test interaction data

August 10, 2018

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Get Glow dataset

```
glow <- read_glow_dataset()</pre>
```

model interactions - main effects

```
model_z1 <- glm(FRACTURE ~ AGE, family = binomial, data = glow)</pre>
model_z2 <- glm(FRACTURE ~ WEIGHT, family = binomial, data = glow)</pre>
model_z3 <- glm(FRACTURE ~ HEIGHT, family = binomial, data = glow)</pre>
model_z4 <- glm(FRACTURE ~ BMI, family = binomial, data = glow)</pre>
model_z5 <- glm(FRACTURE ~ PRIORFRAC, family = binomial, data = glow)</pre>
model_z6 <- glm(FRACTURE ~ PREMENO, family = binomial, data = glow)</pre>
model_z7 <- glm(FRACTURE ~ MOMFRAC, family = binomial, data = glow)</pre>
model_z8 <- glm(FRACTURE ~ ARMASSIST, family = binomial, data = glow)</pre>
model_z9 <- glm(FRACTURE ~ SMOKE, family = binomial, data = glow)</pre>
model_z10 <- glm(FRACTURE ~ RATERISK, family = binomial, data = glow)</pre>
## AGE
                0.05289
                                      4.548 5.42e-06 ***
                            0.01163
## WEIGHT
               -0.005197
                            0.006415 -0.810
## HEIGHT
               -0.05167
                            0.01709 -3.022 0.00251 **
## BMI
                0.005758
                            0.017185 0.335 0.73760
## PRIORFRACYes 1.0638
                            0.2231
                                      4.769 1.85e-06 ***
## PREMENOYes 0.05077
                            0.25921
                                      0.196
               0.6605
                            0.2810
                                      2.351
                                               0.0187 *
## MOMFRACYes
## ARMASSISTYes 0.7091
                            0.2098
                                      3.381 0.000723 ***
## SMOKEYes -0.3077
                            0.4358
                                     -0.706
                                                 0.48
                     0.5462
## RATERISKSame
                                 0.2664
                                         2.050
                                                   0.0404 *
## RATERISKGreater
                     0.9091
                                 0.2711
                                          3.353
                                                   0.0008 ***
```

> code below:

This leads us to consider the covariates above that are significant in the univariate results above at the 25% level.

AGE, HEIGHT, PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK {SAME, GREATER}

```
# fit a univariate logistic regression model for each covariate
# continuous - AGE WEIGHT HEIGHT BMI
# categorical - PRIORFRAC PREMENO MOMFRAC ARMASSIST SMOKE RATERISK
#model_z1 <- glm(FRACTURE ~ AGE, family = binomial, data = glow)</pre>
\#model_z2 \leftarrow glm(FRACTURE \sim WEIGHT, family = binomial, data = glow)
#model_z3 <- glm(FRACTURE ~ HEIGHT, family = binomial, data = glow)</pre>
#model_z4 <- glm(FRACTURE ~ BMI, family = binomial, data = glow)</pre>
\#model\_z5 \leftarrow glm(FRACTURE \sim PRIORFRAC, family = binomial, data = glow)
\#model\_z6 \leftarrow glm(FRACTURE \sim PREMENO, family = binomial, data = glow)
#model_z7 <- qlm(FRACTURE ~ MOMFRAC, family = binomial, data = qlow)</pre>
#model_z8 <- glm(FRACTURE ~ ARMASSIST, family = binomial, data = glow)</pre>
#model_z9 <- glm(FRACTURE ~ SMOKE, family = binomial, data = glow)</pre>
#model_z10 <- qlm(FRACTURE ~ RATERISK, family = binomial, data = qlow)</pre>
#summary(model_z1)
#summary(model_z2)
#summary(model_z3)
#summary(model_z4)
#summary(model z5)
#summary(model z6)
#summary(model_z7)
#summary(model_z8)
#summary(model_z9)
#summary(model z10)
# not interesting due to all variables (i.e. SUB_ID, SITE_ID, PHY_ID)
\# model00 <- glm(FRACTURE \sim ., family = binomial, data = <math>glow)
# summary(model00)
# full model, order by continuous, then factor
model0 <- glm(FRACTURE ~ AGE + WEIGHT + HEIGHT + BMI + PRIORFRAC + PREMENO + MOMFRAC + ARMASSIST + SMOK
summary(model0)
##
## Call:
## glm(formula = FRACTURE ~ AGE + WEIGHT + HEIGHT + BMI + PRIORFRAC +
##
       PREMENO + MOMFRAC + ARMASSIST + SMOKE + RATERISK, family = binomial,
##
       data = glow)
##
## Deviance Residuals:
       Min
                 1Q
                      Median
                                     3Q
                                             Max
## -1.6811 -0.7228 -0.5639 -0.1008
                                          2.2182
##
## Coefficients:
                     Estimate Std. Error z value Pr(>|z|)
##
## (Intercept)
                    -15.74709
                               12.67053 -1.243 0.21394
## AGE
                      0.03895
