Lecture 4: Regression Modelling for Areal Data

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Spatial Regression Models

Y_i is a response variable at spatial unit i. We wish to model:

$$Y_i = \sum_{k=1}^{p} \beta_k x_{ik} + \epsilon_i = \boldsymbol{x}_i \boldsymbol{\beta} + \epsilon_i$$

where $\boldsymbol{x}_i$ is a row vector of covariate and ϵ_i is the residual error.

Goals: Estimate $\boldsymbol{\beta}$ accounting for spatial autocorrelation in ϵ_i.

Methods:

1. Conditional Autoregressive Model (CAR)
2. Simultaneous Autoregressive Model (SAR)

For now, we will focus on the case where Y_i can be modeled as a Gaussian outcome.

Conditional Autoregressive Models

Consider the conditional specification of the random variable Y_i given all the other spatial units as:

$$[\, Y_i \,|\, Y_j : j \neq i \,] \sim \mathsf{N} \left(\rho \sum_{j=1}^{n} b_{ij} Y_j,\, \tau_i^2 \right) .$$

The above model indicates that the *full conditional* distribution of Y_i:

- is Normal;
- has a mean proportional (via $\rho > 0$) to a linear combination of all other random variables. The weights are defined by b_{ij} with $b_{ii} = 0$;
- has a location-specific conditional variance τ_i^2.

What is the induced joint distribution? What conditions on ρ, b_{ij}, and τ_i^2 do we need to ensure a valid joint distribution? [See Appendix.]

Conditional Autoregressive Model

To get a valid joint distribution, the conditional distribution of each Y_i must satisfy

$$[\, Y_i \,|\, Y_j : j \neq i \,] \sim \mathsf{N} \left(\rho \frac{1}{W_{i+}} \sum_{j=1}^{n} W_{ij} Y_j,\ \frac{\tau^2}{W_{i+}} \right) .$$

We typically assume W_{ij} to be binary (indicator for being neighbors).

Then

- The conditional mean of Y_i is the weighted average of all neighbors.
- The conditional variance is proportional to the number of of neighbors.

The induced joint distribution is multivariate Normal:

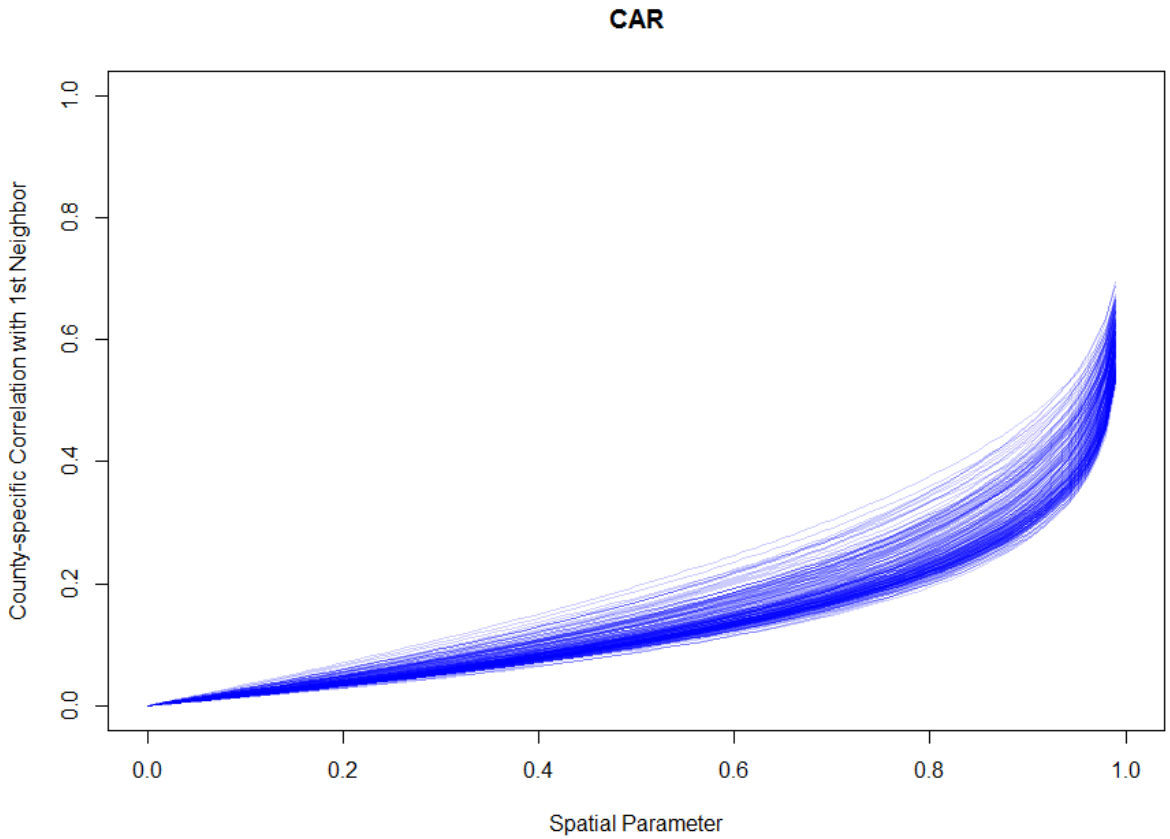
$$[Y_1, Y_2, \ldots, Y_n] \sim N(\, \mathbf{0}, \tau^2 (\mathbf{D}_w - \rho \mathbf{W})^{-1} \,)$$

where $\mathbf{D}_w = diag(W_{1+}, W_{2+}, \ldots, W_{n+})$ and $\mathbf{W}$ is the adjacency matrix.

Impacts of ρ on Average 1st Neighbor Correlation

$$Var[\mathbf{Y}] = \tau^2(\mathbf{D}_w - \rho\mathbf{W})^{-1}, \tau^2 = 1, \mathbf{W} = \text{1st-order}$$

