App stat 2 lab9

Lip cancer

Here is the lip cancer data that was used in the lecture.

- `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 16, what does this mean?

The `expect.i` variable represents the number of deaths from lip cancer that would be expected in a specific region, based on its demographic composition and the national mortality rates for lip cancer by age group. In other words, if a region has an `expect.i` value of 16, it means that, given this region has the same age specific mortality rate at the national level, we would predict 16 lip cancer deaths in this region.

Question 2

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

1. Intercept α_i is same in each region $= \alpha$
2. Intercept α_i is different in each region and modeled separately
3. Intercept α_i is different in each region and the intercept is modeled hierarchically

Note in all three cases, use the proportion of male population working outside in each region as a covariate.

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

Model1

$$\log \theta_i = \alpha + \beta x_i$$
$$\alpha \sim N(0,1)$$

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.2     v readr     2.1.4
v forcats   1.0.0     v stringr   1.5.0
v ggplot2   3.4.2     v tibble    3.2.1
v lubridate 1.9.2     v tidyr     1.3.0
v purrr     1.0.1
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becom
```

```
library(rstan)
```

```
Loading required package: StanHeaders

rstan version 2.32.5 (Stan version 2.32.2)

For execution on a local, multicore CPU with excess RAM we recommend calling
options(mc.cores = parallel::detectCores()).
To avoid recompilation of unchanged Stan programs, we recommend calling
rstan_options(auto_write = TRUE)
For within-chain threading using `reduce_sum()` or `map_rect()` Stan functions,
change `threads_per_chain` option:
rstan_options(threads_per_chain = 1)


Attaching package: 'rstan'

The following object is masked from 'package:tidyr':
```

extract

```r
library(tidybayes)

stan_data <- list(y=observe.i,
             log_e=log(expect.i),
             N=length(observe.i),
             x=aff.i-mean(aff.i)) # Centering
mod1=stan(data=stan_data, file="code/models/lab9_mod1.stan")
```

```
Warning in readLines(file, warn = TRUE): incomplete final line found on
'/Users/euijinbaek/STA2201/labs/code/models/lab9_mod1.stan'
```

```
Trying to compile a simple C file
```

```
Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
using C compiler: ‘Apple clang version 15.0.0 (clang-1500.1.0.2.5)’
using SDK: ‘MacOSX14.2.sdk’
clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG   -I"/Libra
In file included from <built-in>:1:
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/S
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R
/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/
namespace Eigen {
^
/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/
namespace Eigen {
               ^
               ;
In file included from <built-in>:1:
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/S
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R
/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/
#include <complex>
         ^~~~~~~~~
3 errors generated.
make: *** [foo.o] Error 1

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
```

```
Chain 1:
Chain 1: Gradient evaluation took 2.5e-05 seconds
Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.25 seconds.
Chain 1: Adjust your expectations accordingly!
Chain 1:
Chain 1:
Chain 1: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 1: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 1: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 1: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 1: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 1: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 1: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 1: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 1: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 1: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 1: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 1: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 1:
Chain 1:  Elapsed Time: 0.026 seconds (Warm-up)
Chain 1:                0.023 seconds (Sampling)
Chain 1:                0.049 seconds (Total)
Chain 1:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 2).
Chain 2:
Chain 2: Gradient evaluation took 5e-06 seconds
Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.05 seconds.
Chain 2: Adjust your expectations accordingly!
Chain 2:
Chain 2:
Chain 2: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 2: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 2: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 2: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 2: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 2: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 2: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 2: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 2: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 2: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 2: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 2: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 2:
Chain 2:  Elapsed Time: 0.029 seconds (Warm-up)
Chain 2:                0.026 seconds (Sampling)
Chain 2:                0.055 seconds (Total)
Chain 2:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 3).
Chain 3:
Chain 3: Gradient evaluation took 5e-06 seconds
Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.05 seconds.
Chain 3: Adjust your expectations accordingly!
Chain 3:
Chain 3:
Chain 3: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 3: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 3: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 3: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 3: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 3: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 3: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 3: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 3: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 3: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 3: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 3: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 3:
Chain 3:  Elapsed Time: 0.028 seconds (Warm-up)
Chain 3:                0.026 seconds (Sampling)
Chain 3:                0.054 seconds (Total)
Chain 3:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 4).
Chain 4:
Chain 4: Gradient evaluation took 9e-06 seconds
Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.09 seconds.
Chain 4: Adjust your expectations accordingly!
Chain 4:
Chain 4:
Chain 4: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 4: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 4: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 4: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 4: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 4: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 4: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 4: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 4: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 4: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 4: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 4: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 4: 
Chain 4:  Elapsed Time: 0.029 seconds (Warm-up)
Chain 4:                0.024 seconds (Sampling)
Chain 4:                0.053 seconds (Total)
Chain 4: 
```

Model 2

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

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