                                 0.01476
                                            2.640 0.00829 **
## WEIGHT
                     -0.12189
                                 0.08664 -1.407 0.15949
## HEIGHT
                      0.06620
                                 0.07825
                                           0.846 0.39755
## BMI
                                 0.22339
                                            1.485 0.13745
                      0.33181
## PRIORFRACYes
                      0.67577
                                 0.25012
                                            2.702 0.00690 **
```

```
## PREMENOYes
                    0.10080
                               0.28540 0.353 0.72395
                            0.30784
## MOMFRACYes
                    0.63438
                                        2.061 0.03933 *
                                        1.408 0.15924
## ARMASSISTYes
                    0.36102
                               0.25647
## SMOKEYes
                   -0.31228
                               0.46216 -0.676 0.49923
## RATERISKSame
                    0.42256
                               0.28144
                                        1.501 0.13324
                               0.29944
                                        2.526 0.01153 *
## RATERISKGreater 0.75645
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 503.84 on 488 degrees of freedom
## AIC: 527.84
##
## Number of Fisher Scoring iterations: 4
# fit model # note - should remove below model1
model0_fitted <- update(model0, . ~ . - WEIGHT - BMI - PREMENO - SMOKE)
summary(model0_fitted)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##
      ARMASSIST + RATERISK, family = binomial, data = glow)
##
## Deviance Residuals:
       Min
                  1Q
                        Median
                                              Max
## -1.66692 -0.72502 -0.56338 -0.03841
## Coefficients:
##
                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                  2.70935 3.22992 0.839 0.40157
## AGE
                   0.03434
                             0.01305
                                      2.632 0.00848 **
                             0.01827 -2.400 0.01640 *
## HEIGHT
                  -0.04383
## PRIORFRACYes
                   0.64526
                             0.24606
                                      2.622 0.00873 **
                                      2.024 0.04300 *
## MOMFRACYes
                   0.62122 0.30698
## ARMASSISTYes
                   0.44579
                             0.23281
                                      1.915 0.05551 .
## RATERISKSame
                   0.42202
                             0.27925
                                       1.511 0.13071
                                      2.409 0.01599 *
## RATERISKGreater 0.70692
                              0.29342
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 507.50 on 492 degrees of freedom
## AIC: 523.5
## Number of Fisher Scoring iterations: 4
# build model with following covariates (drop WEIGHT, BMI, PREMENO, SMOKE)
# AGE, HEIGHT, PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK {SAME, GREATER}
```

```
model1 <- glm(FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK, family = binomial,
summary(model1)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK, family = binomial, data = glow)
##
## Deviance Residuals:
       Min
                 1Q
                      Median
                                   3Q
                                           Max
## -1.66692 -0.72502 -0.56338 -0.03841
                                       2.22148
##
## Coefficients:
##
                 Estimate Std. Error z value Pr(>|z|)
                 2.70935 3.22992 0.839 0.40157
## (Intercept)
## AGE
                 ## HEIGHT
                 0.64526 0.24606
                                   2.622 0.00873 **
## PRIORFRACYes
                 ## MOMFRACYes
## ARMASSISTYes
                 0.44579 0.23281 1.915 0.05551 .
## RATERISKSame
                 0.42202 0.27925 1.511 0.13071
## RATERISKGreater 0.70692
                           0.29342 2.409 0.01599 *
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 507.50 on 492 degrees of freedom
## AIC: 523.5
##
## Number of Fisher Scoring iterations: 4
# from above result, adding back the removed covariates we see they are not needed to keep the remainin
# this becomes the model, adding back removed covariates WEIGHT, BMI, PREMENO, SMOKE the coefficients d
# this becomes the main effects model
# need to check scale of logit for remaining continous variables AGE HEIGHT
# assume HEIGHT is linearin logit
```