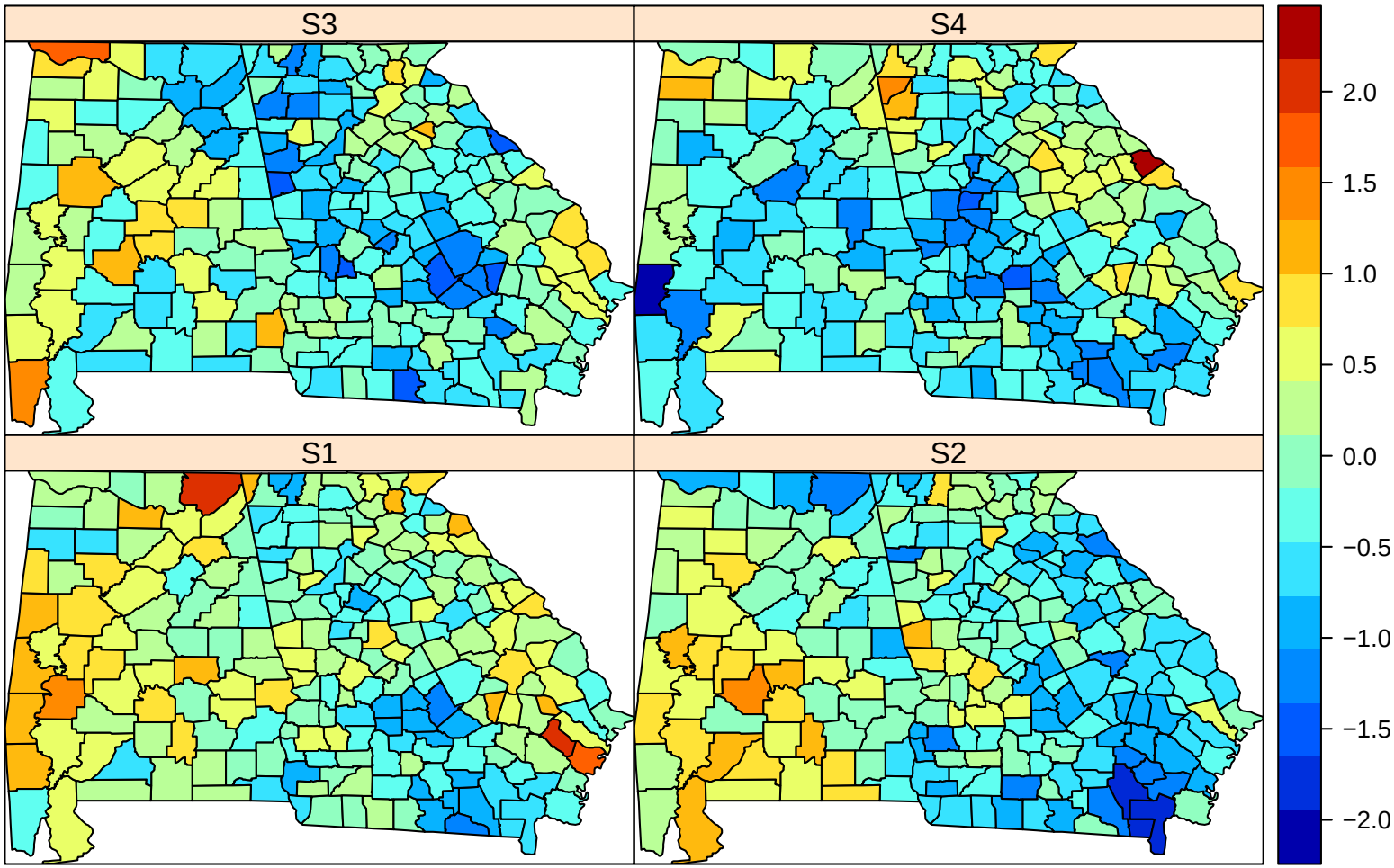
Below we plot the induced average correlation between a county and its neighbors as a function of ρ.



Note that even with $\rho = 0.99$, the correlation is still < 0.8!

