Untitled

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library(pacman)  
p\_load(tidyverse, haven, broom, knitr)

workds <- read\_sav("AFPJ SPSS.sav") %>% mutate\_if(is.labelled, ~(as\_factor(.)))  
workds

## # A tibble: 240 x 26  
## ID GROUP GENDER AGE ONSET RESOLVED BW MAXBILIRUBIN GDM MINFECTION  
## <dbl> <fct> <fct> <dbl> <dbl> <fct> <dbl> <dbl> <fct> <fct>   
## 1 1 CONT~ GIRL 56 0 NO 2150 0 NO NO   
## 2 2 CONT~ GIRL 28 0 NO 3500 0 YES NO   
## 3 3 CONT~ BOY 39 0 NO 3650 0 NO NO   
## 4 4 CONT~ GIRL 58 0 NO 3160 0 NO NO   
## 5 5 CONT~ GIRL 26 0 NO 3430 0 NO NO   
## 6 6 CONT~ BOY 23 0 NO 3850 0 NO NO   
## 7 7 CONT~ GIRL 20 0 NO 3700 0 NO NO   
## 8 8 CONT~ BOY 56 0 NO 2800 0 NO NO   
## 9 9 CONT~ GIRL 33 0 NO 2290 0 NO NO   
## 10 10 CONT~ GIRL 42 0 NO 2530 0 NO NO   
## # ... with 230 more rows, and 16 more variables: OXYTOCIN <fct>,  
## # DELIVERY <fct>, FEEDING <fct>, SIBLINGS <fct>, HYPOTHYROID <fct>,  
## # G6PD <fct>, CEPHALOHEMATOMA <fct>, DELIVERY2 <fct>, BW2 <fct>, ZRE\_1 <dbl>,  
## # ZRE\_2 <dbl>, PRE\_1 <dbl>, PRE\_2 <dbl>, PRE\_3 <dbl>, PRE\_4 <dbl>,  
## # PRE\_5 <dbl>

fit1 <- glm(GROUP ~ GENDER, family = "binomial", workds)  
summary(fit1)

##   
## Call:  
## glm(formula = GROUP ~ GENDER, family = "binomial", data = workds)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.19011 -1.19011 0.00167 1.16476 1.19348   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) -0.03774 0.19429 -0.194 0.846  
## GENDERBOY 0.06759 0.26001 0.260 0.795  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 332.71 on 239 degrees of freedom  
## Residual deviance: 332.64 on 238 degrees of freedom  
## AIC: 336.64  
##   
## Number of Fisher Scoring iterations: 3

tidy(fit1, conf.int = T)

## # A tibble: 2 x 7  
## term estimate std.error statistic p.value conf.low conf.high  
## <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  
## 1 (Intercept) -0.0377 0.194 -0.194 0.846 -0.420 0.344  
## 2 GENDERBOY 0.0676 0.260 0.260 0.795 -0.442 0.578

tidy(fit1, conf.int = T) %>%   
 mutate(OR = exp(estimate),  
 llci = exp(conf.low),  
 ulci = exp(conf.high)) %>%   
 select(variable = term, coef = estimate, OR, llci, ulci, p.value)

## # A tibble: 2 x 6  
## variable coef OR llci ulci p.value  
## <chr> <dbl> <dbl> <dbl> <dbl> <dbl>  
## 1 (Intercept) -0.0377 0.963 0.657 1.41 0.846  
## 2 GENDERBOY 0.0676 1.07 0.643 1.78 0.795

fit2 <- glm(GROUP ~ AGE, family = "binomial", workds)  
summary(fit2)

##   
## Call:  
## glm(formula = GROUP ~ AGE, family = "binomial", data = workds)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.50655 -1.13468 0.03599 1.11158 1.59798   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.26342 0.41364 3.054 0.00226 \*\*  
## AGE -0.03689 0.01150 -3.207 0.00134 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 332.71 on 239 degrees of freedom  
## Residual deviance: 321.82 on 238 degrees of freedom  
## AIC: 325.82  
##   
## Number of Fisher Scoring iterations: 4

tidy(fit2, conf.int = T) %>%   
 mutate(OR = exp(estimate),  
 llci = exp(conf.low),  
 ulci = exp(conf.high)) %>%   
 select(variable = term, coef = estimate, OR, llci, ulci, p.value)

## # A tibble: 2 x 6  
## variable coef OR llci ulci p.value  
## <chr> <dbl> <dbl> <dbl> <dbl> <dbl>  
## 1 (Intercept) 1.26 3.54 1.59 8.09 0.00226  
## 2 AGE -0.0369 0.964 0.942 0.985 0.00134

fit3 <- glm(GROUP ~ BW2, family = "binomial", workds)  
summary(fit3)

##   
## Call:  
## glm(formula = GROUP ~ BW2, family = "binomial", data = workds)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.3174 -1.3174 0.1388 1.0436 1.6550   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.3232 0.1506 2.146 0.0319 \*   
## BW2SGA -1.3994 0.3348 -4.180 2.92e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 332.71 on 239 degrees of freedom  
## Residual deviance: 313.15 on 238 degrees of freedom  
## AIC: 317.15  
##   
## Number of Fisher Scoring iterations: 4

tidy(fit3, conf.int = T) %>%   
 mutate(OR = exp(estimate),  
 llci = exp(conf.low),  
 ulci = exp(conf.high)) %>%   
 select(variable = term, coef = estimate, OR, llci, ulci, p.value)

## # A tibble: 2 x 6  
## variable coef OR llci ulci p.value  
## <chr> <dbl> <dbl> <dbl> <dbl> <dbl>  
## 1 (Intercept) 0.323 1.38 1.03 1.86 0.0319   
## 2 BW2SGA -1.40 0.247 0.125 0.466 0.0000292

gender\_fit <- tidy(fit1, conf.int = T) %>%   
 mutate(OR = exp(estimate),  
 llci = exp(conf.low),  
 ulci = exp(conf.high)) %>%   
 select(variable = term, coef = estimate, OR, llci, ulci, p.value)  
  
age\_fit <- tidy(fit2, conf.int = T) %>%   
 mutate(OR = exp(estimate),  
 llci = exp(conf.low),  
 ulci = exp(conf.high)) %>%   
 select(variable = term, coef = estimate, OR, llci, ulci, p.value)  
  
bw\_fit <- tidy(fit3, conf.int = T) %>%   
 mutate(OR = exp(estimate),  
 llci = exp(conf.low),  
 ulci = exp(conf.high)) %>%   
 select(variable = term, coef = estimate, OR, llci, ulci, p.value)  
  
  
bind\_rows(gender\_fit, age\_fit, bw\_fit) %>%   
 filter(variable != "(Intercept)") %>%   
 kable()

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| variable | coef | OR | llci | ulci | p.value |
| GENDERBOY | 0.0675933 | 1.0699301 | 0.6425170 | 1.7830275 | 0.7948936 |
| AGE | -0.0368861 | 0.9637859 | 0.9417507 | 0.9853351 | 0.0013413 |
| BW2SGA | -1.3993664 | 0.2467532 | 0.1246370 | 0.4663619 | 0.0000292 |