

Ecological Example

- ◆ South Carolina congenital abnormality deaths 1998 by county
- ◆ With number of deaths and number of births and % poverty per county
- ◆ This is a binomial example:

$$y_i \sim \text{bin}(p_i, n_i)$$
$$\text{logit}(p_i) = \alpha_0 + \beta x_i + v_i + u_i$$

```

SCbinomial
#In this case we examine the congenital data
for 1998 with a % of pop classified by the US
#census as in poverty
# Data file is SCcongen_bin_pov.bt
#spatial file:below

model
{
  for( i in 1 : J) {
    y[i] ~ dbin(p[i], n[i])
    logit(p[i]) <- a0+a1* X[i]+b[i]+h[i]
    h[i]~dnorm(0.0,tau.h)
  }
  a0~dflat()
  a1~dnorm(0.0,tau.a1)
  b[1:J]~car.normal(adj[],wei[],num[],tau.b)

  for (i in 1:sumNumNeigh){
    wei[i]<-1.0
  }

  tau.h~dgamma(0.001,0.001)
  tau.a1~dgamma(0.001,0.001)
  tau.b~dgamma(0.001,0.001)

}

# main data is in SCcongen98_data.txt
Main data → click on one of the arrows to open data ←

```

SCcongen_bin_pov.txt

The following data represents the number of cases of congenital abnormality death for 1998 in the counties of South Carolina, the number of births in South Carolina, and a census indicator of percentage of the population below a poverty level within each county for the same period.

cg98	birth98	%poverty
0.0	364.0	13.6
5.0	1797.0	13.8
0.0	177.0	32.3
16.0	2145.0	11.0
0.0	208.0	24.2
0.0	338.0	19.9
3.0	1668.0	12.3
5.0	2017.0	13.3
0.0	168.0	17.0
7.0	4403.0	15.4
1.0	686.0	14.1
5.0	476.0	15.7
1.0	550.0	18.0
2.0	409.0	24.3
1.0	519.0	21.8
3.0	907.0	20.2
2.0	489.0	24.9
5.0	1152.0	12.0
2.0	265.0	17.4
1.0	335.0	18.1
3.0	1867.0	18.7
2.0	736.0	17.5
14.0	5176.0	10.6
7.0	963.0	13.8
1.0	311.0	22.8
9.0	2324.0	13.7
1.0	280.0	21.0
3.0	665.0	12.6
1.0	809.0	14.0
3.0	864.0	14.0
1.0	758.0	26.0

