Hierarchical GLM

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Please hand in Rmd, pdf, and stan files. Due next Wednesday because of delay in lecture.

Lip cancer

Here is the lip cancer data as seen in the lecture.

- `observe.i` is observed deaths in each region
- `expect.i` is expected deaths, based on region-specific age distribution and national-level age-specific mortality rates.

```
observe.i <- c(
  5,13,18,5,10,18,29,10,15,22,4,11,10,22,13,14,17,21,25,6,11,21,13,5,19,18,14,17,3,10,
  7,3,12,11,6,16,13,6,9,10,4,9,11,12,23,18,12,7,13,12,12,13,6,14,7,18,13,9,6,8,7,6,16,4,6,12,5,5,
  17,5,7,2,9,7,6,12,13,17,5,5,6,12,10,16,10,16,15,18,6,12,6,8,33,15,14,18,25,14,2,73,13,14,6,20,8,
  12,10,3,11,3,11,13,11,13,10,5,18,10,23,5,9,2,11,9,11,6,11,5,19,15,4,8,9,6,4,4,2,12,12,11,9,7,7,
  8,12,11,23,7,16,46,9,18,12,13,14,14,3,9,15,6,13,13,12,8,11,5,9,8,22,9,2,10,6,10,12,9,11,32,5,11,
  9,11,11,0,9,3,11,11,11,5,4,8,9,30,110)
expect.i <- c(
    6.17,8.44,7.23,5.62,4.18,29.35,11.79,12.35,7.28,9.40,3.77,3.41,8.70,9.57,8.18,4.35,
    4.91,10.66,16.99,2.94,3.07,5.50,6.47,4.85,9.85,6.95,5.74,5.70,2.22,3.46,4.40,4.05,5.74,6.36,5.13,
    16.99,6.19,5.56,11.69,4.69,6.25,10.84,8.40,13.19,9.25,16.98,8.39,2.86,9.70,12.12,12.94,9.77,
    10.34,5.09,3.29,17.19,5.42,11.39,8.33,4.97,7.14,6.74,17.01,5.80,4.84,12.00,4.50,4.39,16.35,6.02,
    6.42,5.26,4.59,11.86,4.05,5.48,13.13,8.72,2.87,2.13,4.48,5.85,6.67,6.11,5.78,12.31,10.56,10.23,
    2.52,6.22,14.29,5.71,37.93,7.81,9.86,11.61,18.52,12.28,5.41,61.96,8.55,12.07,4.29,19.42,8.25,
    12.90,4.76,5.56,11.11,4.76,10.48,13.13,12.94,14.61,9.26,6.94,16.82,33.49,20.91,5.32,6.77,8.70,
    12.94,16.07,8.87,7.79,14.60,5.10,24.42,17.78,4.04,7.84,9.89,8.45,5.06,4.49,6.25,9.16,12.37,8.40,
    9.57,5.83,9.21,9.64,9.09,12.94,17.42,10.29,7.14,92.50,14.29,15.61,6.00,8.55,15.22,18.42,5.77,
    18.37,13.16,7.69,14.61,15.85,12.77,7.41,14.86,6.94,5.66,9.88,102.16,7.63,5.13,7.58,8.00,12.82,
    18.75,12.33,5.88,64.64,8.62,12.09,11.11,14.10,10.48,7.00,10.23,6.82,15.71,9.65,8.59,8.33,6.06,
    12.31,8.91,50.10,288.00)

stan_data <- list(N = length(observe.i),
                  y = observe.i,
                  e = expect.i)
```

Question 1

Explain a bit more what the `expect.i` variable is. For example, if a particular area has an expected deaths of 6, what does this mean?

Cancer is more likely to occur among eldery population. If we have expected region specific level of 6 it means that the region has relatively young population and we do not expect many cases of lip cancer here.

Question 2

Run three different models in Stan with three different set-up's for estimating θ_i, that is the relative risk of lip cancer in each region:

```
stan_data <- list(N = length(observe.i),
                  y = observe.i,
                  e = expect.i)
```

1. θ_i is same in each region $= \theta$

```
# mod1 <- stan(data = stan_data,
#              file = "lab8_mod1.stan",
#              iter = 500,
#              seed = 161198
#              )
```

```
#saveRDS(mod1, "lab8_mod1_new.rds")
mod1 <- readRDS("lab8_mod1_new.rds")
```

2. θ_i is different in each region and modeled separately

```
# mod2 <- stan(data = stan_data,
#              file = "lab8_mod2.stan",
#              iter = 500,
#              seed = 161198
#              )
```

```
#saveRDS(mod2, "lab8_mod2_new.rds")
mod2 <- readRDS("lab8_mod2_new.rds")
```

3. θ_i is different in each region and modeled hierarchically

```
# mod3 <- stan(data = stan_data,
#              file = "lab8_mod3.stan",
#              iter = 500,
#              seed = 161198
#              )
```

```
#saveRDS(mod3, "lab8_mod3_new.rds")
mod3 <- readRDS("lab8_mod3_new.rds")
```

Question 3

Make three plots (appropriately labeled and described) that illustrate the differences in estimated θ_i's across regions and the differences in θs across models.

```
mod1_thetas = summary(mod1)$summary[c('theta'), c('mean')]
mod2_thetas = summary(mod2)$summary[1:100, c('mean')]
mod3_thetas = summary(mod3)$summary[1:100, c('mean')]
```

