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Bayesian random effects model for disease mapping of relative risks

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ABSTRACT

The use of random effects assumes that every region has some common risk rates and allows estimates to combine information from several regions. This random effect is common in Bayesian approach disease mapping using log-normal model. Bayesian posterior distributions are obtained via Markov Chain Monte Carlo (MCMC) computations. HIV Data was obtained from National Institute for Research in Tuberculosis. The result of the study reveals that the random effects model, gives the smoother values of relative risk than the Poisson gamma model. Spatial analysis is proved to be more useful for studying spread of HIV analysis.

Keywords: Disease mapping, Poisson gamma, Log-normal and random effects model.

INTRODUCTION

The applications of Bayesian methods for disease mapping, risk assessment and prediction within spatial research are numerous. There are two dominant approaches called, empirical and fully Bayesian method. In the Empirical Bayesian (EB) method, parameters of prior distributions are estimated using observed marginal distributions, but in the fully Bayesian approach, the prior and posterior distributions are obtained via Markov Chain Monte Carlo (MCMC) computations. The disease mapping is useful to find the geographical distribution of disease burden and diseases incidence in which disease is shaded according to the high and low risk areas in Chennai ward. Bayesian methods for disease mapping of disease in Chennai ward using Poisson-Gamma model and Log-normal model are explored. The aim is to compare whether Bayesian estimates of random effects model of log normal model are more stable than the Poisson gamma model estimates.

The idea of Empirical Bayesian and Fully Bayesian methods for disease mapping was reviewed and explored in different times point [1,9,16]. Many author discussed about importance of prior and errors in covariates model in disease mapping [2,3]. The comparisons of various models for disease mapping provides a comprehensive review of the recent developments in Bayesian disease mapping[7, 14, 15]. In the Full Bayesian, Inference is made by using MCMC[11,12] techniques that provide an estimate of the posterior distribution of the parameters of the model. Fully Bayesian disease mapping was explored in different situation [4,5,6,10] and Spatio-temporal model was used to find the spatio temporal changes between years and place[20]. The most recent Hierarchical Bayesian models that are used for disease mapping using full Bayes estimation was reviewed by [8]. The several model for infectious disease like HIV and Tuberculosis was done by [18,19]. Geographical analysis of heart diseases for tamilnadu was by studied [17]. Spatial mapping of cholera for Chennai were done by [13].

Poisson-Gamma Model

The Poisson model holds the assumption that mean and variance are same, but it is in the spatial context, the data are over dispersed and variance is higher than mean. A simple way to allow for a higher variance is to use negative binomial distribution instead of Poisson. The negative binomial distribution can also be regarded as a mixed model in which random effect follow a Gamma distribution for each area. This combination is known as Poisson Gamma model. A sample model is;

$Y_i \mid n_i \sim Po(E_i\theta_i), i = 1,...,I$ and $\theta_i \sim Gamma(a,b)$, which denotes gamma distribution with mean $\mu = \frac{a}{b}$ and Variance $\sigma^2 = \frac{a}{b^2}$

The crude SMR rates and RR are often subject to large chance variation when rare diseases are investigated in small areas. Literature on Bayesian disease mapping presents mixed effects Poisson models that are characterized as spatial smoothing. The methods assume spatially varying or randomly varying RRs and the associated joint prior probability for pooling data and borrowing strength. In this section, these considerations are motivated and explored through fully Bayesian mapping models which requires a prior distribution on parameters.

$$\begin{aligned} &Y_i \mid \theta_i, \beta_0 \sim \text{Poisson}(E_i e^{\beta_0}\theta_i) \\ &\theta_i \sim \text{Gamma}(\alpha,\alpha) \end{aligned} \tag{1}$$

here prior for α and β_0 is

$$\begin{aligned} &\beta_0 \sim \text{Norm}(m,v) \\ &\alpha \sim \text{Gamma}(a,b) \end{aligned} \tag{2}$$

two issues is normally arising, when expected count of E_i is small, a small variation in O_i can produce dramatic changes in the value of SMR, secondly, in Poisson model, information is borrowed from all the areas in order to construct the posterior estimates given that a and b are the same for every region.

Log-Normal Model

Clayton and Kaldor (1987) proposed another risk estimator based on assumption that the logarithm of the relative risks ($\beta_i = \log(\theta_i)$ follows multivariate normal distribution with mean μ and variance σ^2. The estimate of the log relative risk is $\log(O_i + 1/2)/E_i$ instead of $\log(O_i)/E_i$, because in the Poisson model is not defined if O_i is zero.

