A Bayesian Approach for Spatial Analysis of Lung Cancer Rates in Ohio

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June 2005

Disease mapping

- Definition

  -Mapping the spatial dispersion of a certain disease across the study area

- Objective

  -Infer the geographic distribution of the rates and then identify areas of higher or lower incidence.

Mapping Relative Risk

- Relative risk measures how much a particular risk factor influences the risk of a specified outcome (e.g., cancer mortality)
- Classical approach is mapping SMRs (standardized mortality/morbidity rates) for subregions based on Poisson model
- Compute P-values for SMRs to identify areas with significantly high (or low) relative risk

Poisson Model

- For rare events a Poisson model is commonly adopted.

$$O_i \mid E_i, y_i \sim Poisson(E_i y_i)$$

- SMR = O_i/E_i is the MLE estimator of Relative Risk from the Poisson model, with estimated standard error $s_i = \sqrt{O_i} / E_i$ asymptotically.
- P-value can then be computed for each area with a certain SMR

Problems of SMR

- More extreme values of the estimates may be based on a few cases only in areas with small population.
- Rare events in small areas can lead to extra-Poisson variation.
- Spatial correlation in the Relative risks is not taken into account.

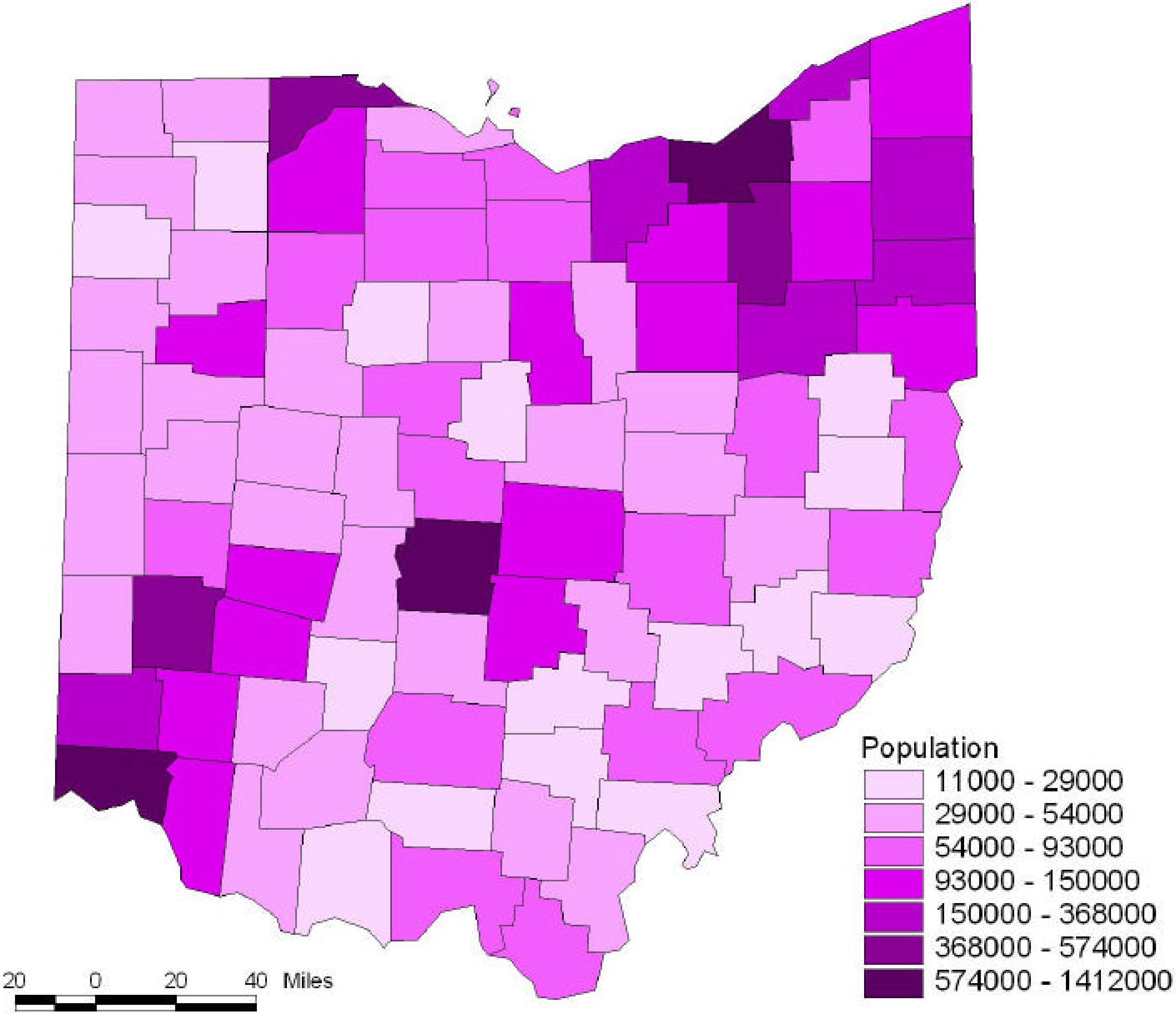
Bayesian approach

- Hierarchical model
  - Enable us to incorporate multiple sources of data and knowledge (e.g., spatial autocorrelation)
- Prior specification
  - Nonspatial random effect to describe unstructured heterogeneity.
  - Spatial random effect can be expressed via Markov random fields models (CAR, Exp)

