eAppendix

Section 1: Spatial weight construction using Delaunay triangulation.

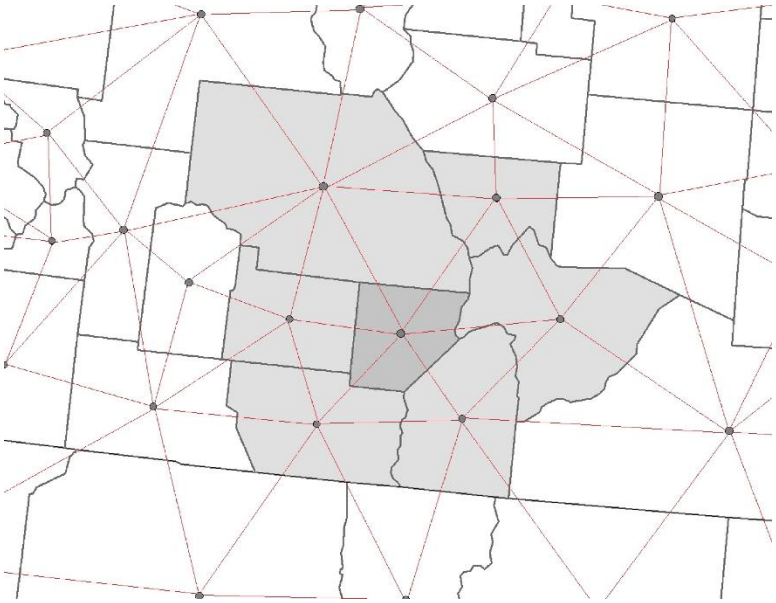


Figure e1. The target county is shown in dark grey in the center. County centroids are connected by red 'edges', those counties that share an edge are considered neighbors (light grey).

Section 2: Model code and evaluation: trace plots, autocorrelation plots, Brooks-Gelman-Rubin plots.

```
model{

for (i in 1:N){

y1[i] ~ dpois(mu1[i])
mu1[i]<-e1[i]*theta1[i]
log(theta1[i])<-ab+w[i]+u[i]*delta

y2[i] ~ dpois(mu2[i])
mu2[i]<-e2[i]*theta2[i]
log(theta2[i])<-aw+u[i]/delta

IMRblack[i]<-theta1[i]*0.0061*1000

          # Multiplied by the background population risk*1,000 to
          # express per 1,000 births

IMRwhite[i]<-theta2[i]*0.0061*1000

          # Multiplied by the background population risk*1,000 to
          # express per 1,000 births

RD[i]<-IMRblack[i]- IMRwhite[i]
RR[i]<-IMRblack[i]/IMRwhite[i]

#Bayesian P-Values and Gelfand and Ghosh statistics
y1rep[i]~ dpois(mu1[i])
D1[i]<- (y1[i]-mu1[i])*(y1[i]-mu1[i]) *mu1[i]
   Dstar1[i] <-  (y1rep[i]-mu1[i])*(y1rep[i]-mu1[i]) *mu1[i]
y2rep[i]~ dpois(mu2[i])
D2[i]<-(y2[i]-mu2[i])*(y2[i]-mu2[i]) *mu2[i]
   Dstar2[i] <-  (y2rep[i]-mu2[i])*(y2rep[i]-mu2[i]) *mu2[i]
}

delta<-exp(sdf)
sdf~dnorm(0,5.9)
u[1:N]~car.normal(adj[],weights[],num[],tauU)
w[1:N]~car.normal(adj[],weights[],num[],tw)

for(i in 1:sumNumNeigh)
{weights[i]<-1}
ab~dflat()
aw~dflat()
tauU<-1/(sigU*sigU)
sigU~dunif(0,1000)
tw<-1/(sdwas*sdwas)
```

```
sdwas~dunif(0,1000)
}

var.shared.bl<-pow(delta,2)*sd(u[])*sd(u[])
var.shared.wh<-pow(delta,-2)*sd(u[])*sd(u[])
var.specific.bl<-sd(w[])*sd(w[])

frac.shared.bl<-var.shared.bl/(var.shared.bl+var.specific.bl)
var.bl<-sd(theta1[])*sd(theta1[])
var.wh<-sd(theta2[])*sd(theta2[])


#Bayesian P-Values and Gelfand and Ghosh statistics
sumDstar1<- sum(Dstar1[])
sumD1<- sum(D1[])

Dp1<- step(sumDstar1-sumD1)
bpvalue1<- mean(Dp1)

sumDstar2<- sum(Dstar2[])
sumD2<- sum(D2[])

Dp2<- step(sumDstar2-sumD2)
bpvalue2<- mean(Dp2)

}

# Gelfand and Ghosh statistics, D1 and D2:
Calculate G1=sum of (y1-y1rep)^2
Calculate G2=sum of (y2-y2rep)^2
Calculate P1= sum of all posterior predictive variances OF Y1REP
Calculate P2= sum of all posterior predictive variances OF Y2REP
Calculate D1=G1+P1
Calculate D2=G2+P2
```

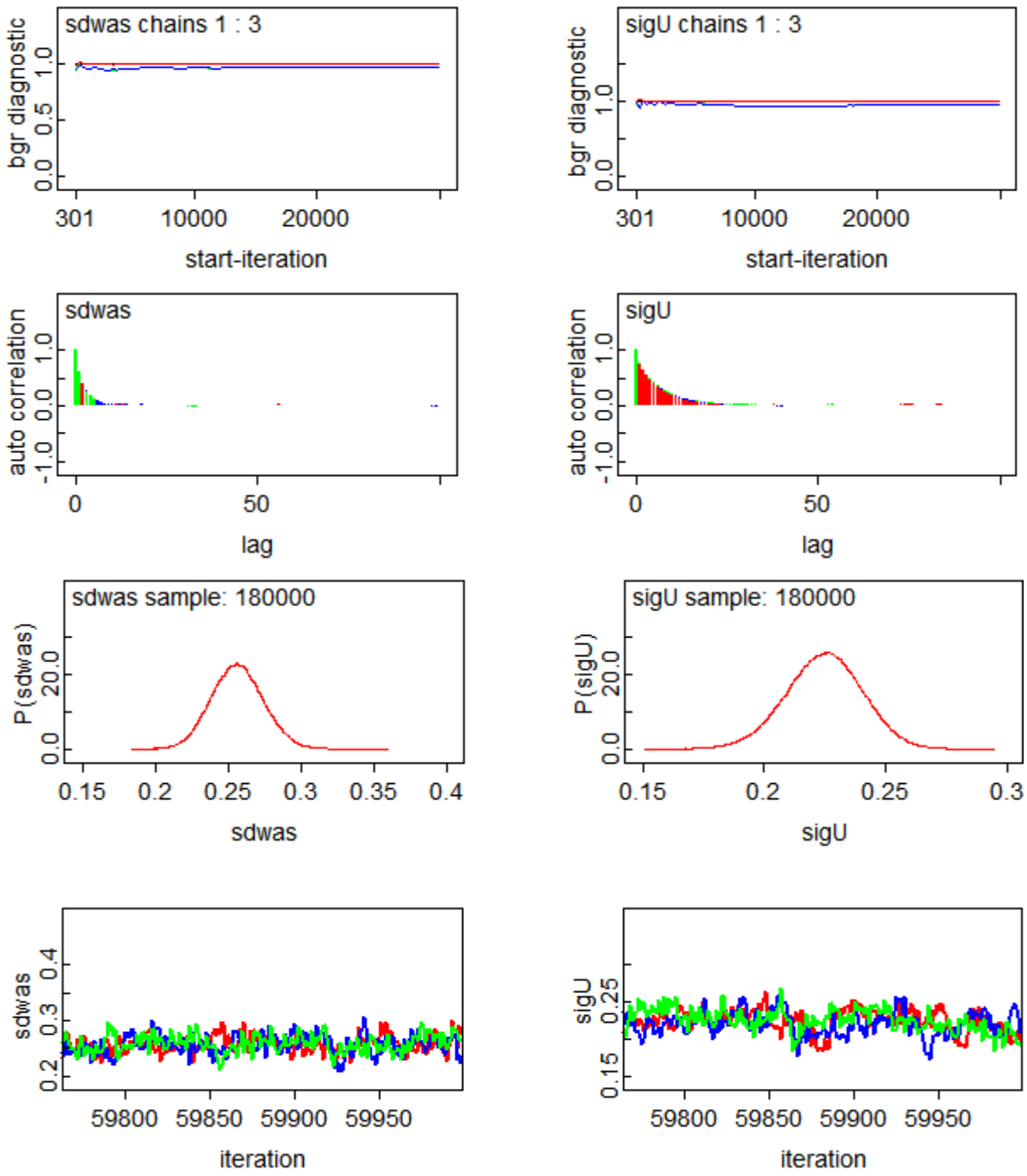


Figure e2. Model evaluation: Brooks-Gelman-Rubin plots (top), autocorrelation (second row), posterior distributions (third row), and trace plots (bottom) from the spatial model. The first column refers to the black-specific component, v_i; the second column refers to the shared component, v_i.

Table e1. Additional Model Fit Statistics:

	Spatial	Non-Spatial
DIC	23900.0	25627.5
Gelfand and Ghosh: black infant mortality	85941	88950
Gelfand and Ghosh: white infant mortality	130583	142800
Bayesian P-Value: black infant mortality	0.48	0.50
Bayesian P-Value: white infant mortality	0.42	0.45

Calculation of additional fit statistics:

Bayesian p-values. Bayesian p-values are used to check whether the model is an adequate representation of the main features in the data (Ntzoufras, 2009). The structural assumptions of the fitted model can be ascertained by the use of posterior predictive model checks.(Gelman, Carlin, Stern & Rubin, 1995; Ntzoufras, 2009) The evaluation of the posterior distribution of the Bayesian model is done by comparing the observed data y^{obs} to the posterior predictive distribution or replicates y^{rep}. We generated replicate datasets y^{rep} for each posterior draw of the model parameters, and then calculated a test quantity $T(y_{it}, \Theta)$, where Θ is the vector of unknown parameters. This represents an omnibus goodness-of-fit measure, defined as follows, where the summation is over all sampled observations (Gelman et al., 1995):

$$T(y_{it}, \theta) = \sum_{i,t} \frac{(y_{it} - E(y_{it}|\theta))^2}{variance(y_{it}|\theta)}$$

Bayesian p-values associated with the test quantity were computed, with values close to zero or one indicating poor fit. Values around 0.5 indicate that the distributions of the replicated and actual data are close while values close to zero or one indicate differences between them.(Carlin & Louis, 2009)

Gelfand and Ghosh statistics. Models were also evaluated using the Gelfand and Ghosh statistic, which compares observed data y^{obs} to the replicates y^{rep}. This approach minimizes the posterior

predictive loss over all possible predictions of future observations y^{rep} .(Ando, 2010; Gelfand & Ghosh, 1998) The replicated dataset is used to compute the posterior predictive mean and variance for each observation. A goodness of fit measure G which is the error sum of squares of the difference between the data and its posterior predictive mean is computed. It's calculated as:

$$G = \sum_{i,t} (y_{it} - E(y_{it}|\theta))^2$$

Again, Θ is the vector of unknown parameters. We then calculate P, which is the sum over all observations of the posterior predictive variances, defined as:

$$P = \sum_{i,t} (variance(y_{it}|\theta))$$

With the increasing complexity in models, G will decrease but P will begin to increase.(Gelfand & Ghosh, 1998) The statistic D is calculated as G+P, which is a combination of goodness of fit and variability.(Barker et al., 2013) Models with smaller D values are selected.

References:

Ando, T. (2010). Bayesian model selection and statistical modeling. New York: Chapman and Hall.

Barker, L. E., et al. (2013). Bayesian Small Area Estimates of Diabetes Incidence by United States County, 2009. J Data Sci 11(1): 269-280.

Carlin, B. P. and Louis, T. A. (2009). Bayesian methods for data analysis. New York: Chapman and Hall.

Gelfand, A.E. and Ghosh, S.K. (1998). Model choice: A minimum posterior predictive loss approach. Biometrika, **85**, 1-11.

Gelman, A., Carlin, J. B., Stern, S. H. and Rubin, D. B. (1995). Bayesian data analysis. New York: Chapman and Hall.

Ntzoufras, I. (2009). Bayesian modeling using winbugs. John Wiley and Sons, Inc., Hoboken, New Jersey.

Section 3. Posterior densities of infant mortality rates for black and white infants from the spatial model.