In the Poisson gamma model which is easy to fit but we cannot include the non-spatial random effect and zero case is not differentiated, so we have to see alternative technique like Poisson log-normal model. A Poisson log-normal non-spatial random effects model is given by

$$\begin{aligned} &Y_i \mid \beta, V_i \sim_{iid} Poisson(E_i \mu_i e^{V_i}) \\ &V_i \sim_{iid} Nor(0,\sigma_v^2) \end{aligned} \tag{3}$$

Where V_i are area-specific random effects that capture the residual or unexplained (log) relative risk of disease in area i, $i = 1...n$.

Here we have

$$\theta = e^{V_i} \sim Lognormal(0,\sigma^2). \tag{4}$$

MATERIALS AND METHODS

The lattice or areal data of Chennai wards for HIV/AIDS disease mapping are considered for this work. Chennai city consists of 155 wards. Let Y_i (i=1, 2,…,155) is the observed count of HIV/AIDS disease and E_i (i=1, 2,…,155) is the expected count in the i^{th} region. If the model follows the Poisson distribution, θ_i (i=1, 2…n) is the relative risk in the i^{th} region. It measures of how much of a risk factor in regions leads to difference in the variance of regional estimates. Here Y_i is a random variable, and E_i is a fixed and known function of θ_i where θ_i is a number of persons at risk for the disease in region i.

We assume that $$E_i = \theta_i \bar{r} \equiv \theta_i \left(\frac{\sum_i y_i}{\sum_i \theta_i} \right), \quad (5)$$

where $\bar{r}$ is the overall disease rates in the entire study region and here we assume that this disease rates constant in all the regions. This method of calculating expected count is called internal standardization or direct standardization. The HIV patients were registered during 2004 to 2006 at the National Institute for Research in Tuberculosis was considered for this work. The observed cases were aggregated for each ward level in Chennai and expected numbers of cases were calculated using indirect standardization method from ward population. The total number of cases recorded during 2004 and 2006 were collected and also the population of each ward was collected from census 2001. In the Poisson gamma model, specified the flat prior for β_0 and gamma (1,1) prior for α and run the iteration for 30000 after discarding initial 3000 as burn-in. The convergence of the model was checked by Gelman Rubin convergence test.

RESULTS

The results are presented in Table 1. The posterior relative risk estimate ranges from 0.512 to 2.74 and highest relative risk shrunk toward the mean. Bayesian Poisson gamma model smoothed towards the global mean and the variations in the map disappeared.

Table 1 Posterior Means of RR under Bayesian Poisson Gamma and Lognormal Model

Ward	Poisson Gamma Model			Lognormal Model		
	Mean	SD	Credible Interval	Mean	SD	Credible Interval
RR[1]	0.730	0.329	0.232, 1.507	0.578	0.287	0.114, 1.221
RR[2]	1.439	0.485	0.651, 2.554	0.850	0.366	0.233, 1.651
RR[3]	0.873	0.391	0.271, 1.786	0.624	0.320	0.125, 1.358
RR[4]	0.975	0.495	0.256, 2.169	0.665	0.380	0.119, 1.581
RR[5]	0.738	0.374	0.189, 1.628	0.579	0.311	0.105, 1.289
RR[6]	0.958	0.486	0.253, 2.113	0.654	0.377	0.114, 1.572
RR[7]	1.693	0.653	0.671, 3.253	0.800	0.458	0.159, 1.907
RR[8]	1.032	0.461	0.327, 2.087	0.663	0.353	0.125, 1.503
RR[9]	1.012	0.513	0.276, 2.250	0.667	0.383	0.115, 1.597
RR[10]	0.548	0.322	0.099, 1.334	0.520	0.282	0.087, 1.175
RR[11]	0.872	0.442	0.226, 1.922	0.624	0.349	0.104, 1.457
RR[12]	0.797	0.464	0.144, 1.926	0.659	0.387	0.116, 1.621
RR[13]	1.950	0.712	0.831, 3.564	0.848	0.503	0.157, 2.071
RR[14]	1.831	0.615	0.842, 3.224	0.929	0.461	0.205, 1.984
RR[15]	0.959	0.481	0.260, 2.099	0.651	0.372	0.108, 1.530
RR[16]	1.164	0.526	0.376, 2.397	0.693	0.387	0.127, 1.611
RR[17]	0.690	0.401	0.130, 1.664	0.602	0.340	0.103, 1.392
RR[18]	1.635	0.680	0.598, 3.233	0.710	0.417	0.129, 1.726
RR[19]	0.787	0.461	0.144, 1.910	0.658	0.380	0.114, 1.582
RR[20]	1.055	0.535	0.283, 2.344	0.682	0.402	0.118, 1.676
RR[21]	1.752	0.675	0.708, 3.323	0.785	0.466	0.144, 1.947
RR[22]	1.095	0.485	0.347, 2.204	0.680	0.374	0.127, 1.572
RR[23]	1.337	0.602	0.422, 2.784	0.704	0.419	0.132, 1.725
RR[24]	2.094	0.767	0.899, 3.880	0.786	0.476	0.140, 1.966
RR[25]	1.048	0.528	0.276, 2.317	0.671	0.387	0.120, 1.613
RR[26]	0.709	0.413	0.130, 1.687	0.609	0.348	0.109, 1.445
RR[27]	1.816	0.709	0.723, 3.450	0.772	0.453	0.140, 1.884
RR[28]	1.608	0.611	0.657, 3.013	0.806	0.447	0.159 1.896
RR[29]	1.595	0.645	0.598, 3.087	0.732	0.433	0.134, 1.782
RR[30]	1.331	0.602	0.429, 2.753	0.703	0.415	0.124, 1.721