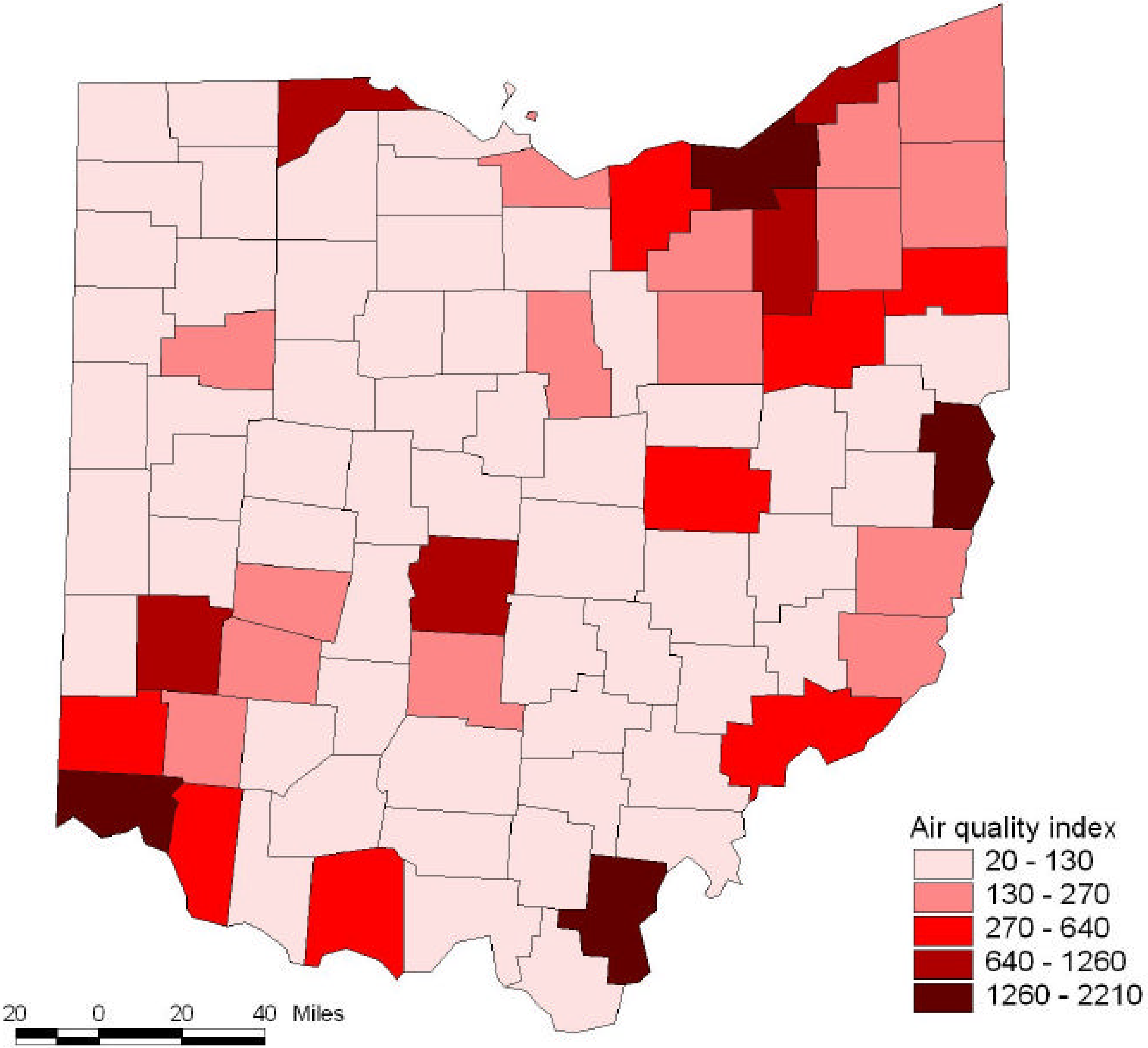
Data

- County map and census population for Ohio
- Observed lung cancer mortality at county level
  - National Cancer Institute
- Expected lung cancer mortality
  - Population in a county multiplied by crude rate
- Covariate variables
  - Air quality data from EPA
  - Poverty level: Census
- Software:
  - ArcView GIS, WinBUGS (GeoBUGS), and R.