The main effects model

```
 \begin{array}{l} model1 <- glm(FRACTURE \sim AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK, family = binomial, data = glow) \\ use lrtest from package lmtest \\ \end{array}
```

test interactions for the following:

5. AGE: [HEIGHT, PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK]

- 6. HEIGHT: [PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK]
- 7. PRIORFRAC: [MOMFRAC, ARMASSIST, RATERISK]
- 8. MOMFRAC: [ARMASSIST, RATERISK]
- 9. ARMASSIST: RATERISK

total 15 interactions

```
library(lmtest)
## Loading required package: zoo
## Attaching package: 'zoo'
## The following objects are masked from 'package:base':
##
##
      as.Date, as.Date.numeric
# model AGE* , HEIGHT* , PRIORFRAC*
model_effects <- glm(FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK, family = bin
lrtest(model_effects)
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK
## Model 2: FRACTURE ~ 1
   #Df LogLik Df Chisq Pr(>Chisq)
## 1 8 -253.75
## 2
     1 -281.17 -7 54.835 1.608e-09 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# (5) AGE: [HEIGHT, PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK]
test <- model_effects</pre>
test <- update(test, . ~ . + AGE:HEIGHT)
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + AGE: HEIGHT, family = binomial, data = glow)
## Deviance Residuals:
                        Median
              1Q
                                      3Q
                                               Max
## -1.66848 -0.73323 -0.56252 0.02069
                                           2.23640
## Coefficients:
                   Estimate Std. Error z value Pr(>|z|)
                 14.749125 23.931667 0.616 0.5377
## (Intercept)
```

```
## AGE
               -0.135869 0.335087 -0.405
                                           0.6851
## HEIGHT
               -0.119095 0.149402 -0.797 0.4254
## PRIORFRACYes
                0.634947 0.246751 2.573 0.0101 *
                ## MOMFRACYes
## ARMASSISTYes
                 0.447271
                         0.232895
                                   1.920
                                          0.0548 .
## RATERISKSame 0.435127 0.280319 1.552 0.1206
## RATERISKGreater 0.707865 0.293394 2.413 0.0158 *
                0.001065 0.002095 0.508 0.6113
## AGE:HEIGHT
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
##
## Residual deviance: 507.24 on 491 degrees of freedom
## AIC: 525.24
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
##
      AGE: HEIGHT
## Model 2: FRACTURE ~ 1
   #Df LogLik Df Chisq Pr(>Chisq)
## 1 9 -253.62
## 2
      1 -281.17 -8 55.096 4.23e-09 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
test <- model_effects</pre>
test <- update(test, . ~ . + AGE:PRIORFRAC)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + AGE: PRIORFRAC, family = binomial,
##
      data = glow)
##
## Deviance Residuals:
                1Q
                     Median
                                          Max
## -1.48423 -0.74080 -0.53895 -0.00078
                                      2.26588
##
## Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                 0.63708 3.35881 0.190 0.849565
## AGE
                  0.05669
                           0.01649
                                   3.437 0.000589 ***
## HEIGHT
                 ## PRIORFRACYes
                 ## MOMFRACYes
```

```
## ARMASSISTYes
                   0.41887
                            0.23395 1.790 0.073391 .
## RATERISKSame
                   ## RATERISKGreater 0.72044
                              0.29561
                                       2.437 0.014804 *
## AGE:PRIORFRACYes -0.05864
                              0.02583 -2.270 0.023188 *
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 502.34 on 491 degrees of freedom
## AIC: 520.34
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
      AGE:PRIORFRAC
## Model 2: FRACTURE ~ 1
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 9 -251.17
      1 -281.17 -8 59.991 4.679e-10 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
test <- model_effects</pre>
test <- update(test, . ~ . + AGE:MOMFRAC)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + AGE: MOMFRAC, family = binomial, data = glow)
## Deviance Residuals:
       Min
                 10
                       Median
                                    30
                                             Max
## -1.58376 -0.72859 -0.56182 -0.02562
                                         2.22962
## Coefficients:
##
                 Estimate Std. Error z value Pr(>|z|)
                 2.59055 3.24368 0.799 0.42450
## (Intercept)
## AGE
                  0.03633
                             0.01393 2.609 0.00908 **
## HEIGHT
                  -0.04402
                             0.01827 -2.409 0.01601 *
## PRIORFRACYes
                             0.24630 2.639 0.00830 **
                  0.65010
## MOMFRACYes
                  1.57119
                             2.31121 0.680 0.49662
                  0.45447
                            0.23374 1.944 0.05185 .
## ARMASSISTYes
## RATERISKSame
                  0.42505
                            0.27940
                                     1.521 0.12819
## RATERISKGreater 0.71044 0.29363 2.420 0.01554 *
## AGE:MOMFRACYes -0.01353 0.03264 -0.414 0.67854
## ---
```

```
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 507.33 on 491 degrees of freedom
## AIC: 525.33
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
      AGE: MOMFRAC
## Model 2: FRACTURE ~ 1
   #Df LogLik Df Chisq Pr(>Chisq)
## 1 9 -253.66
## 2 1 -281.17 -8 55.005 4.406e-09 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
test <- model_effects</pre>
test <- update(test, . ~ . + AGE:ARMASSIST)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + AGE: ARMASSIST, family = binomial,
##
      data = glow)
##
## Deviance Residuals:
      Min
                1Q
                    Median
                                 3Q
                                         Max
## -1.6352 -0.7272 -0.5646 -0.0295
                                      2.2329
## Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                   2.33972 3.33003 0.703 0.48230
## AGE
                   0.01827 -2.406 0.01614 *
## HEIGHT
                   -0.04395
                            0.24609
## PRIORFRACYes
                   0.64031
                                       2.602 0.00927 **
## MOMFRACYes
                    0.63376
                              0.30795
                                       2.058 0.03959 *
## ARMASSISTYes
                              1.76410
                                       0.705 0.48063
                    1.24419
## RATERISKSame
                    0.42815
                             0.27964
                                       1.531 0.12575
## RATERISKGreater 0.71996
                            0.29494
                                       2.441 0.01464 *
## AGE:ARMASSISTYes -0.01132
                              0.02479 -0.457 0.64802
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
```

```
Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 507.29 on 491 degrees of freedom
## AIC: 525.29
##
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
      AGE: ARMASSIST
## Model 2: FRACTURE ~ 1
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 9 -253.65
## 2 1 -281.17 -8 55.043 4.331e-09 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
test <- model_effects</pre>
test <- update(test, . ~ . + AGE:RATERISK)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + AGE: RATERISK, family = binomial, data = glow)
##
## Deviance Residuals:
       Min
                 1Q
                       Median
                                            Max
## -1.68668 -0.74463 -0.56590 -0.02638
                                        2.34976
## Coefficients:
                     Estimate Std. Error z value Pr(>|z|)
                     0.53632 3.53444 0.152 0.87939
## (Intercept)
## AGE
                     0.06673
                              0.02473 2.698 0.00697 **
## HEIGHT
                     ## PRIORFRACYes
                     ## MOMFRACYes
                               0.30765
                                         2.121 0.03395 *
                     0.65241
## ARMASSISTYes
                     0.48569 0.23443 2.072 0.03828 *
## RATERISKSame
                     3.28427 2.27575 1.443 0.14898
## RATERISKGreater
                    4.25804
                             2.28873 1.860 0.06282 .
                                0.03151 -1.269 0.20438
                     -0.03999
## AGE:RATERISKSame
## AGE:RATERISKGreater -0.05021
                                0.03202 -1.568 0.11690
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 504.79 on 490 degrees of freedom
## AIC: 524.79
##
## Number of Fisher Scoring iterations: 5
```