RR[31]	0.679	0.399	0.127,	1.641	0.583	0.324	0.099,	1.344
RR[32]	0.944	0.426	0.304,	1.932	0.645	0.339	0.132,	1.453
RR[33]	1.562	0.558	0.676,	2.831	0.854	0.430	0.182,	1.838
RR[34]	0.921	0.413	0.299,	1.897	0.632	0.329	0.116,	1.375
RR[35]	1.786	0.647	0.764,	3.264	0.871	0.473	0.181,	2.014
RR[36]	0.922	0.411	0.293,	1.874	0.633	0.325	0.124,	1.374
RR[37]	1.426	0.597	0.528,	2.835	0.752	0.424	0.147,	1.793
RR[38]	1.157	0.475	0.412,	2.261	0.718	0.368	0.146,	1.564
RR[39]	0.833	0.422	0.216,	1.850	0.614	0.337	0.110,	1.402
RR[40]	1.235	0.470	0.488,	2.291	0.759	0.361	0.174,	1.568
RR[41]	1.276	0.577	0.416,	2.629	0.704	0.409	0.124,	1.703
RR[42]	0.923	0.463	0.245,	2.030	0.645	0.360	0.114,	1.508
RR[43]	0.844	0.487	0.161,	2.034	0.692	0.410	0.117,	1.684
RR[44]	1.695	0.718	0.622,	3.363	0.690	0.401	0.124,	1.668
RR[45]	0.737	0.428	0.135,	1.778	0.628	0.358	0.106	1.480
RR[46]	1.763	0.742	0.645,	3.494	0.671	0.395	0.116,	1.635
RR[47]	1.447	0.661	0.474,	3.008	0.684	0.409	0.116,	1.675
RR[48]	0.950	0.474	0.250,	2.071	0.654	0.370	0.116,	1.528
RR[49]	1.646	0.697	0.592,	3.276	0.715	0.431	0.130,	1.769
RR[50]	0.518	0.304	0.094,	1.258	0.505	0.272	0.081,	1.135
RR[51]	1.204	0.456	0.481,	2.271	0.750	0.357	0.165,	1.542
RR[52]	1.218	0.550	0.400,	2.512	0.700	0.403	0.125,	1.692
RR[53]	0.935	0.467	0.246,	2.053	0.649	0.364	0.114,	1.514
RR[54]	0.971	0.434	0.314,	1.971	0.641	0.334	0.123,	1.410
RR[55]	0.635	0.370	0.116,	1.533	0.564	0.312	0.098,	1.293
RR[56]	1.004	0.450	0.318,	2.062	0.660	0.355	0.126,	1.495
RR[57]	2.229	0.786	0.983,	3.991	0.892	0.529	0.172,	2.213
RR[58]	0.957	0.426	0.302,	1.954	0.648	0.340	0.126,	1.440
RR[59]	0.964	0.485	0.250,	2.119	0.655	0.377	0.114,	1.576
RR[60]	1.705	0.614	0.730,	3.124	0.861	0.452	0.185,	1.938
RR[61]	1.612	0.671	0.594,	3.178	0.721	0.421	0.135,	1.739
RR[62]	0.623	0.279	0.198,	1.276	0.540	0.259	0.110,	1.105
RR[63]	0.789	0.319	0.278,	1.522	0.613	0.283	0.140,	1.236
RR[64]	0.667	0.300	0.210,	1.365	0.555	0.271	0.105,	1.152
RR[65]	0.665	0.299	0.213,	1.351	0.562	0.271	0.118,	1.164
RR[66]	0.661	0.333	0.171,	1.444	0.545	0.284	0.098,	1.192