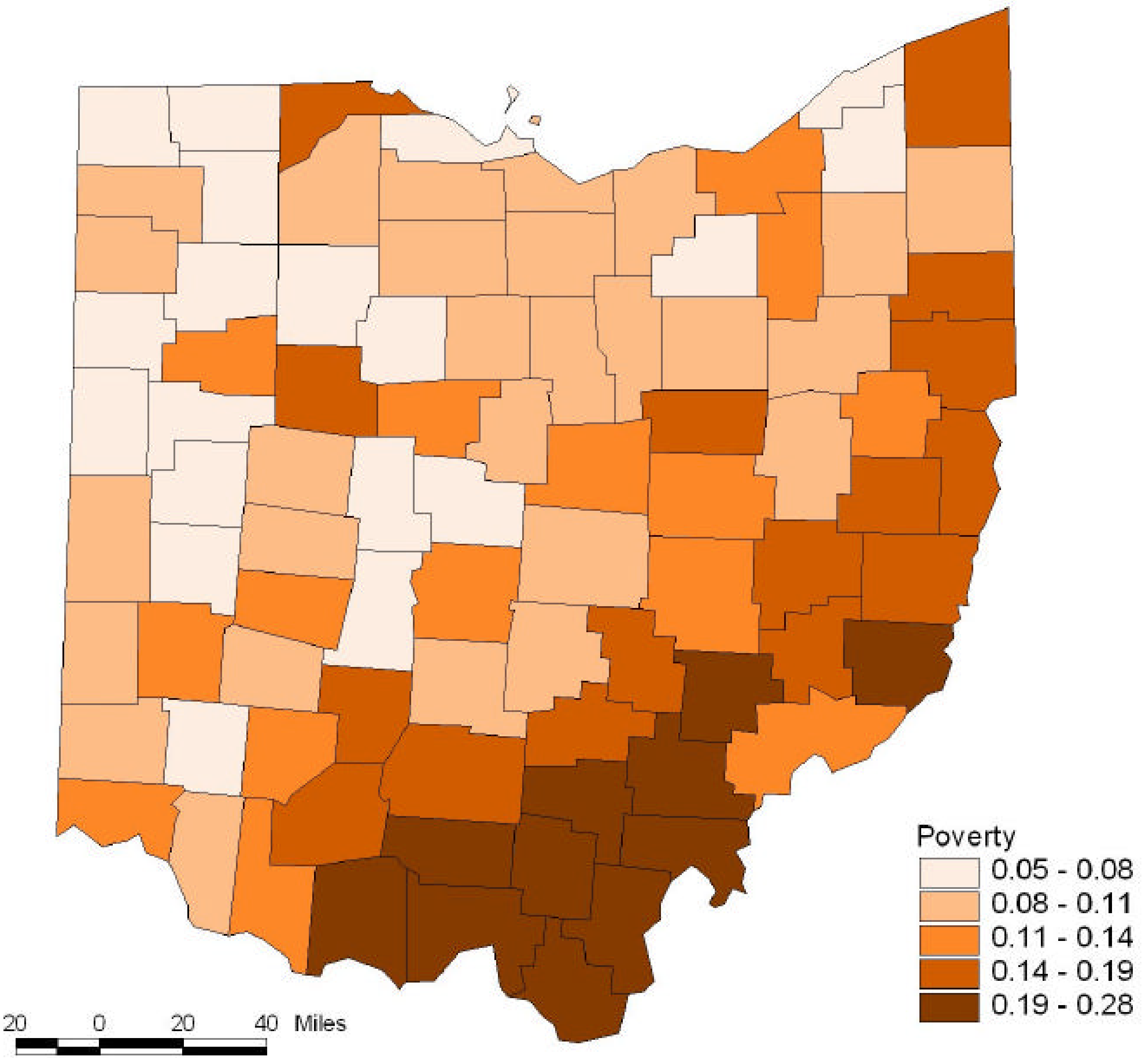
Population Distribution



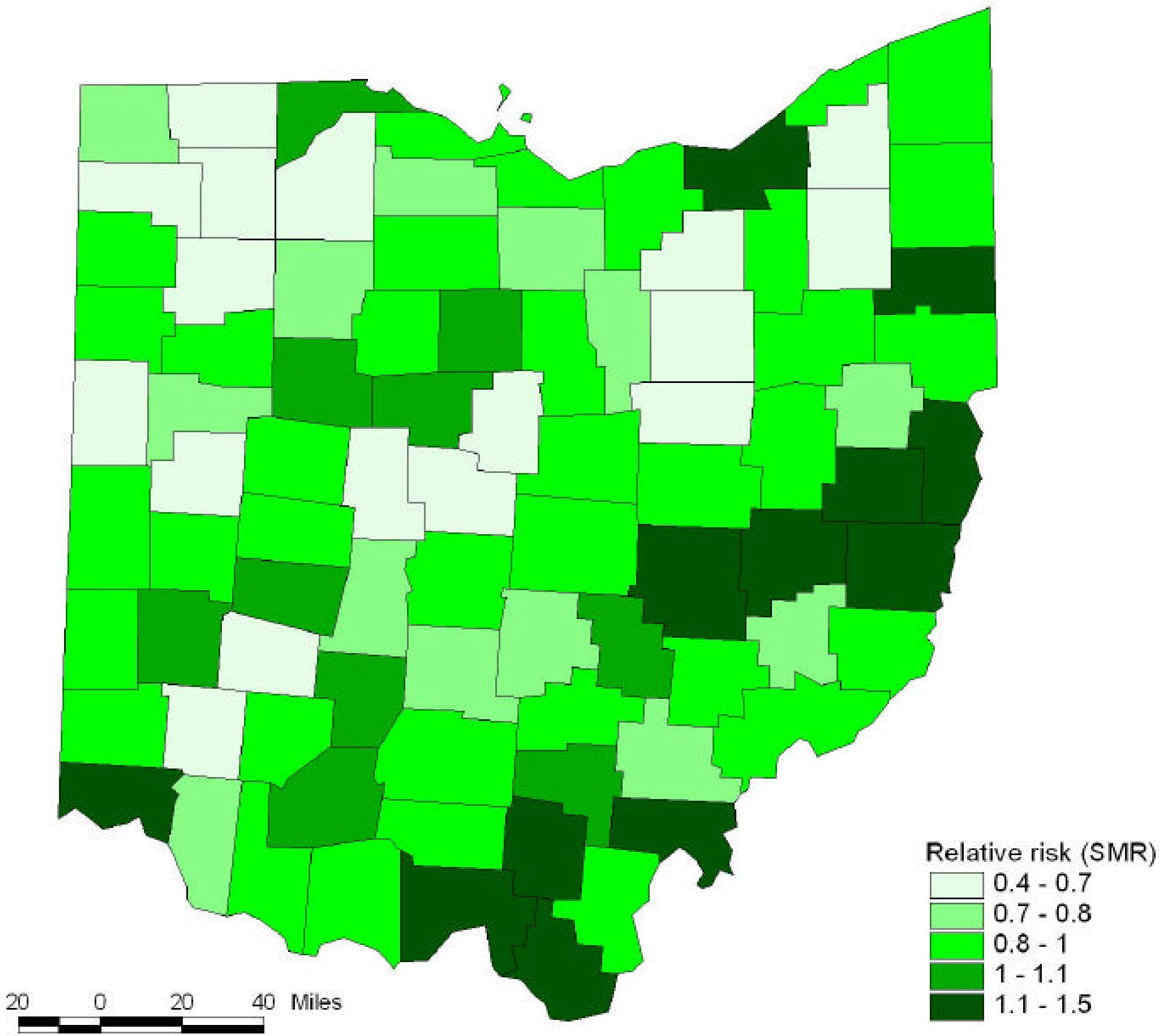