lrtest(test)

```
## Likelihood ratio test
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
      AGE: RATERISK
## Model 2: FRACTURE ~ 1
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 10 -252.40
## 2 1 -281.17 -9 57.54 3.982e-09 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# (4) HEIGHT: [PRIORFRAC, MOMFRAC, ARMASSIST, RATERISK]
test <- model_effects</pre>
test <- update(test, . ~ . + HEIGHT:PRIORFRAC)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + HEIGHT: PRIORFRAC, family = binomial,
##
      data = glow)
##
## Deviance Residuals:
      Min
               1Q
                   Median
                               3Q
## -1.6670 -0.7274 -0.5615 -0.0037
                                    2.2377
##
## Coefficients:
##
                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                    3.79297 3.89138 0.975 0.32970
                                         2.597 0.00941 **
                     0.03395
                               0.01307
## AGE
## HEIGHT
                     -0.05041
                              0.02253 -2.238 0.02524 *
## PRIORFRACYes
                    -2.41864 6.03699 -0.401 0.68869
## MOMFRACYes
                     0.23394
## ARMASSISTYes
                     0.43526
                                         1.861 0.06281 .
                     0.42634 0.27946
## RATERISKSame
                                         1.526 0.12711
## RATERISKGreater
                     ## HEIGHT:PRIORFRACYes 0.01915 0.03770 0.508 0.61146
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 507.24 on 491 degrees of freedom
## AIC: 525.24
## Number of Fisher Scoring iterations: 4
```

```
lrtest(test)
## Likelihood ratio test
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
     HEIGHT: PRIORFRAC
## Model 2: FRACTURE ~ 1
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 9 -253.62
## 2 1 -281.17 -8 55.092 4.236e-09 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
test <- model effects
test <- update(test, . ~ . + HEIGHT:MOMFRAC)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
     ARMASSIST + RATERISK + HEIGHT: MOMFRAC, family = binomial,
##
     data = glow)
##
## Deviance Residuals:
      Min
               1Q
                    Median
                                3Q
                                        Max
## -1.62068 -0.74163 -0.55649 0.06604
                                    2.26717
## Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                  4.73834 3.51132 1.349 0.17719
## AGE
                  ## HEIGHT
## PRIORFRACYes
                  ## MOMFRACYes
                 -11.35526 7.64959 -1.484 0.13770
## ARMASSISTYes
                  0.42455 0.28002
## RATERISKSame
                                   1.516 0.12949
                 ## RATERISKGreater
## HEIGHT: MOMFRACYes 0.07401 0.04718 1.569 0.11675
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
     Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 505.08 on 491 degrees of freedom
## AIC: 523.08
## Number of Fisher Scoring iterations: 4
```

```
## Likelihood ratio test
```

lrtest(test)

```
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
     HEIGHT: MOMFRAC
## Model 2: FRACTURE ~ 1
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 9 -252.54
## 2 1 -281.17 -8 57.258 1.603e-09 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
test <- model_effects</pre>
test <- update(test, . ~ . + HEIGHT:ARMASSIST)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + HEIGHT: ARMASSIST, family = binomial,
##
      data = glow)
## Deviance Residuals:
          1Q Median
     Min
                              30
## -1.6742 -0.7177 -0.5638 -0.1472
                                   2.1734
## Coefficients:
##
                   Estimate Std. Error z value Pr(>|z|)
                  -0.57428 4.12234 -0.139 0.88920
## (Intercept)
## AGE
                    ## HEIGHT
                   -0.02318
                            0.02432 -0.953 0.34051
## PRIORFRACYes
                    ## MOMFRACYes
                    ## ARMASSISTYes
                    7.53985 5.77628 1.305 0.19179
                            0.27981
## RATERISKSame
                    0.41583
                                       1.486 0.13725
## RATERISKGreater
                    ## HEIGHT: ARMASSISTYes -0.04419
                            0.03594 -1.229 0.21890
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 505.98 on 491 degrees of freedom
## AIC: 523.98
##
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
     HEIGHT: ARMASSIST
## Model 2: FRACTURE ~ 1
```

```
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 9 -252.99
## 2 1 -281.17 -8 56.352 2.409e-09 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
test <- model effects
test <- update(test, . ~ . + HEIGHT:RATERISK)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + HEIGHT: RATERISK, family = binomial,
##
      data = glow)
##
## Deviance Residuals:
                 1Q
                      Median
                                   3Q
                                           Max
## -1.64936 -0.72375 -0.57251 -0.05841
                                        2.22612
## Coefficients:
                       Estimate Std. Error z value Pr(>|z|)
                       3.25641 5.81516 0.560 0.57549
## (Intercept)
## AGE
                       ## HEIGHT
                       -0.04674
                                0.03532 -1.323 0.18573
## PRIORFRACYes
                       0.64451
                                0.24655 2.614 0.00895 **
## MOMFRACYes
                       ## ARMASSISTYes
                       0.44610 0.23290 1.915 0.05544 .
## RATERISKSame
                        2.93823
                                  7.29965
                                          0.403 0.68730
                                7.29448 -0.432 0.66581
## RATERISKGreater
                       -3.15056
## HEIGHT:RATERISKSame
                       -0.01577 0.04550 -0.347 0.72890
## HEIGHT:RATERISKGreater 0.02394
                                0.04528 0.529 0.59695
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 506.55 on 490 degrees of freedom
## AIC: 526.55
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
      HEIGHT: RATERISK
## Model 2: FRACTURE ~ 1
   #Df LogLik Df Chisq Pr(>Chisq)
## 1 10 -253.28
     1 -281.17 -9 55.786 8.624e-09 ***
## 2
```

```
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# (3) PRIORFRAC: [MOMFRAC, ARMASSIST, RATERISK]
test <- model effects
test <- update(test, . ~ . + PRIORFRAC:MOMFRAC)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + PRIORFRAC: MOMFRAC, family = binomial,
##
##
      data = glow)
##
## Deviance Residuals:
      Min
            1Q
                     Median
                                  3Q
                                          Max
## -1.52616 -0.73215 -0.54992 0.02399
                                       2.25279
##
## Coefficients:
##
                      Estimate Std. Error z value Pr(>|z|)
                        2.97592 3.23781 0.919 0.35804
## (Intercept)
## AGE
                       ## HEIGHT
                       0.80102
## PRIORFRACYes
                                  0.26285
                                          3.047 0.00231 **
                       ## MOMFRACYes
## ARMASSISTYes
                       0.43294 0.23384 1.851 0.06411 .
                        0.41959 0.28027 1.497 0.13437
## RATERISKSame
                        0.71282 0.29401
                                          2.425 0.01533 *
## RATERISKGreater
## PRIORFRACYes: MOMFRACYes -1.07823 0.65021 -1.658 0.09726 .
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 504.75 on 491 degrees of freedom
## AIC: 522.75
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
      PRIORFRAC: MOMFRAC
## Model 2: FRACTURE ~ 1
   #Df LogLik Df Chisq Pr(>Chisq)
## 1 9 -252.37
## 2 1 -281.17 -8 57.59 1.382e-09 ***
```

Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1

```
test <- model_effects</pre>
test <- update(test, . ~ . + PRIORFRAC:ARMASSIST)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + PRIORFRAC: ARMASSIST, family = binomial,
##
      data = glow)
##
## Deviance Residuals:
                       Median
       Min 10
                                30
                                             Max
## -1.69860 -0.71874 -0.56691 -0.04199 2.21033
## Coefficients:
##
                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                           2.90711 3.25923 0.892 0.37241
                                    0.01306 2.630 0.00854 **
                           0.03434
## AGE
## HEIGHT
                           -0.04486
                                     0.01842 -2.436 0.01487 *
## PRIORFRACYes
                          0.52412
                                    0.34418 1.523 0.12780
## MOMFRACYes
                           0.63247
                                    0.30798 2.054 0.04001 *
                                    0.28322 1.287 0.19803
## ARMASSISTYes
                           0.36456
## RATERISKSame
                           0.42507 0.27929
                                               1.522 0.12802
                           ## RATERISKGreater
## PRIORFRACYes: ARMASSISTYes 0.24587 0.48467 0.507 0.61194
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 507.24 on 491 degrees of freedom
## AIC: 525.24
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
      PRIORFRAC: ARMASSIST
## Model 2: FRACTURE ~ 1
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 9 -253.62
     1 -281.17 -8 55.093 4.235e-09 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
test <- model_effects</pre>
test <- update(test, . ~ . + PRIORFRAC:RATERISK)</pre>
summary(test)
```

```
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + PRIORFRAC: RATERISK, family = binomial,
##
      data = glow)
##
## Deviance Residuals:
       Min
                 1Q
                      Median
                                   3Q
                                           Max
## -1.69776 -0.71989 -0.56384 -0.03822
                                       2.21130
##
## Coefficients:
                             Estimate Std. Error z value Pr(>|z|)
##
## (Intercept)
                             2.733523 3.235459 0.845 0.39819
                             ## AGE
## HEIGHT
                            ## PRIORFRACYes
                             0.564292
                                      0.497212
                                                 1.135 0.25641
                             ## MOMFRACYes
## ARMASSISTYes
                            0.429891 0.236033 1.821 0.06856
## RATERISKSame
                             0.426181 0.324504 1.313 0.18907
## RATERISKGreater
                             0.632806
                                      0.355571
                                                 1.780 0.07513
## PRIORFRACYes:RATERISKSame
                             0.001597 0.625563
                                                0.003 0.99796
## PRIORFRACYes:RATERISKGreater 0.208811 0.624586 0.334 0.73814
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 507.32 on 490 degrees of freedom
## AIC: 527.32
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
      PRIORFRAC: RATERISK
## Model 2: FRACTURE ~ 1
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 10 -253.66
## 2 1 -281.17 -9 55.015 1.21e-08 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# (2) MOMFRAC: [ARMASSIST, RATERISK]
test <- model_effects</pre>
test <- update(test, . ~ . + MOMFRAC:ARMASSIST)</pre>
summary(test)
```

```
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + MOMFRAC: ARMASSIST, family = binomial,
##
      data = glow)
## Deviance Residuals:
                       Median
                10
                                    30
                                             Max
## -1.65273 -0.72683 -0.55140 0.03367
                                         2.27218
##
## Coefficients:
                         Estimate Std. Error z value Pr(>|z|)
                                    3.25148 0.912 0.36160
## (Intercept)
                          2.96640
                                            2.842 0.00448 **
## AGE
                          0.03760
                                    0.01323
## HEIGHT
                         ## PRIORFRACYes
                         0.61633 0.24770
                                            2.488 0.01284 *
## MOMFRACYes
                         1.17111
                                    0.38940
                                             3.007 0.00263 **
                         ## ARMASSISTYes
## RATERISKSame
                         0.41386 0.28032 1.476 0.13985
## RATERISKGreater
                                    0.29445
                                            2.413 0.01582 *
                         0.71051
## MOMFRACYes: ARMASSISTYes -1.33817
                                    0.62405 -2.144 0.03201 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 502.83 on 491 degrees of freedom
## AIC: 520.83
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
      MOMFRAC: ARMASSIST