```r
mod2 = stan(data=stan_data,
            file="code/models/lab9_mod2.stan")
```

```
Warning in readLines(file, warn = TRUE): incomplete final line found on
'/Users/euijinbaek/STA2201/labs/code/models/lab9_mod2.stan'
```

```
Trying to compile a simple C file
```

```
Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
using C compiler: ‘Apple clang version 15.0.0 (clang-1500.1.0.2.5)’
using SDK: ‘MacOSX14.2.sdk’
clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG   -I"/Libra
In file included from <built-in>:1:
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/S
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R
/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/
namespace Eigen {
^
/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/
namespace Eigen {
               ^
               ;
In file included from <built-in>:1:
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/S
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R
/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/
#include <complex>
         ^~~~~~~~~
3 errors generated.
make: *** [foo.o] Error 1

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
Chain 1:
Chain 1: Gradient evaluation took 4.6e-05 seconds
Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.46 seconds.
Chain 1: Adjust your expectations accordingly!
Chain 1:
Chain 1:
Chain 1: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 1: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 1: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 1: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 1: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 1: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 1: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 1: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 1: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 1: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 1: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 1: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 1:
Chain 1:  Elapsed Time: 0.143 seconds (Warm-up)
Chain 1:                0.134 seconds (Sampling)
Chain 1:                0.277 seconds (Total)
Chain 1:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 2).
Chain 2:
Chain 2: Gradient evaluation took 9e-06 seconds
Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.09 seconds.
Chain 2: Adjust your expectations accordingly!
Chain 2:
Chain 2:
Chain 2: Iteration:    1 / 2000 [  0%]  (Warmup)
```

```
Chain 2: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 2: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 2: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 2: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 2: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 2: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 2: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 2: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 2: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 2: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 2: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 2:
Chain 2:  Elapsed Time: 0.145 seconds (Warm-up)
Chain 2:                0.132 seconds (Sampling)
Chain 2:                0.277 seconds (Total)
Chain 2:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 3).
Chain 3:
Chain 3: Gradient evaluation took 7e-06 seconds
Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.07 seconds.
Chain 3: Adjust your expectations accordingly!
Chain 3:
Chain 3:
Chain 3: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 3: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 3: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 3: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 3: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 3: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 3: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 3: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 3: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 3: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 3: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 3: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 3:
Chain 3:  Elapsed Time: 0.137 seconds (Warm-up)
Chain 3:                0.133 seconds (Sampling)
Chain 3:                0.27 seconds (Total)
Chain 3:

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 4).
```

```
Chain 4:
Chain 4: Gradient evaluation took 7e-06 seconds
Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.07 seconds.
Chain 4: Adjust your expectations accordingly!
Chain 4:
Chain 4:
Chain 4: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 4: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 4: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 4: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 4: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 4: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 4: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 4: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 4: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 4: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 4: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 4: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 4:
Chain 4:  Elapsed Time: 0.149 seconds (Warm-up)
Chain 4:                0.134 seconds (Sampling)
Chain 4:                0.283 seconds (Total)
Chain 4:
```

Model 3

$$\log \theta_i = \alpha_i + \beta x_i$$
$$\alpha_i \sim N(\mu, \sigma^2)$$

