{M}, \phi)$ satisifies detailed balance if and only if*

$$\mathcal{M}_j^i \phi_i = \mathcal{M}_i^j \phi_j.$$

This property yields a method of constructing a suitable matrix, by using the result of the following Theorem A.3.2.

Theorem A.3.2 *If $(\mathcal{M}, \phi)$ satisfies detailed balance, then ϕ is the stationary distribution for $\mathcal{M}$.*

Proof.

$$\begin{aligned} &\text{Let} && \mathcal{M}_j^i \phi_i = \mathcal{M}_i^j \phi_j \\ &\text{then} && \textstyle\sum_j \mathcal{M}_i^j \phi_j = \sum_j \mathcal{M}_j^i \phi_i = \phi_i \sum_j \mathcal{M}_j^i = \phi_i \end{aligned}$$

■

This is true for all i thus $\mathcal{M}\phi = \phi$, that is ϕ is the stationary distribution for $\mathcal{M}$. So, given a distribution, π_j, it is possible to construct a Markov matrix with π_j as the stationary distribution, by imposing the condition of detailed balance.

That is, if $\mathcal{M}_j^i$ are chosen so that $\mathcal{M}_j^i \pi_i = \mathcal{M}_i^j \pi_j$, and of course subject to the constraints that $\mathcal{M}_j^i \in [0, 1]$ and $\sum_i \mathcal{M}_j^i = 1$, and that the matrix is aperiodic irreducible, then $\mathcal{M}$ is a transition matrix for a Markov chain whose equilibrium distribution is π. The details of how one might go about such a construction are given in the Metropolis-Hastings Algorithm [Metropolis et al., 1953] [Hastings, 1970].

A.3.6 Metropolis-Hastings Algorithm

The Metropolis-Hastings algorithm is a Markov chain Monte Carlo method as described previously. The algorithm sets about constructing a Markov matrix which has as its equilibrium distribution some target density ϕ, of interest to the operator. The algorithm requires the specification of a proposal density, q_j^i, which is a probability density for j and may depend upon i. This is then used in order to propose transitions from i. The condition of detailed balance is then imposed in the following fashion.

Construct α_j^i, the probability of accepting the proposal density, by imposing detailed balance, so that the matrix with entries given by $\mathcal{M}_j^i = q_j^i \alpha_j^i$ is a Markov matrix. This is done as follows:

$$\begin{aligned} \text{If} \quad & q_j^i \phi_i = q_i^j \phi_j, \\ \text{then} \quad & \alpha_j^i = \alpha_i^j = 1. \end{aligned}$$

Otherwise, assume (without loss of generality) that

$$q_j^i \phi_i \quad > \quad q_i^j \phi_j$$

then setting $\alpha_i^j = 1$, and constructing

$$\alpha_j^i \quad = \quad \frac{q_i^j \phi_j}{q_j^i \phi_i},$$

detailed balance holds.

Thus, by defining in general

$$\alpha_j^i \quad = \quad \min \left\{ \frac{q_i^j \phi_j}{q_j^i \phi_i}, 1 \right\},$$

detailed balance is satisfied.

In order that what has been constructed is a Markov matrix which will generate a chain having ϕ as the invariant distribution, it remains to show that $\mathcal{M}$ is indeed Markov. This imposes conditions on the form of q which is related in turn to ϕ. The conditions are as referred to before, aperiodicity (Definition A.3.7) and connectedness

(Definition A.3.5). These are indeed satisfied for quite a large family of densities [Metropolis et al., 1953], [Tierney, 1994].

The algorithm then, works as follows;

1. Set $i = 1$; Set $N =$ some large value; Choose an initial state x_0.
2. Propose y from $q_y^{x_i}$.
3. Accept the proposal with probability $\alpha_j^{x_i}$.
4. If accepted, set $x_{i+1} = y$, else set $x_{i+1} = x_i$.
5. Let $i = i + 1$. If $i < N$ return to step 2.

Although theory demonstrates that a chain constructed using this algorithm has a limiting distribution which is the target distribution, the question of the rate at which the limiting distribution is attained is still open.

Note that the samples $x_0, x_1, \ldots, x_j, \ldots$ generated by the chain will depend upon the choice of x_0 and only when close to the limiting distribution are the samples to be considered as having come from the target distribution.