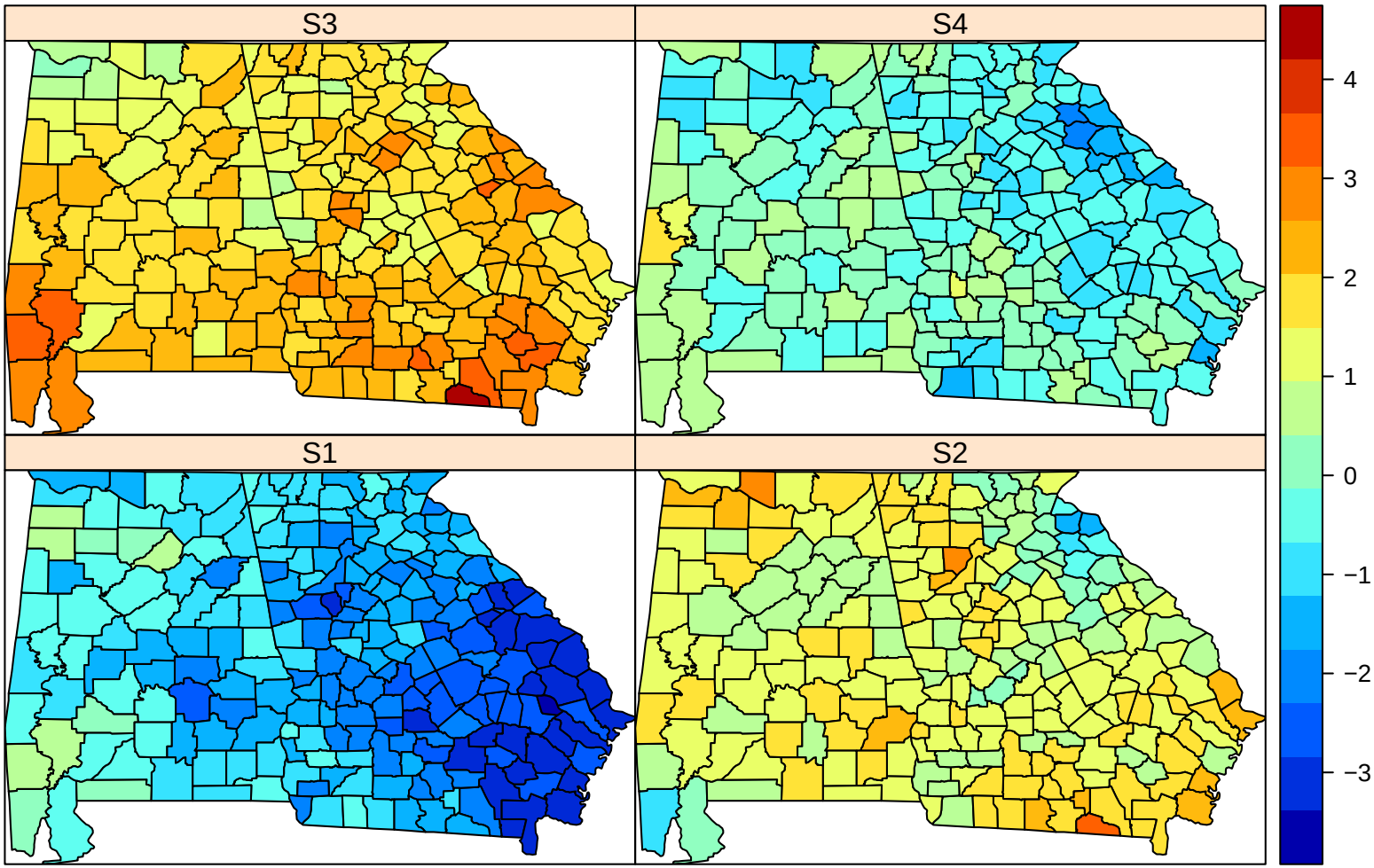
Example Simulations

CAR $(\rho = 0.99, \tau^2 = 1)$



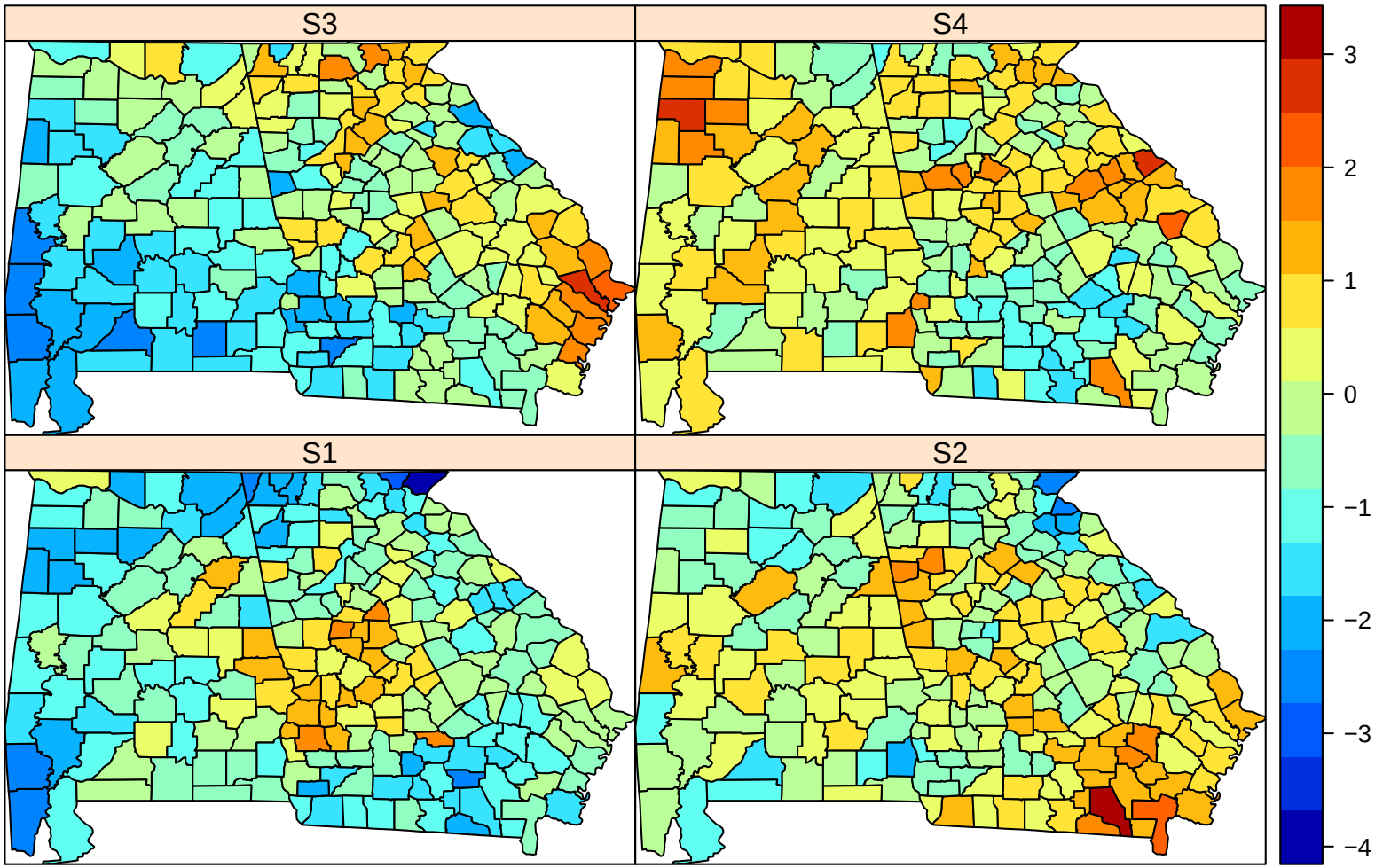
Example Simulations

CAR $(\rho = 0.9999, \tau^2 = 1)$



Example Simulations

CAR $(\rho = 0.99, \tau^2 = 2)$



CAR Parameters

$$[Y_1, Y_2, \ldots, Y_n] \sim N(\mathbf{0}, \tau^2(\mathbf{D}_w - \rho\mathbf{W})^{-1}) .$$

Several important properties of the covariance matrix should be noted.

- τ^2 cannot be interpreted as the variance at each location. This is because $(\mathbf{D}_w - \rho\mathbf{W})^{-1}$ is not a correlation matrix. The variance is dependent on ρ and $\mathbf{W}$.
- $\rho = 0$ implies that Y_i are independent; but the marginal variance $(\tau^2\mathbf{D}_w^{-1})$ is proportional to the number of neighbors. This is not a desirable property for independent data!
- If $\rho = 1$, then the joint distribution is improper because $\mathbf{D}_w - \mathbf{W}$ is not invertible; it is of rank $n - 1$. Therefore, $\rho = 1$ cannot be used to model observed data; but can be used as prior distribution for random effects (particularly in Bayesian analysis later). When $\rho = 1$, we often refer to it as the instrinsic or improper CAR model.

CAR Model Example

$$y_i = \beta_0 + \beta_1 x_i + \epsilon_i \qquad \boldsymbol{\epsilon} \sim N\left(0, \tau^2(\mathbf{D}_w - \rho\mathbf{W})^{-1}\right)$$

- y_i = chlamydia incidence per 10,000.
- x_i = household income (centered and divided by 1,000).

		Estimate (Standard Error)				
	W	β_0	β_1	λ	σ^2	AIC
LM	NA	46 (1.6)	-1.31 (0.18)	NA	24	2089
CAR	1st-order	42 (3.5)	-1.33 (0.22)	0.15	21	2045
CAR	2nd-order	38 (3.9)	-1.14 (0.21)	0.08	21	2051

- Household income and chlamydia incidence are negatively associated.
- Note that standard errors for regression coefficients increase when accounting for spatial correlation.
- Using AIC as a model selection criterion, CARS with 1st-order adjacency is preferred.

Advantages of CAR

The spatial dependence structure is contained entirely in $(\mathbf{D}_w - \rho\mathbf{W})^{-1}$. The matrix $\mathbf{Q} = (\mathbf{D}_w - \rho\mathbf{W})$ is known as the precision matrix. The CAR model falls under a class of Markov network or undirected graphical model known as Gaussian Markov random field (GMRF).

- GMRF theory says that

$$\mathbf{Q}_{ij} = 0 \quad \Leftrightarrow \quad Y_i \perp\!\!\!\perp Y_j \,|\, \mathbf{Y}_k, k \neq i, j$$

  Therefore, if the proximity matrix $\mathbf{W}$ is zero between Y_i and Y_j, it implies that they are conditionally independent. It is often easier to describe conditional dependence then joint dependence.

- In practice, $\mathbf{W}$ contains a large number of zeros. Computation associated with the normal density can be done efficiently with $\mathbf{Q}^{-1}$ using sparse matrix algorithms (e.g. $n > 20,000$).

Goals of Disease Mapping

Setup:

- Counts of disease incidence or prevalence aggregated over some contiguous administrative spatial areal units.
- Each count is associated with certain covariates (e.g.at-risk population size) at the same spatial unit.

Goals:

1. Regression: explain spatial variation in diseases rates as a function of covariates.
2. Smoothing: provide location-specific estimates that have better precision.