```
mod3 = stan(data=stan_data,
            file="code/models/lab9_mod3.stan")
```

```
Trying to compile a simple C file
```

```
Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
using C compiler: ‘Apple clang version 15.0.0 (clang-1500.1.0.2.5)’
using SDK: ‘MacOSX14.2.sdk’
clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG   -I"/Libra
In file included from <built-in>:1:
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/S
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R
/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/
namespace Eigen {
^
/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/
namespace Eigen {
               ^
               ;
In file included from <built-in>:1:
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/S
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R
/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/
#include <complex>
         ^~~~~~~~~
3 errors generated.
make: *** [foo.o] Error 1

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
Chain 1:
Chain 1: Gradient evaluation took 4.2e-05 seconds
Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.42 seconds.
Chain 1: Adjust your expectations accordingly!
Chain 1:
Chain 1:
Chain 1: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 1: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 1: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 1: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 1: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 1: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 1: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 1: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 1: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 1: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 1: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 1: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 1:
Chain 1:  Elapsed Time: 0.154 seconds (Warm-up)
Chain 1:                0.137 seconds (Sampling)
Chain 1:                0.291 seconds (Total)
Chain 1:
```

```
SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 2).
Chain 2: 
Chain 2: Gradient evaluation took 1e-05 seconds
Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.1 seconds.
Chain 2: Adjust your expectations accordingly!
Chain 2: 
Chain 2: 
Chain 2: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 2: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 2: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 2: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 2: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 2: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 2: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 2: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 2: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 2: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 2: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 2: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 2: 
Chain 2:  Elapsed Time: 0.149 seconds (Warm-up)
Chain 2:                0.137 seconds (Sampling)
Chain 2:                0.286 seconds (Total)
Chain 2: 

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 3).
Chain 3: 
Chain 3: Gradient evaluation took 7e-06 seconds
Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.07 seconds.
Chain 3: Adjust your expectations accordingly!
Chain 3: 
Chain 3: 
Chain 3: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 3: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 3: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 3: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 3: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 3: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 3: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 3: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 3: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 3: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 3: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 3: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 3: 
Chain 3:  Elapsed Time: 0.155 seconds (Warm-up)
Chain 3:                0.137 seconds (Sampling)
Chain 3:                0.292 seconds (Total)
Chain 3: 