What size should N be, and for what minimum j should x_j be considered as a sample from the target? A number of methods have been proposed in order to answer these questions. Diagnostic methods of Gelman and Rubin [Gelman and Rubin, 1992] and others are reviewed by Cowles and Carlin [Cowles and Carlin, 1996]. Murdoch and Green have developed methods of demonstrating convergence [Murdoch and Green, 1998], but these methods are far less practical than the heuristic diagnostics described elsewhere. A review of methods to date including those of Murdoch and Green is provided by Brooks and Roberts [Brooks and Roberts, 1998].

The Metropolis-Hastings algorithm is valid for sampling from the $\phi(\underset{\sim}{x})$, for $\underset{\sim}{x} \in \Re^n$, that is for a general vector, $\underset{\sim}{x}$. However, in practice it can be more natural to consider $\underset{\sim}{x}$ as the combination of subvectors $\underset{\sim}{x} = [\underset{\sim}{x}_1, \underset{\sim}{x}_2]'$. It turns out [Chib and Greenberg, 1995] that a transition matrix for a chain which converges to the target $\phi(\underset{\sim}{x})$ may be constructed by considering matrices for a chain which samples from $\phi(\underset{\sim}{x}_1 | \underset{\sim}{x}_2)$ and $\phi(\underset{\sim}{x}_2 | \underset{\sim}{x}_1)$.

A.3.7 Gibbs Sampling

Efficiency of proposal density is an issue, but where the form of the full conditional distributions is known, these may be used to obtain proposals for the above algorithm.

The special case of the Metropolis-Hastings algorithm, where the proposal density, q is the product of full conditional distributions is called the Gibbs sampler. For example, consider the case of sampling from a target $\phi(X, Y)$, with the knowledge of the conditional distributions, $\phi(X|\,Y)$, and $\phi(Y|\,X)$. Now, since $\phi(X, Y) = \phi(X|\,Y)\phi(Y)$, detailed balance holds and the proposal is always accepted. In practice, it is possible that $\phi(X|\,Y)$ is known, but that $\phi(Y|\,X)$ has to be sampled using more general methods. In this case Gibbs sampling is combined with for example Metropolis-Hastings techniques. Such a sampling method is sometimes referred to as Metropolis-Hastings within Gibbs; although since Gibbs sampling is a special case of Metropolis-Hastings, this terminology is incorrect [Chib and Greenberg, 1995].

A.4 Issues of Convergence

For any of the sampling schemes outlined above, it should be remembered that although the target distribution is the invariant distribution, and that the sequence generated by the algorithms will tend in distribution to the invariant distribution, issues of rate of convergence will be important.

Specifically there are two main important considerations:

1. When will the samples be independent of the initial value, x_0?
2. What number of samples, N are needed?

The first question refers to the fact that x_0 is just some (operator chosen) possible value for X and is unlikely to come from the target distribution. Indeed, it may be some time before x_j is from ϕ, (call this time J), only after which time the samples

may be used. This time is called burn-in. The chain is said to have converged after time J.

While it is possible to determine burn-in exactly in principle, certainly for a limited number of cases [Murdoch and Green, 1998], analytical methods of determining J are tedious if not wholly impractical. Even in such cases the question then arises as to whether one should use the outputs of multiple chains or a single long chain [Murdoch and Rosenthal, 1998].

For practical applications, time series plots of the chain can give an idea of J. In the literature, a review of a number of diagnostic tools is provided in [Cowles and Carlin, 1996] and [Brooks and Roberts, 1998] to assess convergence.

The second question is as to how many samples should be taken. This depends on what the samples are being used for, that is, what is being estimated, and how accurate the estimator needs to be. Of course, N depends on J also, since only $N-J$ samples come from the target distribution.

Again, diagnostics exist for determining how many samples are needed. A comparison of estimates based on two different chains started at different points is one method of checking the variance of the estimators used.

The choice of the proposal distribution is fundamental to the rate of convergence. Common choices for the proposal density include the normal, centred on x_{old}, choice of variance to be decided; uniform, centred on x_{old}; normal centred on x_i; uniform centred on x_0. In the case of the last two of these, the proposal, x_{i+1} is independent of x_i, and hence they are known as independence samplers [Tierney, 1994].