Air quality index



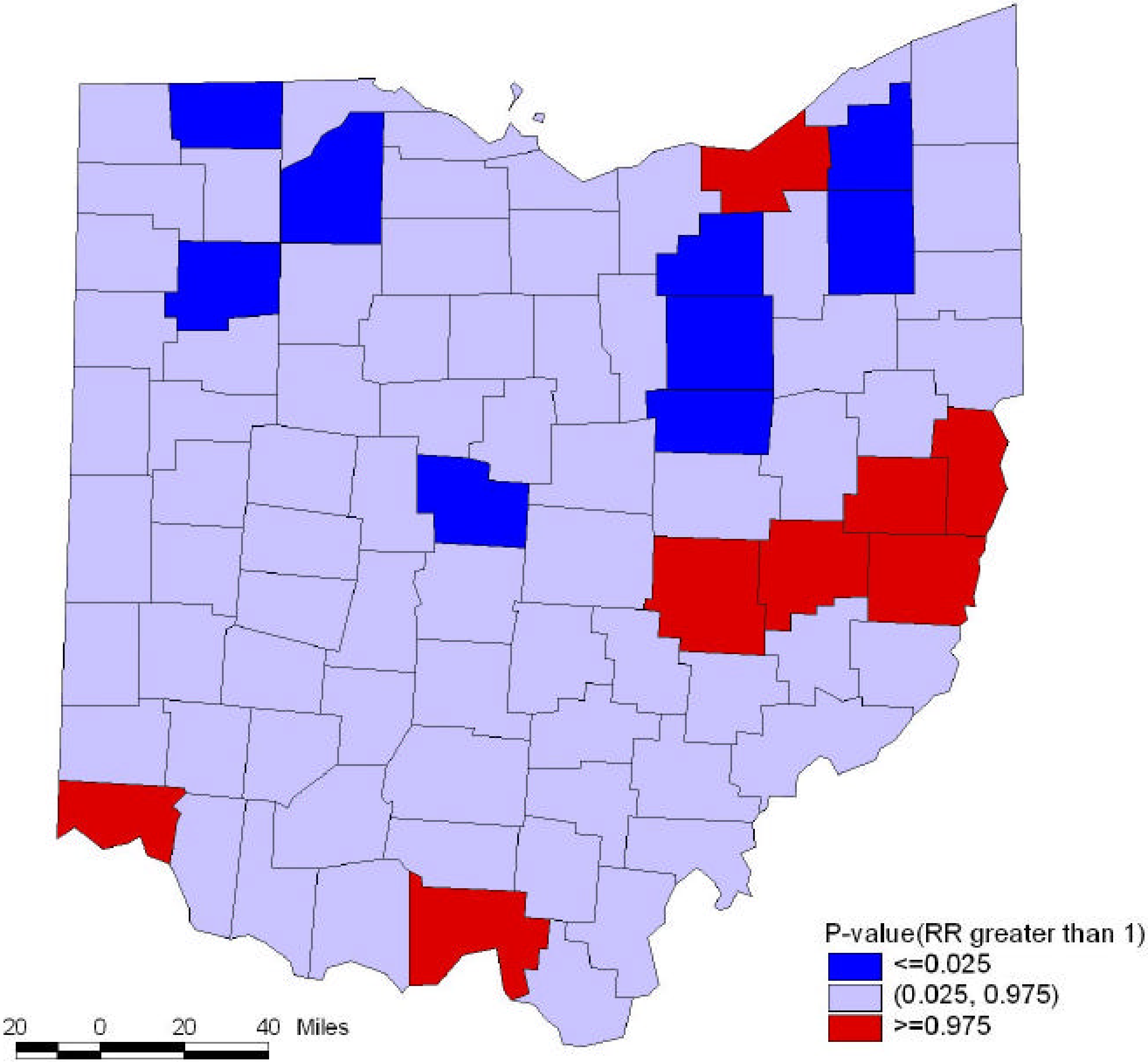
Poverty percentage



Standard mortality rate (SMR)