Smoothing = Borrowing Information

Poisson Generalized Linear Model

For spatial unit $i = 1, \ldots, n$, assume the following Poisson log-linear model

$$Y_i \sim \text{Poisson } (\lambda_i)$$
$$\log(\lambda_i) = \mathbf{X}_i' \boldsymbol{\beta} \, .$$

- Y_i is the observed case count.
- λ_i is the location-specific Poisson mean with fixed-effect $\boldsymbol{\beta}$ and covariates $\mathbf{X}$.

Problems with this model:

1. λ_i is completely determined by the covariates and $\boldsymbol{\beta}$ is shared across ALL spatial units.
2. Does not account for spatial variability/dependence not explained by $\mathbf{X}$ (often leading to over/under-dispersion).

Poisson Generalized Linear Model

First, we can include a location-specific effect (u_i) in the mean structure:

$$Y_i \sim \text{Poisson } (\lambda_i)$$
$$\log(\lambda_i) = \mathbf{X}_i'\boldsymbol{\beta} + u_i \ .$$

- u_i can be interpreted as the location-specific log baseline mean count.
- u_i is difficult (almost impossible) to estimate well because we only have one observation at each location!

Under a hierarchical modeling framework, we treat u_i as random effects:

$$u_i \overset{iid}{\sim} N(0, \sigma^2) \ .$$

This allows shrinkage, information-borrowing, or penalization on u_i based on the value of σ^2. Smaller σ^2 results in higher shrinkage towards 0.

A Note on Offset

In the Poisson mean, we often include an offset $\log P_i$:

$$\log(\lambda_i) = \log P_i + \mathbf{X}_i'\boldsymbol{\beta} + u_i \ .$$

This implies the Poisson model

$$Y_i \sim \text{Poisson } \left(P_i \exp\{\mathbf{X}_i'\boldsymbol{\beta} + u_i\}\right) .$$

Two typical choices for P_i:

1. at-risk population size; or
2. expected disease count.

With offsets, $\exp\{\mathbf{X}_i'\boldsymbol{\beta} + u_i\}$ can be interpreted as

1. prevalence/incidence rates for the at-risk population; or
2. relative deviation from the expected counts.

Spatial Random Effects

$$\log(\lambda_i) = \log P_i + \mathbf{X}_i'\boldsymbol{\beta} + u_i \ .$$

Often $\mathbf{X}$ is not able to remove all the spatial dependence in u_i. So we can also consider u_i's as spatially-dependent random effects.

Let $\mathbf{u}' = (u_1, \ldots, u_n)$, we assume the joint distribution is Normal with covariance $\boldsymbol{\Sigma}$:

$$\mathbf{u} \sim N(\mathbf{0}, \boldsymbol{\Sigma}) \ .$$

For areal data, the most commonly used spatial random effect specification is the conditional autoregressive (CAR) model.

Let $\mathbf{W}$ denote the symmetric adjacency matrix. The CAR model is given by two parameters ρ and τ^2:

$$\mathbf{u} \sim N(\mathbf{0}, \tau^2[\mathbf{D} - \rho\mathbf{W}]^{-1} \ )$$

is equivalent to a conditional specification, for $i = 1, \ldots, n$

$$u_i | u_{j \neq i} \sim N\left(\rho \frac{\sum_{j \neq i} W_{ij} u_j}{D_{ii}}, \ \frac{\tau^2}{D_{ii}}\right)$$

Proper versus Improper CAR

An improper or intrinsic CAR is a special case where $\rho = 1$

$$u_i | u_{j \neq i} \sim N\left(\frac{\sum_{j \neq i} W_{ij} u_j}{D_{ii}}, \frac{\tau^2}{D_{ii}} \right) .$$

However, this does not correspond to a valid joint distribution, i.e. $\mathbf{u} \sim N(\mathbf{0}, \tau^2[\mathbf{D} - \mathbf{W}]^{-1})$, because $\mathbf{D} - \mathbf{W}$ is not invertible (it has rank $n - 1$).

We can see that if we add a constant k to all the u_i, the above distribution still holds.

$$u_i + k | u_{j \neq i} + k \sim N\left(\frac{\sum_{j \neq i} W_{ij} (u_j + k)}{D_{ii}}, \frac{\tau^2}{D_{ii}} \right) .$$

To get around this, we often impose a constraint for improper CAR:

$$\sum_{i=1}^{n} u_i = 0 .$$

Improper CAR in Bayesian Analysis

The improper CAR is usually used under a Bayesian framework, which makes inference on the posterior distribution of u_i:

$$[\mathbf{u} \mid \mathbf{Y}] = \frac{[\mathbf{Y}, \mathbf{u}]}{[\mathbf{y}]} = \frac{[\mathbf{Y} \mid \mathbf{u}] \times [\mathbf{u}]}{[\mathbf{y}]} \propto [\mathbf{Y} \mid \mathbf{u}] \times [\mathbf{u}].$$

So we can use CAR as a prior for $[\mathbf{u}]$ and the posterior distribution will be valid as long as we have data $\mathbf{Y}$.

Note: The reason we can do this here is because

- We assume u_i is a random effect.
- Conditioned on u_i, the stochastic nature of Y_i is given by the Poisson likelihood - NOT by the CAR prior.

Leroux's Proper CAR

Recall that one disadvantage of the proper CAR model

$$\mathbf{u} \sim N(\mathbf{0}, \tau^2[\mathbf{D} - \rho\mathbf{W}]^{-1})$$

is that it does not reduce to an independent model with $\rho = 0$.

Another commonly used structure is the Leroux's form:

$$\mathbf{u} \sim N(\mathbf{0}, \tau^2[(1-\rho)\mathbf{I} + \rho(\mathbf{D} - \mathbf{W})]^{-1})$$

The above reduces to iCAR when $\rho = 1$ and an exchangeable model when $\rho = 0$. One challenge is that the conditional distribution becomes a bit less intuitive:

$$u_i | u_{j \neq i} \sim N\left(\frac{\rho \sum_{j \neq i} W_{ij} u_j}{1 - \rho + \rho D_{ii}}, \frac{\tau^2}{1 - \rho + \rho D_{ii}}\right).$$

The above conditional mean/variance can be seen as weighted mean between the iCAR and exchangeable model with weight (for iCAR) $= \rho D_{ii}/(1 - \rho + \rho D_{ii}$.

Convolution Model

A convolution model (aka Besag-York-Mollie, BYM) includes both spatially-dependent and unstructured/exchangeable random effects.

$$\log(\lambda_i) = \log P_i + \mathbf{X}_i'\boldsymbol{\beta} + u_i + v_i \ .$$

$$\mathbf{u} \sim N(\mathbf{0}, \tau^2[\mathbf{D} - \mathbf{W}]^{-1} \ )$$

$$v_i \overset{iid}{\sim} N(0, \sigma^2) \ .$$

Challenge!!! We are asking our model to partition a location-specific random effect into a spatial and a non-spatial component. With only one Y_i at each location, this is a very difficult task. In this setting, our main inferential interest may be on $u_i + \nu_i$.

Chlamydia Application

First consider models without covariates:

$$Y_i \sim \text{Poisson}\ (\lambda_i) \qquad \log(\lambda_i) = \log P_i + \beta_0 + u_i\ .$$

where Y_i is the chlamydia counts and P_i is the population size.

