

proj651

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```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.1.3
```

```
## -- Attaching packages ----- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.5    v purrr  0.3.4
## v tibble  3.1.6    v dplyr  1.0.8
## v tidyr   1.2.0    v stringr 1.4.0
## v readr   2.1.2    v forcats 0.5.1
```

```
## Warning: package 'ggplot2' was built under R version 4.1.3
```

```
## Warning: package 'readr' was built under R version 4.1.3
```

```
## Warning: package 'dplyr' was built under R version 4.1.3
```

```
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
```

```
library(gtable)
library(gtsummary)
```

```
## Warning: package 'gtsummary' was built under R version 4.1.3
```

```
library(gridExtra)
```

```
## Warning: package 'gridExtra' was built under R version 4.1.3
```

```
##
```

```
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
```

```
##
```

```
##      combine
```

```
library(knitr)
library(car)
```

```
## Warning: package 'car' was built under R version 4.1.3
```

```
## Loading required package: carData
```

```
## Warning: package 'carData' was built under R version 4.1.3
```

```
##
```

```
## Attaching package: 'car'
```

```
## The following object is masked from 'package:dplyr':
```

```
##
```

```
##      recode
```

```
## The following object is masked from 'package:purrr':
```

```
##
```

```
##      some
```

```
library(boot)
```

```
## Warning: package 'boot' was built under R version 4.1.3
```

```
##
```

```
## Attaching package: 'boot'
```

```
## The following object is masked from 'package:car':
```

```
##
```

```
##      logit
```

```
data <- readRDS("Dataset.RData")
```

Interaction using age/sex/age and sex

```
melanoma <- data %>% mutate(age_c = age - median(age),
                           trans_class_bin = ifelse(trans_class == 'immune',1,0),
                           prop_infiltrated = infiltration_count/tile_count)

model3a <- glm(infiltration_count/tile_count ~ KLRD1+RFX5+DDX58+EIF2AK2+CCL28+CD86+C5+DCK+
              IL17RB+TLR4+IL17C +age_c+gender+stage+trans_class_bin +
              age_c:KLRD1 + age_c:RFX5 + age_c:DDX58 + age_c:EIF2AK2 + age_c:CCL28
              +age_c:CD86+age_c:C5+age_c:DCK+age_c:IL17RB+age_c:TLR4+age_c:IL17C,
              data = melanoma,
              weights = tile_count,
              family = binomial(link=logit))
summary(model3a)
```

```
##
## Call:
## glm(formula = infiltration_count/tile_count ~ KLRD1 + RFX5 +
##      DDX58 + EIF2AK2 + CCL28 + CD86 + C5 + DCK + IL17RB + TLR4 +
##      IL17C + age_c + gender + stage + trans_class_bin + age_c:KLRD1 +
##      age_c:RFX5 + age_c:DDX58 + age_c:EIF2AK2 + age_c:CCL28 +
##      age_c:CD86 + age_c:C5 + age_c:DCK + age_c:IL17RB + age_c:TLR4 +
##      age_c:IL17C, family = binomial(link = logit), data = melanoma,
##      weights = tile_count)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -22.084  -2.117   1.362   4.419  13.242
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.9228326  0.0295171  31.264 < 2e-16 ***
## KLRD1          -0.1378845  0.0136228 -10.122 < 2e-16 ***
## RFX5           -0.0902380  0.0100405  -8.987 < 2e-16 ***
## DDX58           0.1232737  0.0111707  11.035 < 2e-16 ***
## EIF2AK2        -0.0547992  0.0097376  -5.628 1.83e-08 ***
## CCL28          -0.0909403  0.0079420 -11.450 < 2e-16 ***
## CD86            0.1046159  0.0162283   6.446 1.14e-10 ***
## C5             -0.0042051  0.0087735  -0.479 0.631731
## DCK            -0.1554395  0.0096548 -16.100 < 2e-16 ***
## IL17RB         -0.0609868  0.0078319  -7.787 6.86e-15 ***
## TLR4           -0.1159999  0.0097659 -11.878 < 2e-16 ***
## IL17C           0.0899113  0.0084592  10.629 < 2e-16 ***
## age_c           0.0011360  0.0005506   2.063 0.039098 *
## gendermale     -0.1701383  0.0160580 -10.595 < 2e-16 ***
## stage           0.0171486  0.0105302   1.629 0.103414
## trans_class_bin -0.2822991  0.0192395 -14.673 < 2e-16 ***
## KLRD1:age_c     0.0017810  0.0008628   2.064 0.039002 *
## RFX5:age_c      0.0033914  0.0006567   5.164 2.41e-07 ***
## DDX58:age_c     0.0023661  0.0009527   2.484 0.013009 *
## EIF2AK2:age_c  -0.0044938  0.0007149  -6.286 3.26e-10 ***
## CCL28:age_c     -0.0051720  0.0004925 -10.501 < 2e-16 ***
## CD86:age_c      -0.0049517  0.0011732  -4.221 2.44e-05 ***
## C5:age_c        0.0019242  0.0005679   3.388 0.000703 ***
## DCK:age_c       0.0052004  0.0006201   8.387 < 2e-16 ***
## IL17RB:age_c    -0.0011650  0.0004781  -2.437 0.014827 *
## TLR4:age_c      -0.0034182  0.0009973  -3.428 0.000609 ***
## IL17C:age_c     0.0017285  0.0008191   2.110 0.034846 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 10648.2  on 239  degrees of freedom
## Residual deviance:  7502.3  on 213  degrees of freedom
## AIC: 8910.2
##
## Number of Fisher Scoring iterations: 4
```

