Supplement 1 – Model Code

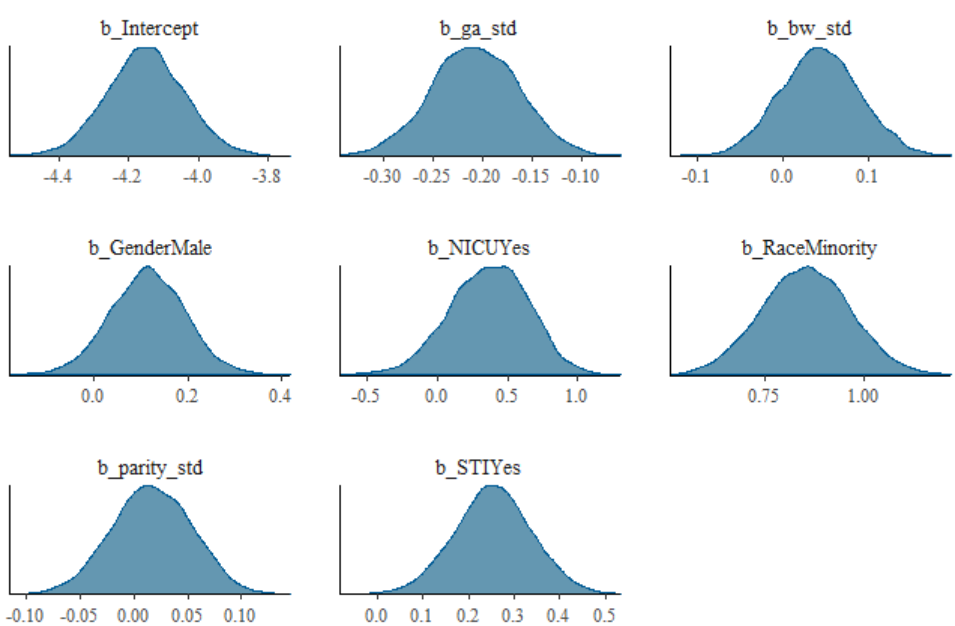
The analyses we present in this paper were performed using *brms*, an R package that delivers models to the Markov chain Monte Carlo sampler Stan. The model variables are:

ga_std = gestational age (standardized and centered around 0)
bw_std = birth weight (standardized and centered around 0)
parity_std = maternal parity (standardized and centered around 0)
Gender (reference level = Female)
Race (reference level = non-Hispanic white)
NICU (reference level = no)
STI = maternal STI (reference level = no)

Nonspatial Models

These models are shown to illustrate the syntax used to assess non-spatial predictor variables.

```
> Model1 <- brm(Result ~ ga_std + bw_std + Gender + NICU + Race + parity_std + STI,
family="Bernoulli", data=dat)
> summary(Model1)

Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup samples = 4000

Population-Level Effects:
              Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
Intercept        -4.15      0.11    -4.37    -3.93       3197    1
ga_std           -0.21      0.04    -0.29    -0.12       3584    1
bw_std            0.04      0.05    -0.04     0.13       3491    1
GenderMale        0.11      0.08    -0.04     0.28       4000    1
NICUYes           0.37      0.28    -0.21     0.89       4000    1
RaceMinority      0.85      0.11     0.63     1.07       3549    1
parity_std        0.02      0.04    -0.06     0.09       4000    1
STIYes            0.25      0.08     0.09     0.42       4000    1

> stanplot(Model1, type="dens")  ## Note that interval plots are presented in the paper
```



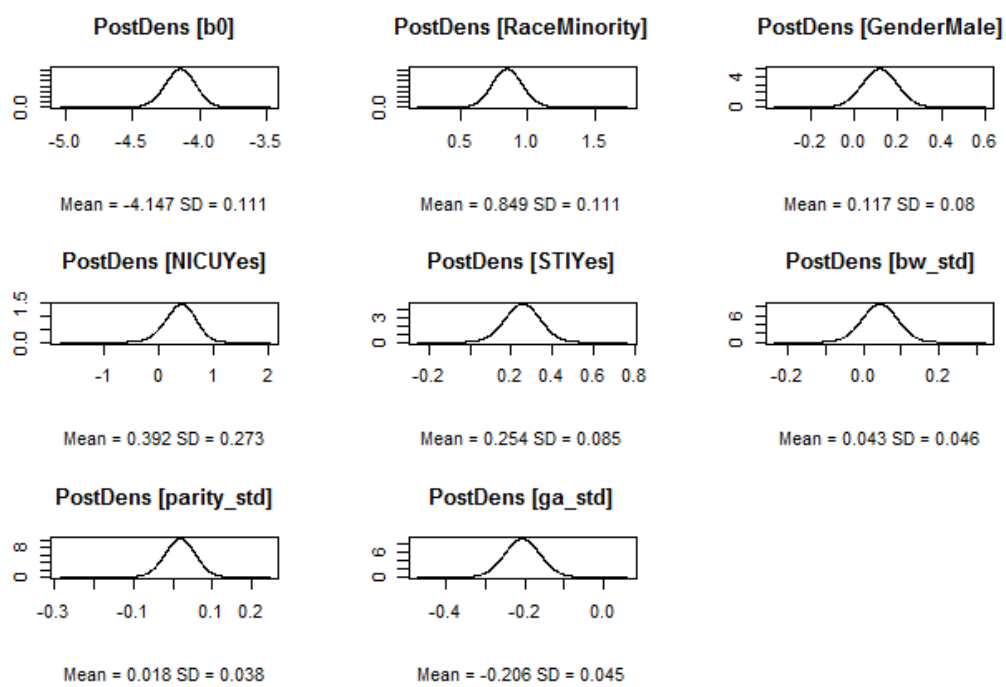
We additionally ran models using different estimation methods to confirm the important predictors of hearing loss. Here we show two models, first using standard frequentist logistic regression, and second using the novel Bayesian estimation method INLA (integrated nested Laplace approximation). These show close concordance with the results of our Markov chain Monte Carlo-based methods presented in this paper.