RR[67]	0.993	0.446	0.307,	2.040	0.656	0.348	0.124,	1.452
RR[68]	0.977	0.438	0.313,	2.017	0.652	0.339	0.125,	1.447
RR[69]	0.906	0.456	0.235,	2.000	0.636	0.357	0.109,	1.480
RR[70]	1.129	0.507	0.360,	2.310	0.685	0.381	0.123,	1.578
RR[71]	0.847	0.496	0.153,	2.066	0.693	0.413	0.120,	1.691
RR[72]	1.069	0.480	0.339,	2.197	0.671	0.363	0.123,	1.532
RR[73]	1.167	0.528	0.370,	2.394	0.696	0.395	0.125,	1.650
RR[74]	1.012	0.417	0.371,	1.958	0.674	0.327	0.146,	1.411
RR[75]	0.754	0.335	0.239,	1.522	0.586	0.289	0.117,	1.228
RR[76]	1.182	0.531	0.374,	2.416	0.692	0.388	0.132,	1.637
RR[77]	1.194	0.540	0.388,	2.456	0.699	0.397	0.129,	1.659
RR[78]	0.898	0.449	0.239,	1.972	0.637	0.357	0.116,	1.479
RR[79]	0.681	0.401	0.126,	1.645	0.591	0.336	0.106,	1.409
RR[80]	1.047	0.470	0.340,	2.146	0.666	0.358	0.126,	1.499
RR[81]	1.689	0.651	0.676,	3.215	0.804	0.462	0.152,	1.934
RR[82]	1.230	0.557	0.395,	2.528	0.702	0.401	0.120,	1.670
RR[83]	0.723	0.420	0.137,	1.743	0.622	0.357	0.103,	1.464
RR[84]	1.348	0.604	0.451,	2.730	0.698	0.412	0.122,	1.702
RR[85]	2.284	0.850	0.972,	4.306	0.687	0.405	0.118,	1.655
RR[86]	2.738	0.926	1.290,	4.842	0.764	0.468	0.142,	1.905
RR[87]	1.365	0.623	0.427,	2.844	0.698	0.408	0.128,	1.677
RR[88]	0.728	0.430	0.136,	1.773	0.625	0.355	0.112,	1.485
RR[89]	2.164	0.793	0.912,	3.991	0.765	0.463	0.142,	1.908
RR[90]	1.058	0.532	0.279,	2.327	0.688	0.416	0.121,	1.730
RR[91]	0.728	0.427	0.138,	1.754	0.622	0.357	0.106,	1.490
RR[92]	0.770	0.446	0.154,	1.863	0.648	0.379	0.111,	1.581
RR[93]	1.312	0.596	0.412,	2.708	0.707	0.420	0.122,	1.745
RR[94]	1.926	0.700	0.839,	3.552	0.856	0.496	0.165,	2.096
RR[95]	1.451	0.665	0.469,	3.016	0.681	0.399	0.123,	1.677
RR[96]	2.408	0.837	1.094,	4.365	0.798	0.490	0.146,	2.007
RR[97]	1.122	0.500	0.369,	2.286	0.694	0.389	0.129,	1.624
RR[98]	0.776	0.458	0.150,	1.888	0.646	0.374	0.111,	1.567
RR[99]	1.251	0.577	0.399,	2.625	0.710	0.407	0.127,	1.679
RR[100]	0.838	0.490	0.161,	2.038	0.688	0.405	0.119,	1.669
RR[101]	1.060	0.534	0.275,	2.307	0.684	0.401	0.114,	1.665