As well as the question of when the chain has converged, of interest is the rate of mixing of the chain. Mixing is the speed at which the chain explores the target distribution. If the chain mixes slowly, then it requires very many samples to explore the whole support of the target. In the case of the first proposal mentioned, mixing depends upon the variance. The acceptance rate is the number of times a move is made divided by the total number of steps in the chain. If the acceptance rate is too high, this indicates that the chain does not have the opportunity to sample

from the tails of the distribution. If the acceptance rate is too low, this indicates that the chain is too stationary, and thus does not move around much. Both these cases would indicate insufficient mixing. Experience has shown that an optimum acceptance rate is between 0.25 and 0.5 [Gelman et al., 1996] for the case of normal target and proposals, with lower rates acceptable for higher dimensions [Chib and Greenberg, 1995].

B. APPENDICES

B.1 Specification of Hyper-parameter constants used in Section 3.1

Letting $\tilde{\lambda}_i = d_i/n_i$, an estimator of λ_i is

$$\hat{\lambda}_i \;=\; \begin{cases} \tilde{\lambda}_i & , d_i > 0 \\ \hat{d}/\hat{n} & , d_i = 0 \end{cases}, \tag{B.1}$$

where $\hat{n} = \ell^{-1}\sum_{i=1}^{\ell} n_i$ and $\hat{d} = \ell^{-1}\sum_{i=1}^{\ell} d_i$. By the Poisson assumption (3.1), given λ_i,

$$\mathrm{E}\{\log(\tilde{\lambda}_i)\} \;\approx\; \lambda_i \tag{B.2}$$

$$\mathrm{Var}\{\log(\tilde{\lambda}_i)\} \;\approx\; \frac{1}{n_i\lambda_i}. \tag{B.3}$$

Using the prior density for the λ_i (3.2), and the properties of the gamma distribution, the expectation of λ_i is

$$\mathrm{E}(\lambda_i |\, \alpha, \underset{\sim}{\beta}) \;=\; \frac{\alpha}{\alpha e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}} = e^{\underset{\sim}{x}_i'\underset{\sim}{\beta}}. \tag{B.4}$$

Taking the logarithm of both sides of this expectation we have

$$\mathrm{E}(\log(\lambda_i) |\, \alpha, \underset{\sim}{\beta}) \;\approx\; \underset{\sim}{x}_i'\underset{\sim}{\beta}. \tag{B.5}$$

Thus, we assume that

$$\log(\hat{\lambda}_i) \;\approx\; \underset{\sim}{x}_i'\underset{\sim}{\beta} + e_i, \tag{B.6}$$

$$e_i \;\overset{ind}{\sim}\; \mathrm{Normal}(0, \gamma^2/(n_i\lambda_i)), \qquad i = 1, \ldots, \ell,$$

where γ^2 is an unknown scale factor.

We compute weighted least square estimators in (B.6). Let $\underset{\sim}{Y} = (\log(\hat{\lambda}_1), \ldots, \log(\hat{\lambda}_\ell))'$ be the response vector, $\mathbf{X} = (\underset{\sim}{x}_1, \ldots, \underset{\sim}{x}_\ell)'$ be the matrix of covariates and $\mathbf{W} = \mathrm{diagonal}(n_1\lambda_1, \ldots, n_\ell\lambda_\ell)$ be the weight matrix for the vector $(\log(\lambda_1), \ldots, \log(\lambda_\ell))'$.

Then the least square estimator of $\underset{\sim}{\beta}$ is

$$\underset{\sim}{\hat{\beta}} = (\mathbf{X}'\mathbf{W}^{-1}\mathbf{X})^{-1}(\mathbf{X}'\mathbf{W}^{-1}\underset{\sim}{Y}) \tag{B.7}$$

and $\mathrm{Cov}(\underset{\sim}{\hat{\beta}})$ is estimated by

$$\begin{aligned} \widehat{\mathrm{Cov}}(\underset{\sim}{\hat{\beta}}) &= (\mathbf{X}'\mathbf{W}^{-1}\mathbf{X})^{-1}\hat{\gamma}^2 \\ \hat{\gamma}^2 &= \frac{(\underset{\sim}{Y} - \mathbf{X}\underset{\sim}{\hat{\beta}})'\mathbf{W}^{-1}(\underset{\sim}{Y} - \mathbf{X}\underset{\sim}{\hat{\beta}})}{n-p}. \end{aligned} \tag{B.8}$$

Finally, we specify $\mu_{\underset{\sim}{\beta}}$ and $\Delta_{\underset{\sim}{\beta}}$ by taking the means of $\underset{\sim}{\beta}$, $\mu_{\underset{\sim}{\beta}} = \underset{\sim}{\hat{\beta}}$ in (B.7) and $\Delta_{\underset{\sim}{\beta}} = \kappa_{\mathrm{v}}\widehat{\mathrm{Cov}}(\underset{\sim}{\hat{\beta}})$ in (B.8), where κ_{v} is a variance inflation factor. By experimentation, we choose κ_{v} to be large so that the prior density for $\underset{\sim}{\beta}$ is proper and barely informative. For our data analysis, after a sensitivity analysis revealing a lack of sensitivity to the value of κ_{v}, we choose $\kappa_{\mathrm{v}} = 100000$.

