STA2201 Lab 9

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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,
  7,3,12,11,6,16,13,6,9,10,4,9,11,12,23,18,12,7,13,12,12,13,6,14,7,18,13,9,6,8,7,6,16,4,6,12,5,5,
  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)
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?

Answer

Expected deaths = # of deaths implied for a particular region given that region's age structure aand national age-specific mortality rates for lip caancer.

E.g. an expected deaths of 6 would mean we expect 6 lip cancer deaths if the region were to experience the **same age-specific mortality rates as 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 = α
2. α_i is different in each region and modeled separately (with covariate)
3. α_i is different in each region and the intercept is modeled hierarchically (with covariate)

$$y_i|\theta \sim Poisson()$$
$$log\theta_i = \alpha + \beta x_i$$
$$log\theta_i = \alpha_i + \beta x_i$$

$$\alpha_i$$

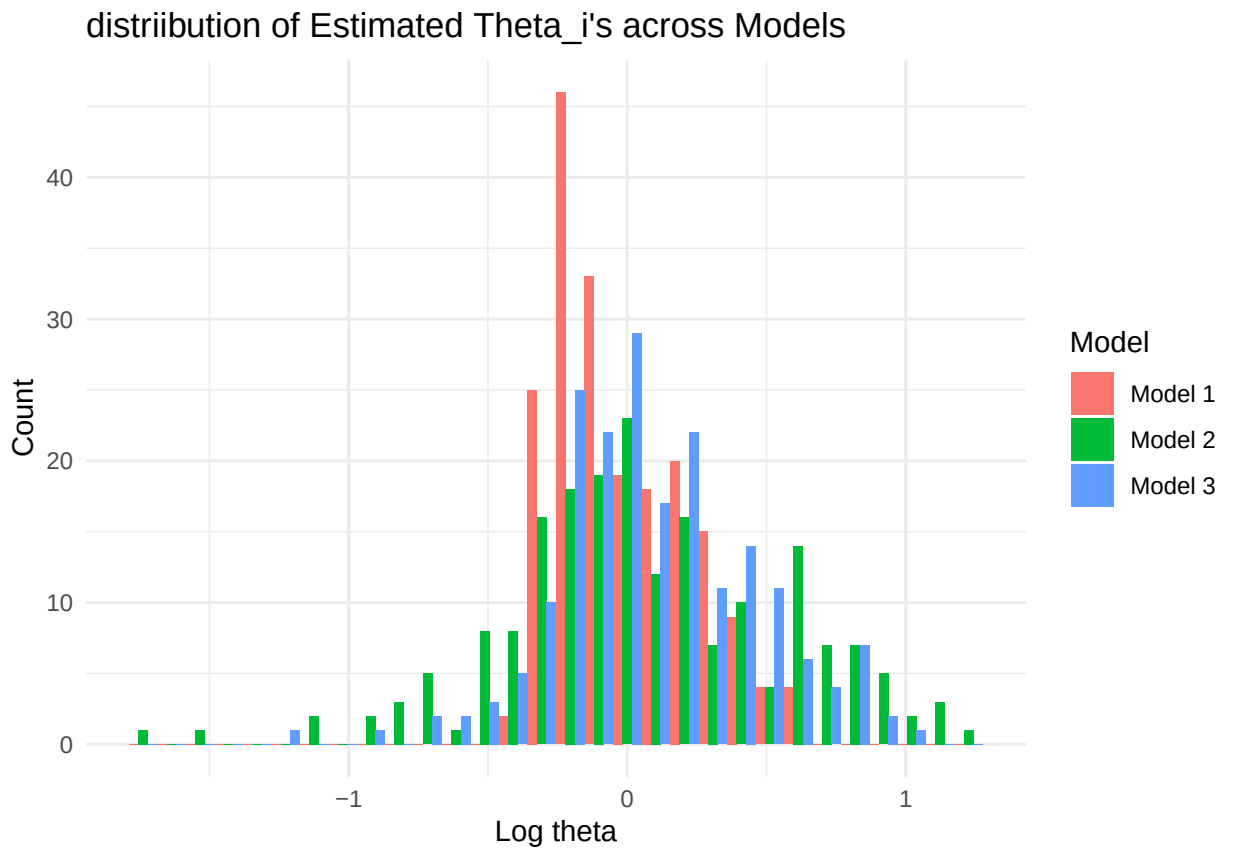
Question 3

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.

```r
res91 = model_L91 %>% gather_draws(log_theta[i]) %>%
  median_qi() %>%
  rename(median_mod1 = .value,
         lower_mod1 = .lower,
         upper_mod1 = .upper) %>%
  dplyr::select(i, median_mod1:upper_mod1)

res92 = model_L92 %>% gather_draws(log_theta[i]) %>%
  median_qi() %>%
  rename(median_mod2 = .value,
         lower_mod2 = .lower,
         upper_mod2 = .upper) %>%
  dplyr::select(i, median_mod2:upper_mod2)

res93 = model_L93 %>% gather_draws(log_theta[i]) %>%
  median_qi() %>%
  rename(median_mod3 = .value,
         lower_mod3 = .lower,