P-value



Hierarchical Bayesian Model using CAR prior

Likelihood:

O[i] ~ Poisson(mu[i])

First stage:

Log(mu[i]) = Log(E[i]) + phi[i] + theta[i]

RR[i] = exp(phi[i])

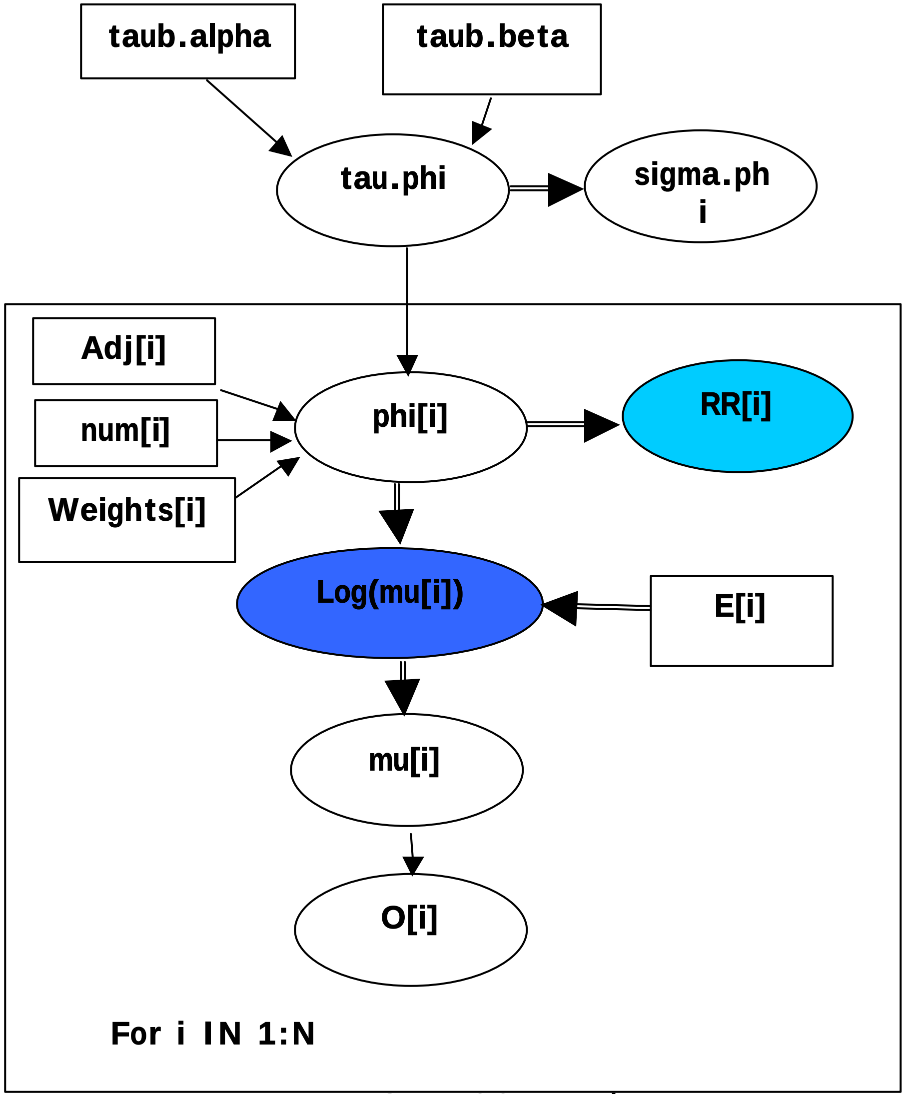
Second stage:

phi[1:N] ~ car.normal(adj[], weights[], num[], tau.phi)

Priors:

tau.phi ~ Gamma(taub.alpha, taub.beta)