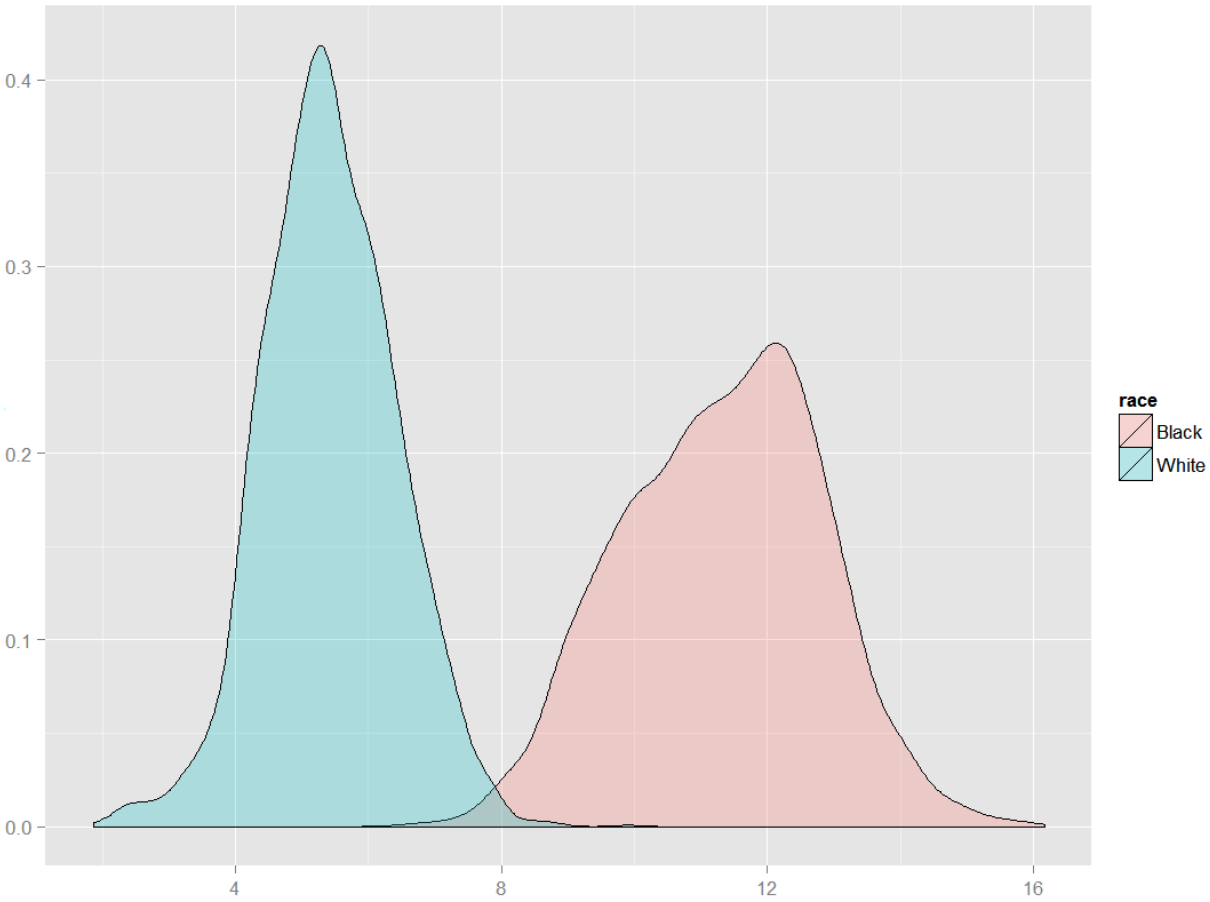


Figure e3. Posterior densities of infant mortality rates (x-axis) for black and white infants.

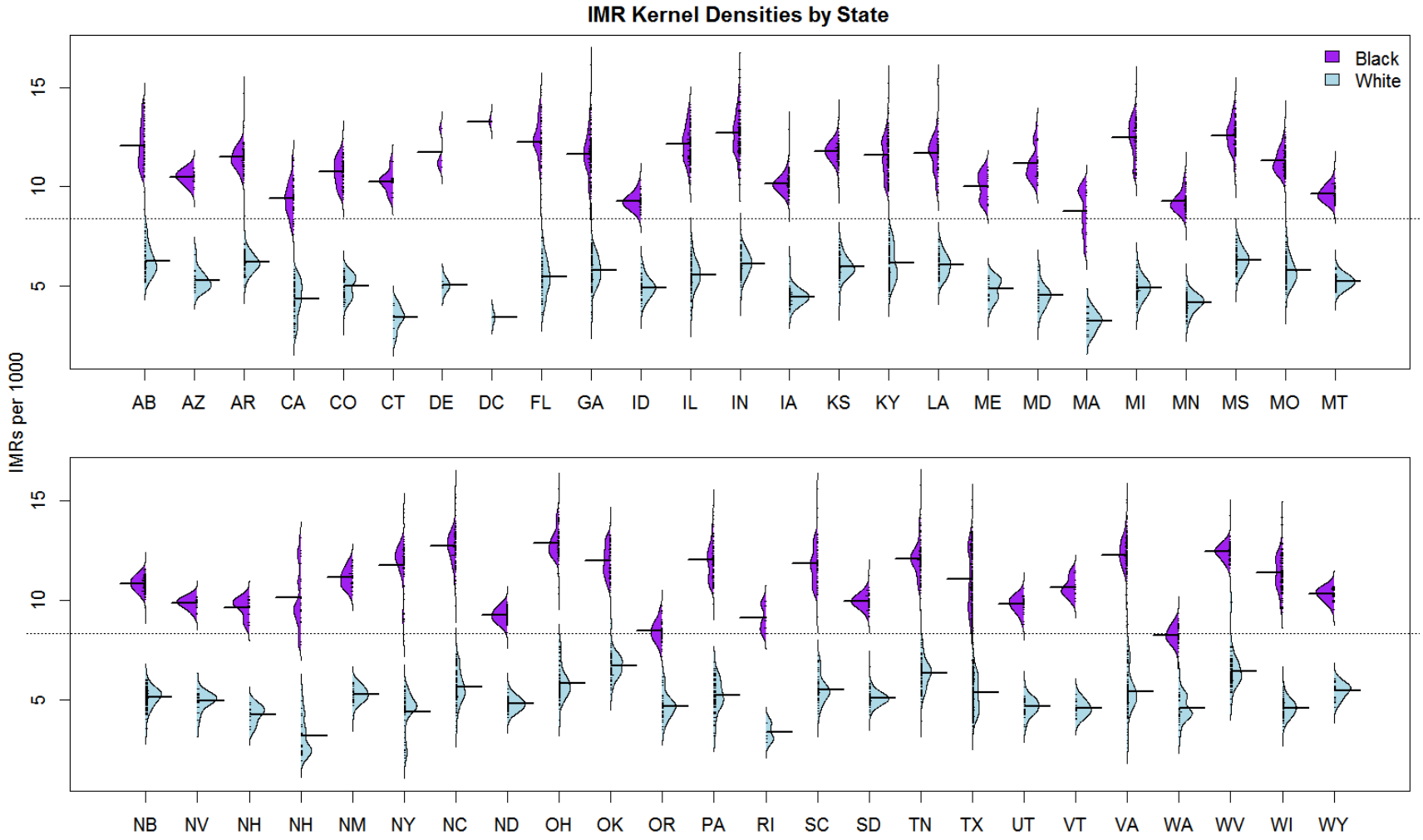


Figure e4. Kernel densities of posterior infant mortality rate estimates for black and white infants from the spatial model, by state.

Section 4. County rankings from the spatial model.

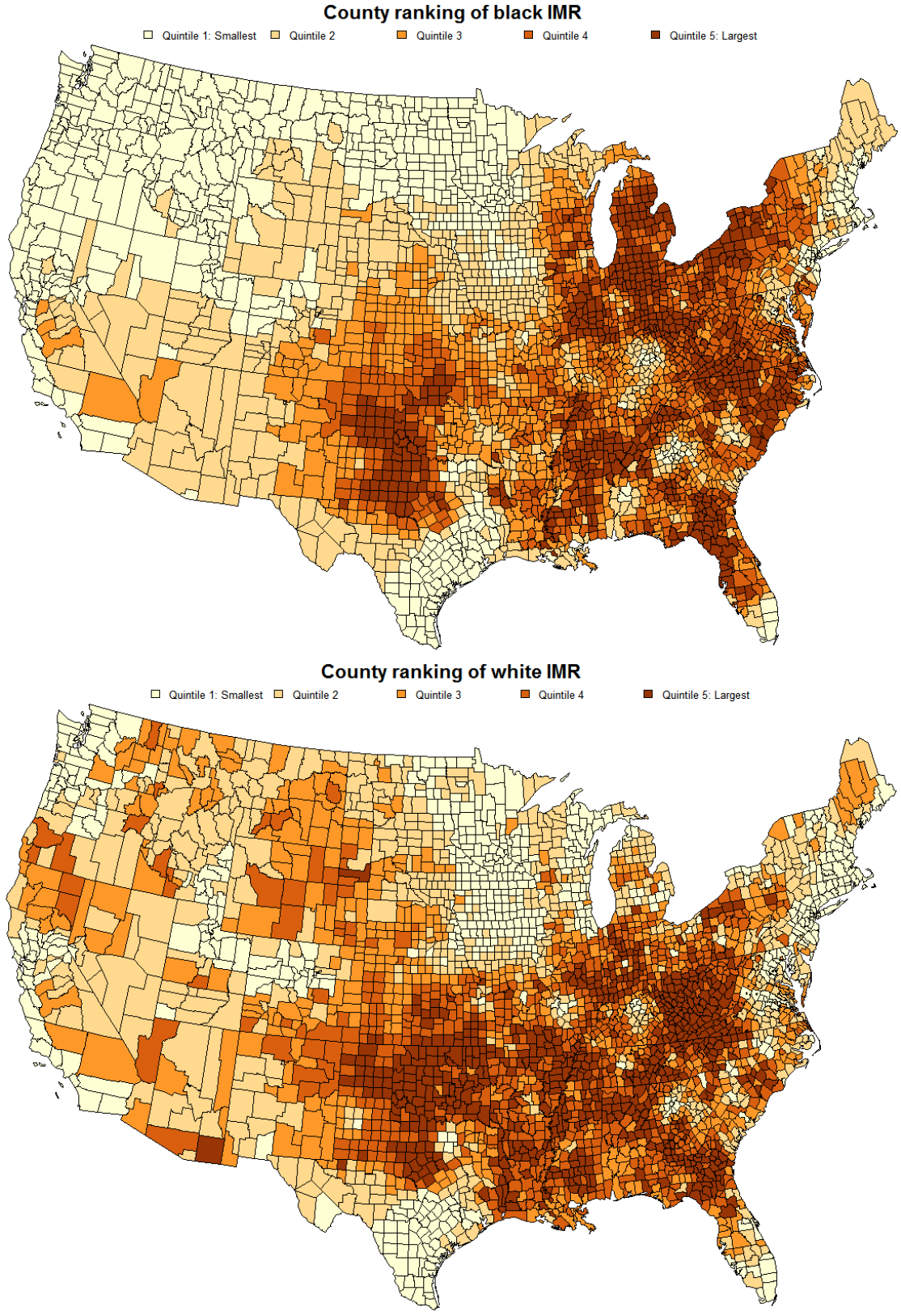


Figure e5. Median county rankings for black infant mortality (top) and white infant mortality (bottom) from the spatial SCM.

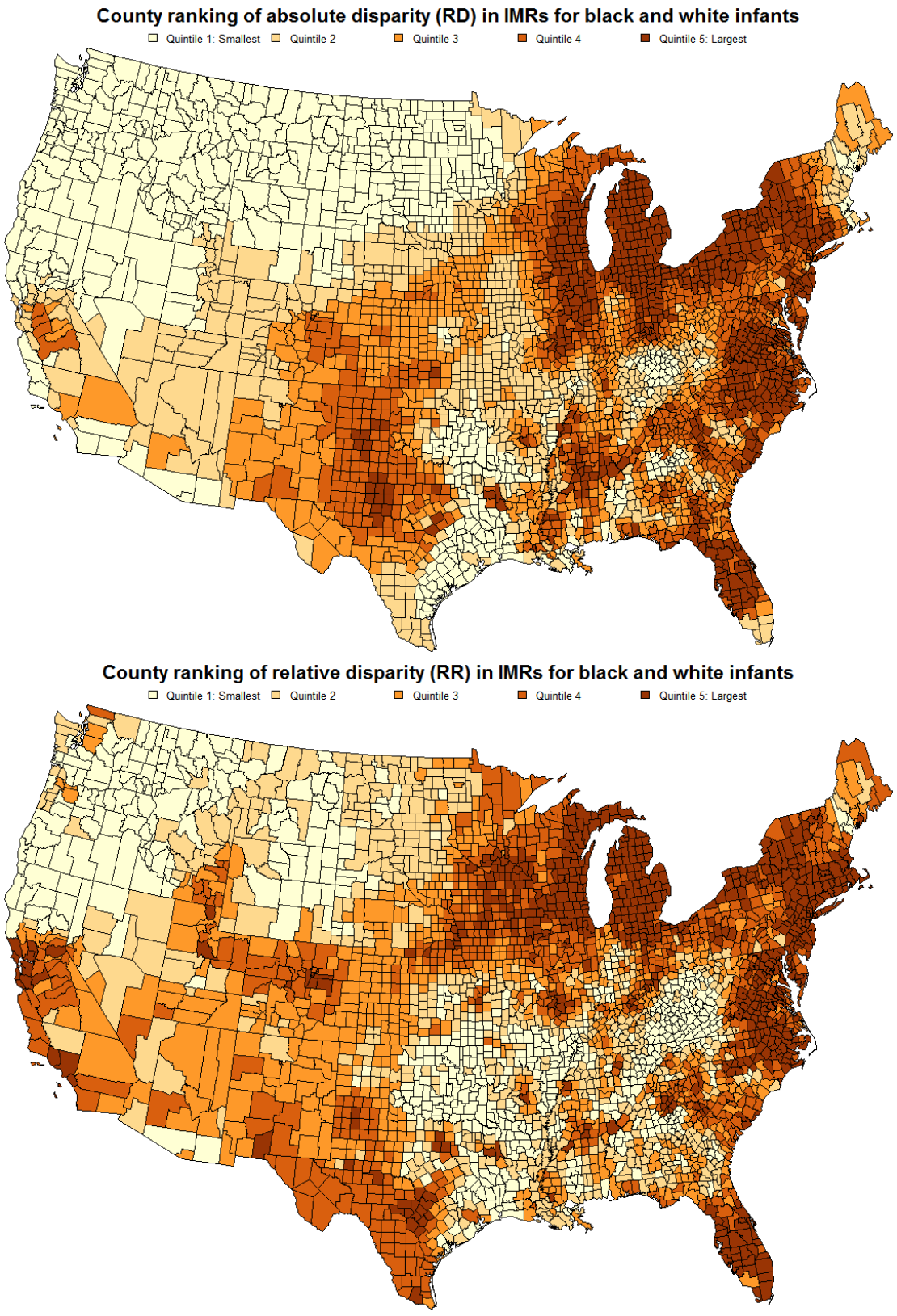


Figure e6. Median county rankings for the risk difference (top) and relative risk (bottom) comparing black and white infant mortality rates from the spatial SCM.

