Week 9: Hierarchical GLM

19/03/23

Lip cancer

Here is the lip cancer data given to you in terribly unreproducible and error-prone format.

- `aff.i` is proportion of male population working outside in each region
- `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,
  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
  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
  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,
  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
    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
    10.34,5.09,3.29,17.19,5.42,11.39,8.33,4.97,7.14,6.74,17.01,5.80,4.84,12.00,4.50,4.39,1
    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.
    2.52,6.22,14.29,5.71,37.93,7.81,9.86,11.61,18.52,12.28,5.41,61.96,8.55,12.07,4.29,19.4
    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.
    12.94,16.07,8.87,7.79,14.60,5.10,24.42,17.78,4.04,7.84,9.89,8.45,5.06,4.49,6.25,9.16,1
    9.57,5.83,9.21,9.64,9.09,12.94,17.42,10.29,7.14,92.50,14.29,15.61,6.00,8.55,15.22,18.4
    18.37,13.16,7.69,14.61,15.85,12.77,7.41,14.86,6.94,5.66,9.88,102.16,7.63,5.13,7.58,8.0
    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.
    12.31,8.91,50.10,288.00)
aff.i <- c(0.2415,0.2309,0.3999,0.2977,0.3264,0.3346,0.4150,0.4202,0.1023,0.1752,
        0.2548,0.3248,0.2287,0.2520,0.2058,0.2785,0.2528,0.1847,0.3736,0.2411,
        0.3700,0.2997,0.2883,0.2427,0.3782,0.1865,0.2633,0.2978,0.3541,0.4176,
        0.2910,0.3431,0.1168,0.2195,0.2911,0.4297,0.2119,0.2698,0.0874,0.3204,
        0.1839,0.1796,0.2471,0.2016,0.1560,0.3162,0.0732,0.1490,0.2283,0.1187,
        0.3500,0.2915,0.1339,0.0995,0.2355,0.2392,0.0877,0.3571,0.1014,0.0363,
        0.1665,0.1226,0.2186,0.1279,0.0842,0.0733,0.0377,0.2216,0.3062,0.0310,
        0.0755,0.0583,0.2546,0.2933,0.1682,0.2518,0.1971,0.1473,0.2311,0.2471,
        0.3063,0.1526,0.1487,0.3537,0.2753,0.0849,0.1013,0.1622,0.1267,0.2376,
        0.0737,0.2755,0.0152,0.1415,0.1344,0.1058,0.0545,0.1047,0.1335,0.3134,
        0.1326,0.1222,0.1992,0.0620,0.1313,0.0848,0.2687,0.1396,0.1234,0.0997,
        0.0694,0.1022,0.0779,0.0253,0.1012,0.0999,0.0828,0.2950,0.0778,0.1388,
        0.2449,0.0978,0.1144,0.1038,0.1613,0.1921,0.2714,0.1467,0.1783,0.1790,
        0.1482,0.1383,0.0805,0.0619,0.1934,0.1315,0.1050,0.0702,0.1002,0.1445,
        0.0353,0.0400,0.1385,0.0491,0.0520,0.0640,0.1017,0.0837,0.1462,0.0958,
        0.0745,0.2942,0.2278,0.1347,0.0907,0.1238,0.1773,0.0623,0.0742,0.1003,
        0.0590,0.0719,0.0652,0.1687,0.1199,0.1768,0.1638,0.1360,0.0832,0.2174,
        0.1662,0.2023,0.1319,0.0526,0.0287,0.0405,0.1616,0.0730,0.1005,0.0743,
        0.0577,0.0481,0.1002,0.0433,0.0838,0.1124,0.2265,0.0436,0.1402,0.0313,
        0.0359,0.0696,0.0618,0.0932,0.0097)
```

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?

The expected deaths is the implied number of lip cancer deaths for a particular region, given that region's age structure and the national level age-specific mortality rates for lip cancer.For example, an expected number of deaths of 6 would mean that for that particular region,we would expect 6 lip cancer deaths if this region were to experience the same age specific mortality rates as at the national level.

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:

1. Intercept α_i is same in each region $= \alpha$

$$y_i|\theta_i \sim \text{Poisson}(\theta_i \cdot e_i)$$

Model1:

$$\log \theta_i = \alpha + \beta x_i$$

with

$$\alpha \sim N(0,1) \beta \sim N(0,1)$$