```

model3b <- glm(prop_infiltrated ~ KLRD1+RFX5+DDX58+EIF2AK2+CCL28+CD86+C5+DCK+
  IL17RB+TLR4+IL17C +age_c+gender+stage+trans_class_bin +
  gender:KLRD1 + gender:RFX5 + gender:DDX58 + gender:EIF2AK2 + gender:CCL28
  +gender:CD86+gender:C5+gender:DCK+gender:IL17RB+gender:TLR4+gender:IL17C,
  data = melanoma,
  weights = tile_count,
  family = binomial(link=logit))
summary(model3b)

```

```

##
## Call:
## glm(formula = prop_infiltrated ~ KLRD1 + RFX5 + DDX58 + EIF2AK2 +
##   CCL28 + CD86 + C5 + DCK + IL17RB + TLR4 + IL17C + age_c +
##   gender + stage + trans_class_bin + gender:KLRD1 + gender:RFX5 +
##   gender:DDX58 + gender:EIF2AK2 + gender:CCL28 + gender:CD86 +
##   gender:C5 + gender:DCK + gender:IL17RB + gender:TLR4 + gender:IL17C,
##   family = binomial(link = logit), data = melanoma, weights = tile_count)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -21.591  -2.236   1.280   4.219  12.305
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      8.483e-01  2.956e-02  28.692  < 2e-16 ***
## KLRD1             9.196e-02  2.305e-02   3.990  6.61e-05 ***
## RFX5             -7.111e-02  1.531e-02  -4.645  3.40e-06 ***
## DDX58             1.093e-01  2.199e-02   4.971  6.67e-07 ***
## EIF2AK2          -2.500e-02  1.586e-02  -1.576  0.114973
## CCL28            -1.463e-01  1.277e-02 -11.456  < 2e-16 ***
## CD86            -1.812e-01  3.071e-02  -5.902  3.60e-09 ***
## C5              -1.184e-01  1.625e-02  -7.288  3.15e-13 ***
## DCK              -7.696e-02  1.291e-02  -5.961  2.51e-09 ***
## IL17RB          -1.419e-01  1.008e-02 -14.074  < 2e-16 ***
## TLR4            -8.658e-02  1.630e-02  -5.311  1.09e-07 ***
## IL17C            1.191e-01  2.008e-02   5.928  3.06e-09 ***
## age_c            2.674e-05  5.232e-04   0.051  0.959245
## gendermale       -1.088e-01  1.603e-02  -6.788  1.14e-11 ***
## stage            3.031e-02  1.045e-02   2.901  0.003717 **
## trans_class_bin  -2.792e-01  1.931e-02 -14.457  < 2e-16 ***
## KLRD1:gendermale -3.213e-01  2.764e-02 -11.625  < 2e-16 ***
## RFX5:gendermale  -6.997e-02  1.952e-02  -3.586  0.000336 ***
## DDX58:gendermale  2.882e-02  2.566e-02   1.123  0.261440
## EIF2AK2:gendermale -2.830e-02  2.060e-02  -1.374  0.169569
## CCL28:gendermale  9.105e-02  1.636e-02   5.566  2.61e-08 ***
## CD86:gendermale  3.743e-01  3.496e-02  10.708  < 2e-16 ***
## C5:gendermale    1.363e-01  1.857e-02   7.338  2.17e-13 ***
## DCK:gendermale   -7.007e-02  1.834e-02  -3.822  0.000133 ***
## IL17RB:gendermale 8.630e-02  1.567e-02   5.506  3.67e-08 ***
## TLR4:gendermale  -1.867e-02  2.032e-02  -0.919  0.358237
## IL17C:gendermale -3.401e-02  2.216e-02  -1.535  0.124874
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 10648.2 on 239 degrees of freedom
## Residual deviance: 7524.5 on 213 degrees of freedom
## AIC: 8932.4
##
## Number of Fisher Scoring iterations: 4

model3c <- glm(prop_infiltrated ~ KLRD1+RFX5+DDX58+EIF2AK2+CCL28+CD86+C5+DCK+
  IL17RB+TLR4+IL17C +age_c+gender+stage+trans_class_bin +
  age_c:KLRD1 + age_c:RFX5 + age_c:DDX58 + age_c:EIF2AK2 + age_c:CCL28
+age_c:CD86+age_c:C5+age_c:DCK+age_c:IL17RB+age_c:TLR4+age_c:IL17C
+gender:KLRD1 + gender:RFX5 + gender:DDX58 + gender:EIF2AK2 + gender:CCL28
+gender:CD86+gender:C5+gender:DCK+gender:IL17RB+gender:TLR4+gender:IL17C,
  data = melanoma,
  weights = tile_count,
  family = binomial(link=logit))
summary(model3c)
```