B.2 Poisson-Gamma model as a weighted average of prior mean and sample mean

The Poisson-Gamma model is an example of a famous result in Bayesian analysis, namely that the posterior mean is a weighted average of the prior mean and the sample mean. The details for our situation follow. For Poisson data $d_i|\,\lambda_i \overset{ind}{\sim}$ Poisson$(n_i\lambda_i)$, $i = 1, \ldots, \ell$, the likelihood is

$$\begin{aligned} f(\underset{\sim}{d}|\,\underset{\sim}{\lambda}) &= \prod_{i=1}^{\ell} \frac{e^{-n_i\lambda_i}(n_i\lambda_i)^{d_i}}{d_i!} \\ &\propto \exp\left\{-\sum_{i=1}^{\ell} n_i\lambda_i\right\} \prod_{i=1}^{\ell}(n_i\lambda_i)^{d_i}. \end{aligned}$$

The estimator of λ_i using the maximum likelihood estimator (MLE) is $\hat{\lambda}_i = d_i/n_i = r_i$, $i = 1, \ldots, \ell$. The prior on λ_i is Gamma(a, b), where $a = \alpha$ and $b = \alpha e^{-\underset{\sim}{x}_i'\underset{\sim}{\beta}}$. So

$$\begin{aligned} f(\lambda_i|\,a, b) &= \frac{b^a\lambda_i^{a-1}e^{-b\lambda_i}}{\Gamma(a)} \\ &\propto \lambda_i^{a-1}e^{-b\lambda_i}. \end{aligned}$$

The estimate of λ_i using this prior is $\tilde{\lambda}_i = a/b$. Therefore, the posterior distribution of λ_i is

$$\begin{aligned} f(\lambda_i|\,d_i, a, b) &\propto \lambda_i^{a-1}e^{-b\lambda_i}e^{-n_i\lambda_i}(n_i\lambda_i)^{d_i} \\ &= \lambda_i^{d_i+a-1}n_i^{d_i}e^{-\lambda_i(n_i+b)}. \end{aligned}$$

This we recognize as the functional part of another gamma density (gamma is conjugate for Poisson data). The posterior is $\lambda_i|\,d_i, a, b \sim$ Gamma$(d_i + a, n_i + b)$. The Bayes' estimator, that is the estimate of λ_i using the posterior mean, is $\lambda_i^* = \frac{d_i+a}{n_i+b}$. The value of the prior information can be thought of as follows: it is as though we had b extra observations which sum to a. The Bayes' estimator can again be written as a weighted average of the data-based estimator and the prior mean,

$$\lambda_i^* = \frac{n_i}{n_i+b}\frac{d_i}{n_i} + \frac{b}{n_i+b}\frac{a}{b}.$$

Note that as n_i increases ("more data") the weight attached to the data-based estimator increases.

B.3 Besag Simultaneous Credible Regions Based on Order Statistics

This description is taken from the original paper [Besag et al., 1995] (p.30).

Denoting the stored sample by $\{x_i^{(t)} : i = 1, \ldots, \ell; t = 1, \ldots, M\}$, order $\{x_i^{(t)} : t = 1, \ldots, M\}$ separately for each component i, to obtain order statistics $x_i^{[t]}$ and ranks $r_i^{(t)}, t = 1, \ldots, M$. For fixed $k \in \{1, \ldots, M\}$, let t^* be the smallest integer such that $x_i^{[M+1-t^*]} \leq x_i^{(t)} \leq x_i^{[t^*]}$, for all i, for at least k values of t. It is equal to the kth order statistic from the set $a^{(t)} = \max\{\max_i r_i^{(t)}, M + 1 - \min_i r_i^{(t)}\}, t = 1, \ldots, M$, that is, $t^* = a^{[k]}$.

Then $\{[x_i^{[M+1-t^*]}, x_i^{[t^*]}] : i = 1, \ldots, \ell\}$ are a set of simultaneous credible regions containing at least $100k/M\%$ of the empirical distribution.