Section 5. Scatterplots of county rankings from the spatial model.

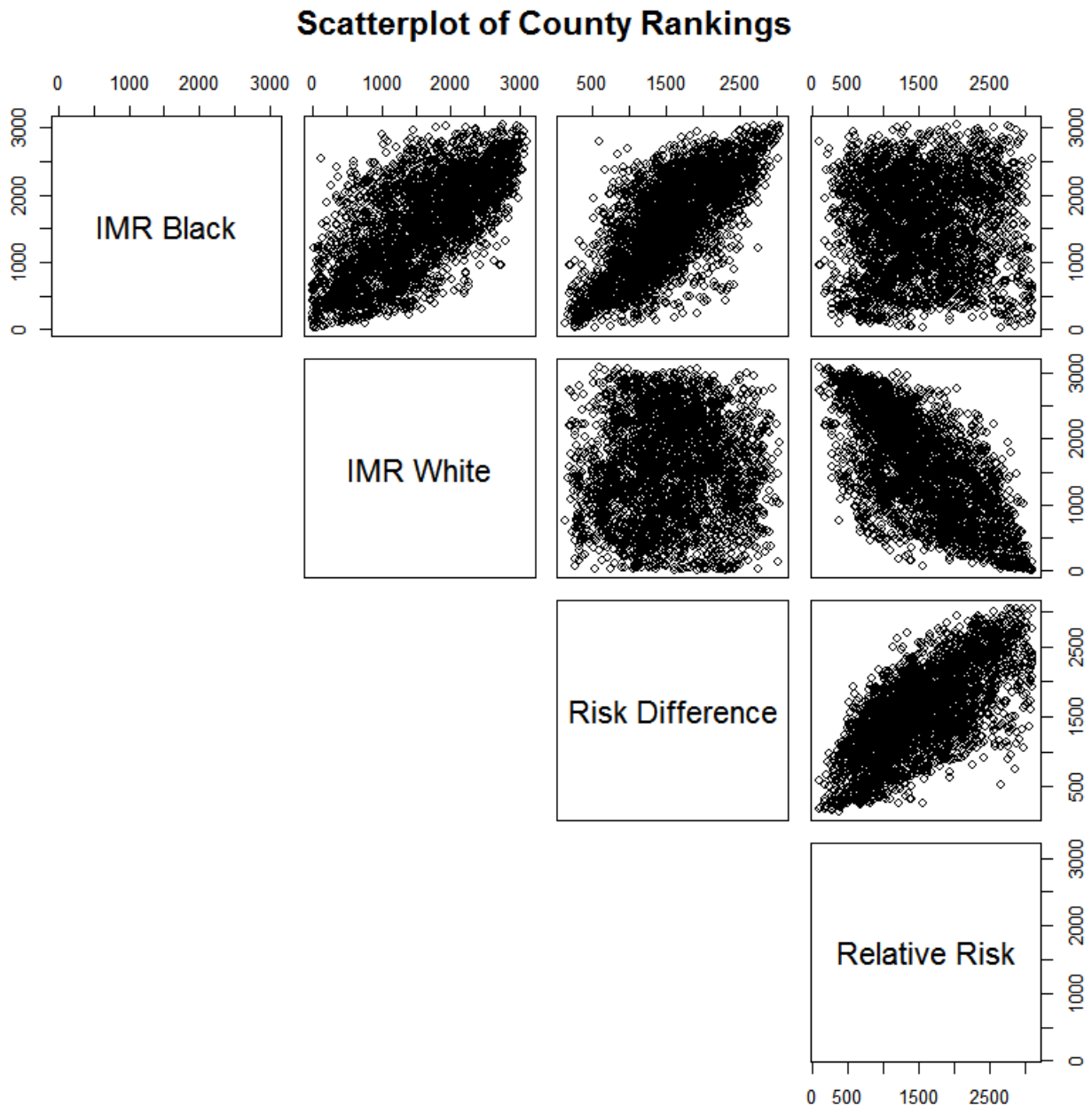


Figure e7. Scatter plots of median county rankings on four outcomes of interest from the spatial shared component model.

Section 6. Comparison of model-based estimates to state direct estimates from the spatial model.

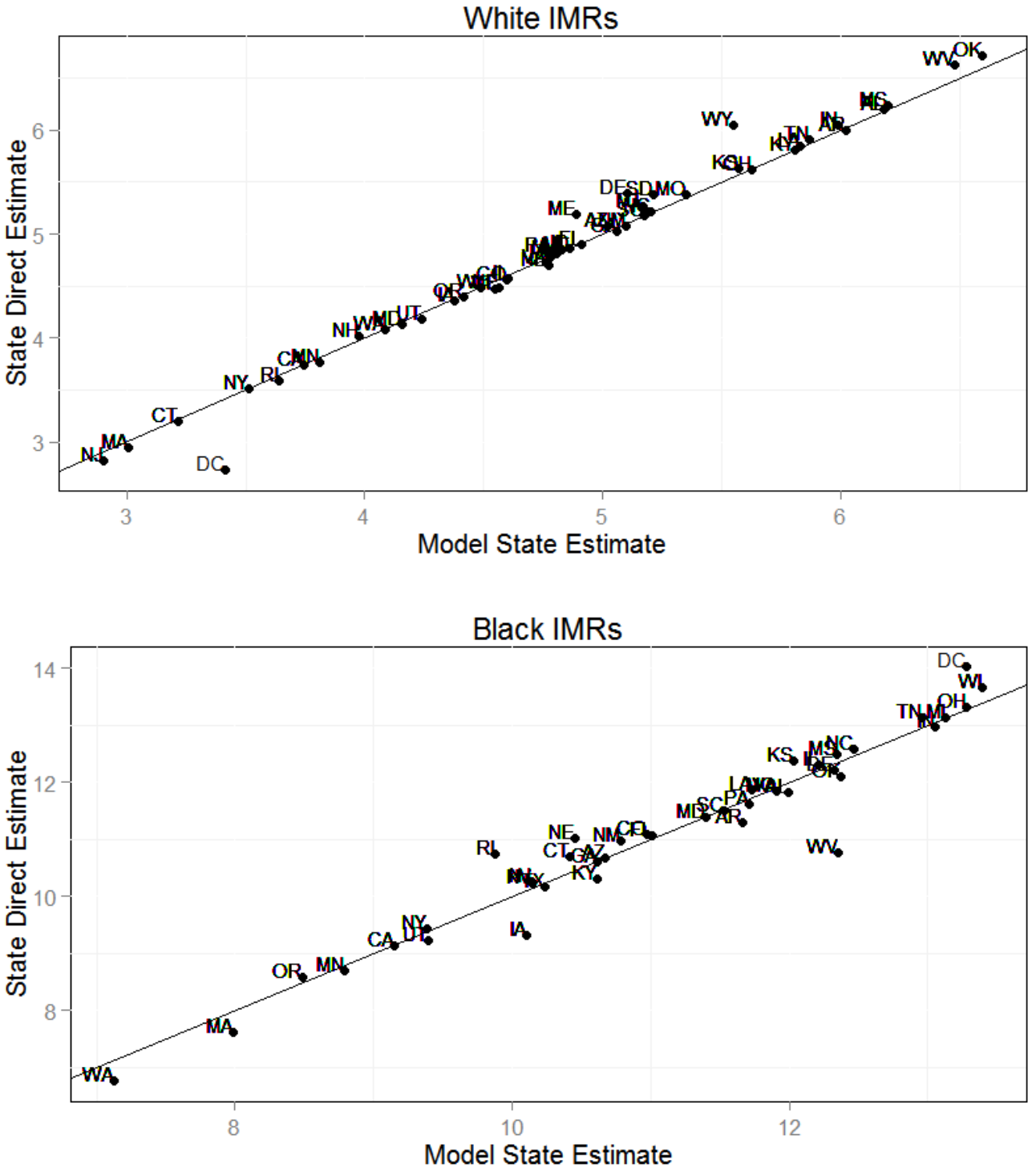


Figure e8. Comparison of state direct estimates for white infant mortality rates (top) and black infant mortality rates (bottom) with model-based estimates. Data for states with fewer than 20 deaths are suppressed.

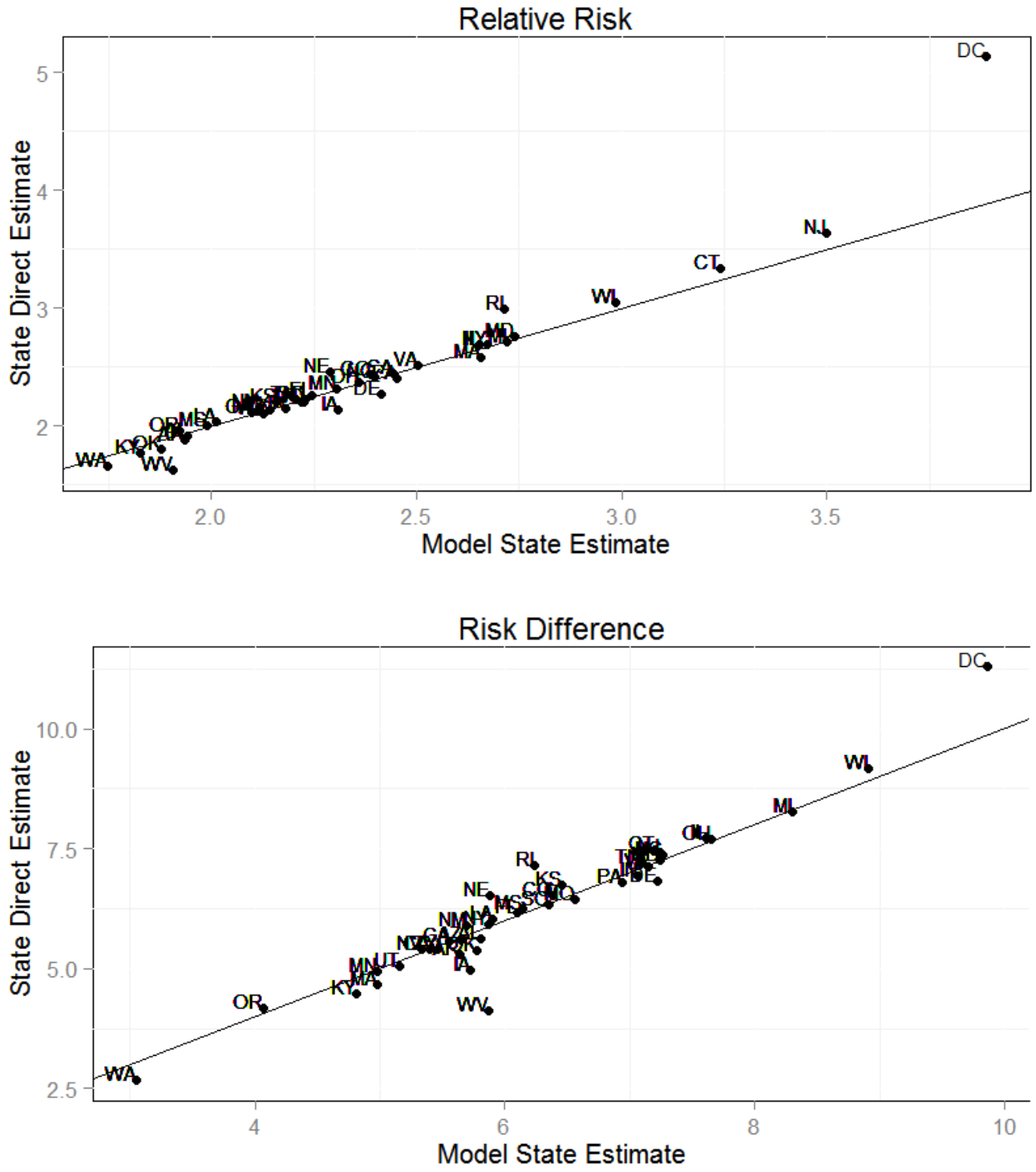


Figure e9. Comparison of state direct estimates and model-based estimates for relative rates (RR, top) and rate differences (RD, bottom). Data for states with fewer than 20 deaths are suppressed.

Section 7. Results from shared component models (SCM) with non-spatial priors.