```
##
## Call:
## glm(formula = prop_infiltrated ~ KLRD1 + RFX5 + DDX58 + EIF2AK2 +
## CCL28 + CD86 + C5 + DCK + IL17RB + TLR4 + IL17C + age_c +
## gender + stage + trans_class_bin + age_c:KLRD1 + age_c:RFX5 +
## age_c:DDX58 + age_c:EIF2AK2 + age_c:CCL28 + age_c:CD86 +
## age_c:C5 + age_c:DCK + age_c:IL17RB + age_c:TLR4 + age_c:IL17C +
## gender:KLRD1 + gender:RFX5 + gender:DDX58 + gender:EIF2AK2 +
## gender:CCL28 + gender:CD86 + gender:C5 + gender:DCK + gender:IL17RB +
## gender:TLR4 + gender:IL17C, family = binomial(link = logit),
## data = melanoma, weights = tile_count)
##
## Deviance Residuals:
## Min 1Q Median 3Q Max
## -21.507 -2.248 1.169 4.121 12.516
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) 0.8850202 0.0306121 28.911 < 2e-16 ***
## KLRD1 0.0446504 0.0244239 1.828 0.067528 .
## RFX5 -0.0083215 0.0163780 -0.508 0.611392
## DDX58 0.1028395 0.0225003 4.571 4.86e-06 ***
## EIF2AK2 -0.0493387 0.0162627 -3.034 0.002415 **
## CCL28 -0.1052747 0.0142616 -7.382 1.56e-13 ***
## CD86 -0.1597435 0.0318162 -5.021 5.14e-07 ***
## C5 -0.0605134 0.0194363 -3.113 0.001849 **
## DCK -0.1145816 0.0140578 -8.151 3.62e-16 ***
## IL17RB -0.1058307 0.0127637 -8.292 < 2e-16 ***
## TLR4 -0.0674300 0.0165198 -4.082 4.47e-05 ***
## IL17C 0.1641257 0.0213362 7.692 1.44e-14 ***
## age_c 0.0006394 0.0005730 1.116 0.264477
## gendermale -0.1429258 0.0165916 -8.614 < 2e-16 ***
## stage 0.0258210 0.0108616 2.377 0.017441 *
## trans_class_bin -0.3001700 0.0199109 -15.076 < 2e-16 ***
```

```

## KLRD1:age_c      -0.0021284  0.0009409  -2.262  0.023691  *
## RFX5:age_c       0.0044430  0.0006802   6.532  6.51e-11  ***
## DDX58:age_c      0.0005345  0.0010074   0.531  0.595679
## EIF2AK2:age_c    -0.0038000  0.0007378  -5.151  2.59e-07  ***
## CCL28:age_c      -0.0046073  0.0005702  -8.080  6.50e-16  ***
## CD86:age_c       -0.0017560  0.0012512  -1.403  0.160479
## C5:age_c         0.0025565  0.0006104   4.188  2.81e-05  ***
## DCK:age_c        0.0036262  0.0006558   5.530  3.21e-08  ***
## IL17RB:age_c     -0.0020995  0.0006339  -3.312  0.000927  ***
## TLR4:age_c       -0.0038370  0.0010920  -3.514  0.000442  ***
## IL17C:age_c      0.0038365  0.0008515   4.506  6.62e-06  ***
## KLRD1:gendermale -0.3127115  0.0306765 -10.194 < 2e-16 ***
## RFX5:gendermale  -0.1427905  0.0203162  -7.028  2.09e-12  ***
## DDX58:gendermale  0.0439922  0.0266384   1.651  0.098645  .
## EIF2AK2:gendermale -0.0034443  0.0209788  -0.164  0.869590
## CCL28:gendermale  0.0433685  0.0192293   2.255  0.024113  *
## CD86:gendermale   0.3774205  0.0369502  10.214 < 2e-16 ***
## C5:gendermale     0.0836214  0.0211551   3.953  7.73e-05  ***
## DCK:gendermale    -0.0455027  0.0192157  -2.368  0.017885  *
## IL17RB:gendermale  0.0340830  0.0205552   1.658  0.097293  .
## TLR4:gendermale   -0.0416249  0.0214183  -1.943  0.051965  .
## IL17C:gendermale  -0.0802411  0.0233731  -3.433  0.000597  ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 10648 on 239 degrees of freedom
## Residual deviance: 7248 on 202 degrees of freedom
## AIC: 8677.9
##
## Number of Fisher Scoring iterations: 4

```