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 4).
Chain 4: 
Chain 4: Gradient evaluation took 7e-06 seconds
Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.07 seconds.
Chain 4: Adjust your expectations accordingly!
Chain 4: 
Chain 4: 
Chain 4: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 4: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 4: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 4: Iteration:  600 / 2000 [ 30%]  (Warmup)
Chain 4: Iteration:  800 / 2000 [ 40%]  (Warmup)
Chain 4: Iteration: 1000 / 2000 [ 50%]  (Warmup)
Chain 4: Iteration: 1001 / 2000 [ 50%]  (Sampling)
Chain 4: Iteration: 1200 / 2000 [ 60%]  (Sampling)
Chain 4: Iteration: 1400 / 2000 [ 70%]  (Sampling)
Chain 4: Iteration: 1600 / 2000 [ 80%]  (Sampling)
Chain 4: Iteration: 1800 / 2000 [ 90%]  (Sampling)
Chain 4: Iteration: 2000 / 2000 [100%]  (Sampling)
Chain 4: 
Chain 4:  Elapsed Time: 0.153 seconds (Warm-up)
Chain 4:                0.137 seconds (Sampling)
Chain 4:                0.29 seconds (Total)
Chain 4: 
```

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.

We generate two plots to compare the estimated relative risks (θ_i) across different regions and to visualize how these estimates differ across the three models.

First, we aggregate results from the three models. For each model, we gather draws of the logarithm of θ_i (log_theta[i]), calculate their median and a credible interval (quantile interval), and then rename and select relevant columns for further analysis:

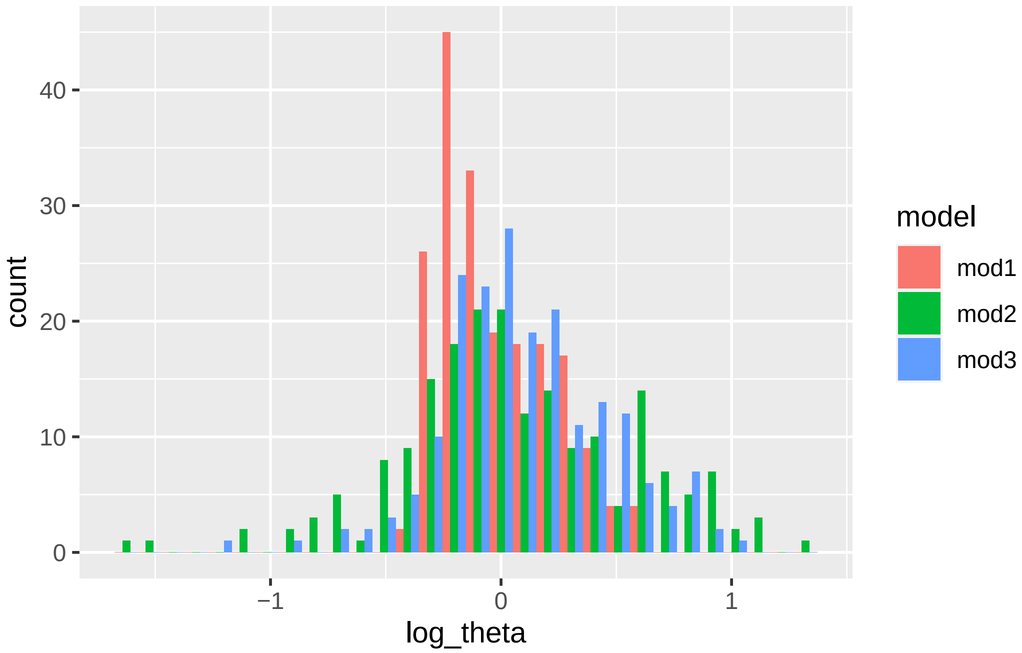
```r
# Aggregate results from models 1, 2, and 3
res_mod1 <- mod1 |>
  gather_draws(log_theta[i]) |>
  median_qi() |>
  rename(median_mod1 = .value,
         lower_mod1 = .lower,
         upper_mod1 = .upper) |>
  select(i, median_mod1:upper_mod1)