Main data is in SCcongen98_data.txt

```

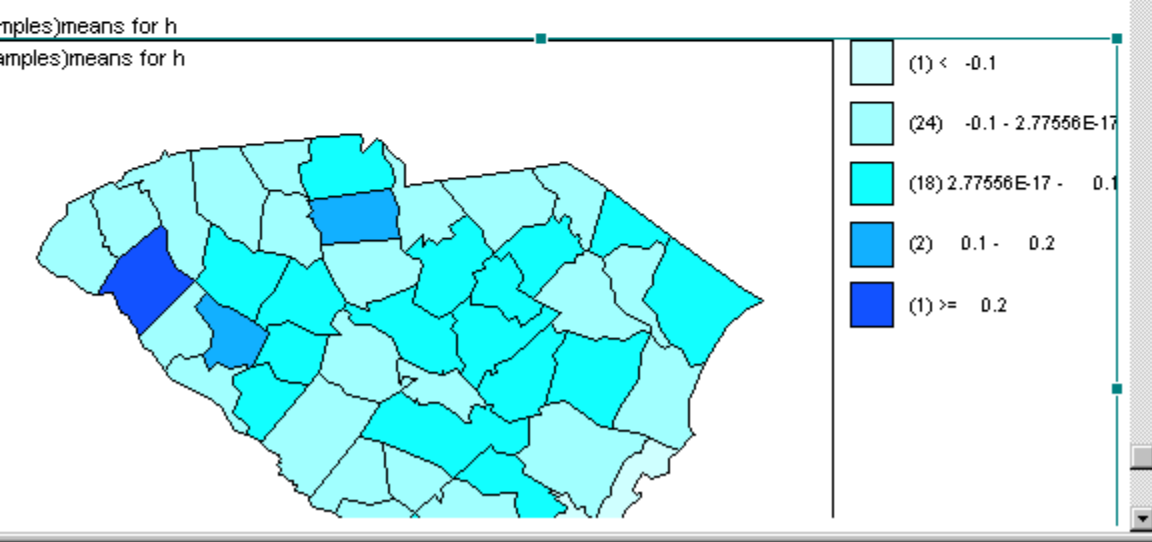
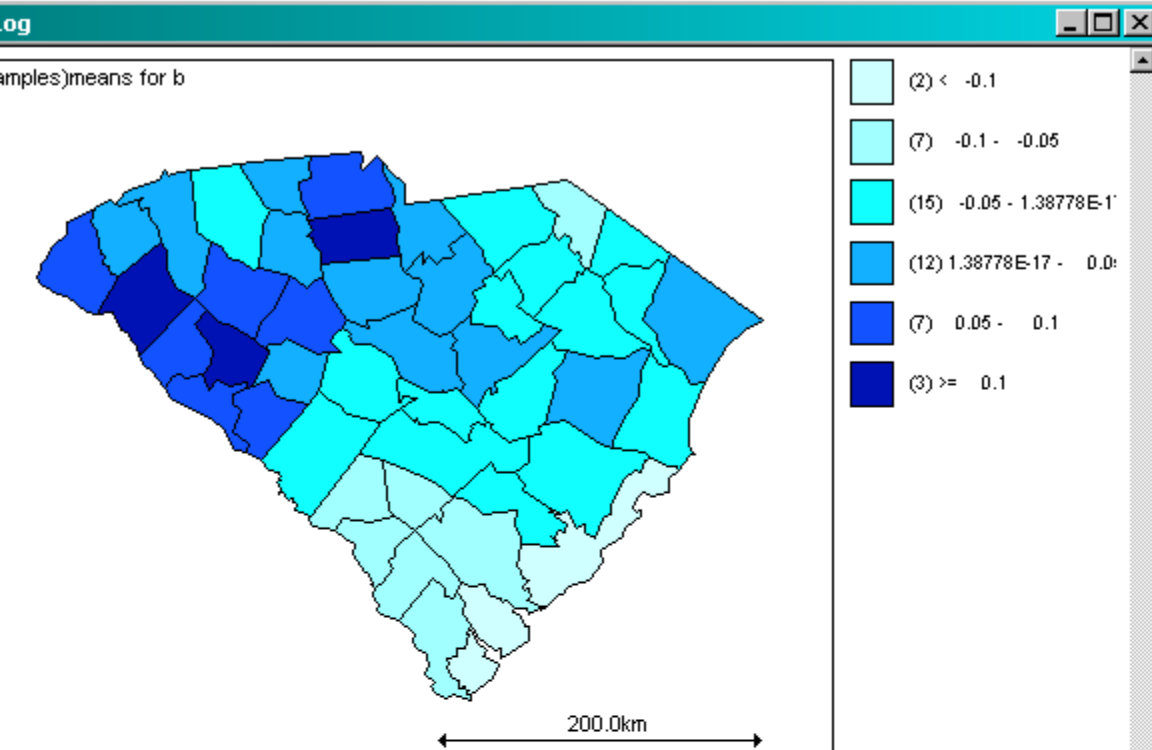
n data ⇨
y=c(0,5,0,16,0,0,3,5,0,7,1,5,1,2,1,3,2,5,2,1,3,2,14,7,1,9,
1,3,1,7,0,1,0,4,2,7,3,14,1,7,7,0,4,10),
(364,1797,177,2145,208,338,1668,2017,168,4403,686,476,550,40
19,907,489,1152,265,335,1867,736,5176,963,311,2324,280,665,8
864,258,3028,83,478,433,523,796,1265,1379,4286,256,3288,1699,369,502,2122),
c(13.6,13.8,32.3,11,24.2,19.9,12.3,13.3,17,15.4,14.1,15.7,18,
3,21.8,20.2,24.9,12,17.4,18.1,18.7,17.5,10.6,13.8,22.8,13.7,
12.6,14,14,26.9,9.4,17.8,23.1,23.1,14.4,10.8,22.1,10.1,13.6,15.9,11.2,18.3,14,26.4,10.6))
    
```

```

Spatial Data ⇨
J=46, num = c(5, 5, 4, 5, 5, 4, 3, 6, 5, 4,
5, 6, 7, 5, 4, 4, 4, 6,
5, 6, 5, 3, 2, 7, 5, 7,
3, 5, 4, 7, 2, 9, 3, 6,
6, 7, 5, 4
    
```

```

= c(
80, 24, 23, 4,
88, 32, 19, 6,
15, 6, 5,
37, 30, 23, 1,
25, 15, 6, 3,
5, 3, 2,
25, 15,
88, 22, 18, 14, 10,
40, 38, 32, 14,
18, 15, 8,
44, 42,
44, 29, 20,
31, 29, 28, 16,
43, 38, 21, 9, 8,
25, 18, 10, 7, 5, 3,
31, 28, 21, 13,
84 26 21
    
```