RR[102]	1.782	0.753	0.660,	3.560	0.660	0.383	0.117,	1.582
RR[103]	1.315	0.593	0.419,	2.731	0.708	0.419	0.123,	1.728
RR[104]	1.142	0.517	0.363,	2.370	0.694	0.392	0.126,	1.638
RR[105]	1.754	0.676	0.696,	3.336	0.787	0.463	0.137,	1.924
RR[106]	1.196	0.534	0.386,	2.473	0.695	0.396	0.126,	1.665
RR[107]	1.559	0.601	0.636,	2.960	0.808	0.441	0.165,	1.889
RR[108]	1.886	0.646	0.855,	3.343	0.934	0.480	0.210,	2.069
RR[109]	1.176	0.530	0.368,	2.416	0.697	0.397	0.123,	1.653
RR[110]	1.056	0.533	0.276,	2.337	0.675	0.391	0.120,	1.634
RR[111]	0.716	0.422	0.131,	1.754	0.621	0.352	0.107,	1.455
RR[112]	2.091	0.768	0.892,	3.861	0.800	0.493	0.144,	2.014
RR[113]	1.157	0.517	0.376,	2.391	0.690	0.388	0.128,	1.624
RR[114]	0.779	0.390	0.201,	1.704	0.593	0.321	0.106,	1.334
RR[115]	0.671	0.392	0.124,	1.630	0.595	0.338	0.102,	1.400
RR[116]	0.895	0.445	0.236,	1.943	0.630	0.349	0.108,	1.461
RR[117]	1.256	0.513	0.458,	2.454	0.734	0.391	0.146,	1.660
RR[118]	1.058	0.475	0.340,	2.148	0.670	0.360	0.126,	1.528
RR[119]	0.690	0.402	0.131,	1.672	0.598	0.336	0.102,	1.394
RR[120]	0.838	0.418	0.219,	1.816	0.614	0.334	0.111,	1.397
RR[121]	1.107	0.496	0.361,	2.265	0.685	0.378	0.130,	1.572
RR[122]	1.212	0.505	0.434,	2.402	0.720	0.378	0.141,	1.605
RR[123]	2.151	0.745	0.975,	3.841	0.909	0.529	0.178,	2.222
RR[124]	1.239	0.561	0.393,	2.583	0.708	0.404	0.129,	1.702
RR[125]	0.861	0.439	0.220,	1.935	0.619	0.342	0.105,	1.424
RR[126]	1.693	0.653	0.669,	3.219	0.793	0.464	0.146,	1.918
RR[127]	0.679	0.395	0.128,	1.623	0.592	0.331	0.100,	1.383
RR[128]	0.850	0.378	0.270,	1.712	0.612	0.313	0.118,	1.329
RR[129]	0.690	0.347	0.182,	1.506	0.557	0.291	0.104,	1.230
RR[130]	0.858	0.383	0.279,	1.757	0.621	0.320	0.115,	1.370
RR[131]	1.287	0.457	0.555,	2.348	0.794	0.350	0.206,	1.548
RR[132]	0.935	0.425	0.292,	1.918	0.634	0.331	0.121,	1.399
RR[133]	0.697	0.406	0.126,	1.677	0.607	0.341	0.105,	1.433
RR[134]	1.142	0.515	0.353,	2.379	0.690	0.386	0.123	1.621
RR[135]	0.895	0.395	0.286,	1.814	0.627	0.323	0.125,	1.374
RR[136]	1.376	0.570	0.507,	2.699	0.745	0.416	0.145,	1.751
RR[137]	2.134	0.733	0.955,	3.817	0.916	0.523	0.188,	2.222
RR[138]	0.947	0.423	0.301,	1.927	0.642	0.334	0.124,	1.411
RR[139]	1.020	0.466	0.319,	2.112	0.655	0.349	0.124,	1.468
RR[140]	0.629	0.368	0.114,	1.513	0.568	0.313	0.095,	1.306
RR[141]	0.841	0.373	0.268,	1.703	0.615	0.309	0.120,	1.304
RR[142]	1.584	0.611	0.646	2.995	0.808	0.445	0.156,	1.878
RR[143]	1.606	0.668	0.597,	3.189	0.723	0.429	0.131,	1.771
RR[144]	1.268	0.572	0.412,	2.643	0.704	0.406	0.128,	1.690
RR[145]	1.974	0.717	0.841,	3.636	0.836	0.494	0.164,	2.047
RR[146]	2.092	0.716	0.952,	3.743	0.926	0.522	0.185,	2.198
RR[147]	1.285	0.583	0.411,	2.663	0.704	0.414	0.126,	1.707
RR[148]	1.700	0.658	0.671,	3.243	0.799	0.463	0.147,	1.922
RR[149]	0.614	0.358	0.109,	1.469	0.554	0.308	0.090	1.273
RR[150]	1.022	0.461	0.325,	2.112	0.660	0.356	0.122,	1.490
RR[151]	1.299	0.494	0.523,	2.433	0.770	0.375	0.175,	1.626
RR[152]	1.159	0.516	0.387,	2.356	0.691	0.386	0.129,	1.603
RR[153]	0.835	0.292	0.359,	1.494	0.674	0.267	0.197,	1.235
RR[154]	0.885	0.399	0.283,	1.819	0.624	0.318	0.118,	1.343
RR[155]	1.083	0.362	0.500,	1.915	0.780	0.300	0.236,	1.400