Model 1: No Shrinkage (MLE estimates):

$$\hat{\beta}_0 + \hat{u}_i = \log(Y_i/P_i).$$

Model 2: Exchangeable (independent)

$$u_i \sim N(0, \sigma^2)$$

Model 3: Only Spatial (improper CAR)

$$u_i \sim iCAR(\tau^2)$$

Model 4: Only Spatial (proper Leroux)

$$u_i \sim pCAR(\tau^2)$$

Model 5: Convolution (iCAR + exchangeable)

$$u_i = \gamma_i + \theta_i$$

$$\gamma_i \sim iCAR(\tau^2) \qquad \theta_i \sim N(0, \sigma^2)$$

Bayesian Inference

We often frame estimation in disease mapping under a Bayesian framework to get uncertainty estimates for random effects.

Typical priors (we will use later)

- $\beta_0 \sim \text{Normal}(0, \sigma^2_\beta)$ where σ^2_β can be 0 (improper flat prior) or be very large (e.g., 100^2).
- Variance components $\tau \sim \text{Inv-Gamma}(a, b)$ with small a and b (e.g. 0.0001).
- $\text{Logit}(\rho) \sim \text{Normal}(0, \sigma^2_\rho)$.

Estimation can be done using MCMC-based methods (JAGS, Stan, custome code) or approximation methods (INLA).

Model Estimates

Posterior Median and 95% Posterior Interval

	β_0	τ^2	σ^2
Exch.	-5.57 (-5.66, -5.57)		0.42 (0.35, 0.51)
iCAR	-5.57 (-5.58, -5.55)	1.21 (1.13, 1.48)	
pCAR	-5.57 (-5.95, -5.19)	1.08 (0.85, 1.37)	
Conv.	-5.57 (-5.62, -5.52)	0.60 (0.34, 1.03)	0.12 (0.06, 0.19)

For pCAR, estimate of ρ is 0.81 (0.59, 0.95).

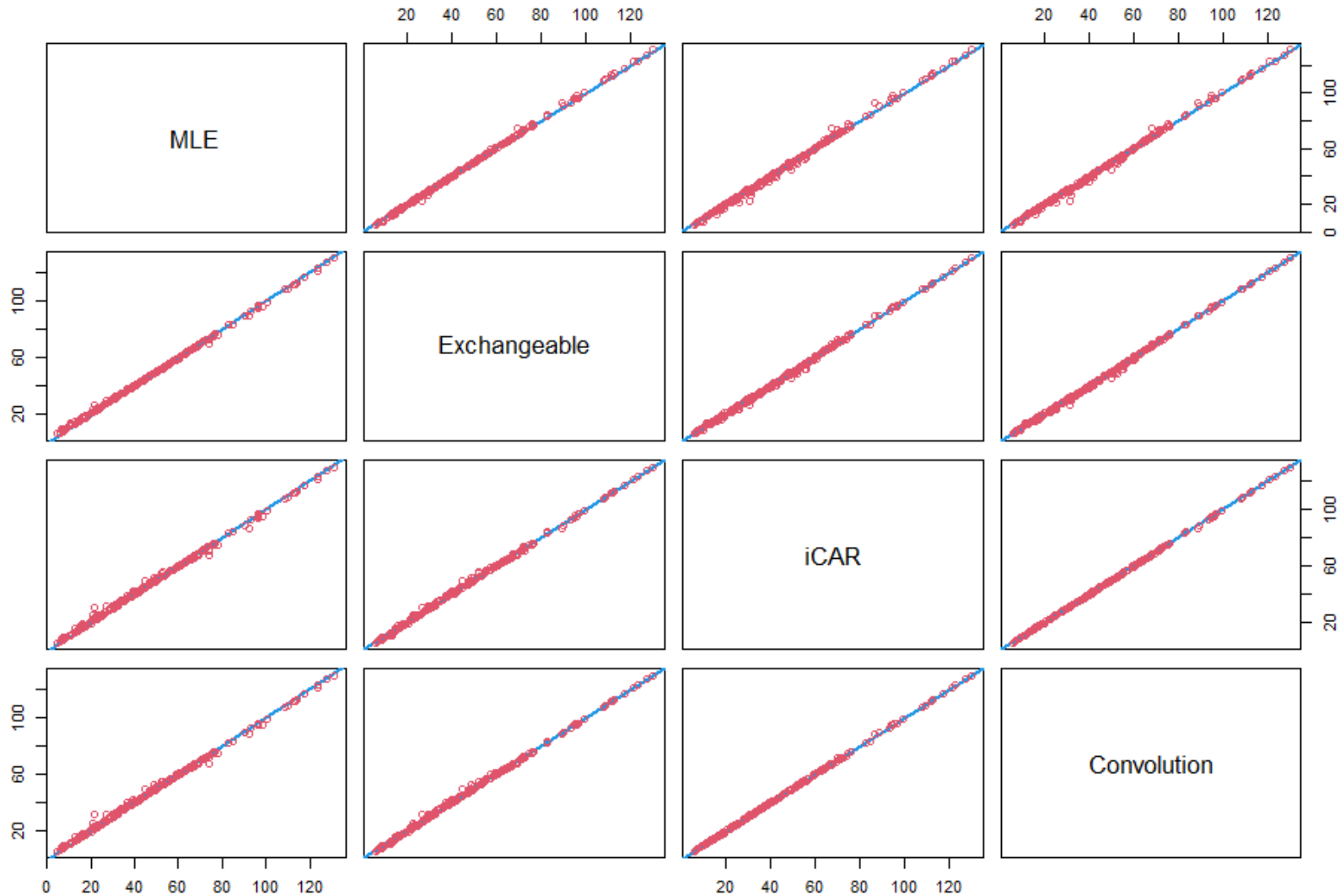
Model Comparison

	DIC	pD	WAIC	pWAIC
Exch.	1926	218	1873	118
iCAR	1917	211	1864	114
pCAR	1920	213	1870	117
Conv.	1919	213	1868	116