## Model 2: FRACTURE ~ 1
   #Df LogLik Df Chisq Pr(>Chisq)
## 1 9 -251.41
      1 -281.17 -8 59.509 5.818e-10 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
test <- model_effects</pre>
test <- update(test, . ~ . + MOMFRAC:RATERISK)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + MOMFRAC: RATERISK, family = binomial,
##
      data = glow)
```

```
##
## Deviance Residuals:
                     Median 3Q
      Min
               1Q
## -1.73530 -0.73156 -0.56262 -0.02886
                                     2.20217
## Coefficients:
                        Estimate Std. Error z value Pr(>|z|)
                                   3.23715 0.856 0.39221
## (Intercept)
                          2.76974
## AGE
                          ## HEIGHT
## PRIORFRACYes
                          0.02648 0.83795 0.032 0.97479
## MOMFRACYes
                          0.44890 0.23340 1.923 0.05444
## ARMASSISTYes
## RATERISKSame
                          0.29742 0.29700 1.001 0.31663
## RATERISKGreater
                          ## MOMFRACYes:RATERISKSame 1.04615 0.95957 1.090 0.27561
## MOMFRACYes:RATERISKGreater 0.36775 0.96207 0.382 0.70227
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 505.79 on 490 degrees of freedom
## AIC: 525.79
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
      MOMFRAC: RATERISK
## Model 2: FRACTURE ~ 1
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 10 -252.90
## 2 1 -281.17 -9 56.542 6.183e-09 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# (1) ARMASSIST: RATERISK
test <- model effects
test <- update(test, . ~ . + ARMASSIST:RATERISK)</pre>
summary(test)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##
      ARMASSIST + RATERISK + ARMASSIST: RATERISK, family = binomial,
##
      data = glow)
##
```

```
## Deviance Residuals:
##
      Min 1Q Median
                          30
                                      Max
## -1.6586 -0.7419 -0.5544 -0.0470
                                   2.2531
##
## Coefficients:
                            Estimate Std. Error z value Pr(>|z|)
##
                                     3.22529 0.739 0.45988
## (Intercept)
                            2.38363
                                       0.01314 2.691 0.00713 **
## AGE
                             0.03534
## HEIGHT
                            -0.04274
                                     0.01819 -2.349 0.01883 *
## PRIORFRACYes
                            ## MOMFRACYes
                             0.61378
                                       0.30782 1.994 0.04616 *
                                       0.44193 1.375 0.16906
## ARMASSISTYes
                             0.60776
## RATERISKSame
                             ## RATERISKGreater
                             0.98400 0.38373 2.564 0.01034 *
## ARMASSISTYes:RATERISKSame
                             0.10760 0.56723 0.190 0.84956
## ARMASSISTYes:RATERISKGreater -0.60953
                                     0.58200 -1.047 0.29496
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
##
## Residual deviance: 505.42 on 490 degrees of freedom
## AIC: 525.42
##
## Number of Fisher Scoring iterations: 4
lrtest(test)
## Likelihood ratio test
##
## Model 1: FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
      ARMASSIST: RATERISK
## Model 2: FRACTURE ~ 1
   #Df LogLik Df Chisq Pr(>Chisq)
## 1 10 -252.71
      1 -281.17 -9 56.912 5.253e-09 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Results from interactions
## AGE:HEIGHT
                     0.001065 0.002095 0.508 0.6113
  AGE:PRIORFRACYes
                    -0.01353
                               0.03264 -0.414 0.67854
## AGE:MOMFRACYes
## AGE:ARMASSISTYes
                    -0.01132
                              0.02479 -0.457
                                              0.64802
                    -0.03999
                              0.03151 -1.269 0.20438
## AGE:RATERISKSame
## AGE:RATERISKGreater -0.05021
                              0.03202 -1.568 0.11690
## HEIGHT:PRIORFRACYes 0.01915
                              0.03770
                                       0.508 0.61146
## HEIGHT:MOMFRACYes
                     0.07401
                               0.04718
                                       1.569 0.11675
## HEIGHT: ARMASSISTYes -0.04419
                              0.03594 -1.229 0.21890
## HEIGHT:RATERISKSame
                     -0.01577
                                   0.04550 -0.347 0.72890
## HEIGHT:RATERISKGreater 0.02394
                                   0.04528 0.529 0.59695
```

```
## PRIORFRACYes:RATERISKSame 0.001597
                                  0.625563
                                          0.003 0.99796
## PRIORFRACYes:RATERISKGreater 0.208811
                                   0.624586
                                          0.334 0.73814
  MOMFRACYes: ARMASSISTYes -1.33817 0.62405 -2.144 0.03201 *
## MOMFRACYes:RATERISKSame 1.04615 0.95957
                                        1.090 0.27561
## MOMFRACYes:RATERISKGreater 0.36775 0.96207
                                         0.382 0.70227
## ARMASSISTYes:RATERISKSame
                        0.10760 0.56723 0.190 0.84956
## ARMASSISTYes:RATERISKGreater -0.60953
                                   0.58200 -1.047 0.29496
```

