

# Hierarchical GLM

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PLEASE HAND IN RMD, PDF AND STAN MODELS!!!!

## 1 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)
```

## 1.1 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: The expected death is the death number calculated by the age distribution of the target example times the mortality rate of the whole population. If a particular area has an expected deaths of 6, which means if there are no special circumstances, this area should have an appoxiamatly 6 deaths among all the people.

## 1.2 Question 2

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

1.  $\theta_i$  is same in each region =  $\theta$
2.  $\theta_i$  is different in each region and modeled separately
3.  $\theta_i$  is different in each region and modeled hierarchically

```
x <- aff.i - mean(aff.i)
offset <- expect.i
deaths <- observe.i
N <- length(x)
```

```
data <- list(x = x,
            offset = offset,
            deaths = deaths,
            N = N)
```

```
fit1 <- stan(file = "./case1.stan", data = data)
```

```
## Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
## clang -mmacosx-version-min=10.13 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG -I
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/StanHeaders/inc
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/inclu
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/inclu
## /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/include/Eigen/src/Core/util
## namespace Eigen {
## ^
## /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/include/Eigen/src/Core/util
## namespace Eigen {
## ^
## ;
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/StanHeaders/inc
```

```

## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/include/Eigen/Core:96:10: f
## /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/include/Eigen/Core:96:10: f
## #include <complex>
##      ~~~~~
## 3 errors generated.
## make: *** [foo.o] Error 1
##
## SAMPLING FOR MODEL 'case1' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 3e-05 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.3 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: 0.026422 seconds (Warm-up)
## Chain 1:                0.02399 seconds (Sampling)
## Chain 1:                0.050412 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL 'case1' 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: 0.024795 seconds (Warm-up)
## Chain 2:                0.022938 seconds (Sampling)

```

```

## Chain 2:          0.047733 seconds (Total)
## Chain 2:
##
## SAMPLING FOR MODEL 'case1' NOW (CHAIN 3).
## Chain 3:
## Chain 3: Gradient evaluation took 1.6e-05 seconds
## Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.16 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: 0.027778 seconds (Warm-up)
## Chain 3:          0.027143 seconds (Sampling)
## Chain 3:          0.054921 seconds (Total)
## Chain 3:
##
## SAMPLING FOR MODEL 'case1' NOW (CHAIN 4).
## Chain 4:
## Chain 4: Gradient evaluation took 1e-05 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.1 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: 0.027631 seconds (Warm-up)
## Chain 4:          0.023047 seconds (Sampling)
## Chain 4:          0.050678 seconds (Total)
## Chain 4:

```

```
summary(fit1)$summary[c("theta"),]
```

```
##           mean      se_mean      sd      2.5%      25%      50%
## 9.539957e-01 5.526801e-04 1.956073e-02 9.152893e-01 9.409703e-01 9.541151e-01
##           75%      97.5%      n_eff      Rhat
## 9.671937e-01 9.909394e-01 1.252630e+03 1.000762e+00
```

```
x <- aff.i - mean(aff.i)
offset <- expect.i
deaths <- observe.i
N <- length(x)
```

```
data <- list(x = x,
             offset = offset,
             deaths = deaths,
             N = N)
```

```
fit2 <- stan(file = "./case2.stan", data = data)
```

```
## Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
## clang -mmacosx-version-min=10.13 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG -I
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/StanHeaders/inc
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/inclu
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/inclu
## /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/include/Eigen/src/Core/util
## namespace Eigen {
## ~
## /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/include/Eigen/src/Core/util
## namespace Eigen {
## ~
## ;
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/StanHeaders/inc
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/inclu
## /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/include/Eigen/Core:96:10: f
## #include <complex>
## ~~~~~
## 3 errors generated.
## make: *** [foo.o] Error 1
##
## SAMPLING FOR MODEL 'case2' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 4.5e-05 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.45 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: 0.268331 seconds (Warm-up)
## Chain 1: 0.273694 seconds (Sampling)
## Chain 1: 0.542025 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL 'case2' NOW (CHAIN 2).
## Chain 2:
## Chain 2: Gradient evaluation took 1.7e-05 seconds
## Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.17 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: 0.267178 seconds (Warm-up)
## Chain 2: 0.274066 seconds (Sampling)
## Chain 2: 0.541244 seconds (Total)
## Chain 2:
##
## SAMPLING FOR MODEL 'case2' NOW (CHAIN 3).
## Chain 3:
## Chain 3: Gradient evaluation took 2e-05 seconds
## Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.2 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: 0.267606 seconds (Warm-up)
## Chain 3: 0.272564 seconds (Sampling)
## Chain 3: 0.54017 seconds (Total)
## Chain 3:
##
## SAMPLING FOR MODEL 'case2' NOW (CHAIN 4).
## Chain 4:
## Chain 4: Gradient evaluation took 1.6e-05 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.16 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: 0.25963 seconds (Warm-up)
## Chain 4: 0.272942 seconds (Sampling)
## Chain 4: 0.532572 seconds (Total)
## Chain 4:

```