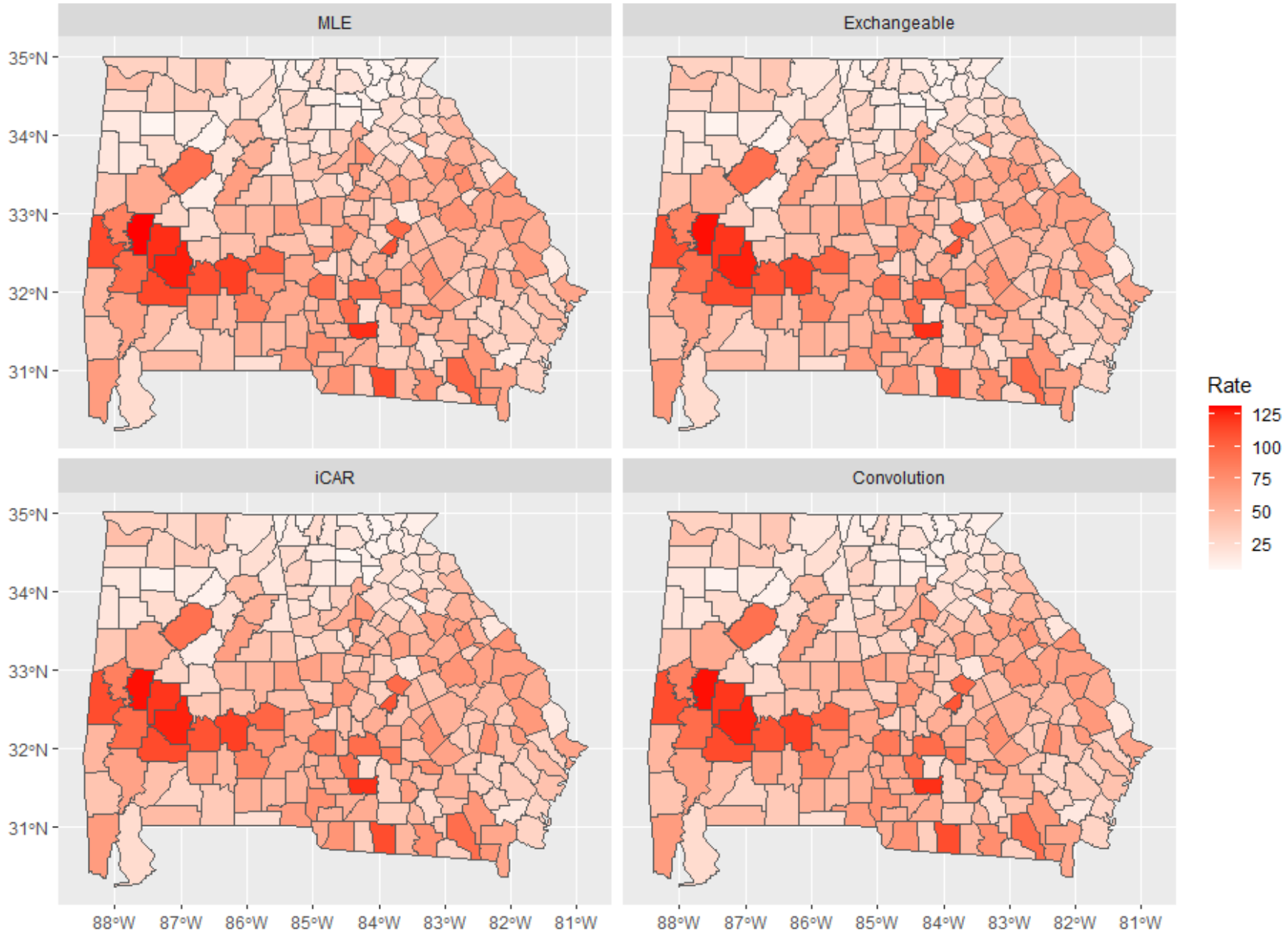
DIC/WAIC prefers the iCAR model, which also gives the smallest number of effet degrees of freedom.

Estimated Relative Risk (per 10,000)

County-specific estimates are very similar.

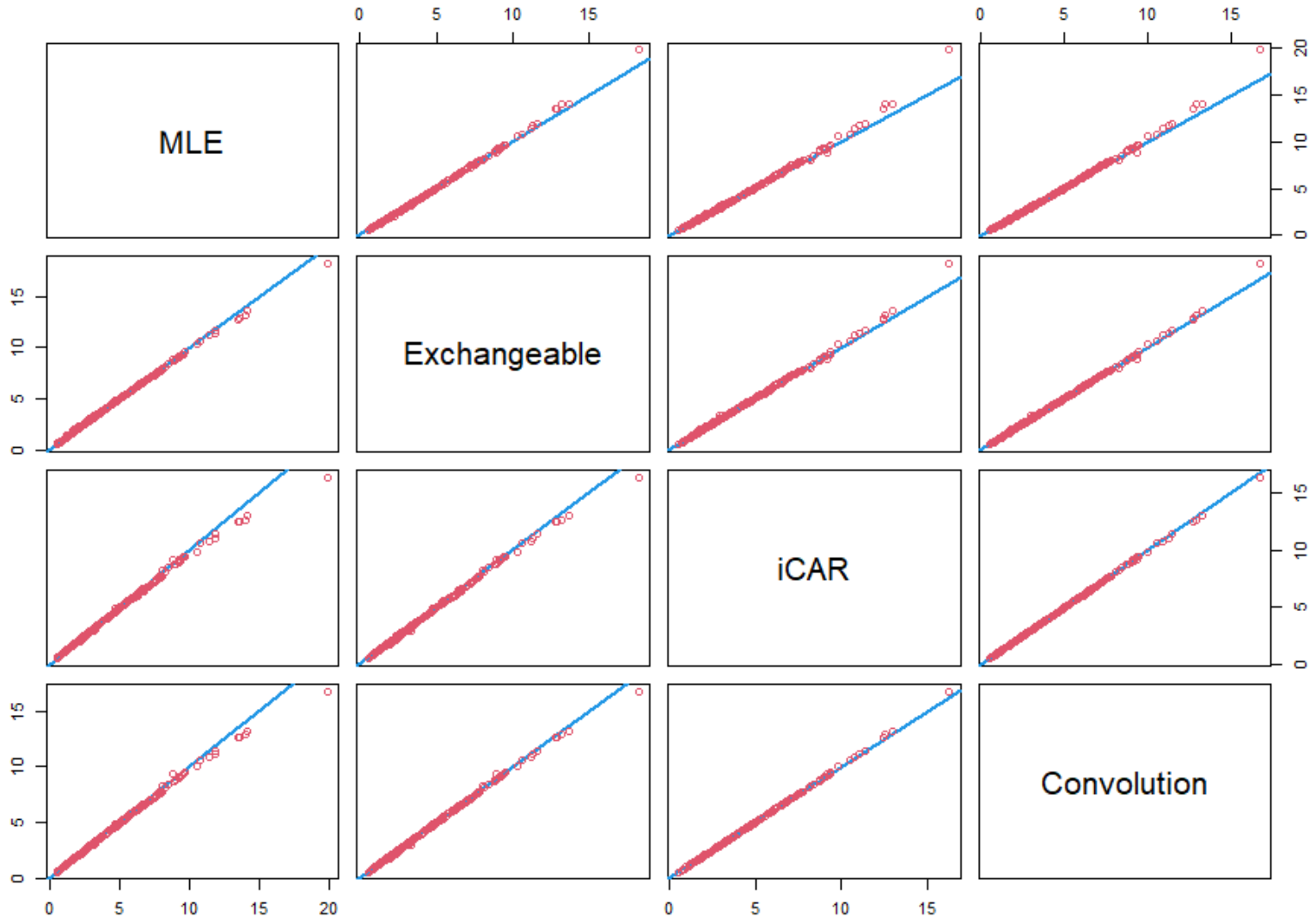


Estimated Relative Risk (per 10,000)