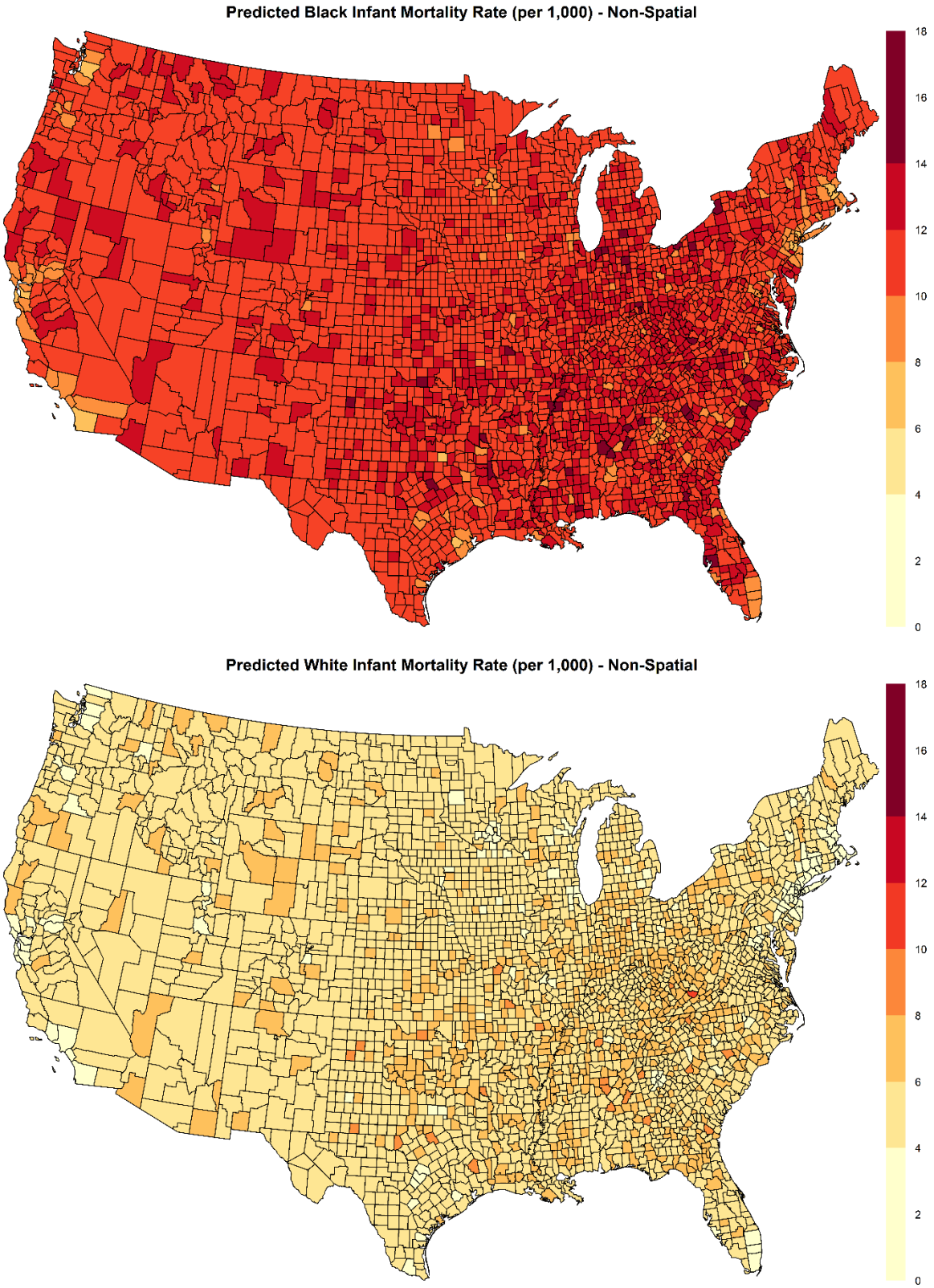


Figure e10. Posterior mean predicted black infant mortality rate (per 1,000) by county, 2004-2011 (top) and posterior mean predicted white infant mortality rate (per 1,000) by county, 2004-2011 (bottom) from the non-spatial SCM.

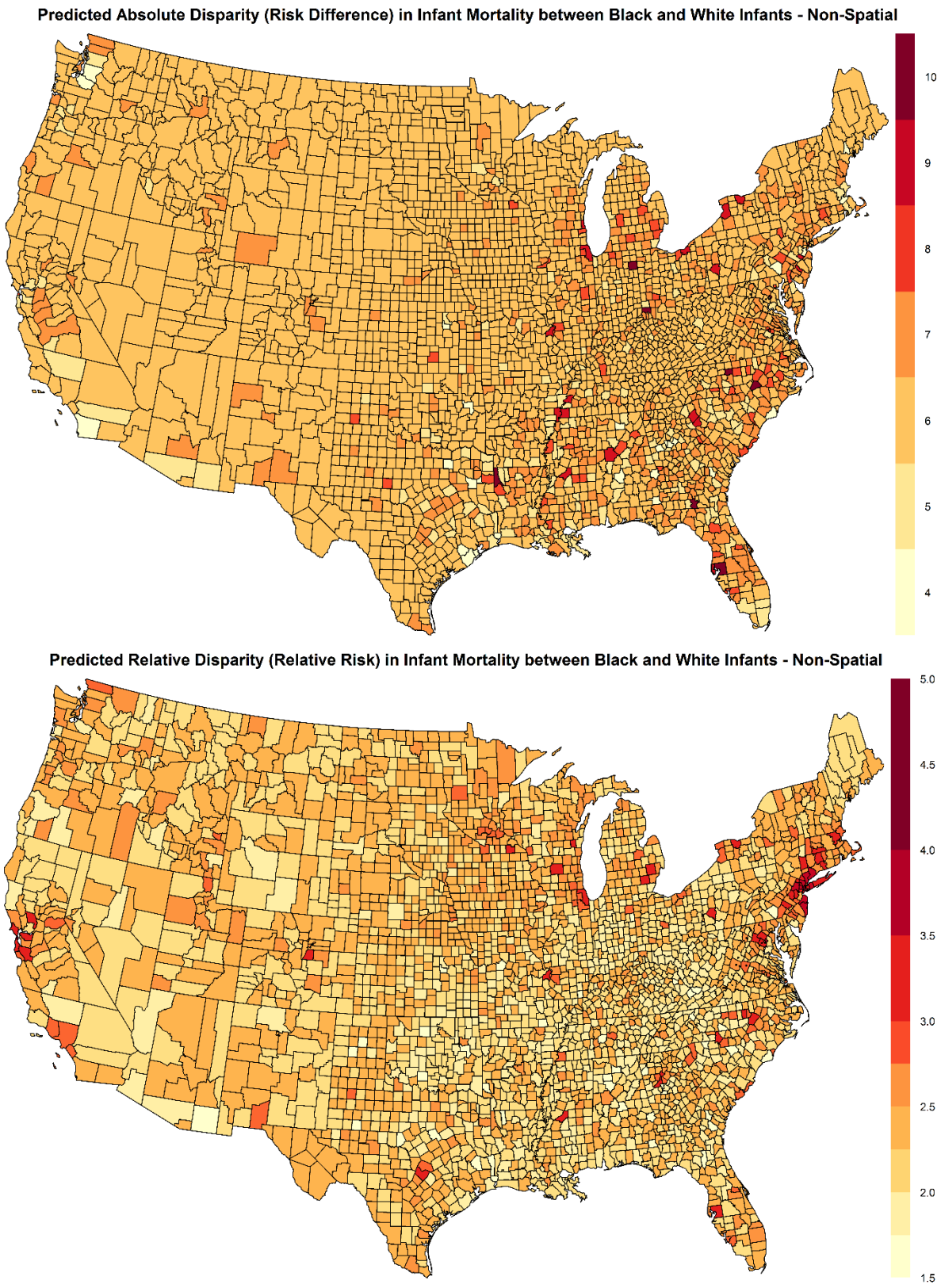


Figure e11. Posterior mean predicted absolute disparities (risk difference) by county in infant mortality rates (per 1,000) comparing black and white infants, 2004-2011 (top) and posterior mean predicted relative disparities (relative risk) by county in infant mortality rates comparing black and white infants, 2004-2011 (top) from the non-spatial SCM.

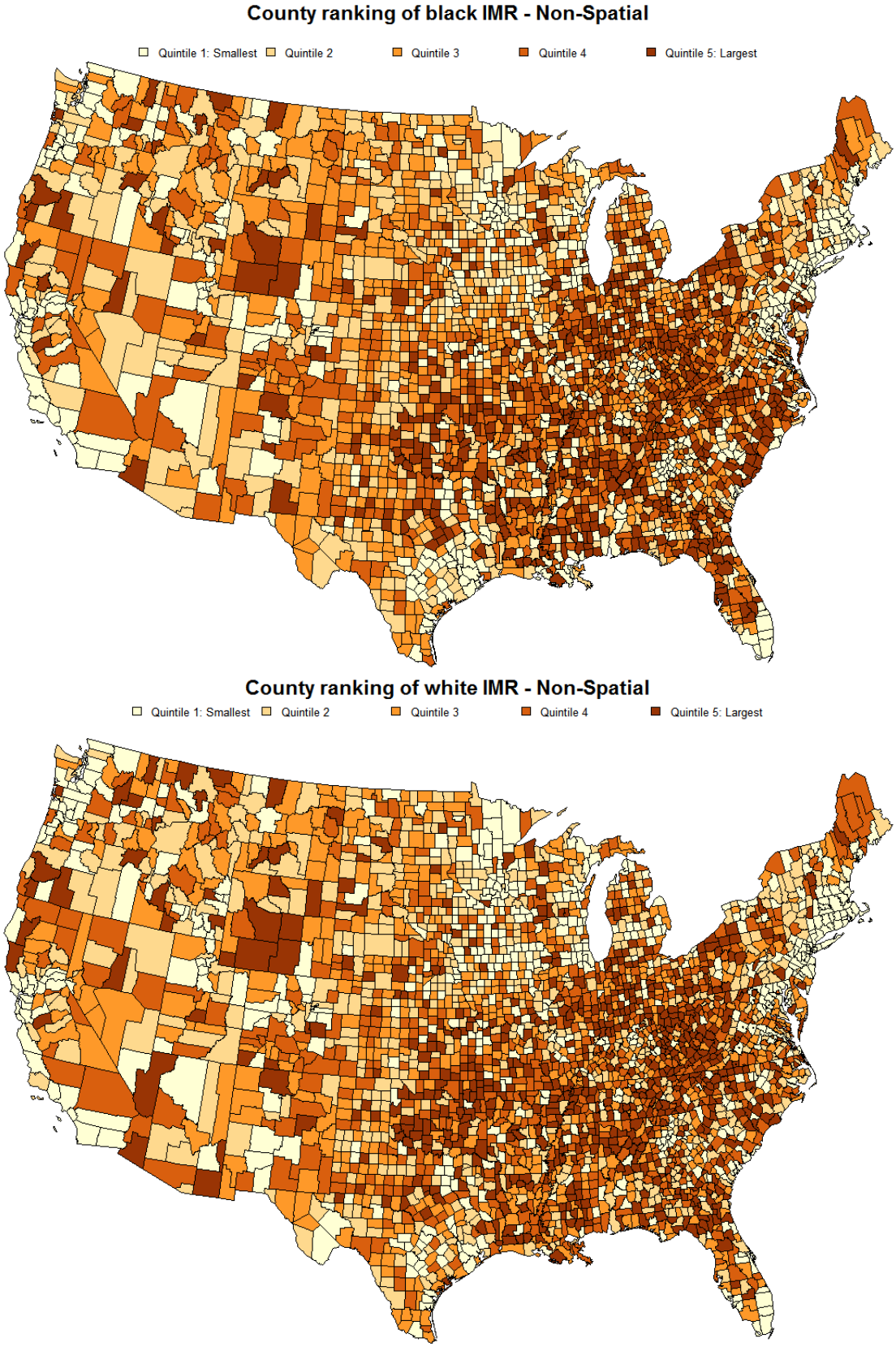


Figure e12. Median county rankings for black infant mortality (top) and white infant mortality (bottom) from the non-spatial SCM.

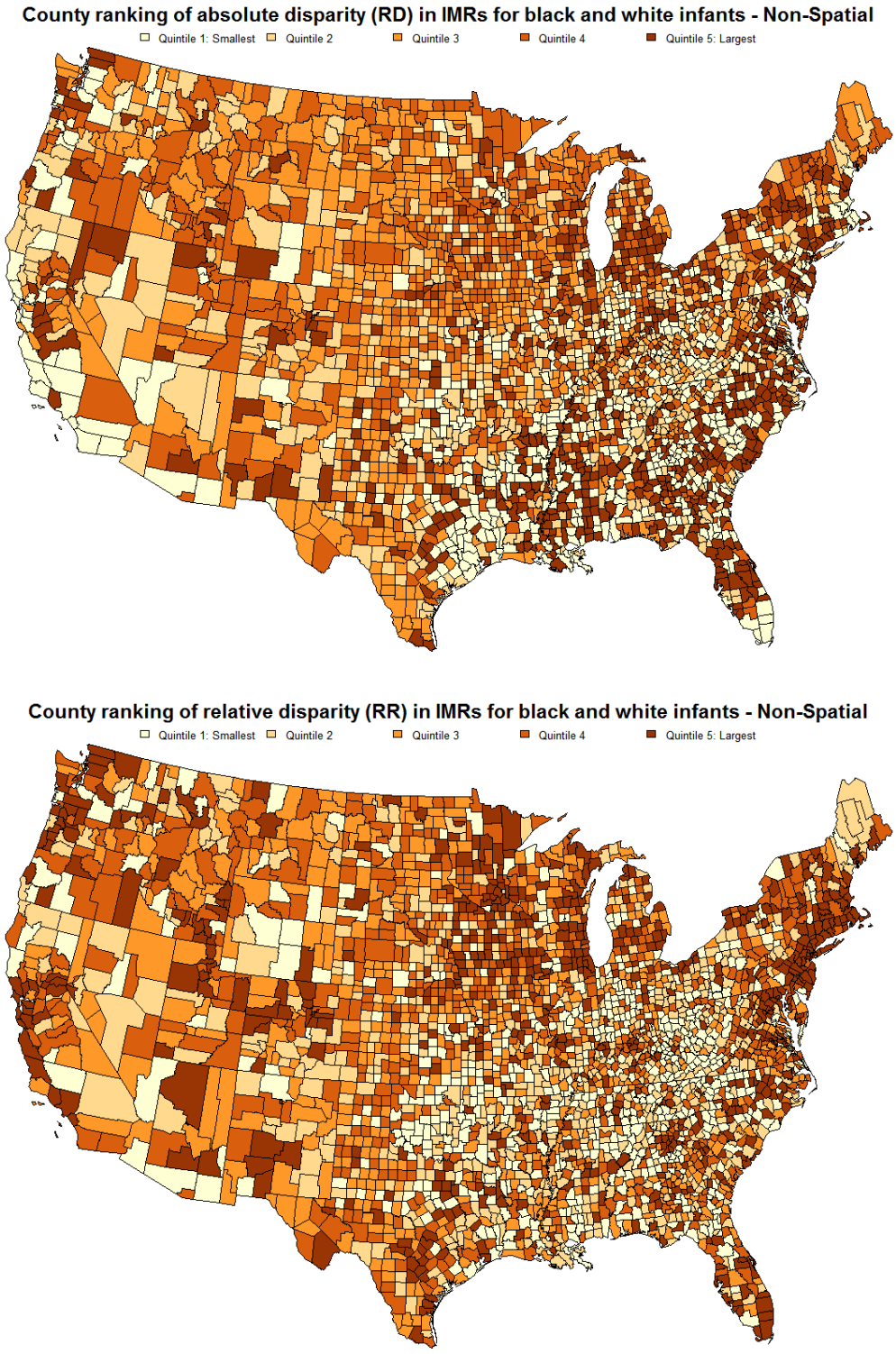


Figure e13. Median county rankings for the risk difference (top) and relative risk (bottom) comparing black and white infant mortality rates from the non-spatial SCM.