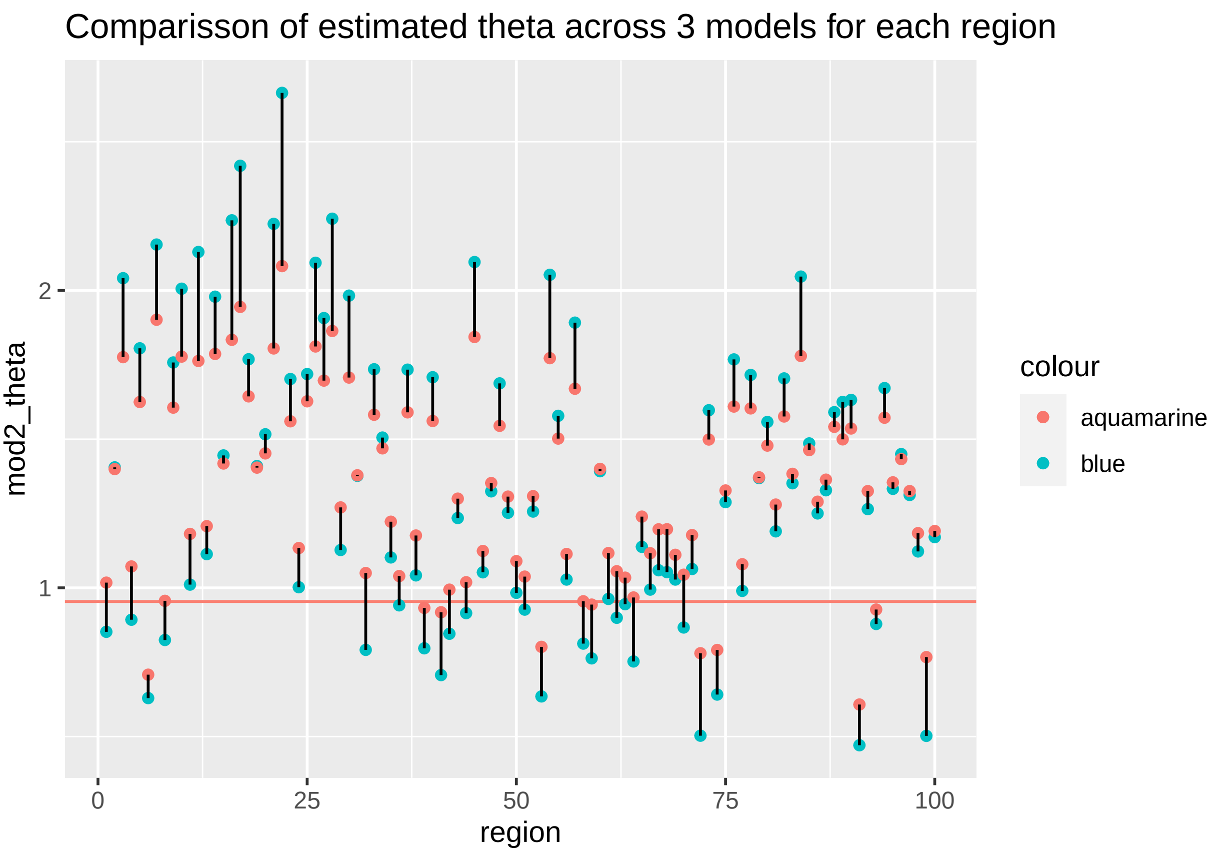
```
region <- seq(1,100,1)
region
```

```
##   [1]   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18
##  [19]  19  20  21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36
##  [37]  37  38  39  40  41  42  43  44  45  46  47  48  49  50  51  52  53  54
##  [55]  55  56  57  58  59  60  61  62  63  64  65  66  67  68  69  70  71  72
##  [73]  73  74  75  76  77  78  79  80  81  82  83  84  85  86  87  88  89  90
##  [91]  91  92  93  94  95  96  97  98  99 100
```

```
tdf <- data.frame(region)
```

```
tdf$mod1_theta <- mod1_thetas
tdf$mod2_theta <- mod2_thetas
tdf$mod3_theta <- mod3_thetas
```

```
ggplot(data = tdf)+
  geom_hline(yintercept = tdf$mod1_theta, color = 'salmon') +
  geom_point(aes(x = region, y = mod2_theta, color = 'blue'))+
  geom_point(aes(x = region, y = mod3_theta, color = 'aquamarine'))+
  geom_segment(aes(x = region,
                   y = mod2_theta,
                   xend =region,
                   yend = mod3_theta))+
  ggtitle('Comparisson of estimated theta across 3 models for each region')
```



Question 4

Rerun model 3 (the hierarchical model), but also including an overdispersion parameter. Compare the two models and decide which is more appropriate.

```
# mod4 <- stan(data = stan_data,
#              file = "lab8_mod4.stan",
#              iter = 500,
#              seed = 161198
#              )
```

```
#saveRDS(mod4, "lab8_mod4_new.rds")
mod4 <- readRDS("lab8_mod4_new.rds")
```

```
loglik3 <- rstan::extract(mod3)[["log_lik"]]
loglik4 <- rstan::extract(mod4)[["log_lik"]]
```

```
loo3 = loo(loglik3, save_psis = T )
loo4 = loo(loglik4, save_psis = T )
```

```
loo_compare(loo3, loo4)
```

```
##        elpd_diff se_diff
## model2  0.0       0.0
## model1 -8.1       8.3
```