The posterior RR for Poisson gamma model ranges between 0.518 – 2.735 comparing to lognormal model 0.505 – 0.934 which implies that log normal model gives better smoothing for this HIV data due to adding random effect in Chennai ward. After incorporating the random effects in the log normal model, the extreme values disappear and relative risk extremely shrunk toward the global mean. Figure (2) displays the relative risk estimates for all the wards in Chennai after convergence was achieved. The spatial pattern in relative risk is very similar to the one obtained using the Poisson-gamma model but more smoother map with less extremes in the relative risk estimates. The relative risk ranges from 0.52 to 0.934.

The map of the Poisson model revealed that the extreme values shrunk towards the mean and there is no ward comes under RR > 1.

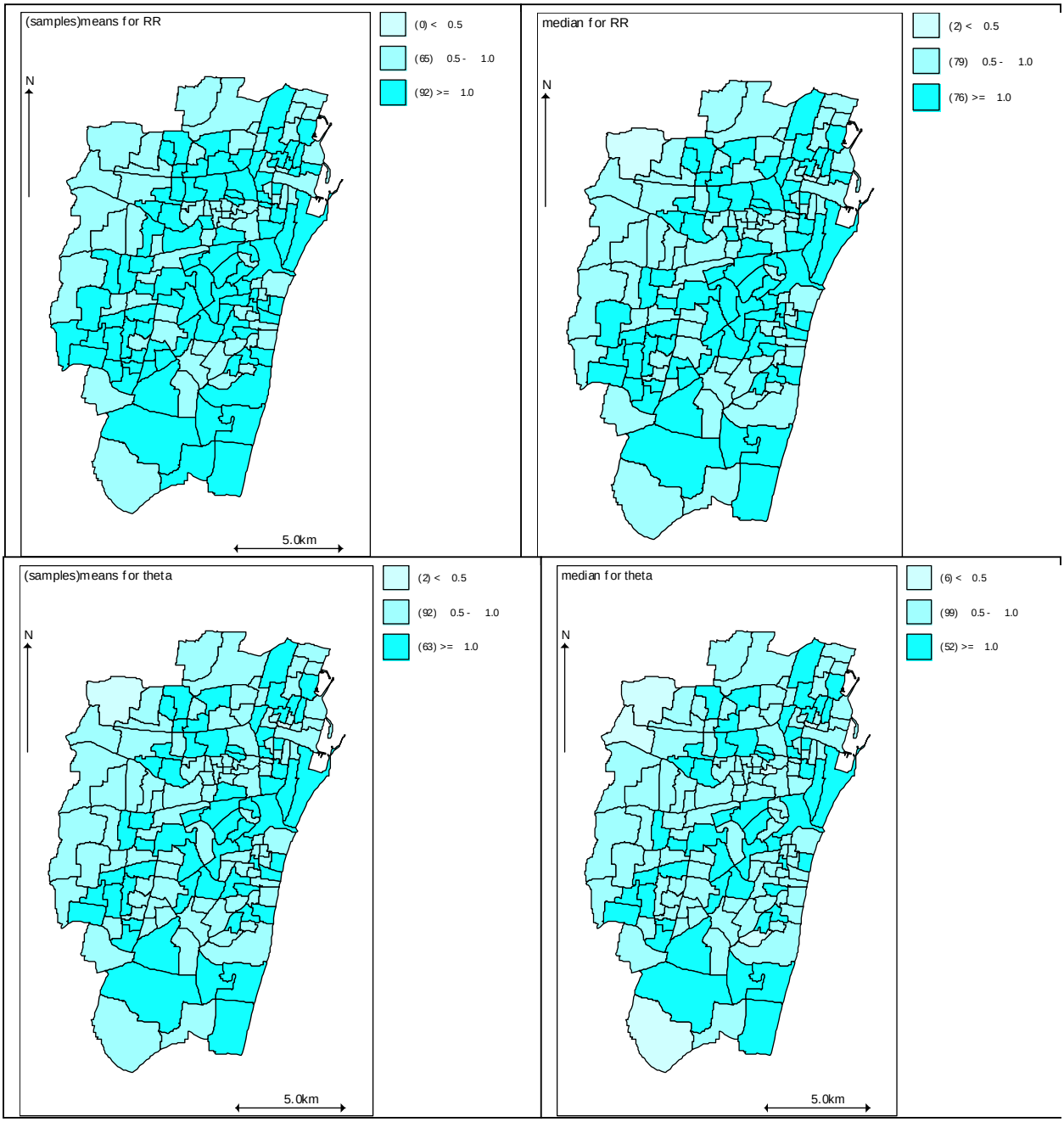

Figure 1 Posterior Expected Relative (Mean and Median) and Posterior Probability of Theta (Mean and Median) under Poisson Gamma Model

Table 2 Posterior summaries for Poisson gamma model and Log normal model

Parameter	Poisson Gamma model					Log-normal model				
	Mean	SD	MC error	Credible Interval		Mean	SD	MC error	Credible Interval	
α	3.07	0.75	0.022	1.91	4.86	3.17	1.69	0.05	1.34,	4.68
β_0	0.17	0.07	0.001	0.03	0.31	-0.4	0.18	0.01	-0.80,	-0.10
σ	0.58	0.07	0.002	0.45	0.72	0.44	1.3	0.05	0.38,	0.68