Add to main effects model

we find three interactions, AGE:PRIORFRACYes, PRIORFRACYes:MOMFRACYes, MOMFRACYes:ARMASSISTYes

```
model_effects_new <- glm(FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
                    AGE:PRIORFRAC + PRIORFRAC:MOMFRAC + MOMFRAC:ARMASSIST, family = binomial, data =
summary(model_effects_new)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + AGE:PRIORFRAC + PRIORFRAC:MOMFRAC +
      MOMFRAC: ARMASSIST, family = binomial, data = glow)
##
##
## Deviance Residuals:
##
      Min
                1Q
                     Median
                                 3Q
                                         Max
## -1.47664 -0.74929 -0.51571 0.07753
                                      2.33224
##
## Coefficients:
                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                       1.20626 3.38765 0.356 0.721785
                       ## AGE
                       -0.04610 0.01854 -2.487 0.012886 *
## HEIGHT
## PRIORFRACYes
                      4.63031 1.88158 2.461 0.013860 *
                       ## MOMFRACYes
                      ## ARMASSISTYes
                       0.42125 0.28217 1.493 0.135462
## RATERISKSame
                       ## RATERISKGreater
## AGE:PRIORFRACYes -0.05408 0.02602 -2.079 0.037662 *
## PRIORFRACYes:MOMFRACYes -0.83184 0.64852 -1.283 0.199606
## MOMFRACYes:ARMASSISTYes -1.15254 0.61838 -1.864 0.062350 .
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 496.53 on 489 degrees of freedom
## AIC: 518.53
##
## Number of Fisher Scoring iterations: 4
```

```
# create final model with interactions terms AGE:PRIORFRAC + MOMFRAC:ARMASSIST
model_effects_final <- glm(FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK +
                     AGE: PRIORFRAC + MOMFRAC: ARMASSIST, family = binomial, data = glow)
summary(model effects final)
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
      ARMASSIST + RATERISK + AGE:PRIORFRAC + MOMFRAC:ARMASSIST,
##
      family = binomial, data = glow)
##
## Deviance Residuals:
      Min
             1Q
                   Median
                               3Q
                                       Max
## -1.6995 -0.7459 -0.5238
                            0.0620
                                    2.3123
##
## Coefficients:
##
                        Estimate Std. Error z value Pr(>|z|)
                                   3.38252 0.287 0.774392
## (Intercept)
                         0.96955
## AGE
                         0.05890
                                   0.01666
                                           3.535 0.000408 ***
## HEIGHT
                        ## PRIORFRACYes
                         4.65073 1.88342 2.469 0.013538 *
                         1.19902
## MOMFRACYes
                                   0.39487
                                            3.036 0.002393 **
## ARMASSISTYes
                                   0.25358
                                            2.422 0.015426 *
                         0.61423
## RATERISKSame
                         0.42626
                                  0.28154 1.514 0.130012
## RATERISKGreater
                         ## AGE:PRIORFRACYes
                        ## MOMFRACYes:ARMASSISTYes -1.26534 0.62377 -2.029 0.042507 *
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##
      Null deviance: 562.34 on 499 degrees of freedom
## Residual deviance: 498.17 on 490 degrees of freedom
## AIC: 518.17
##
## Number of Fisher Scoring iterations: 4
Final Interaction Model
(Intercept)
AGE
                      0.05890
                                0.01666
                                         3.535 0.000408 ***
HEIGHT
                                0.01848 -2.388 0.016949 *
                     -0.04413
PRIORFRACYes
                      4.65073
                                1.88342
                                        2.469 0.013538 *
```

FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC + ARMASSIST + RATERISK + AGE:PRIORFRAC + MOMFRAC:ARMASSIS

0.02600 -2.158 0.030950 *

0.62377 -2.029 0.042507 *

3.036 0.002393 **

2.422 0.015426 *

0.39487

0.25358

1.19902

0.61423

-0.05610

MOMFRACYes

ARMASSISTYes

RATERISKGreater

AGE:PRIORFRACYes

MOMFRACYes: ARMASSISTYes -1.26534

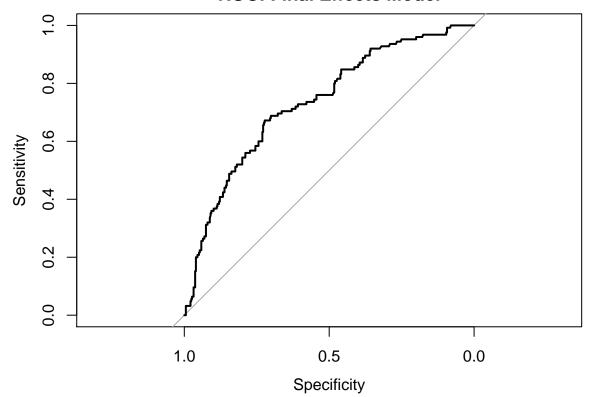
```
library(pROC)
## Type 'citation("pROC")' for a citation.
##
## Attaching package: 'pROC'
## The following objects are masked from 'package:stats':
##
##
       cov, smooth, var
library(vcdExtra)
## Loading required package: vcd
## Loading required package: grid
##
## Attaching package: 'vcd'
## The following object is masked from 'package: ISLR':
##
##
       Hitters
## Loading required package: gnm
# vcov(model_effects_final)
HLtest(model_effects_final)
## Hosmer and Lemeshow Goodness-of-Fit Test
##
## Call:
## glm(formula = FRACTURE ~ AGE + HEIGHT + PRIORFRAC + MOMFRAC +
##
       ARMASSIST + RATERISK + AGE:PRIORFRAC + MOMFRAC:ARMASSIST,
##
       family = binomial, data = glow)
## ChiSquare df
                  P_{value}
   7.268011 8 0.5080118
glow$predict_mfinal <- predict(model_effects_final, type = "response")</pre>
with(glow, addmargins(table(glow$predict_mfinal > 0.5, glow$FRACTURE)))
##
##
            No Yes Sum
##
     FALSE 354 97 451
##
     TRUE
          21 28 49
     Sum 375 125 500
##
```

```
(roc_final_model <- roc(glow$FRACTURE ~ glow$predict_mfinal, data = glow))

##
## Call:
## roc.formula(formula = glow$FRACTURE ~ glow$predict_mfinal, data = glow)
##
## Data: glow$predict_mfinal in 375 controls (glow$FRACTURE No) < 125 cases (glow$FRACTURE Yes).
## Area under the curve: 0.7331

plot(roc_final_model, main = "ROC: Final Effects Model")</pre>
```