```
library(tidyverse)
library(rstan)
library(tidybayes)
library(here)


stan_data <- list(y=observe.i,
                  log_e=log(expect.i),
                  N=length(observe.i),
                  x=aff.i-mean(aff.i))

mod1<-stan(data=stan_data,file="D:\\lab9\\lab9_1.stan",refresh = 0)
```

2. α_i is different in each region and modeled separately (with covariate)

Model2:

$$\log \theta_i = \alpha_i + \beta x_i$$

with

$$\alpha_i \sim N(0,1) \beta \sim N(0,1)$$

```
mod2<-stan(data=stan_data,file="D:\\lab9\\lab9_2.stan",refresh = 0)
```

3. α_i is different in each region and the intercept is modeled hierarchically (with covariate)

Model3:

$$\log \theta_i = \alpha_i + \beta x_i$$

with

$$\alpha_i \sim N(\mu, \sigma^2) \beta \sim N(0,1) \mu \sim N(0,1) \sigma \sim N(0,1)$$

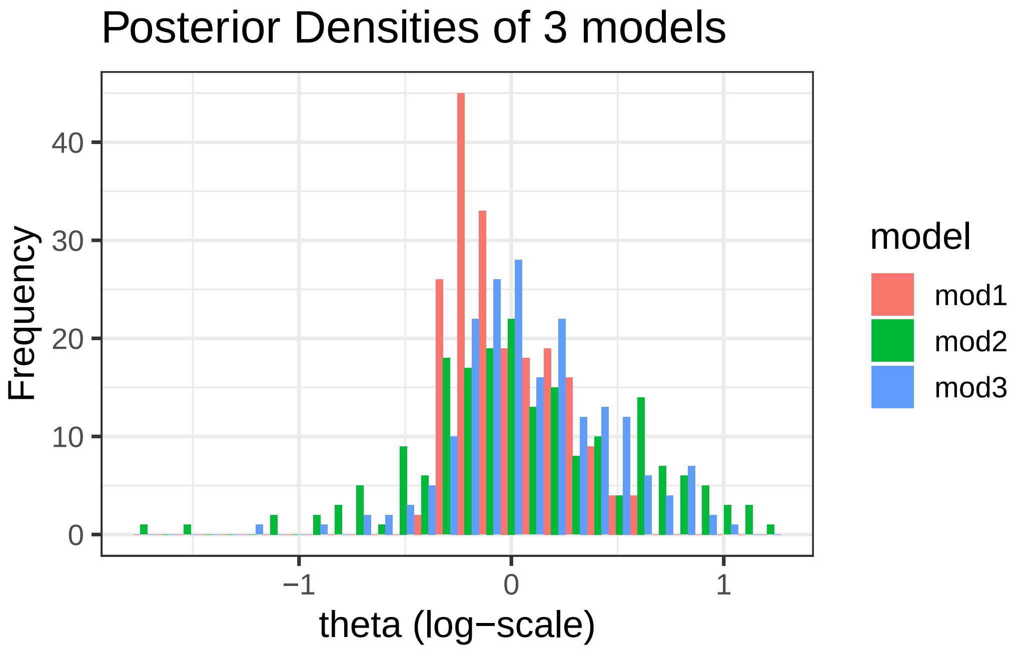
```
mod3<-stan(data=stan_data,file="D:\\lab9\\lab9_3.stan",refresh = 0)
```

Question 3

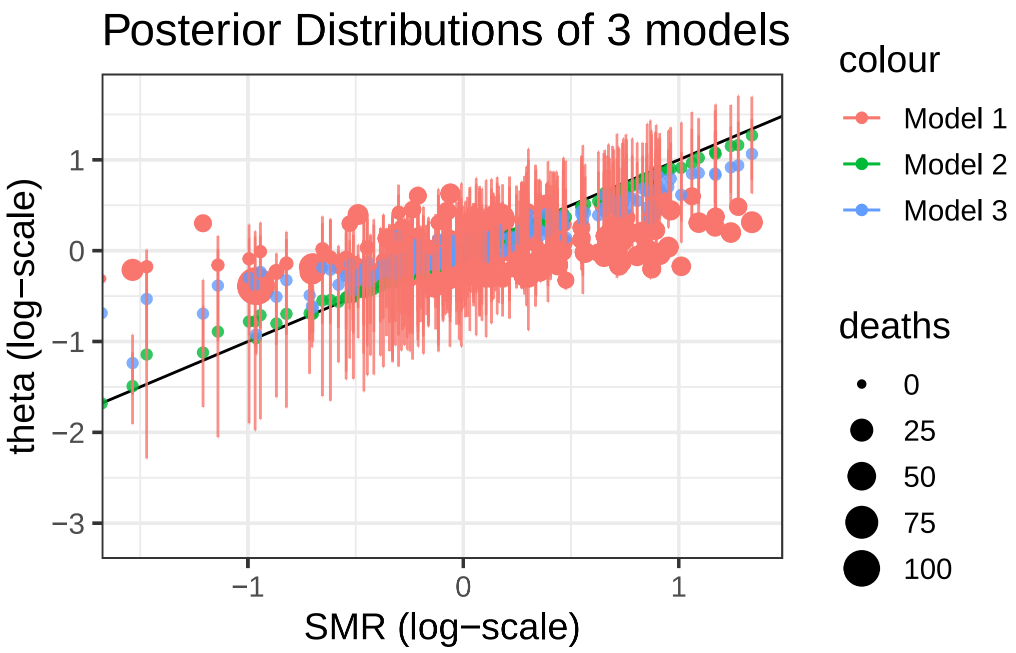
Make two plots (appropriately labeled and described) that illustrate the differences in estimated θ_i's across regions and the differences in θs across models.