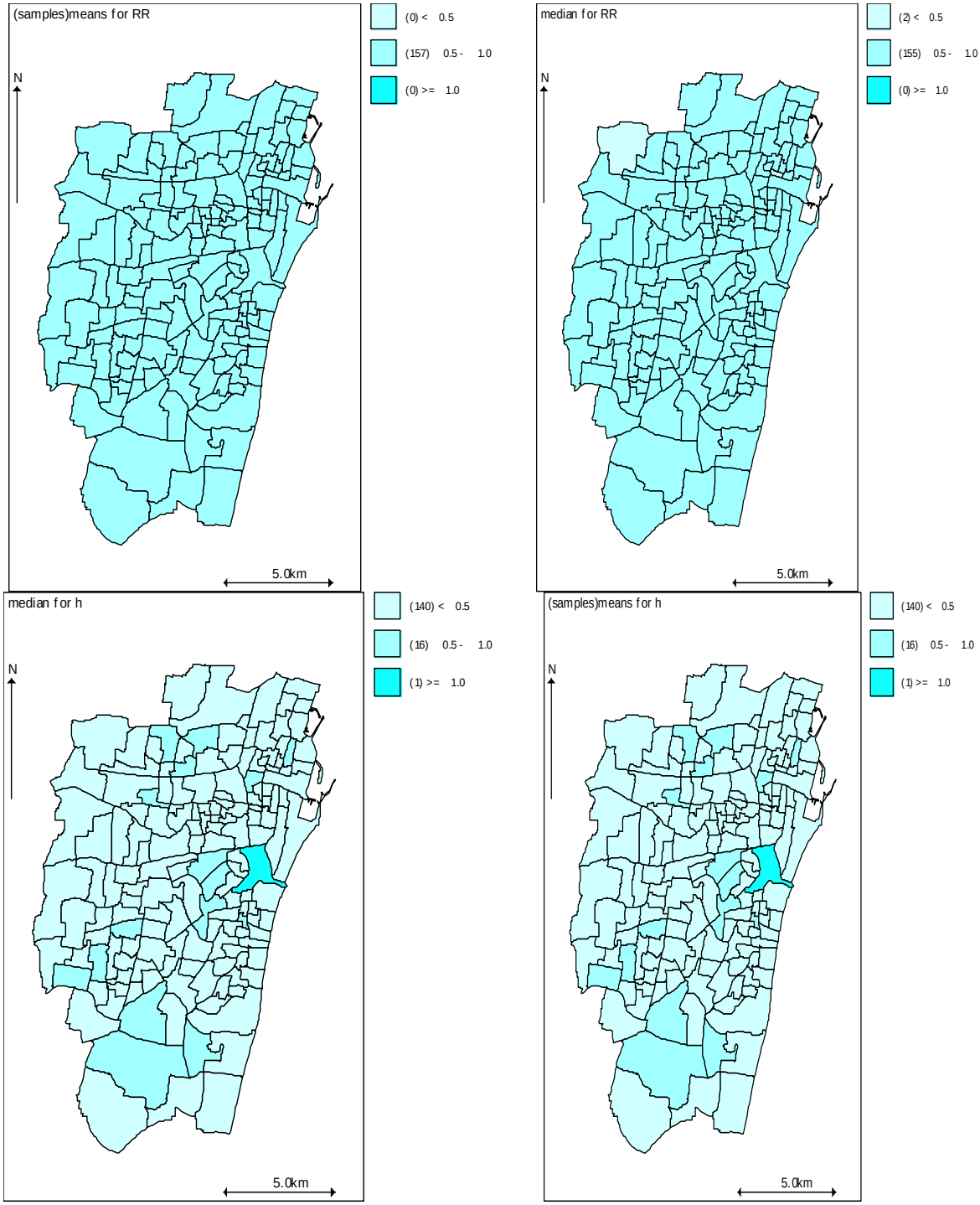

Figure 2 Posterior Expected Relative Risk (Mean and Median) and Residual (Mean and Median) under Lognormal Model

The posterior estimates of the parameter for Bayesian Poisson gamma and Log-normal model are given in Table 2. The posterior mean for α is 3.07, compared to 3.17 under log-normal, and the posterior mean for β is 0.17, compared to -0.4. The MC error for Poisson gamma model is high compared with random effect log-normal model. Also, Credible Interval for log normal model is very narrow.

Table 3 Deviance values for Poisson gamma and Log normal models

Model	$\overline{D}$	$\hat{D}$	D_p	DIC
Poisson-gamma	537.907	476.492	61.415	599.322
Log-normal	512.881	441.413	71.468	584.359

The Deviance Information Criterion (DIC) for log-normal model is less (584.35) compared with Poisson-gamma model which implies that log-normal model has the advantage of spatial random effect and better fit for this HIV disease mapping model.

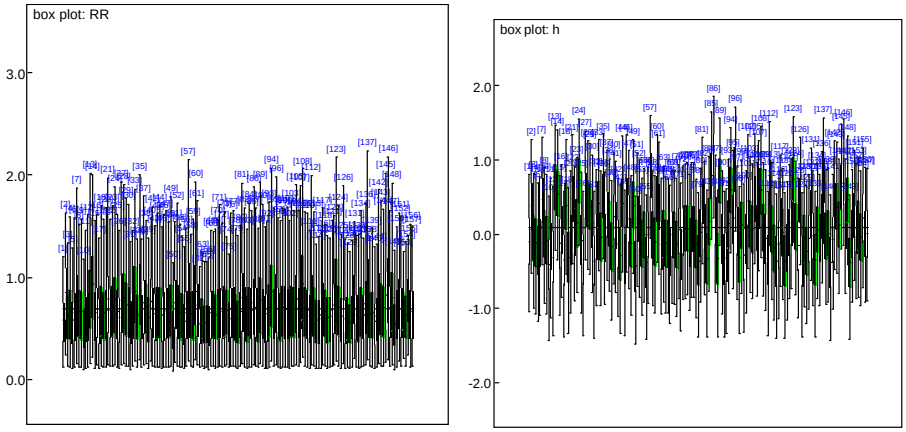

Figure 3 Box plot for Relative risk and residual using Lognormal Model

CONCLUSION

Bayesian disease mapping techniques in which the random effect model method gives smoother relative risk, especially when rare diseases are investigated in an area with a small population. The result reveals that there are 82 wards having no risk HIV/AIDS ward and 75 wards having higher risk which was scattered throughout Chennai. Bayesian model with random effect gives better shrinkage and smaller DIC than Poisson gamma model. This approach would observe the unobserved and unexplained spatial variation of interest. Bayesian random effect disease mapping of RR shrunk extreme towards the global mean and lowest RR pulls upwards and highest RR pulls downwards. The MC error and credible Interval for Bayesian random effect model is very narrow and posterior median also close with posterior mean which implies that random effect model is better for disease mapping of HIV/AIDS data.

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