Logistic Regression

```
> glm1 <- glm(Result ~ Race + Gender + NICU + STI + bw_std + parity_std + ga_std, family=
binomial("logit"))
> summary(glm1)

Call:
glm(formula = Result ~ Race + Gender + NICU + STI + bw_std +
    parity_std + ga_std, family = binomial("logit"))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.7425  -0.2982  -0.2677  -0.1979   3.0267

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  -4.14362    0.11138 -37.203  < 2e-16 ***
RaceMinority  0.84848    0.11145   7.613 2.67e-14 ***
GenderMale    0.11730    0.07980   1.470  0.14161
NICUYes       0.39250    0.27274   1.439  0.15012
STIYes        0.25425    0.08492   2.994  0.00275 **
bw_std        0.04277    0.04638   0.922  0.35647
parity_std    0.01803    0.03809   0.473  0.63606
ga_std       -0.20636    0.04451  -4.636 3.54e-06 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

INLA

```
> table<-model.matrix(~long + lat + Race + Gender + NICU + STI + bw_std + parity_std + ga
_std, data=data)[,-1]
> formula_1 <- y ~ 0 + b0 + RaceMinority + GenderMale + NICUYes + STIYes + bw_std + parit
y_std + ga_std
> stk.est.a <- inla.stack(tag='estimation',
+                         data=list(y=data$result),
+                         A=list(1),
+                         effects=list(data.frame(b0=1,
+                                                 table)))
> model_1 <- inla(formula_1,
+                 data=inla.stack.data(stk.est.a),
+                 family="binomial",
+                 control.predictor=list(A =inla.stack.A(stk.est.a), compute=TRUE))
> summary(model_1)

Fixed effects:
               mean     sd 0.025quant 0.5quant 0.975quant    mode kld
b0          -4.1474 0.1114    -4.3709  -4.1458    -3.9332 -4.1425   0
RaceMinority 0.8488 0.1115     0.6342   0.8474     1.0718  0.8445   0
GenderMale   0.1174 0.0798    -0.0391   0.1173     0.2741  0.1172   0
NICUYes      0.3917 0.2727    -0.1751   0.4026     0.8971  0.4249   0
STIYes       0.2544 0.0849     0.0865   0.2548     0.4199  0.2556   0
bw_std       0.0429 0.0464    -0.0485   0.0431     0.1336  0.0433   0
parity_std   0.0181 0.0381    -0.0576   0.0184     0.0921  0.0190   0
ga_std      -0.2062 0.0445    -0.2933  -0.2063    -0.1186 -0.2066   0


> plot(model_1)
```



Spatial Models

This is the syntax used to assess the odds of hearing loss over space.

```
#Fit model using spline-based isotropic smoothing of coordinates
#Adjusted models are the same, but include other covariates (see above examples)
> Model2 <- brm(Result ~ s(Longitude, Latitude), family="Bernoulli", data=dat)

#Predict model to a coordinate grid
> pred1 <- fitted(Model2, grid)

#Join coordinate columns from grid to prediction
> pred1 <- cbind(grid[,1:2], pred1)

#Compute grid points where estimate is different than average with 95% confidence
> fv<-fitted(Model1, grid, summary=FALSE)
> m <- mean(fv)
> p <- colMeans(fv > m)
> pred1<-cbind(pred1, p)
> str(pred1)
'data.frame':   5921 obs. of  7 variables:
 $ Longitude: int  616173 616479 616785 615867 618315 618621 618927 619233 619233 619539
...
 $ Latitude : int  249972 249972 249972 250398 240594 240594 240594 240594 241020 241020
...
 $ Estimate : num  0.0368 0.0368 0.0369 0.0367 0.0336 ...
 $ Est.Error: num  0.00296 0.0029 0.00282 0.00313 0.00331 ...
 $ 2.5%ile  : num  0.0302 0.0304 0.0307 0.0296 0.0269 ...
 $ 97.5%ile : num  0.0419 0.0418 0.0418 0.0421 0.0402 ...
 $ p        : num  0.447 0.452 0.457 0.435 0.112 ...


#Plot results
> ggplot(pred1) +
        geom_raster(aes(long, lat, fill = Estimate))+
        scale_fill_viridis(option = "B") +
        theme_bw()+
        geom_contour(aes(x=long, y=lat, z=p), breaks=c(0.025), color="Blue",
                cex=1.2, lty=1) +
        geom_contour(aes(x=long, y=lat, z=p), breaks=c(0.975), color="Red",
                cex=1.2, lty=1)
```