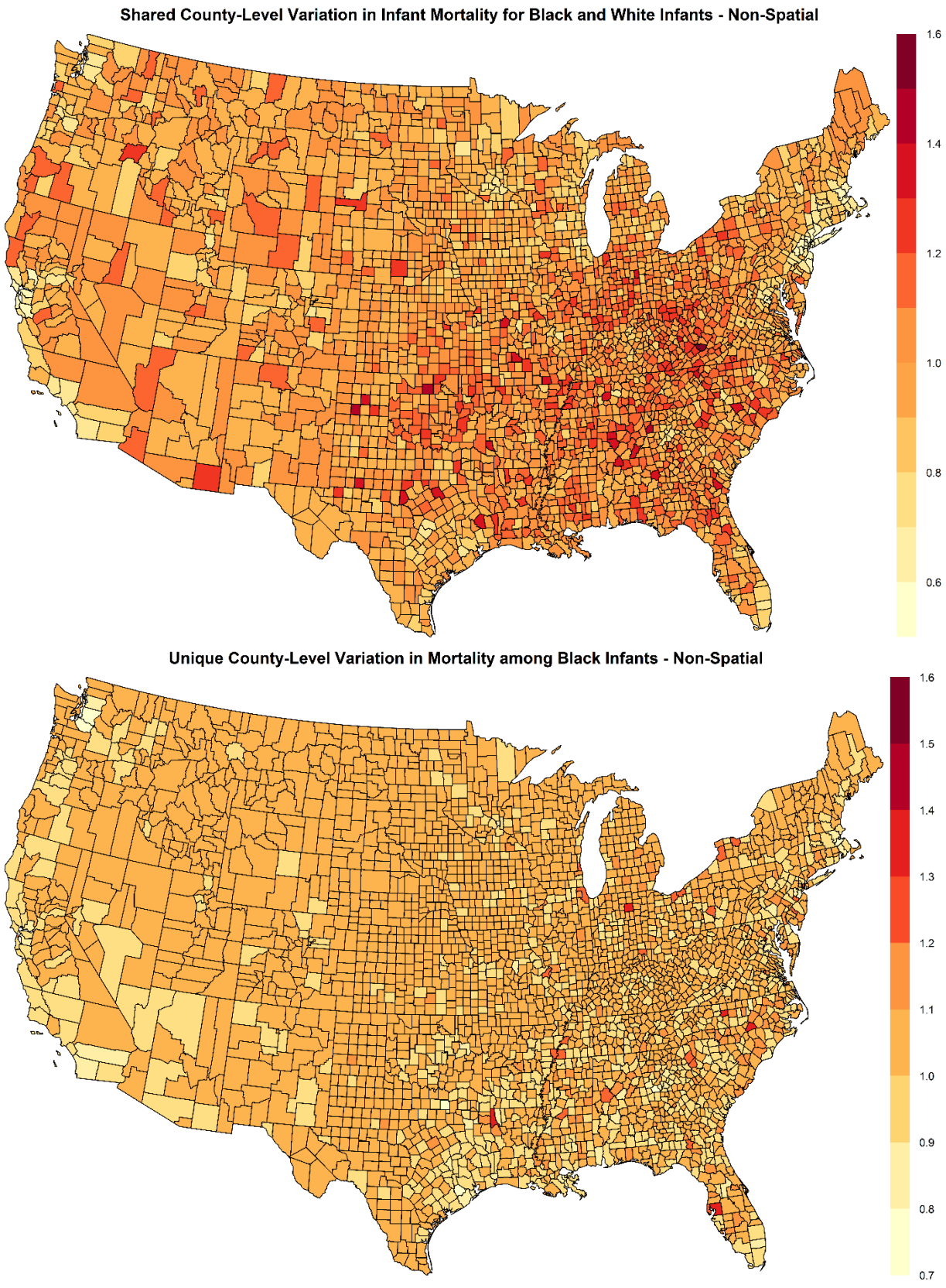


Figure e14. Shared risk (correlated heterogeneity) in infant mortality between black and white infants, 2004-2011 (top) and excess risk (uncorrelated heterogeneity) experienced by black infants (bottom) from the non-spatial SCM.

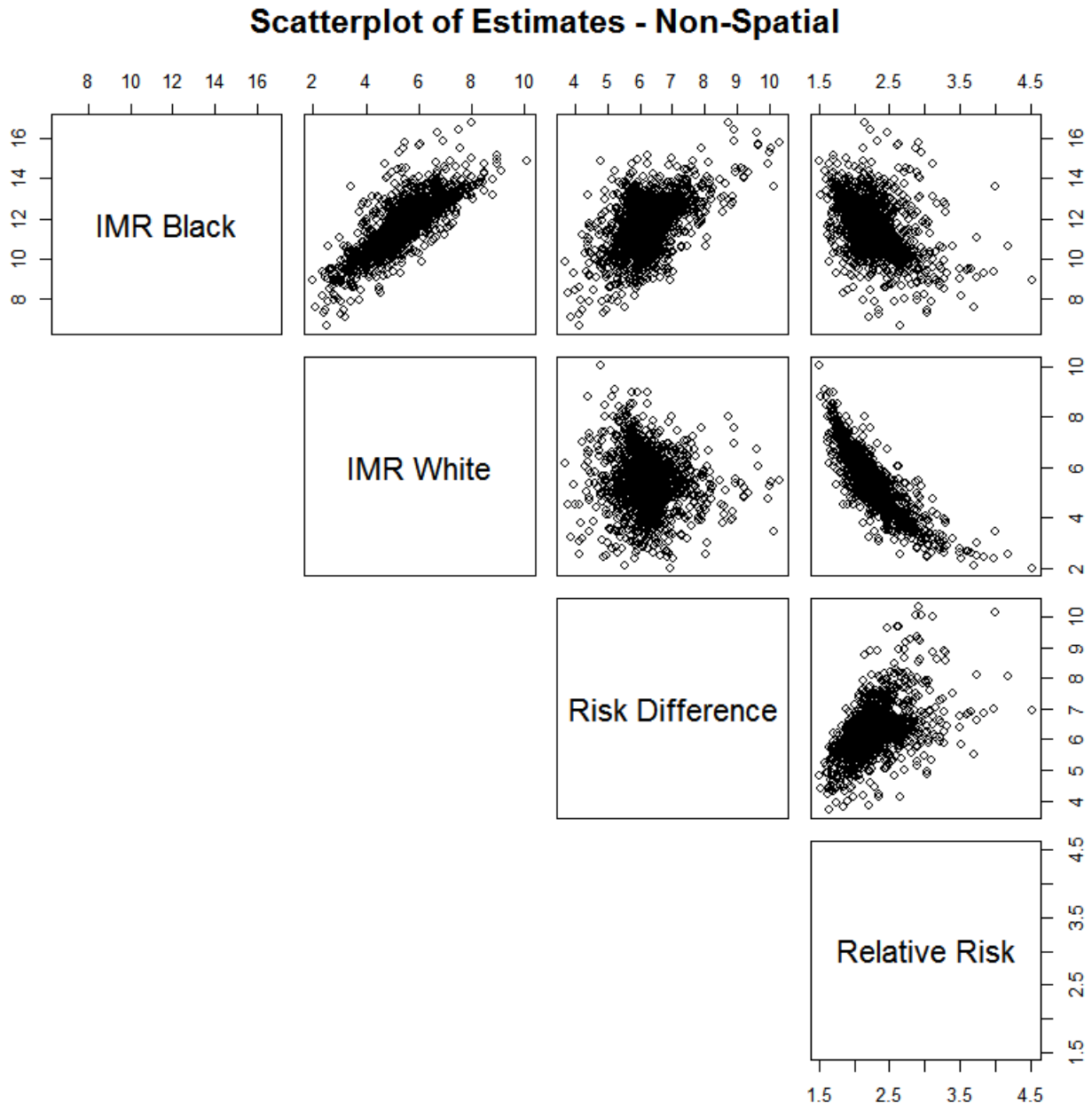


Figure e15. Scatterplots of county estimates for the outcomes of interest from the non-spatial SCM.

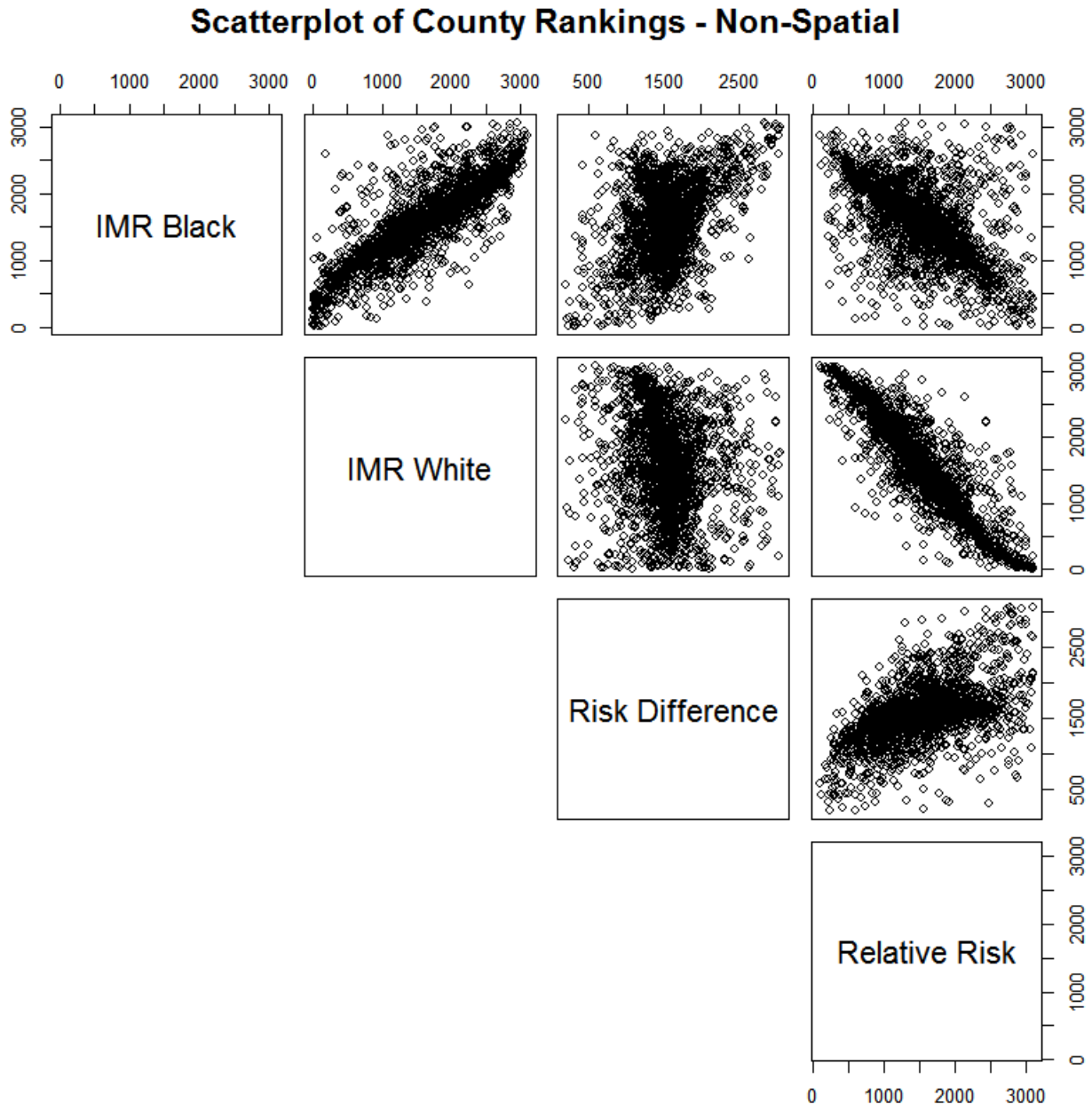


Figure e16. Scatterplots of median county rankings for the outcomes of interest from the non-spatial SCM.