         upper_mod3 = .upper) %>%
  dplyr::select(i, median_mod3:upper_mod3)

res9 = left_join(left_join(res91, res92, by = "i"), res93, by = "i")
head(res9)
```

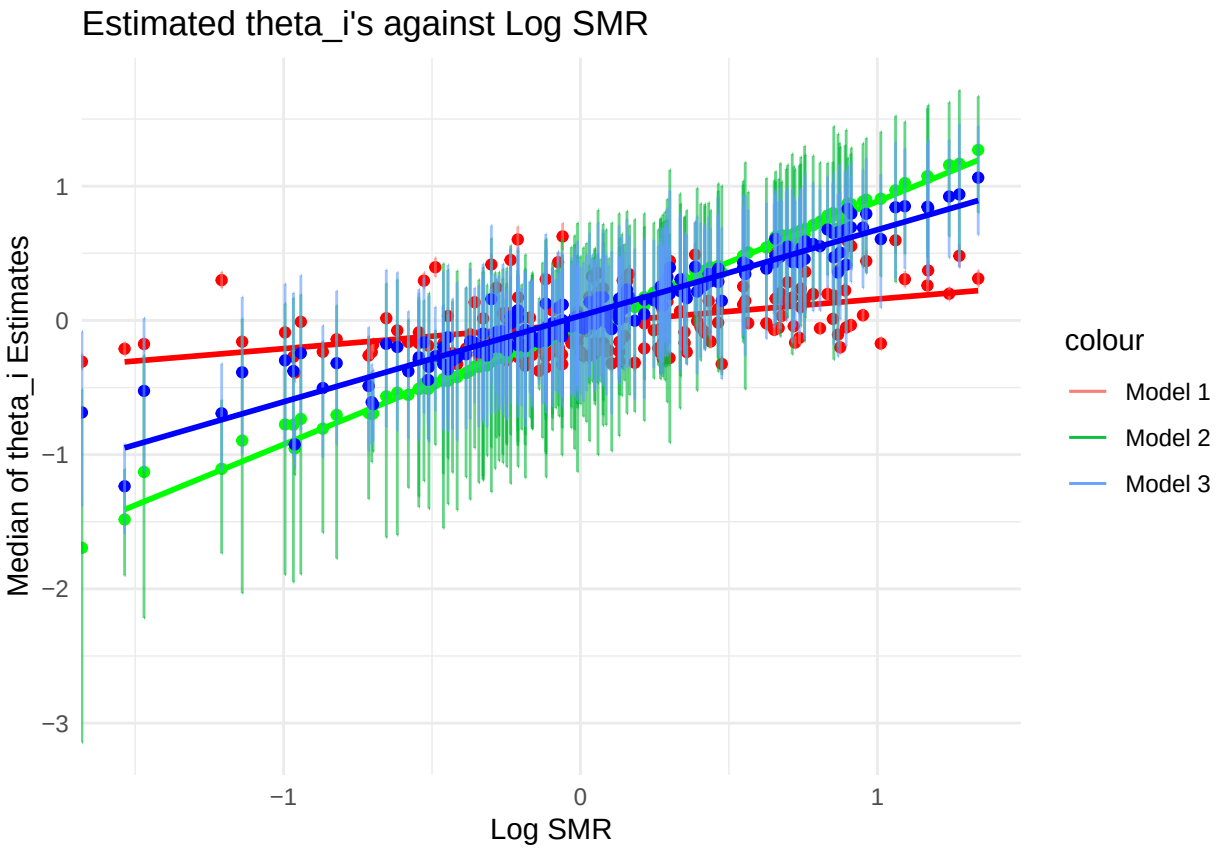
```
## # A tibble: 6 x 10
##       i median~1 lower~2 upper~3 media~4 lower~5 upper~6 media~7 lower~8 upper~9
##   <int>    <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
## 1     1    0.171  0.123    0.220  -0.193  -1.09   0.520   0.0188  -0.560   0.544
## 2     2    0.146  0.0988   0.192   0.384  -0.199  0.877   0.346   -0.112   0.773
## 3     3    0.554  0.464    0.644   0.866   0.388  1.29    0.795    0.380   1.18
## 4     4    0.307  0.247    0.368  -0.113  -0.979  0.598   0.125   -0.455   0.644
## 5     5    0.376  0.307    0.445   0.788   0.115  1.32    0.661    0.110   1.16
## 6     6    0.396  0.325    0.467  -0.467  -0.928 -0.0736 -0.267   -0.673   0.100
## # ... with abbreviated variable names 1: median_mod1, 2: lower_mod1,
## #   3: upper_mod1, 4: median_mod2, 5: lower_mod2, 6: upper_mod2,
## #   7: median_mod3, 8: lower_mod3, 9: upper_mod3
```

```r
res9 %>%
  dplyr::select(median_mod1, median_mod2, median_mod3) %>%
  rename("Model 1" = median_mod1, "Model 2" = median_mod2, "Model 3" = median_mod3) %>%
  pivot_longer(1:3, names_to = "Model", values_to = "log_theta_i") %>%
  #mutate(model = str_remove(model, "median_")) %>%
  ggplot(aes(log_theta_i, fill = Model)) +
  geom_histogram(position = "dodge") +
  labs(title = "distriibution of Estimated Theta_i's across Models", x = "Log theta", y = "Count") +
  theme(plot.title = element_text(hjust = 0.5, size=11)) +
  theme_minimal()
```