Model diagram



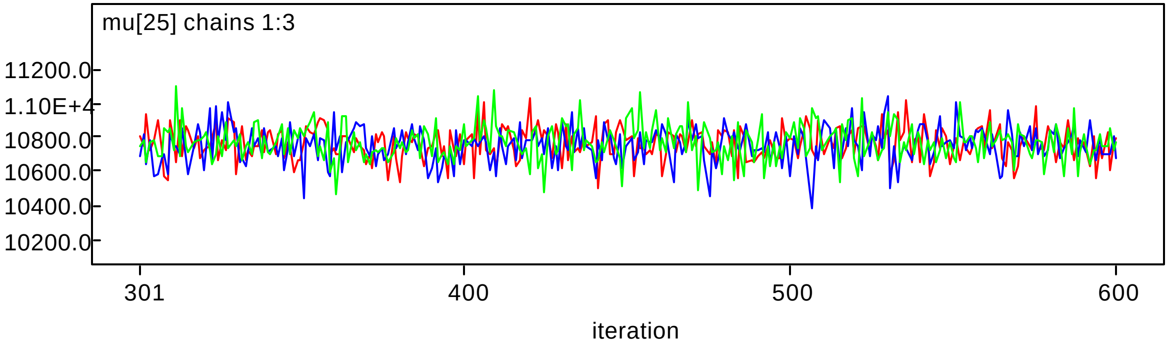
Example of Source Code

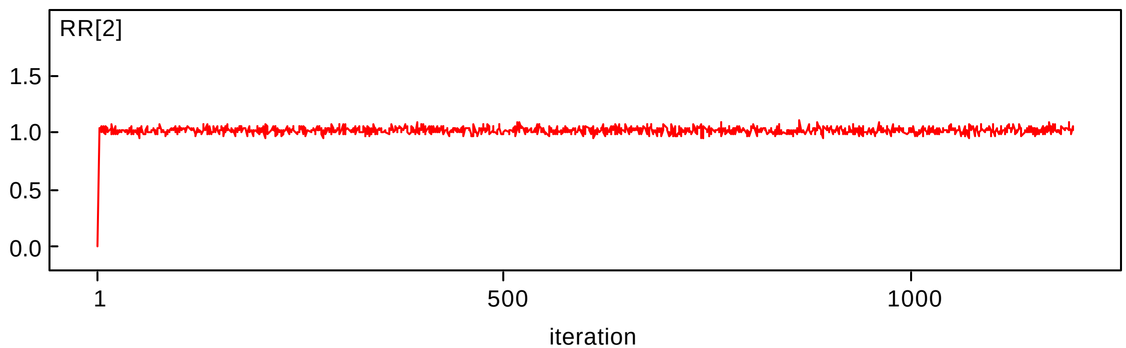
```
model {
    # Likelihood
    for (i in 1 : N) {
        obs.m[i]  ~ dpois(mu[i])
        theta[i]  ~ dnorm(0, tau.theta)
        log(mu[i]) <- log(e.m[i]) + beta0 + beta1*log.emis[i] + phi[i] + theta[i]
        RR[i] <- exp(beta0 + beta1*pov[i] + phi[i] + theta[i])
    }
    # CAR prior distribution for relative risk:
    phi[1:N] ~ car.normal(adj[], weights[], num[], tau.phi)
    for(k in 1:sumNumNeigh) { weights[k] <- 1}
    # Other priors:
    beta0 ~ dflat()
    beta1 ~ dnorm(0.0, 1.0E-5)
    #beta2 ~ dnorm(0.0, 1.0E-5)
    tau.phi  ~ dgamma(0.5, 0.0005)
    tau.theta  ~ dgamma(0.5, 0.0005)
    sigma.phi <- sqrt(1 / tau.phi)
}
```

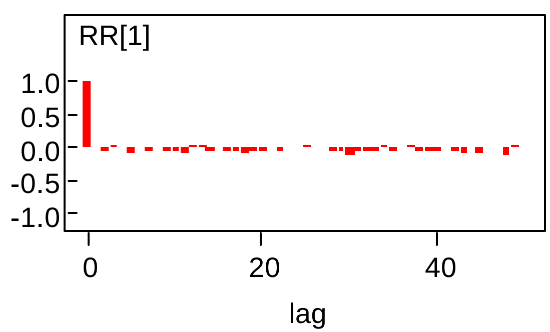
Model selection

Model		DIC	pD
No spatial structured variance		922.3	87.7
Structured & unstructured	CAR	926.5	93.5
	EXP	916.3	83.4
1 covariate log.emis	CAR	923.6	89.7
	EXP	916.7	83.3
1 covariate pov	CAR	924.3	90.6
	EXP	916.2	82.9
2 covariates log.emis and pov	CAR	921.7	88.5
	EXP	917.4	84.5