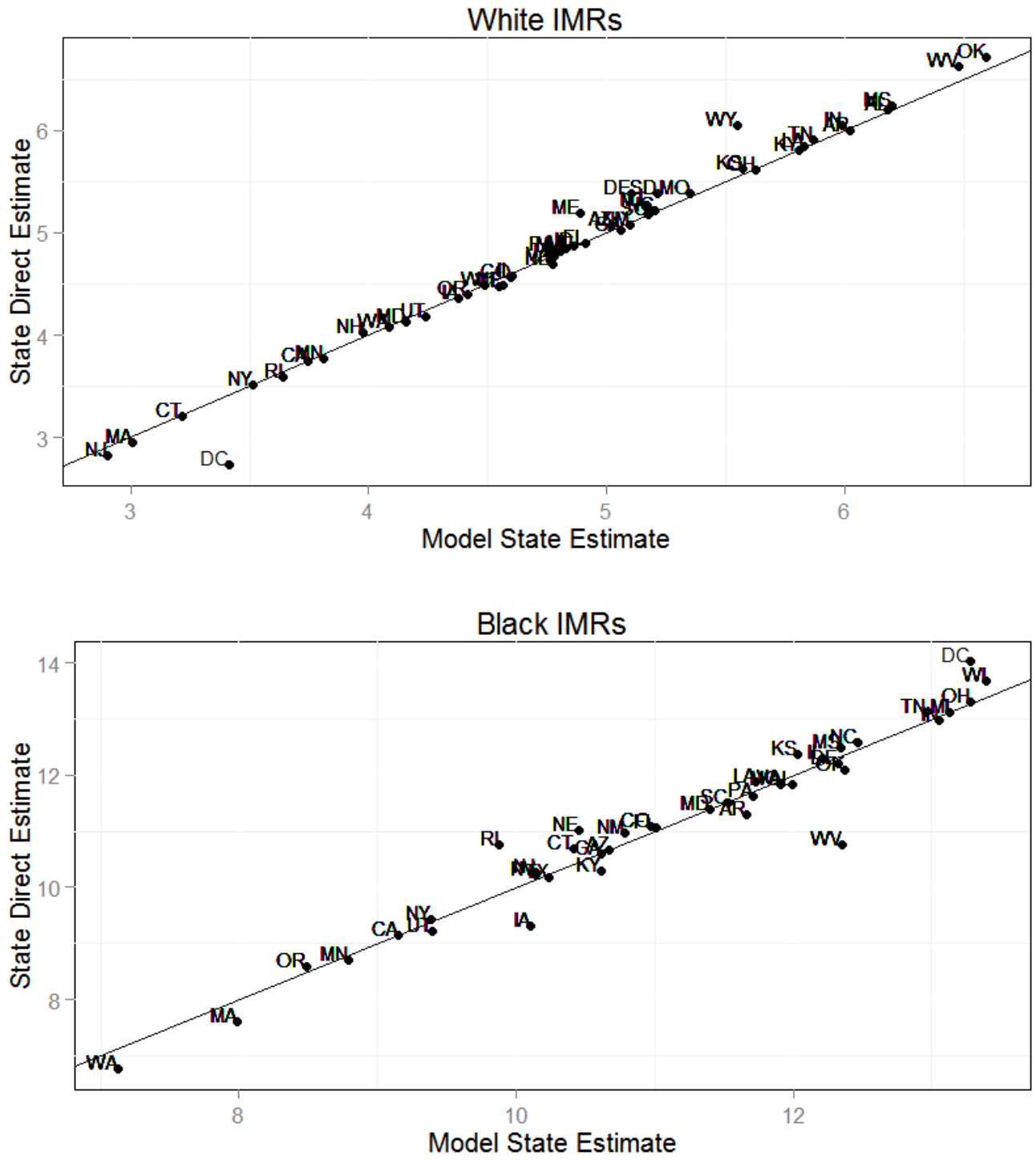


Figure e17. Comparison of state direct estimates for white infant mortality rates (top) and black infant mortality rates (bottom) with model-based estimates for the non-spatial model. Data for states with fewer than 20 deaths are suppressed.

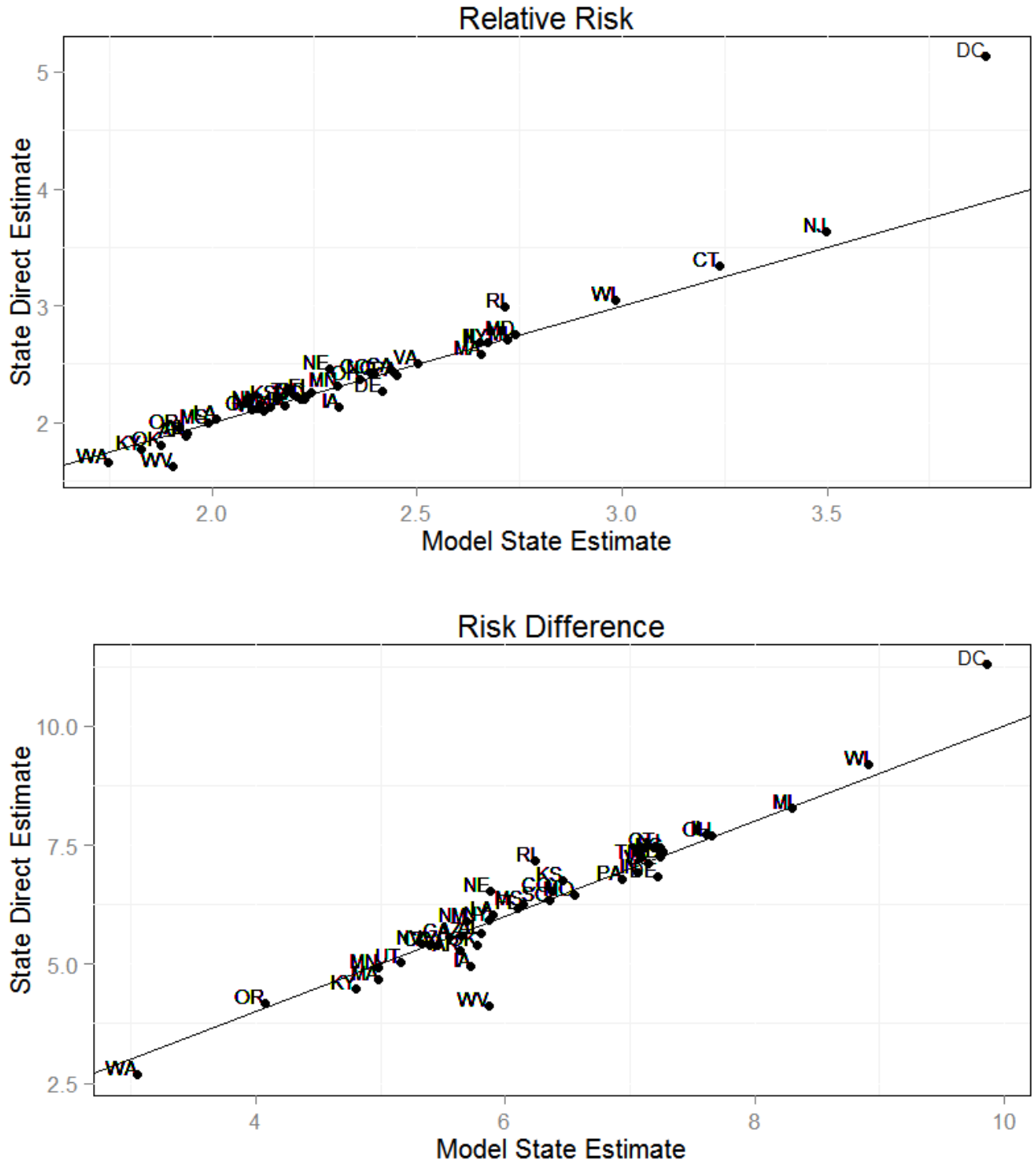


Figure e18. Comparison of state direct estimates and model-based estimates for relative rates (RR, top) and rate differences (RD, bottom) for the non-spatial model. Data for states with fewer than 20 deaths are suppressed.

Section 8. Uncertainty estimates from shared component models (SCM) with spatial priors

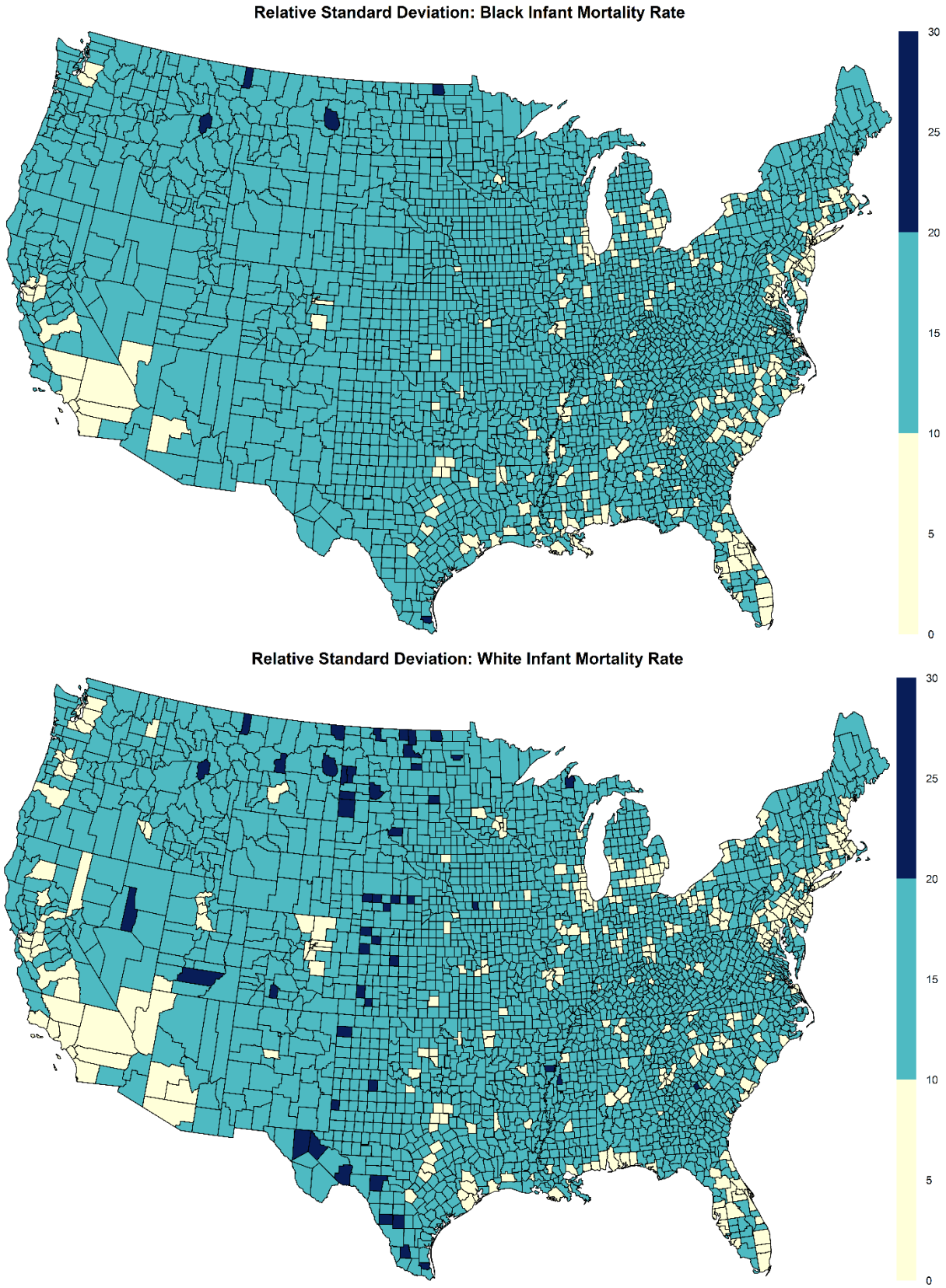


Figure e19. Coefficients of variation (relative standard deviations = 100*SD/estimate) for black (top) and white (bottom) infant mortality rates from the spatial SCM.

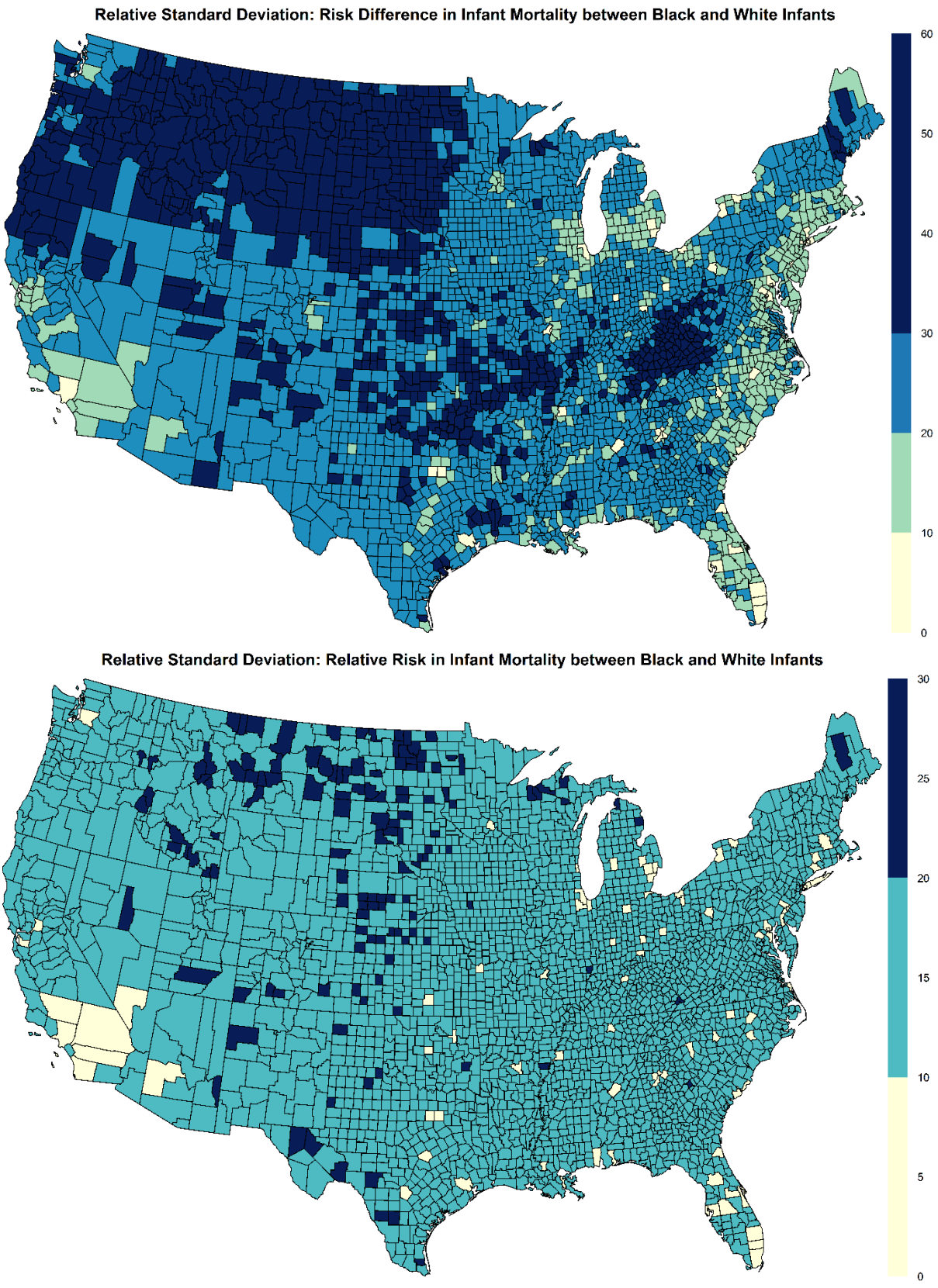


Figure e20. Coefficients of variation (relative standard deviations = 100*SD/estimate) for the risk difference (top) and relative risk of infant mortality (bottom) comparing black and white infant mortality rates from the spatial SCM.