As we can see in our first plot, each model has a slightly different distribution of their estimates for theta. Firstly, we see that for model 1, this has the tightest distribution, with very high masses around 0, and peaking just below 0. From model 2, we see the widest distribution, as estimates reach further out on either end, but still with a significant mass around its center at 0. Lastly, in model 3, we see a high mass around 0 again at its center, but with a medium level of variance just between models 1 and 3.

```
res9 %>%
  mutate(log_smr = log(observe.i/expect.i), aff = aff.i) %>%
  ggplot(aes(x= log_smr, y = median_mod1)) +
  geom_point(color = "red") +
  geom_errorbar(aes(ymin=lower_mod1, ymax=upper_mod1, color = "Model 1"), alpha=0.6) +
  geom_smooth( method = lm, color = "red", se=FALSE) +
  geom_point(aes(y = median_mod2), color = "green")  +
  geom_errorbar(aes(ymin=lower_mod2, ymax=upper_mod2, color= "Model 2"), alpha=0.6) +
  geom_smooth(aes(x = log_smr, y = median_mod2), method = lm, color = "green", se=FALSE) +
  geom_point(aes(y = median_mod3), color =  "blue") +
  geom_errorbar(aes(ymin=lower_mod3, ymax=upper_mod3, color= "Model 3"), alpha=0.6) +
  geom_smooth(aes(x = log_smr, y = median_mod3), method = lm, color = "blue", se=FALSE) +
  labs(title = "Estimated theta_i's against Log SMR", x = "Log SMR", y="Median of theta_i Estimates") +
  theme_minimal()
```



In our next plot, we compare the estimated thetas from each model against the log smr values. We have also included lines of best fit for these estimates to more clearly interpret their trends. As we can see, each model has significantly different characteristics. Model 1 has the highest intercept, but a very shallow slope, whereas model 2 has the lowest intercept, but the steepest slope. Again, we see model 3 sitting in the middle, with an intercept and slope that are both estimated between those from models 1 and 3. We can also see the clear difference in variance of our estimates as we compare the error bars on each model, where model 1 again has the lowest variance, model 2 the highest, and model 3 sitting just slightly lower than model 2.