ROC: Final Effects Model



 misc

##

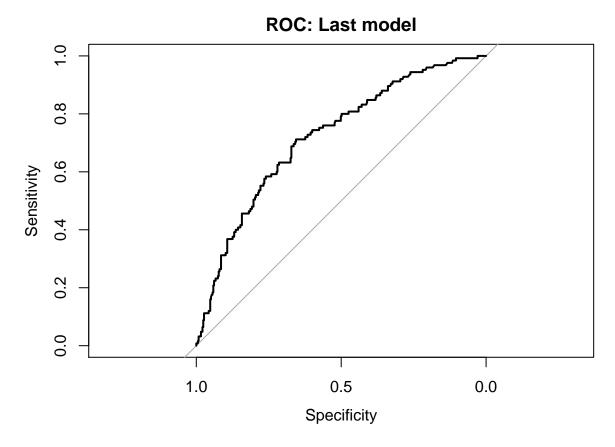
3.10152 8 0.9278259

```
## restart with clean data
glow <- read_glow_dataset()

model_last <- glm(FRACTURE ~ AGE:PRIORFRAC + HEIGHT + MOMFRAC:ARMASSIST + I(as.integer(RATERISK) == 3),
HLtest(model_last)

## Hosmer and Lemeshow Goodness-of-Fit Test
##
## Call:
## glm(formula = FRACTURE ~ AGE:PRIORFRAC + HEIGHT + MOMFRAC:ARMASSIST +
## I(as.integer(RATERISK) == 3), family = binomial, data = glow)
## ChiSquare df P_value</pre>
```

```
summary(HLtest(model_last))
## Partition for Hosmer and Lemeshow Goodness-of-Fit Test
##
##
                  cut total obs
                                                chi
                                     exp
## 1 [0.0243,0.0967]
                         50 47 45.97075 0.1518032
## 2
       (0.0967, 0.123]
                         50 46 44.35914 0.2463653
## 3
        (0.123,0.152] 50 42 43.19969 -0.1825284
## 4
        (0.152, 0.18]
                         50 41 41.81265 -0.1256745
         (0.18, 0.213]
                         50 42 40.34124 0.2611609
## 5
## 6
        (0.213, 0.251]
                         50 36 38.55936 -0.4121599
## 7
        (0.251, 0.292]
                         50 38 36.55362 0.2392312
        (0.292,0.372]
## 8
                         50 32 33.67421 -0.2885110
## 9
         (0.372, 0.47]
                         50 28 29.25398 -0.2318447
## 10
         (0.47, 0.724]
                         50 23 21.27536 0.3739034
## Hosmer and Lemeshow Goodness-of-Fit Test
## Call:
## glm(formula = FRACTURE ~ AGE:PRIORFRAC + HEIGHT + MOMFRAC:ARMASSIST +
       I(as.integer(RATERISK) == 3), family = binomial, data = glow)
##
##
   ChiSquare df
                 P_{value}
      3.10152 8 0.9278259
##
# classification table
glow$predict_last <- predict(model_last, type = "response")</pre>
with(glow, addmargins(table(predict_last > 0.5, FRACTURE)))
          FRACTURE
##
##
            No Yes Sum
##
     FALSE 355 103 458
##
     TRUE
           20 22 42
##
     Sum
           375 125 500
# Sensitivy, specificity, ROC (using pROC)
roc_model_last <- roc(glow$FRACTURE ~ glow$predict_last, data = glow)</pre>
plot(roc_model_last, main = "ROC: Last model")
```



```
# create table
vars <- c("thresholds", "sensitivities", "specificities")
model_table <- data.frame(roc_model_last[vars])

findIndex <- function(x, y) which.min( (x-y)^2 )
cutPoints <- seq(0.05, 0.75, by = 0.05)

tableIndex <- mapply(findIndex, y = cutPoints, MoreArgs = list(x = roc_model_last$thresholds))
model_table[tableIndex, ]</pre>
```

```
thresholds sensitivities specificities
##
## 3
       0.05165803
                           1.000
                                   0.005333333
## 43 0.09905744
                           0.976
                                   0.128000000
## 120 0.15054070
                           0.880
                                   0.349333333
## 202 0.20014367
                           0.760
                                   0.549333333
## 259 0.25035362
                           0.640
                                   0.674666667
## 316 0.29918726
                           0.520
                                   0.789333333
## 349 0.34952747
                           0.416
                                   0.842666667
## 379 0.40012793
                           0.320
                                   0.893333333
## 401 0.44487716
                           0.240
                                   0.925333333
                                   0.94400000
## 416 0.49400138
                           0.176
## 426 0.55045683
                           0.120
                                   0.954666667
                           0.056
                                   0.978666667
## 443 0.59996390
## 452 0.65801860
                           0.024
                                   0.992000000
## 455 0.69417409
                           0.008
                                   0.994666667
```

```
# plot
plot(specificities ~ thresholds, xlim = c(0, 1), type = "l",
xlab = "probability cutoff", ylab = "sensitivity / specificity",
ylim = c(0, 1), data = model_table, main = "probability sensitivity")
with(model_table, lines(thresholds, sensitivities, col = "red"))
legend(x = 0.75, y = 0.55, legend = c("Sensitivity", "Specificity"),
lty = 1, col = c("red", "black"))
abline(h = c(0, 1), col = "grey80", lty = "dotted")
```

probability sensitivity