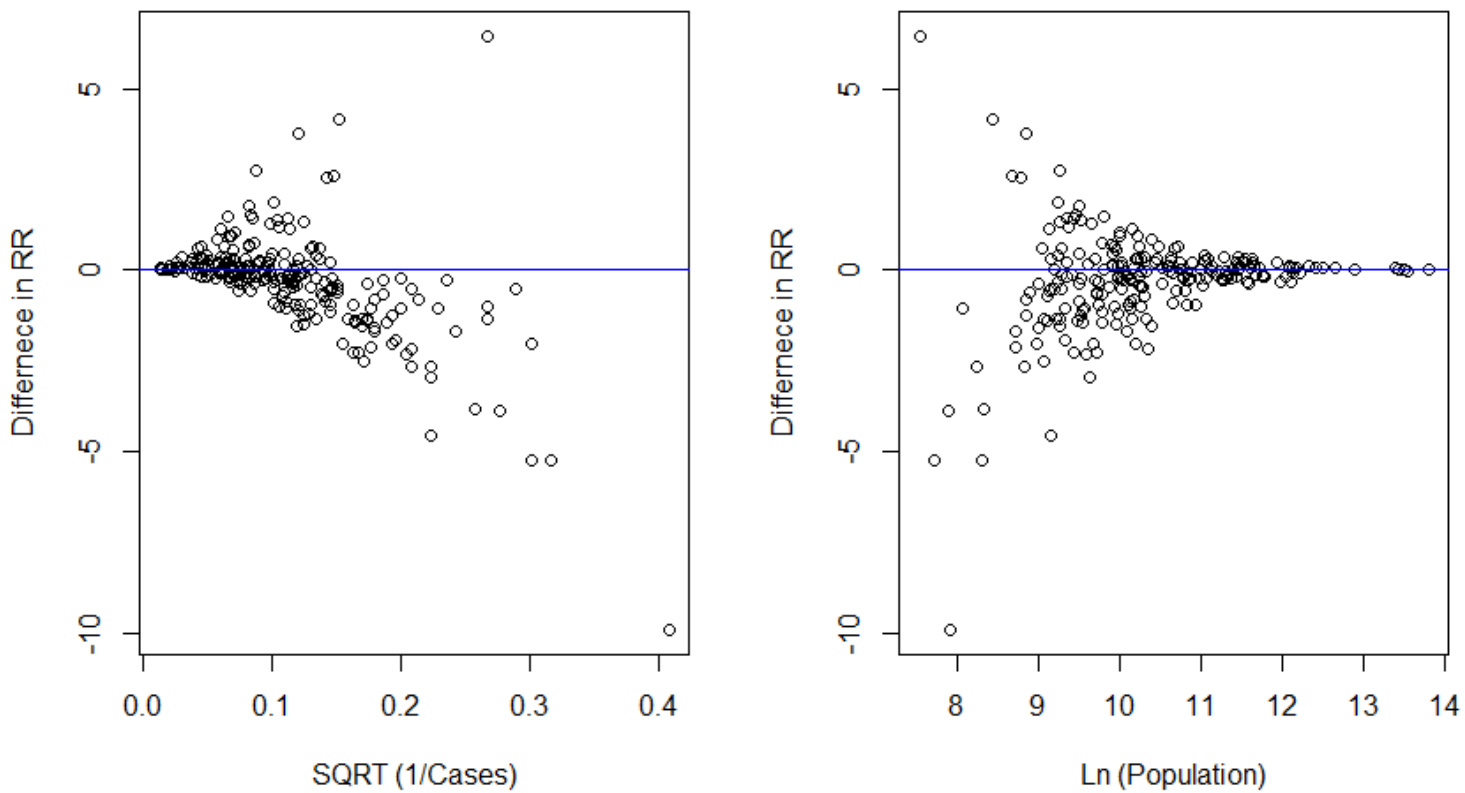
Comparison of County-Specific Standard Error

Large SE's from MLE are reduced in random effect models.



Difference in $\hat{\beta}_0 + \hat{u}_i$

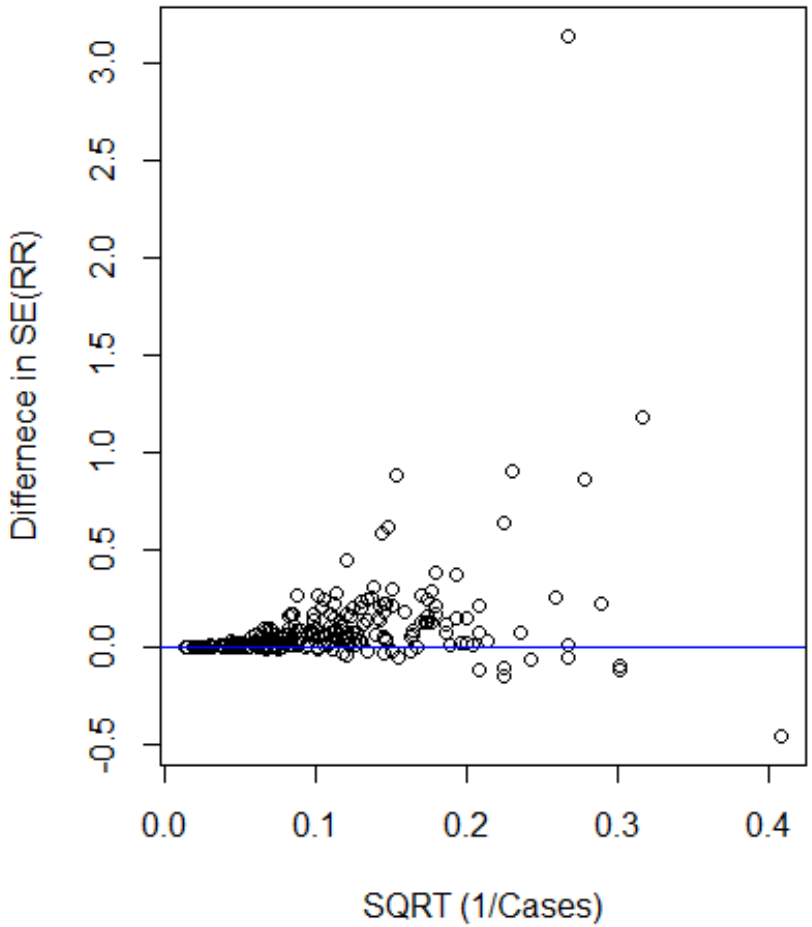
MLE (Model 1) - Convolution (Model 5)