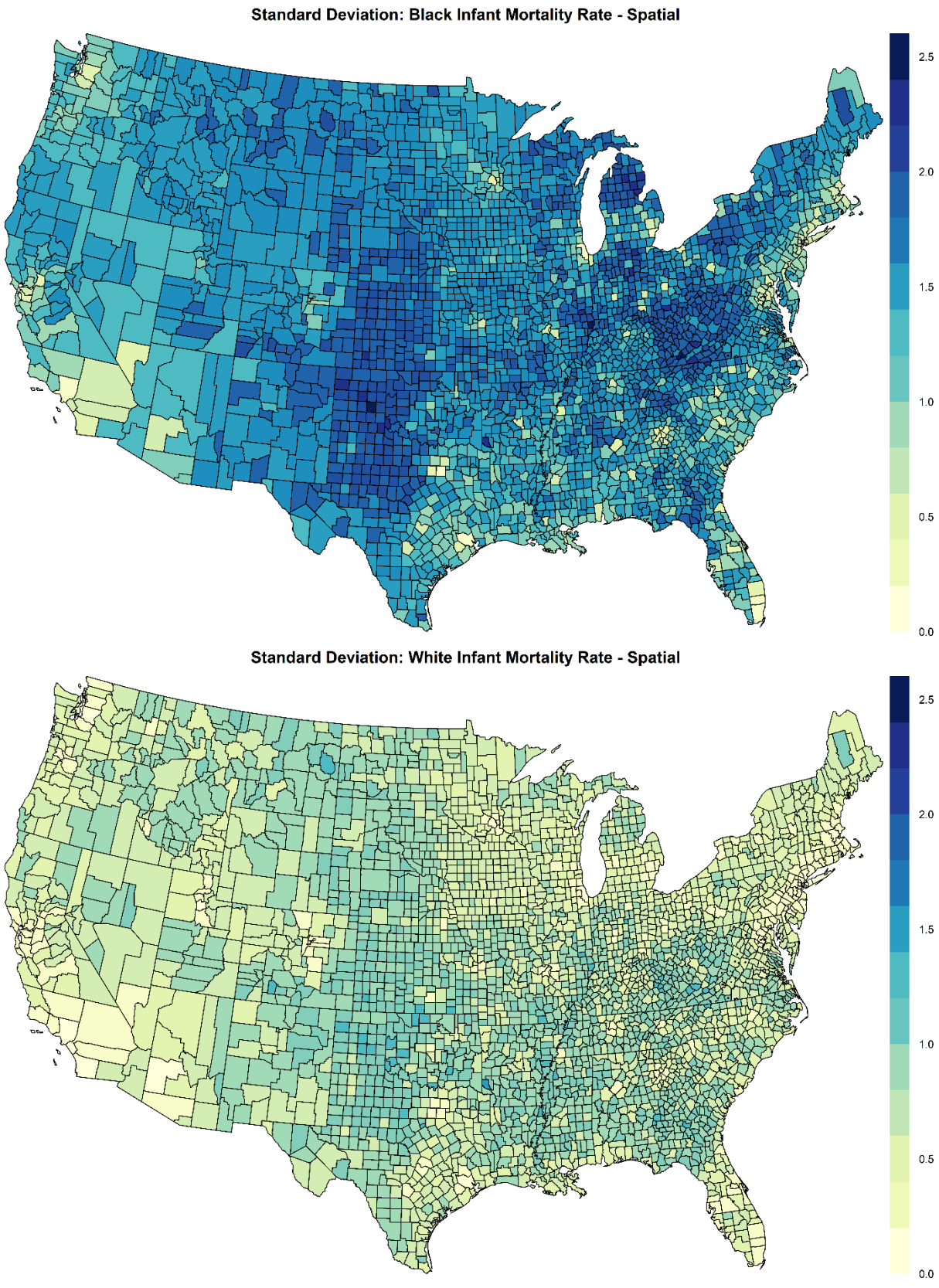


Figure e21. Absolute standard deviations for black (top) and white (bottom) infant mortality rates from the spatial SCM.

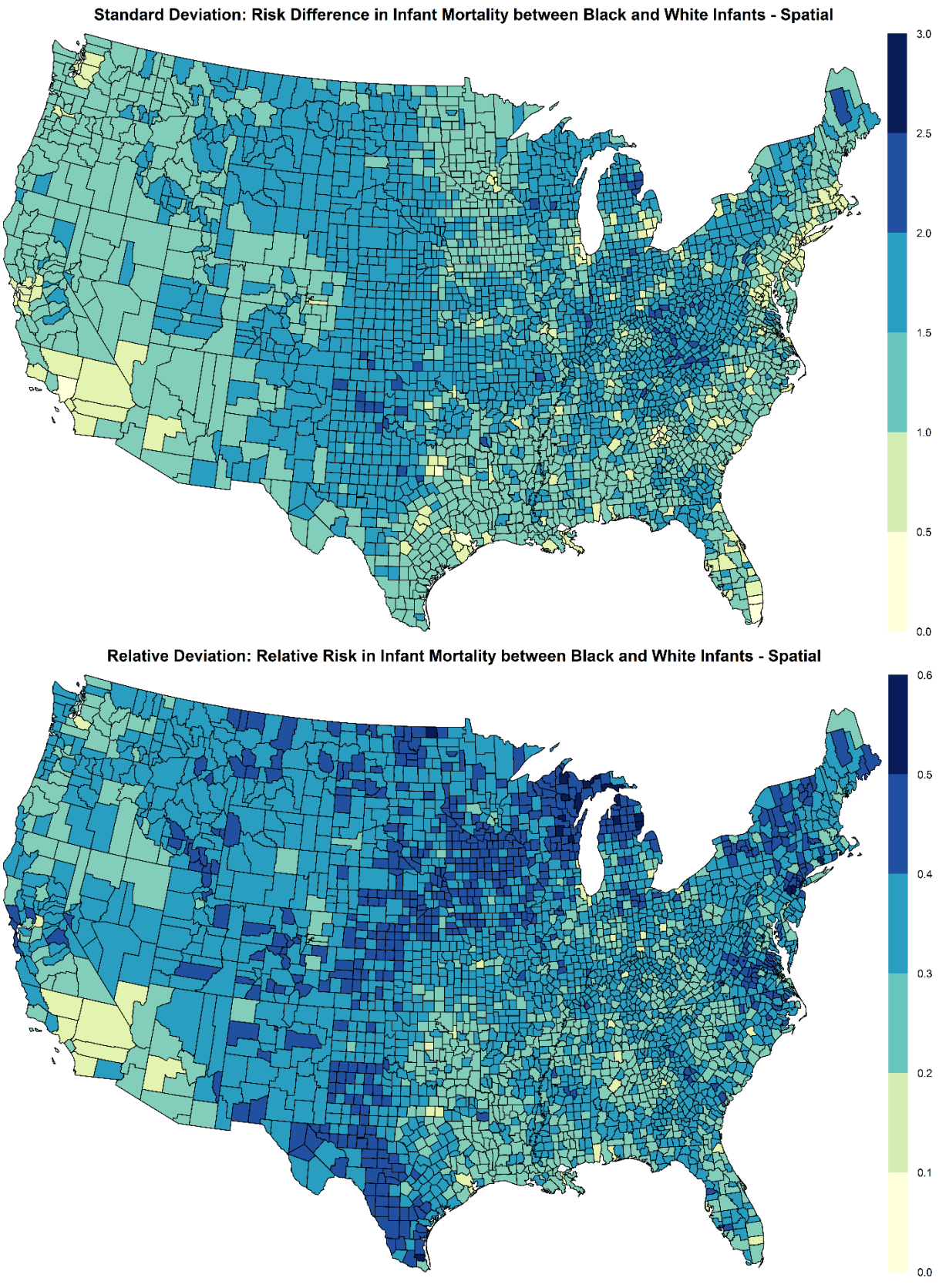
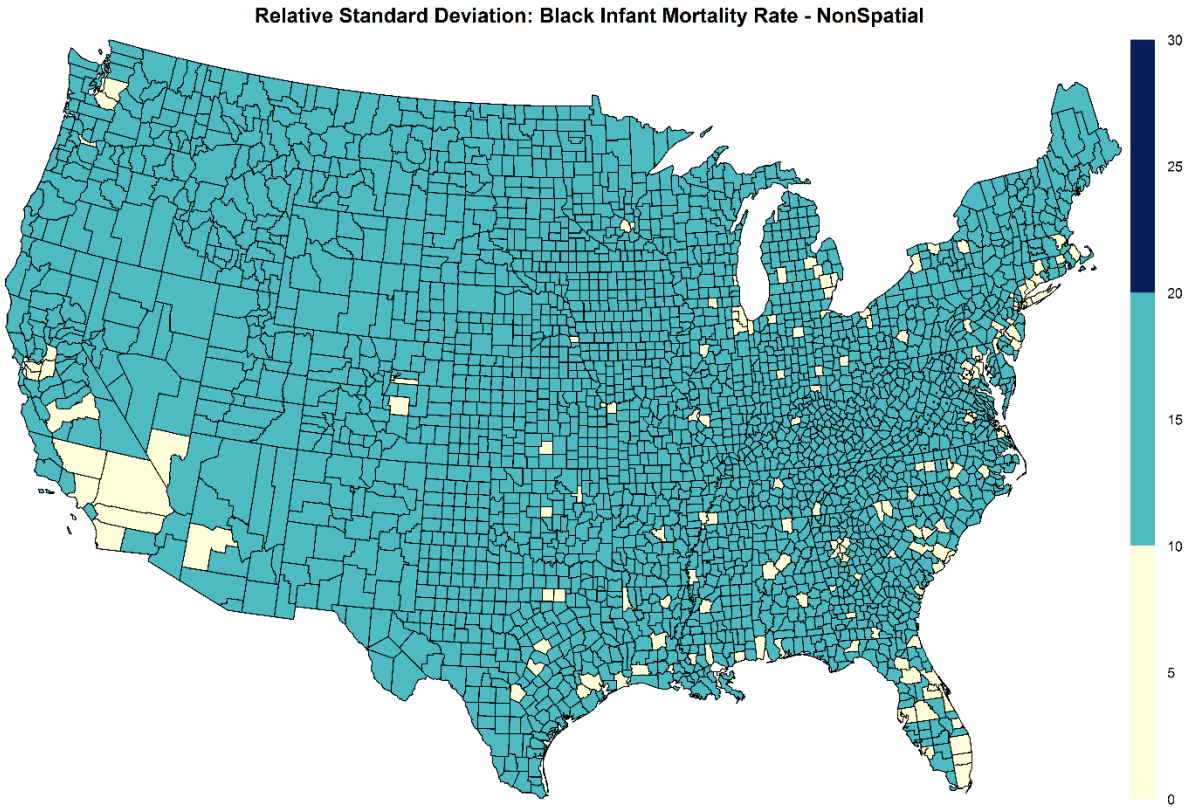


Figure e22. Absolute standard deviations for the risk difference (top) and relative risk of infant mortality (bottom) comparing black and white infant mortality rates from the spatial SCM.

Section 9. Uncertainty estimates from shared component models (SCM) with non-spatial priors.