```
summary(fit2)$summary[c(1:5),]
```

```

##           mean      se_mean      sd      2.5%      25%      50%      75%
## theta[1] 0.8404790 0.003295185 0.3184172 0.3316046 0.6133308 0.8019298 1.034929
## theta[2] 1.4162826 0.003699631 0.3447225 0.8014737 1.1722070 1.3906796 1.630296
## theta[3] 2.0341961 0.004084921 0.4269127 1.2912206 1.7314186 2.0060018 2.306883
## theta[4] 0.8997405 0.003448001 0.3408440 0.3409785 0.6542481 0.8583188 1.109165
## theta[5] 1.7982589 0.005008526 0.4747770 0.9617516 1.4465108 1.7646491 2.119309
##           97.5%      n_eff      Rhat
## theta[1] 1.563217 9337.561 0.9996738
## theta[2] 2.167726 8682.049 0.9992120
## theta[3] 2.953697 10922.216 0.9991428
## theta[4] 1.665766 9771.850 0.9993418
## theta[5] 2.807244 8985.857 0.9996245

```

```

x <- aff.i - mean(aff.i)
offset <- log(expect.i)
deaths <- observe.i
N <- length(x)

data <- list(x = x,
             offset = offset,

```

```

        deaths = deaths,
        N = N)

fit3 <- stan(file = "./case3.stan", data = data)

## Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c
## clang -mmacosx-version-min=10.13 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG -I
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/StanHeaders/inc
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/inclu
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/inclu
## /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/include/Eigen/src/Core/util
## namespace Eigen {
## ~
## /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/include/Eigen/src/Core/util
## namespace Eigen {
## ~
## ~
## In file included from <built-in>:1:
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/StanHeaders/inc
## In file included from /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/inclu
## /Library/Frameworks/R.framework/Versions/4.0/Resources/library/RcppEigen/include/Eigen/Core:96:10: f
## #include <complex>
## ~~~~~
## 3 errors generated.
## make: *** [foo.o] Error 1
##
## SAMPLING FOR MODEL 'case3' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 4.9e-05 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.49 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: 0.304049 seconds (Warm-up)
## Chain 1: 0.278505 seconds (Sampling)
## Chain 1: 0.582554 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL 'case3' NOW (CHAIN 2).
## Chain 2:

```



```

## Chain 2: Gradient evaluation took 1.8e-05 seconds
## Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.18 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: 0.309853 seconds (Warm-up)
## Chain 2:                0.27755 seconds (Sampling)
## Chain 2:                0.587403 seconds (Total)
## Chain 2:
##
## SAMPLING FOR MODEL 'case3' NOW (CHAIN 3).
## Chain 3:
## Chain 3: Gradient evaluation took 1.8e-05 seconds
## Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.18 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: 0.297046 seconds (Warm-up)
## Chain 3:                0.272104 seconds (Sampling)
## Chain 3:                0.56915 seconds (Total)
## Chain 3:
##
## SAMPLING FOR MODEL 'case3' NOW (CHAIN 4).
## Chain 4:
## Chain 4: Gradient evaluation took 2.7e-05 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.27 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: 0.305171 seconds (Warm-up)
## Chain 4: 0.272774 seconds (Sampling)
## Chain 4: 0.577945 seconds (Total)
## Chain 4:
```