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)
```

```
Joining with `by = join_by(i)`
Joining with `by = join_by(i)`
```

Next, we create a histogram to display the distribution of median log_theta estimates for each model. This plot allows us to visualize the spread and central tendency of the estimates across models:

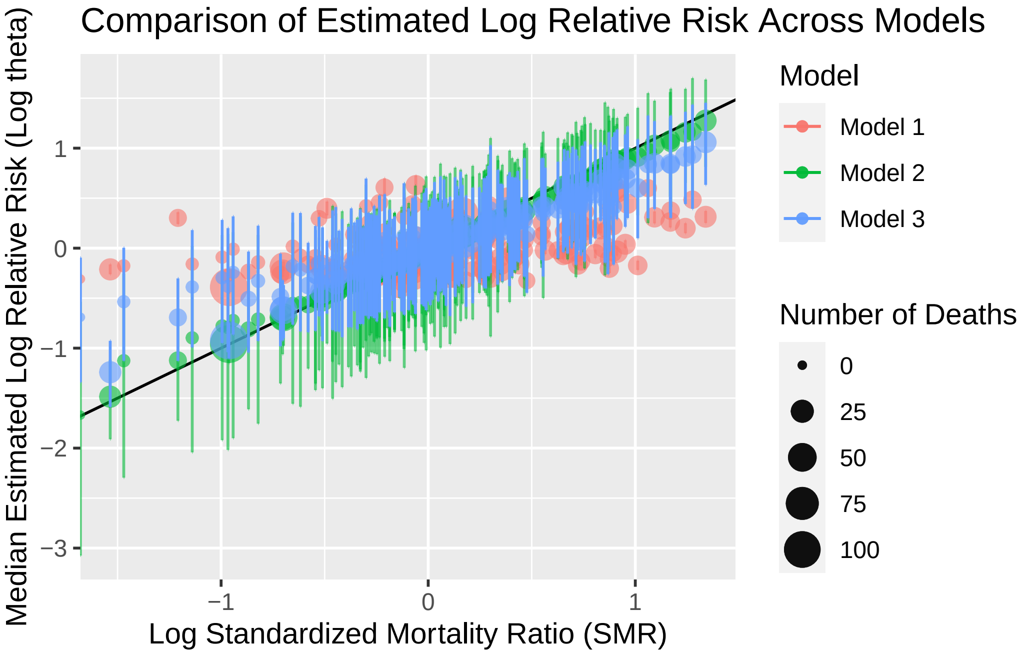
```r
# Histogram of median log_theta estimates for each model
res |>
  select(median_mod1, median_mod2, median_mod3) |>
  pivot_longer(median_mod1:median_mod3, names_to = "model", values_to = "log_theta") |>
  mutate(model = str_remove(model, "median_")) |>
  ggplot(aes(log_theta, fill = model)) +
  geom_histogram(position = "dodge")
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Finally, we plot the medians of simulated log_theta values against the log of the standardized mortality ratio (SMR) for each region. The size of the points reflects the number of observed deaths, providing insight into the relationship between the estimated and observed relative risks:

```
# Scatter plot of median log_theta vs. log SMR, with error bars and point sizes based on o
res |>
  mutate(deaths = observe.i) |>
  mutate(log_smr = log(observe.i / expect.i)) |>
  ggplot(aes(log_smr, median_mod1, color = "Model 1")) +
  geom_point(aes(size = deaths), alpha = 0.6) +
  geom_errorbar(aes(ymin = lower_mod1, ymax = upper_mod1, color = "Model 1"), alpha = 0.6)
  geom_abline(slope = 1, intercept = 0) +
  geom_point(aes(log_smr, median_mod2, color = "Model 2", size = deaths), alpha = 0.6) +
  geom_errorbar(aes(ymin = lower_mod2, ymax = upper_mod2, color = "Model 2"), alpha = 0.6)
  geom_point(aes(log_smr, median_mod3, color = "Model 3", size = deaths), alpha = 0.6) +
  geom_errorbar(aes(ymin = lower_mod3, ymax = upper_mod3, color = "Model 3")) +
  labs(
    title = "Comparison of Estimated Log Relative Risk Across Models",
    x = "Log Standardized Mortality Ratio (SMR)",
    y = "Median Estimated Log Relative Risk (Log theta)",
    color = "Model",
    size = "Number of Deaths"
  )
```



Question 4

Using tool of your choice, decide which model is the best, and justify your choice.

Based on the plots in Question 3, we could determine which model is the best.

Fit to Data: Model 2 (green) points on the scatter plot are generally closer to the black line compared to Models 1 and 3. This suggests Model 2 might have a better fit to the observed data since its estimates are closer to the line of perfect agreement.

Consistency: Model 2 also appears to show a consistent spread of estimates across the range of log SMR values, which might indicate it captures the variability in the data without overfitting or underfitting.

Distribution of Estimates: The histogram shows that Model 2's estimates are more centrally distributed around zero, indicating less bias in the estimates. Model 1 has a distribution with a noticeable peak, and Model 3 shows a more uniform distribution, possibly indicating more variability.

Taking these observations into account, Model 2 might be considered the best out of the three because it appears to provide a balance between fit to the observed data and consistency of estimates across regions.