History graphs







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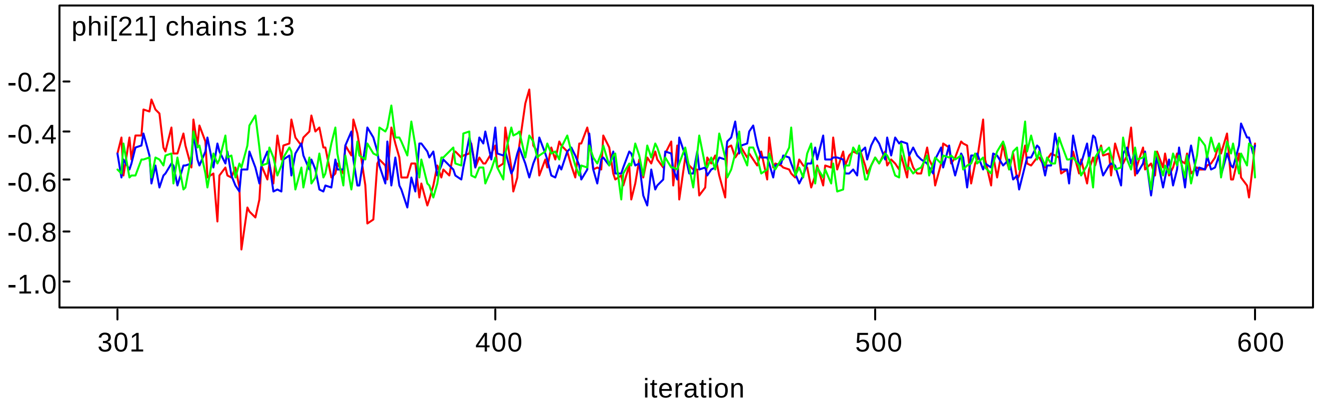
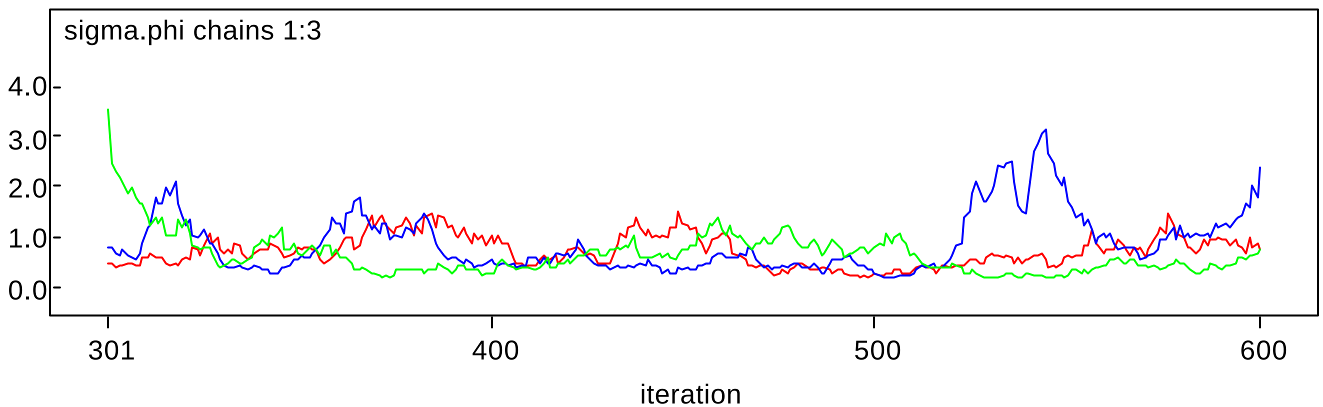