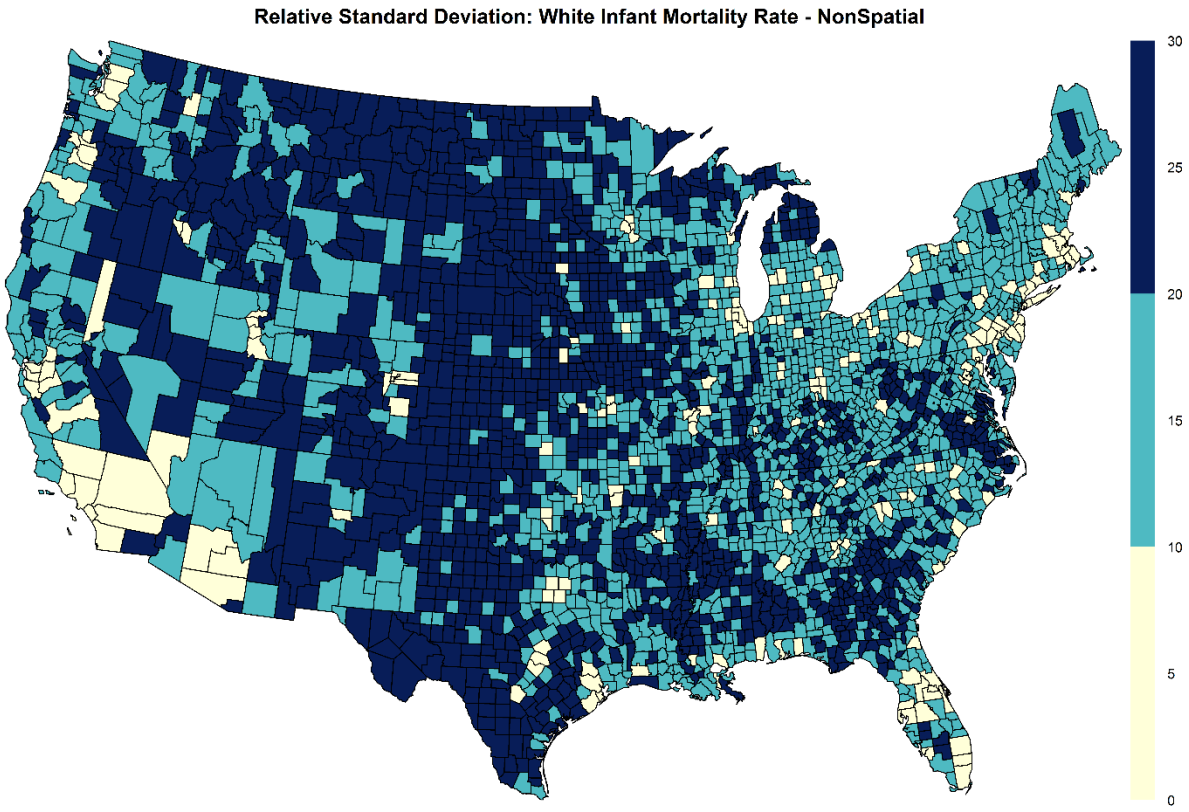


Figure e23. Coefficients of variation (relative standard deviations = 100*SD/estimate) for black (top) and white (bottom) infant mortality rates from the non-spatial SCM.

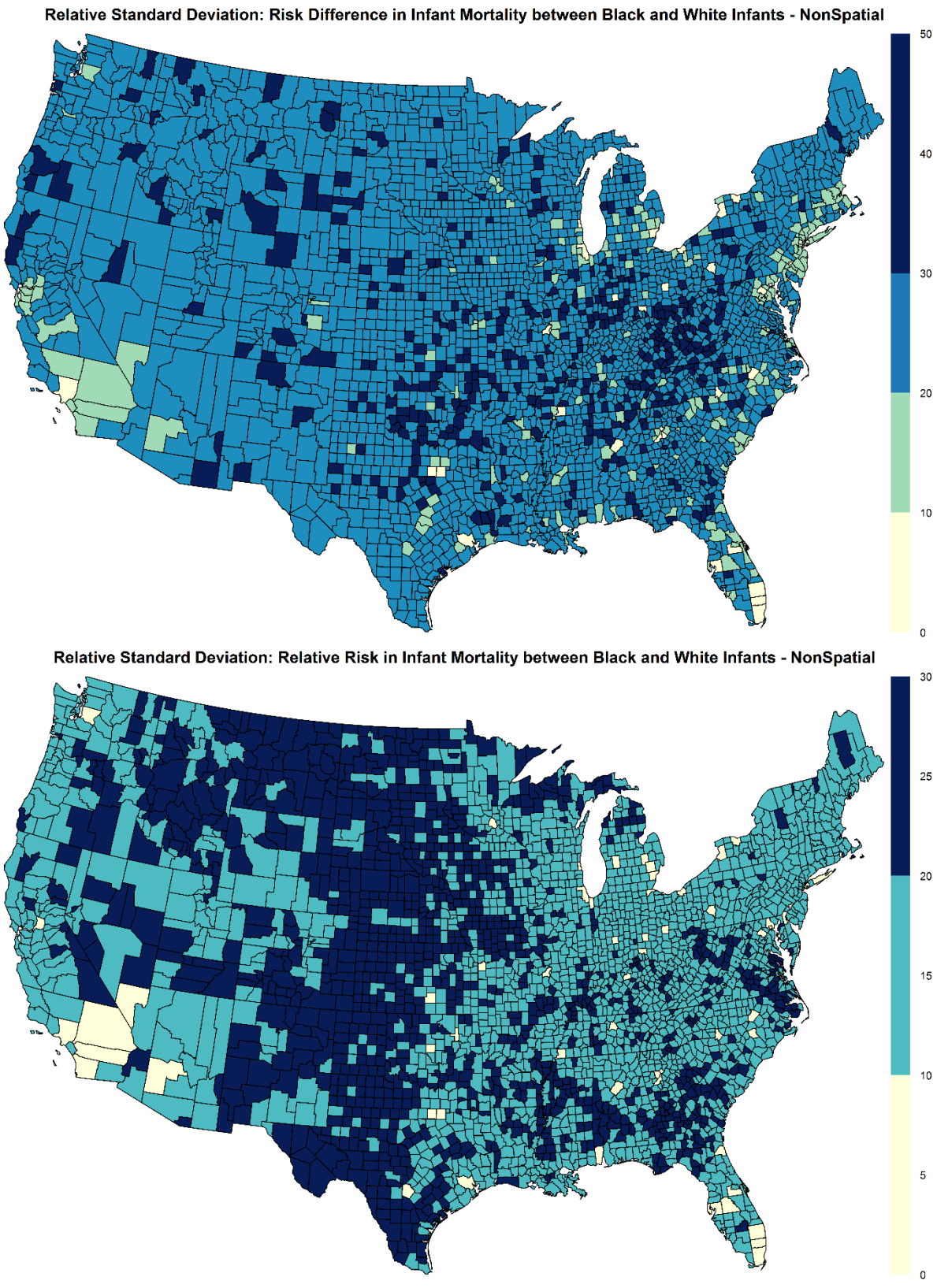


Figure e24. Coefficients of variation (relative standard deviations = 100*SD/estimate) for the risk difference (top) and relative risk of infant mortality (bottom) comparing black and white infant mortality rates from the non-spatial SCM.

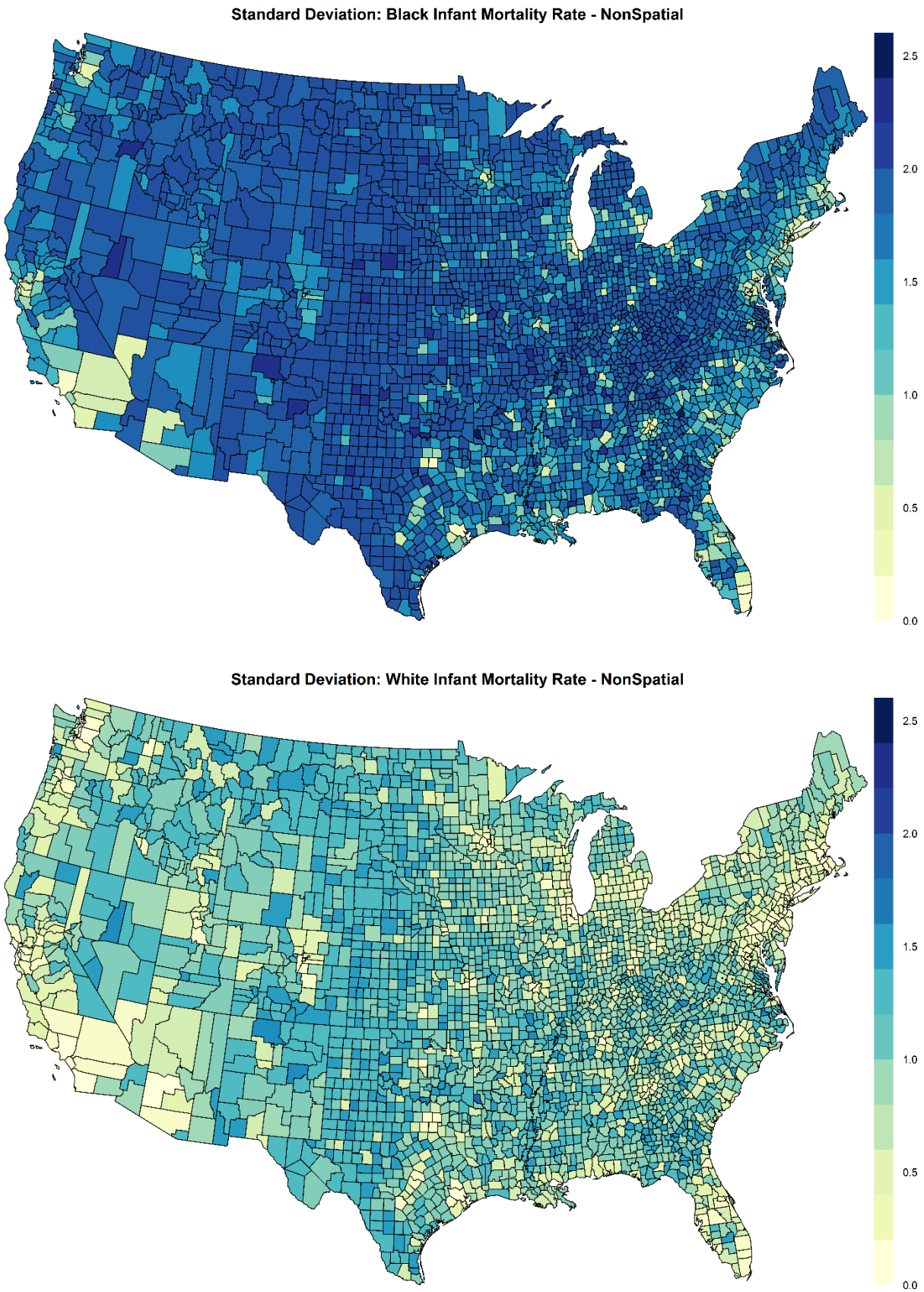


Figure e25. Absolute standard deviations for black (top) and white (bottom) infant mortality rates from the non-spatial SCM.

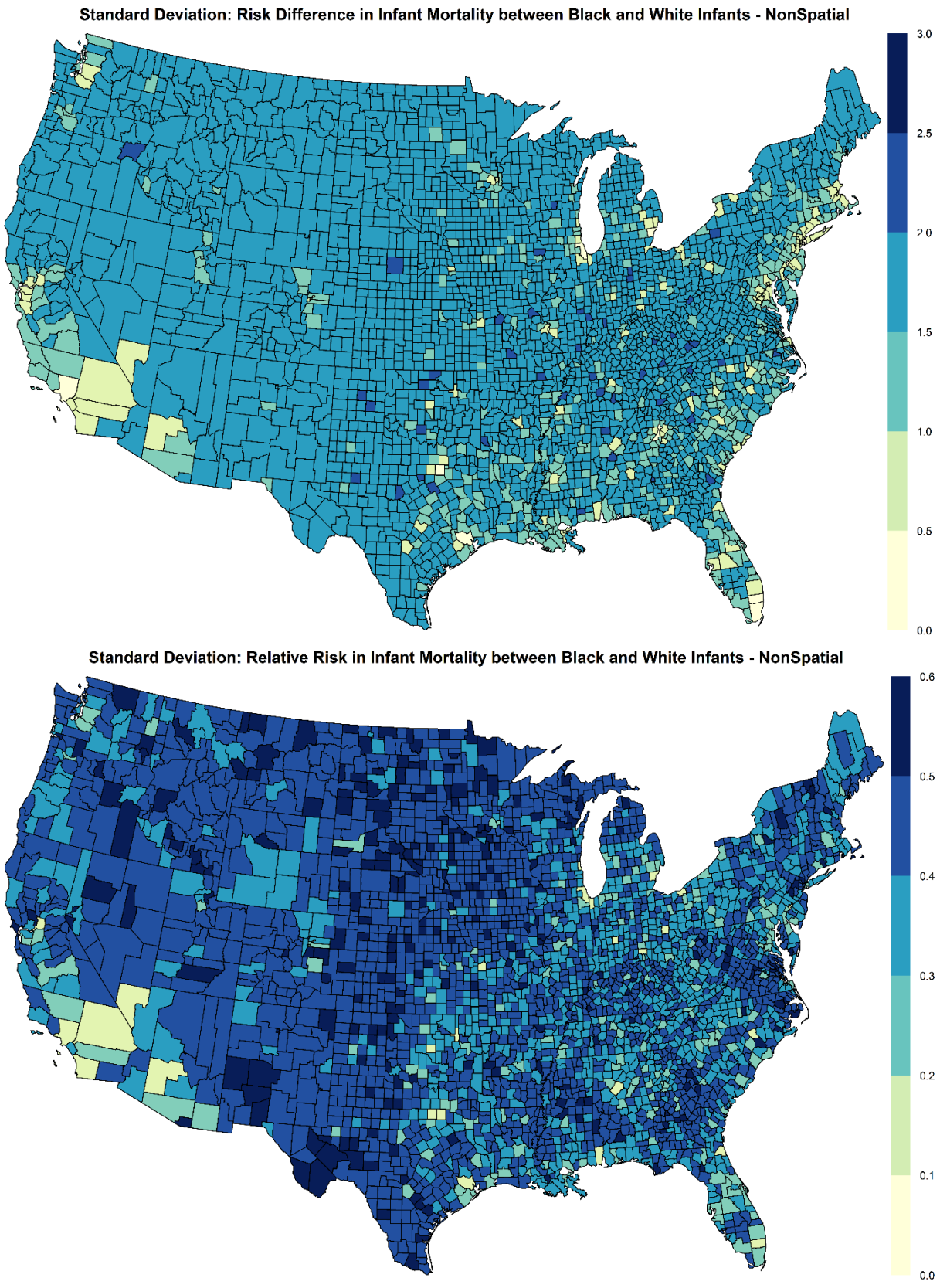


Figure e26. Absolute standard deviations for the risk difference (top) and relative risk of infant mortality (bottom) comparing black and white infant mortality rates from the non-spatial SCM.