Sample Monitor Tool

node chains to

beg end thin

clear set trace history density

stats coda quantiles bgr diag auto cor

percentile

2.5

5

10

25

median

75

90

95

97.5

Map Tool

map SC

variable h

quantity mean(sample)

cut points abs value percentile

threshold quantile

beg end

plot get cuts set cuts

cuts

num cuts default

cut1 -0.09999999

cut2 2.77555756

cut3 0.1

cut4 0.2

cut5

cut6

Specification Tool

check model load data

compile

num of chains 1

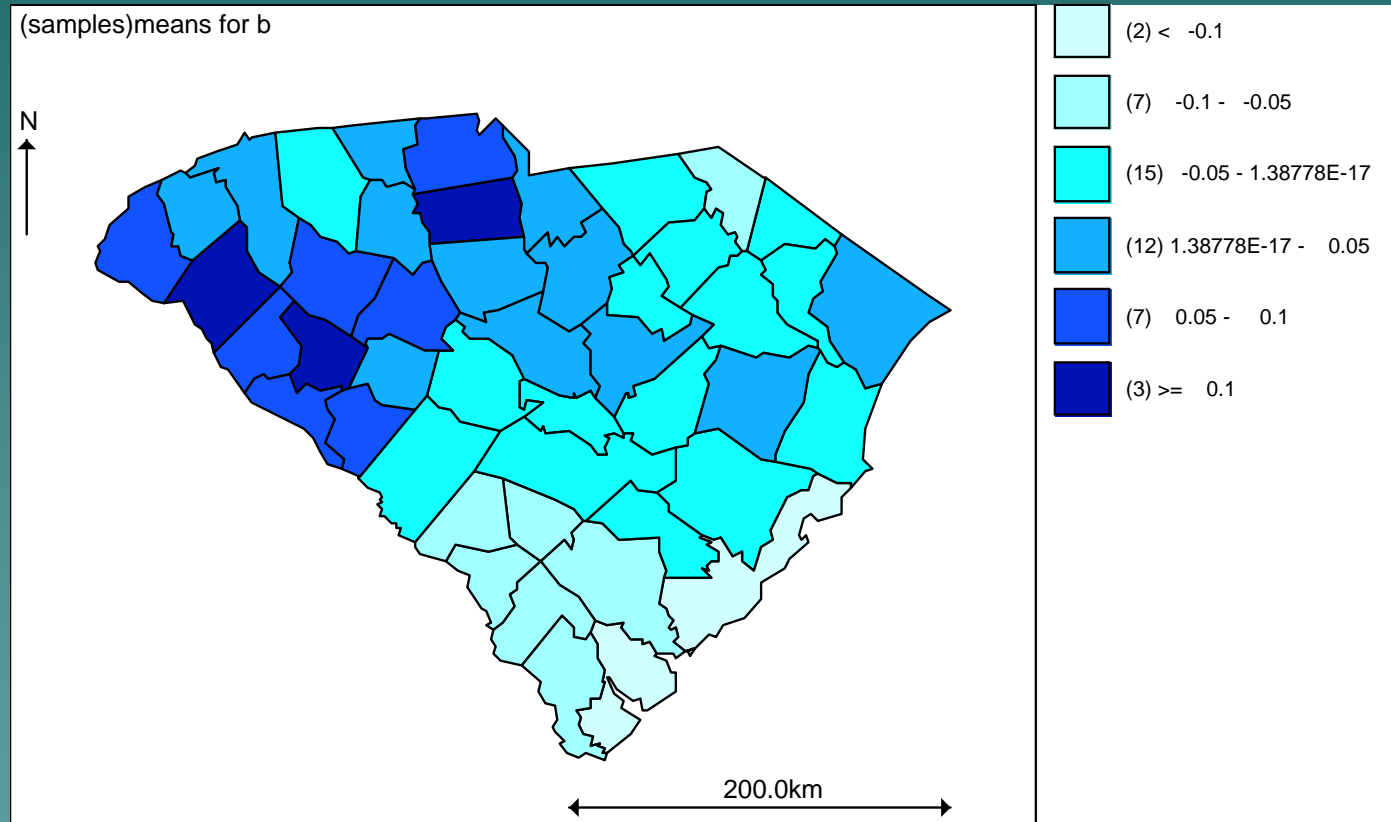
Update Tool

updates 10000 refresh 100

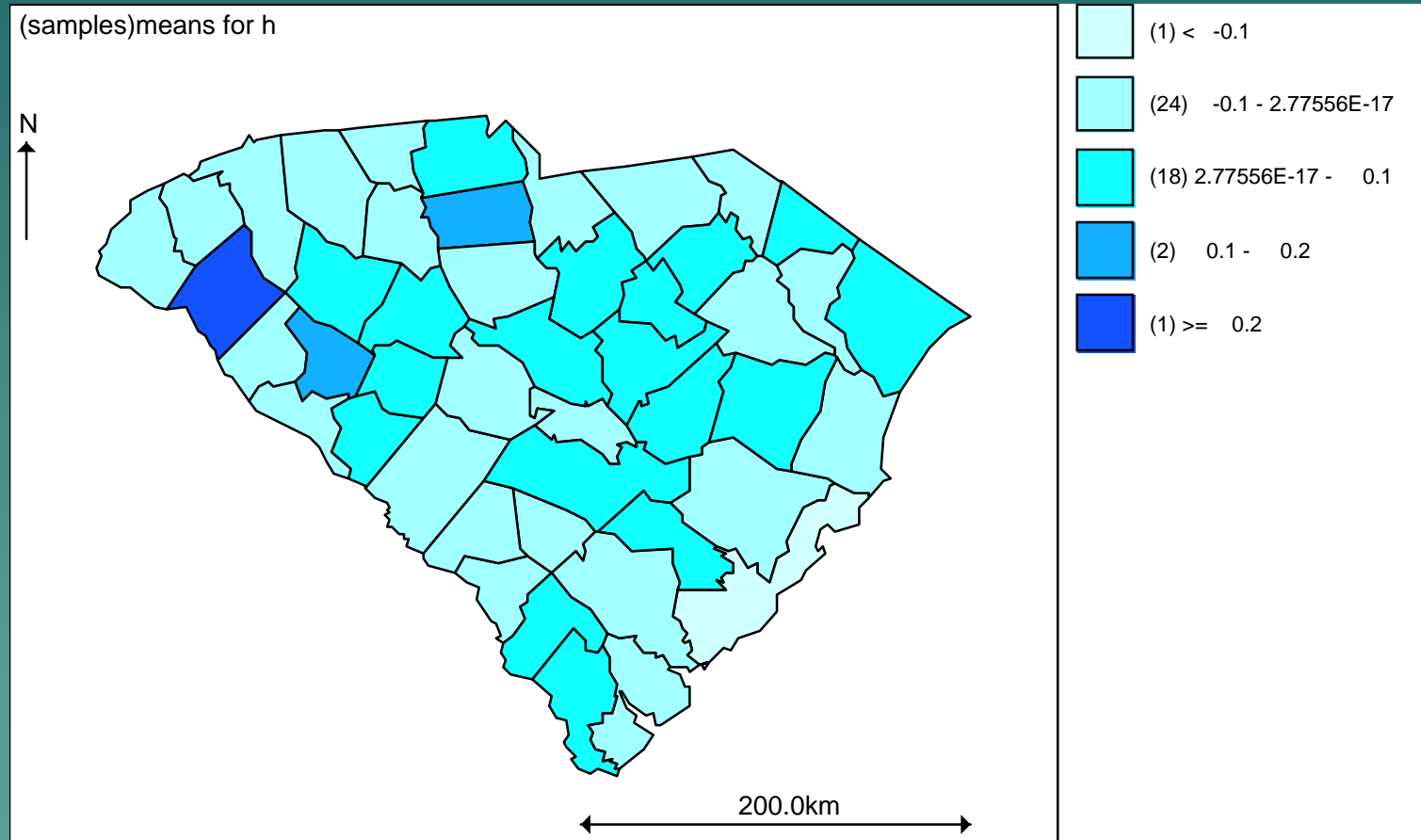
update thin 1 iteration 11000

over relax adapting

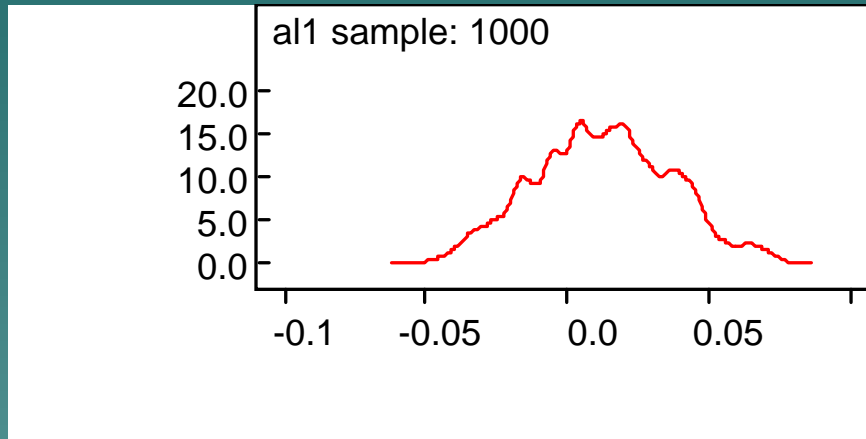
CAR (CH) component



UH component



Is %poverty significant?



Node statistics

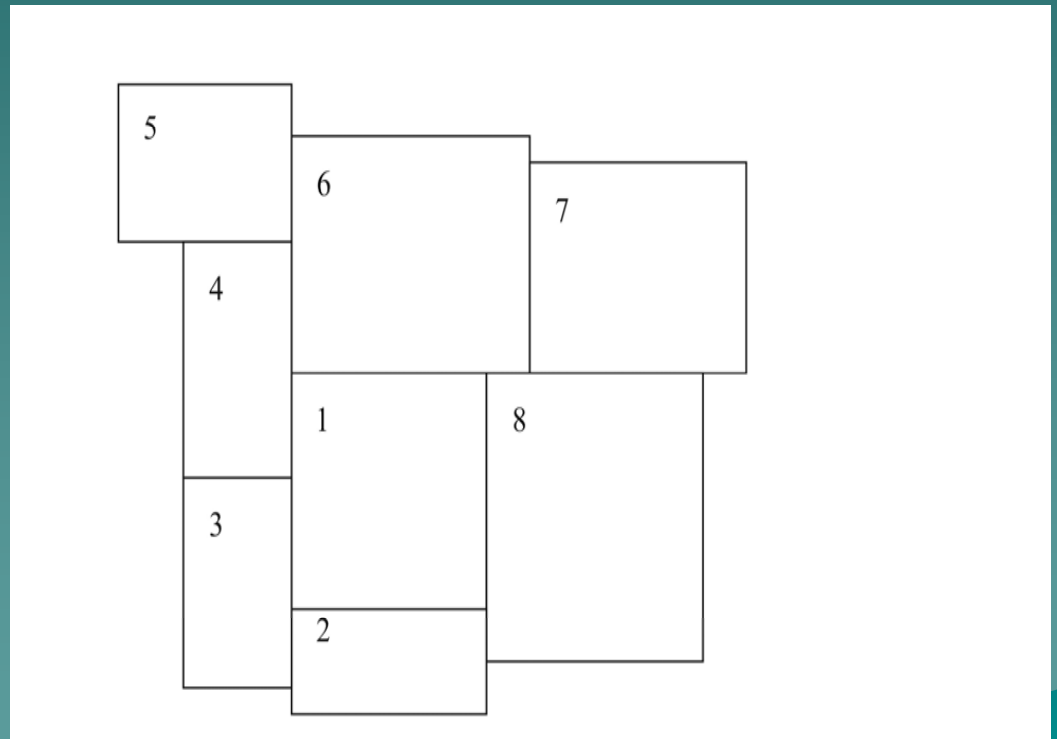
node	mean	sd	MC error	2.5%	median	97.5%	start	sample
al1	0.01258	0.02437	0.003607	-0.03415	0.01262	0.06251	11001	1000

CAR and other models

- ◆ The CAR model is available on WinBUGS
- ◆ Other correlation models can also be used and are available: for example a full Multivariate Normal model can be used (similar to Bayesian Kriging). A proper CAR can also be used

Dependencies

- ◆ adjacency: 2,3 ,4 ,6, 8 neighbors of 1:
- ◆ hence



$$\bar{\mu}_{\delta_i} = \sum_{j \in \delta_i} \mu_j / n_{\delta_i}$$

$$\bar{\mu}_{\delta_1} = (\mu_2 + \mu_3 + \mu_4 + \mu_6 + \mu_8) / 5$$