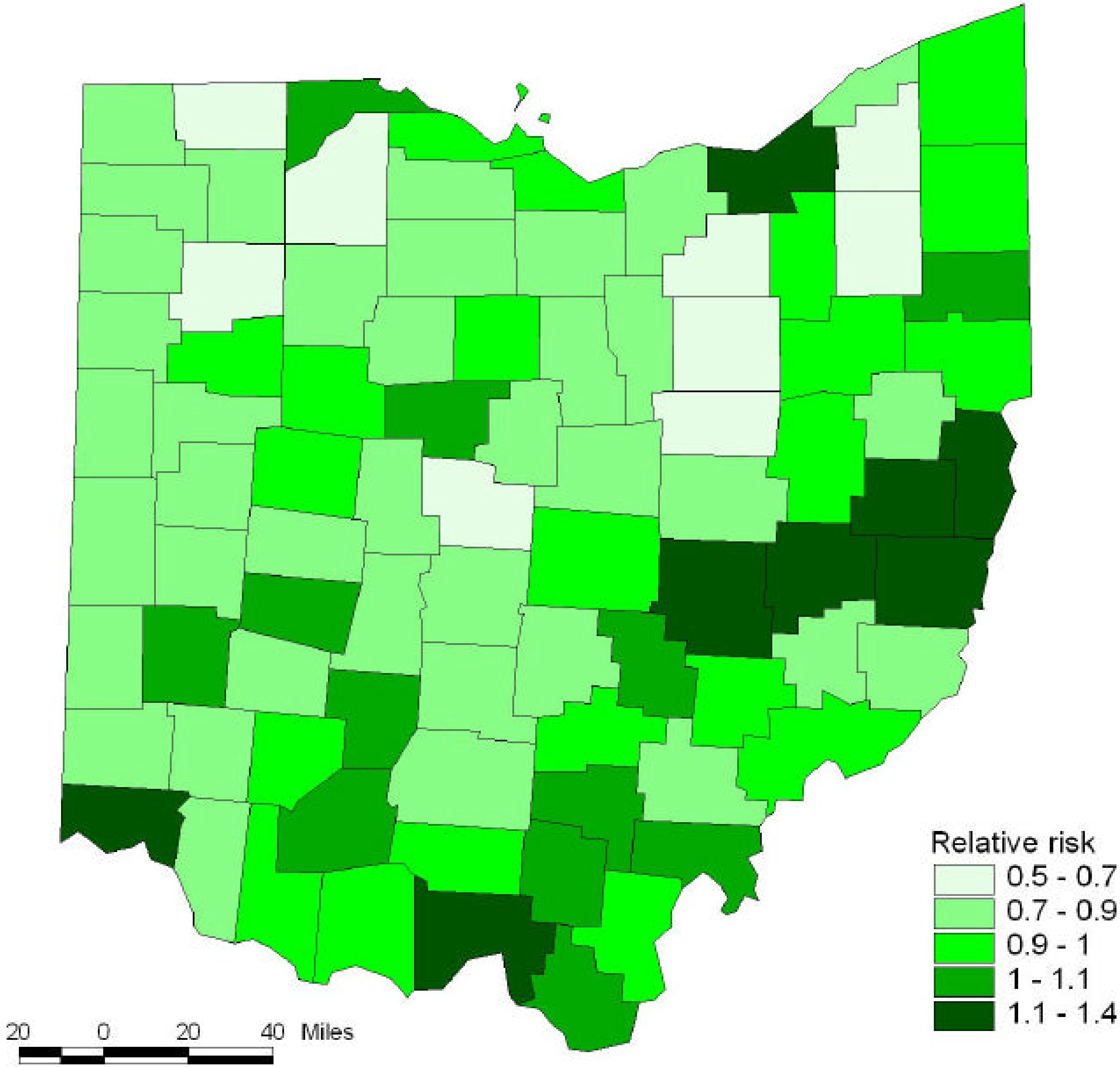
Statistical results

One covariate (pov) with spatial structured variance

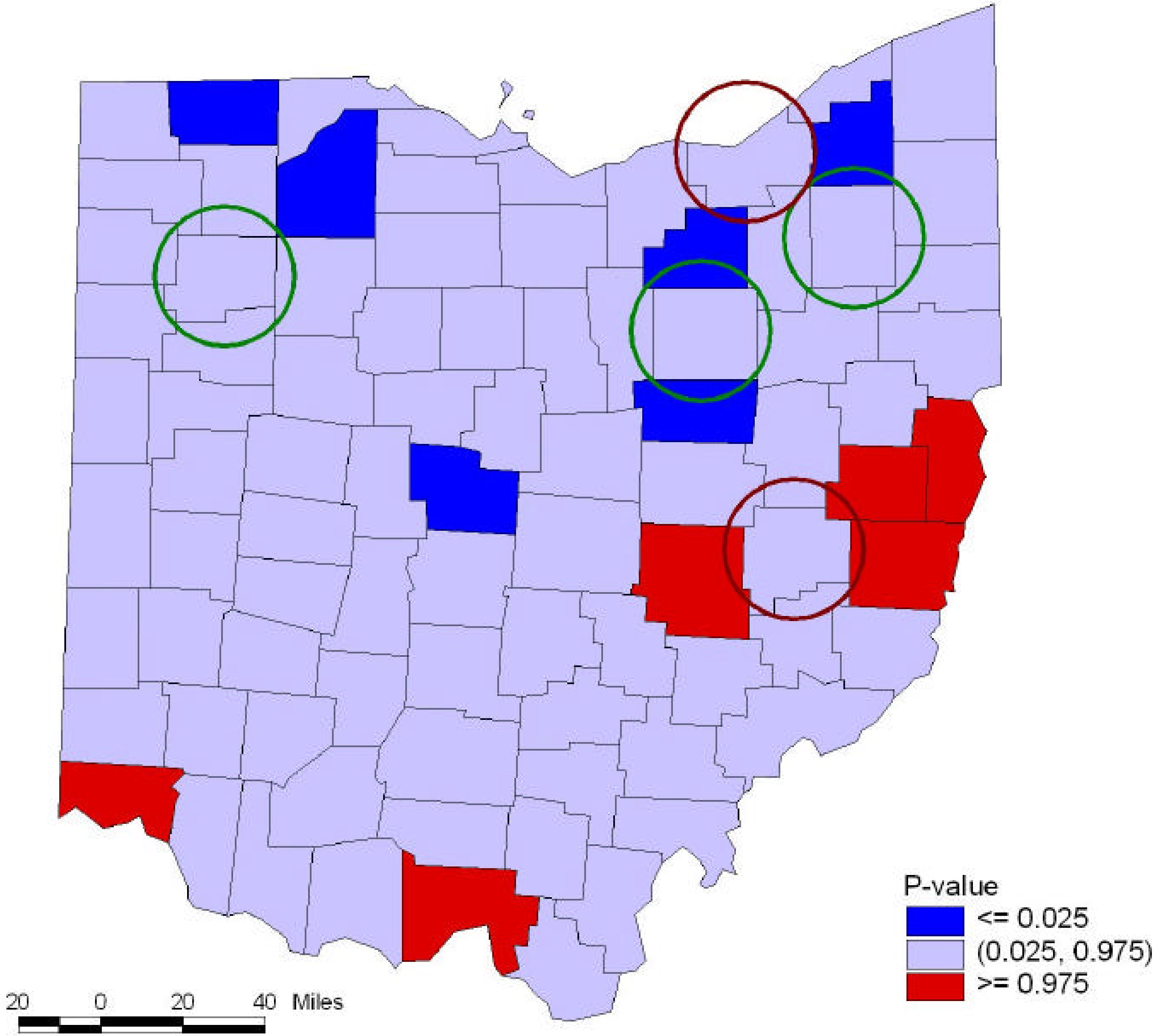
sigma.phi	210.8	56.5	120.3	141.5	234.4	254.6	286.8	7.0	3
deviance	833.3	12.9	809.8	824.7	832.6	841.9	859.4	1.0	900

pD = 82.9 and DIC = 916.2 (using the rule, pD = var(deviance)/2)

Relative risks



P-value of RR>1



Discussion and Conclusions

- Bayesian approach helps create more interpretable map by:
  - Applying priors
  - Incorporate covariates
- p-value map identify several potential hotspots.
- Age and race adjusted rates may be used to compute expected number of cases.
- Space and time