```
param <- extract(fit3)
summary(fit3)$summary[c(1:5),]
```

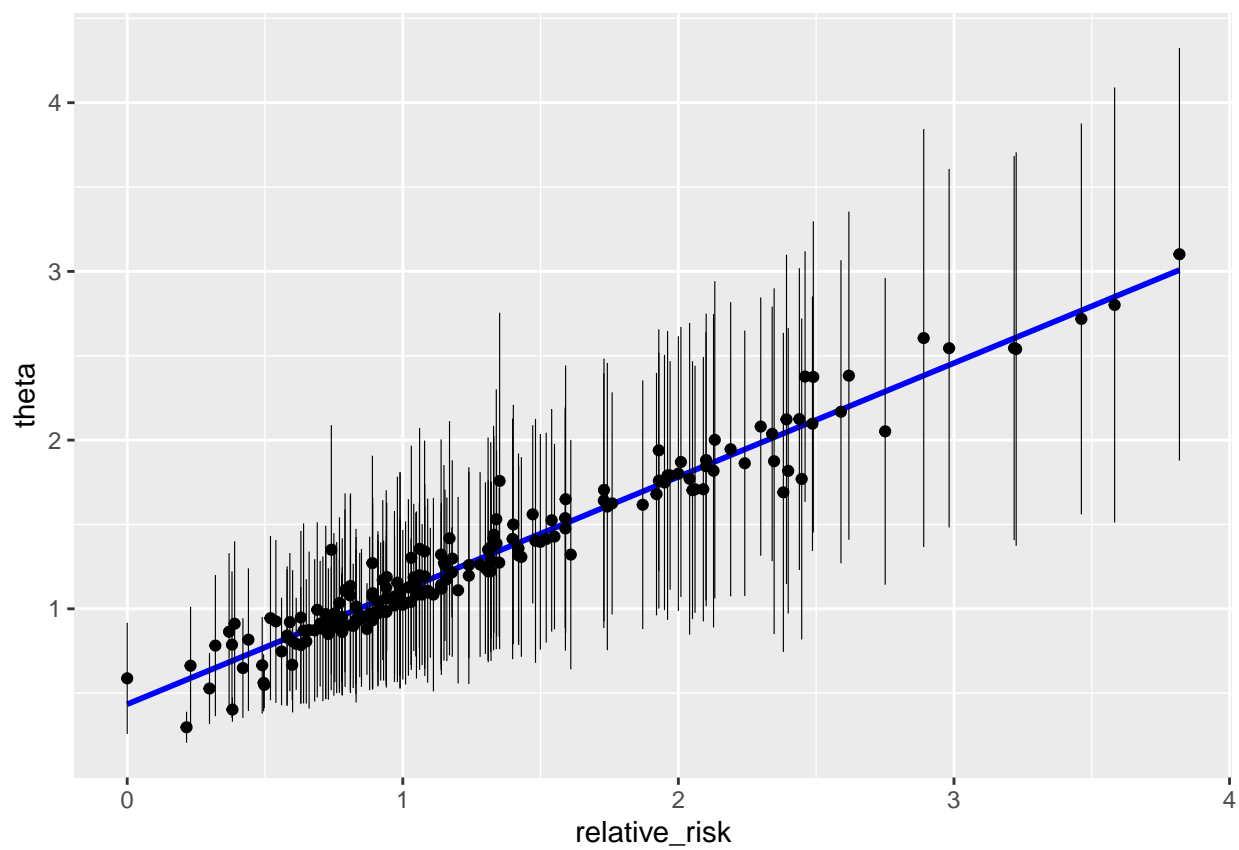
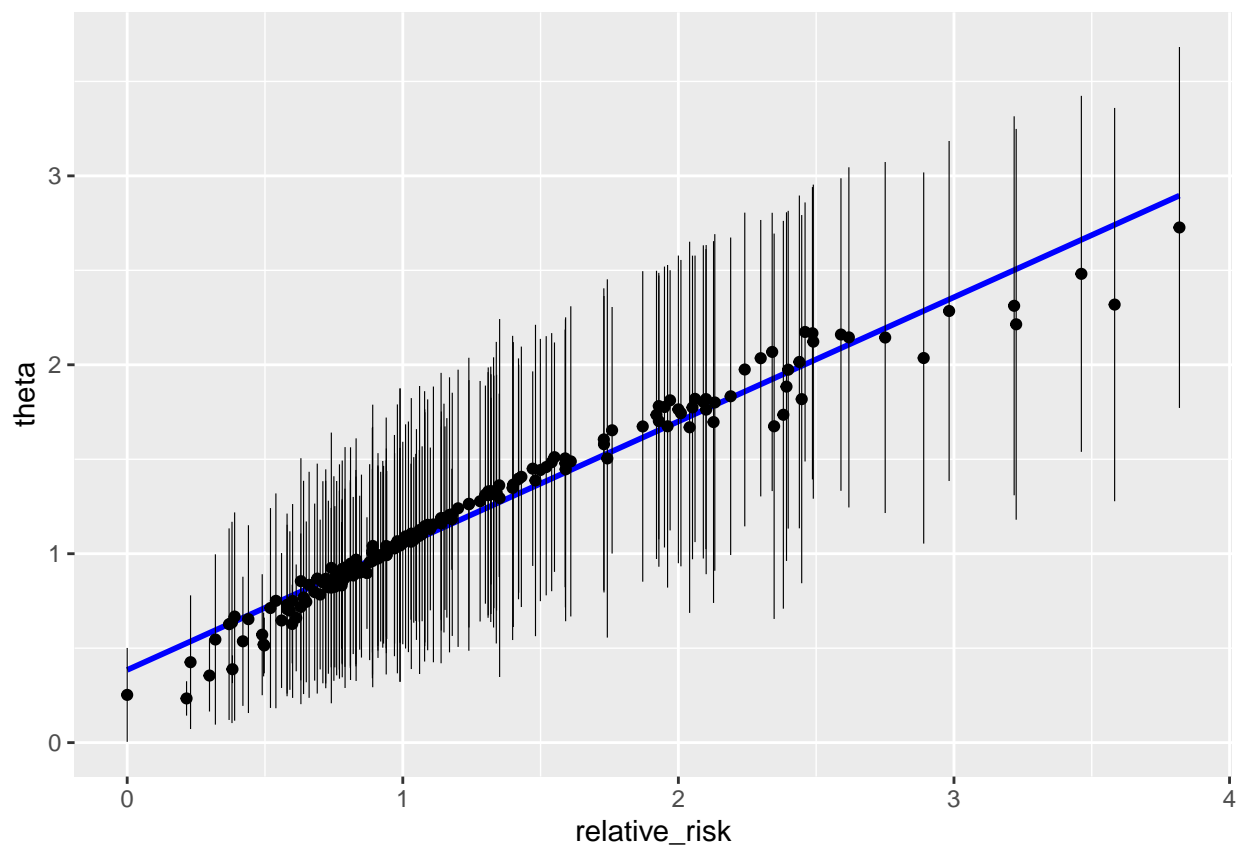
##	mean	se_mean	sd	2.5%	25%	50%
## alpha[1]	-0.1314888	0.002753668	0.2722248	-0.6775428	-0.31273193	-0.1224897
## alpha[2]	0.2138706	0.002371783	0.2351834	-0.2651069	0.06573769	0.2186241
## alpha[3]	0.3356703	0.002539494	0.2154841	-0.1014081	0.19521470	0.3385879
## alpha[4]	-0.1487320	0.002952479	0.2772856	-0.7188995	-0.33121380	-0.1426641
## alpha[5]	0.3361968	0.002826871	0.2590396	-0.1861158	0.16789635	0.3441852
##	75%	97.5%	n_eff	Rhat		
## alpha[1]	0.05309756	0.3789161	9773.099	0.9992542		
## alpha[2]	0.37215742	0.6520526	9832.490	0.9995823		
## alpha[3]	0.48467826	0.7460675	7200.059	0.9994568		
## alpha[4]	0.04117453	0.3838319	8820.252	0.9993052		
## alpha[5]	0.51377329	0.8198201	8396.926	0.9994183		

### 1.3 Question 3

Make three plots (appropriately labeled and described) that illustrate the differences in estimated  $\theta_i$ 's across regions and the differences in  $\theta$ s across models.

- Answer: For the first graph. We plot the sample distribution of 195 different independent theta for the second models. The y axis are the distribution of theta and the x axis are the relative risks.

For the Second graph. We plot the sample distribution of the third models. The x axis and the y axis are the same definition as above. For plot 1&2 we could see the differences between region and their relative risks.



- On the third plot we could plot the estimation of theta from three models on the same graph. The black line indicate the estimation of theta from model 1(no pooling, same value for all theta). We could see the hierarchical model (model 3, half pooling) has a better estimation(more concentrated) than separate model (model 2, complete pooling) .