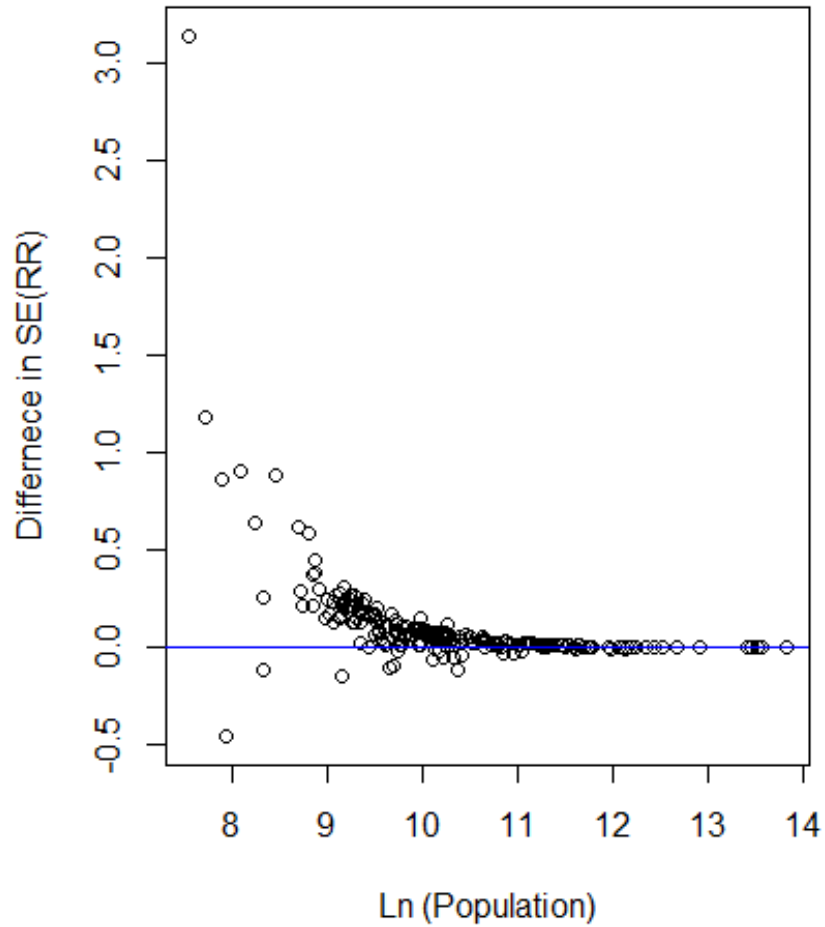


Largest differences observed when the population is smaller or the cases are larger.

Difference in SE($\hat{\beta}_0 + \hat{u}_i$)

MLE (Model 1) - Convolution (Model 5)





Convolution Model with Covariate

$$Y_i \sim \text{Poisson } (\lambda_i)$$

$$\log(\lambda_i) = \log P_i + \beta_0 + \beta_1 \text{Income}_i + u_i + v_i$$

$$u_i \sim ICAR(\tau^2) \qquad v_i \sim N(0, \sigma^2)$$

	Posterior Mean	95% Post Int
β_0	-5.56	(-5.60, -5.53)
$\beta_1(\times 1,000)$	-0.034	(-0.043, -0.024)
τ^2	0.69	(0.41, 1.15)
σ^2	0.06	(0.02, 0.11)

- σ^2 decreased with the inclusion of income in the model.
- We found that a \$1,000 increase in county-level median household income was associated with a 3.4% (95% PI: 2.4%, 4.3%) decrease in chlamydia incidence, controlling for county-level baseline heterogeneity.

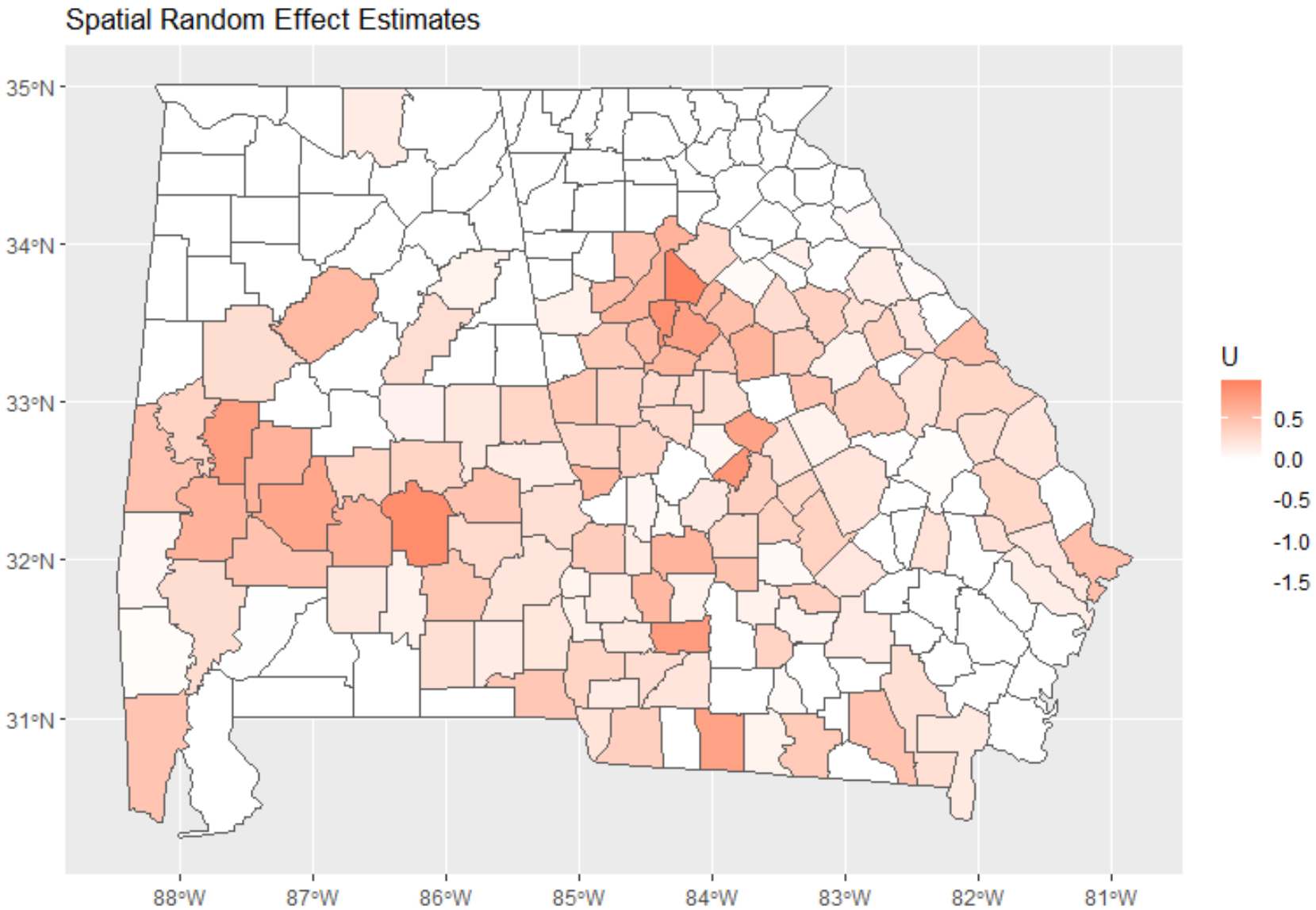
Comparison with Other Models

Estimates of $\beta_1(\times 1,000)$

	Posterior Mean	SE	95% PI/CI
Spatial Convolution	-0.034	0.0049	$(-0.043, -0.024)$
Poisson Regression	-0.023	0.0004	(-0.024, -0.022)
Quasi-poisson Regression	-0.023	0.0033	(-0.016, -0.029)

- A standard Poisson regression under-estimates the uncertainty considerably.
- Using quasi-Poisson to account for over-dispersion increases confidence interval length (by a lot).
- The point estimates differ as well.

Posterior Mean of Spatial Residuals γ_i



Posterior Mean of Independent Residuals θ_i