```
res_mod1<- mod1 |>
gather_draws(log_theta[i]) |>
median_qi()|>
rename(median_mod1=.value,
       lower_mod1=.lower,
          upper_mod1=.upper)|>
select(i,median_mod1:upper_mod1)


res_mod2<- mod2 |>
gather_draws(log_theta[i]) |>
median_qi()|>
rename(median_mod2=.value,
       lower_mod2=.lower,
         upper_mod2=.upper)|>
select(i,median_mod2:upper_mod2)


res_mod3<- mod3|>
gather_draws(log_theta[i]) |>
median_qi()|>
rename(median_mod3=.value,
       lower_mod3=.lower,
         upper_mod3=.upper)|>
select(i,median_mod3:upper_mod3)
```

```
#res <- res_mod1 |>left_join(res_mod2)|> left_join(res_mod3)
res_mod<- as.data.frame(cbind(res_mod1,res_mod2[,c(2,3,4)],res_mod3[,c(2,3,4)]))

res_mod|>
  select(median_mod1, median_mod2, median_mod3)|>
  pivot_longer(median_mod1:median_mod3, names_to='model', values_to='log_theta')|>
  mutate(model = str_remove(model, 'median_'))|>
  ggplot(aes(log_theta, fill=model))+
  geom_histogram(position = 'dodge') +
  labs(x ="theta (log-scale)", y = "Frequency", title = "Posterior Densities of 3 models")
  theme_bw(base_size = 14)
```



```
res_mod |>
  mutate(deaths=observe.i)|>
  mutate(log_smr=log(observe.i/expect.i))|>
  ggplot(aes(log_smr,median_mod1,color="Model 1"),alpha=0.8)+
  geom_point(aes(size=deaths))+
  geom_errorbar(aes(ymin=lower_mod1,ymax=upper_mod1),alpha=0.8)+
  geom_abline(slope=1,intercept=0)+
  geom_point(aes(log_smr,median_mod2,color="Model 2"),alpha=0.8)+
  geom_errorbar(aes(ymin=lower_mod2,ymax=upper_mod2),alpha=0.8)+
  geom_point(aes(log_smr,median_mod3,color="Model 3"),alpha=0.8)+
  geom_errorbar(aes(ymin=lower_mod3,ymax=upper_mod3),alpha=0.8)+
  labs(x = "SMR (log-scale)", y = "theta (log-scale)", title = "Posterior Distributions of
  theme_bw(base_size = 14)
```



The differences in estimated θ_i's across regions were there were the different morality rates for different 200 regions.

The differences in θs across models were there were the different morality rates for different 3 models.We can assume that each morality rate of the model was the average of respondent the model.