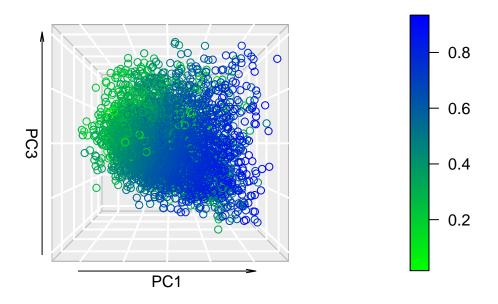
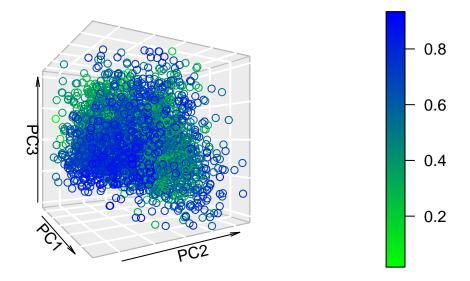
#### PCA glmm

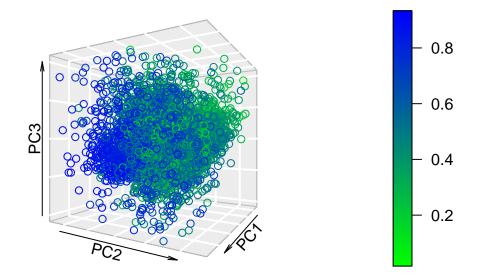
```
setwd("C:/Users/Helen/Desktop/Stats/Pruned3_big")
pcaData = read.csv("3factorPCA.csv")
Let's try removing outliers
PC1mean = mean(pcaData$PC1)
PC1sd = sd(pcaData$PC1)
PC2mean = mean(pcaData$PC2)
PC2sd = sd(pcaData$PC2)
PC3mean = mean(pcaData$PC3)
PC3sd = sd(pcaData$PC3)
pcaData = filter(pcaData, PC1 >= PC1mean - (2.5 * PC1sd))
pcaData = filter(pcaData, PC1 <= PC1mean + (2.5 * PC1sd))</pre>
pcaData = filter(pcaData, PC2 >= PC2mean - (2.5 * PC2sd))
pcaData = filter(pcaData, PC2 <= PC2mean + (2.5 * PC2sd))</pre>
pcaData = filter(pcaData, PC3 >= PC3mean - (2.5 * PC3sd))
pcaData = filter(pcaData, PC3 <= PC3mean + (2.5 * PC3sd))</pre>
pcaData$speaker = as.factor(pcaData$speaker)
m3 = glmer(label ~ PC1 + PC2 + PC3 + (1|speaker), data = pcaData, family=binomial)
r.squaredGLMM(m3)
## Warning: 'r.squaredGLMM' now calculates a revised statistic. See the help page.
## Warning: The null model is correct only if all variables used by the original
## model remain unchanged.
##
                      R2m
                                 R2c
## theoretical 0.10789239 0.3977706
## delta
               0.09226173 0.3401445
summary(m3)
## Generalized linear mixed model fit by maximum likelihood (Laplace
     Approximation) [glmerMod]
## Family: binomial (logit)
## Formula: label ~ PC1 + PC2 + PC3 + (1 | speaker)
      Data: pcaData
##
```

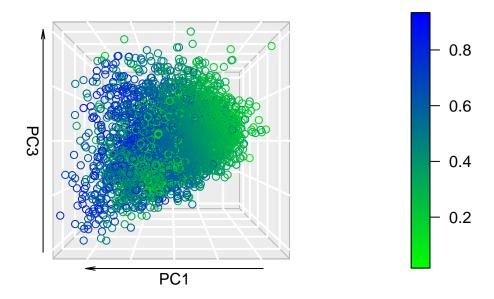
```
##
                BIC logLik deviance df.resid
##
     6987.4
             7020.5 -3488.7
                               6977.4
                                          5541
##
## Scaled residuals:
      Min
               1Q Median
                               3Q
## -3.5309 -0.8583 -0.3503 0.8693 3.9519
## Random effects:
## Groups Name
                       Variance Std.Dev.
## speaker (Intercept) 1.584
                                1.258
## Number of obs: 5546, groups: speaker, 12
##
## Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.85757
                          0.37104 -2.311
                                            0.0208 *
## PC1
               0.35593
                          0.01874 18.998 < 2e-16 ***
## PC2
                                    0.837
               0.01554
                          0.01857
                                            0.4027
## PC3
              -0.16700
                          0.02392 -6.980 2.95e-12 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##
       (Intr) PC1
                    PC2
## PC1 -0.038
## PC2 -0.038 0.107
## PC3 0.037 0.025 -0.029
coefs = coef(m3)
coefs
## $speaker
     (Intercept)
                      PC1
                                 PC2
## c 0.05517477 0.3559334 0.01553552 -0.1670019
## d 0.55343542 0.3559334 0.01553552 -0.1670019
## e -1.96344250 0.3559334 0.01553552 -0.1670019
## f -2.47981958 0.3559334 0.01553552 -0.1670019
## h -1.13184884 0.3559334 0.01553552 -0.1670019
## j -1.04611501 0.3559334 0.01553552 -0.1670019
## k 1.02870220 0.3559334 0.01553552 -0.1670019
## o -1.39473840 0.3559334 0.01553552 -0.1670019
## q -1.58285807 0.3559334 0.01553552 -0.1670019
## s -1.27280420 0.3559334 0.01553552 -0.1670019
## t 1.32014281 0.3559334 0.01553552 -0.1670019
## u -2.25778799 0.3559334 0.01553552 -0.1670019
##
## attr(,"class")
## [1] "coef.mer"
exp(coefs$speaker)
##
     (Intercept)
                     PC1
                              PC2
                                       PC3
## c 1.05672528 1.427512 1.015657 0.846198
## d 1.73921772 1.427512 1.015657 0.846198
```

```
## e 0.14037435 1.427512 1.015657 0.846198
## f 0.08375834 1.427512 1.015657 0.846198
## h 0.32243657 1.427512 1.015657 0.846198
## j 0.35129990 1.427512 1.015657 0.846198
## k 2.79743296 1.427512 1.015657 0.846198
## o 0.24789788 1.427512 1.015657 0.846198
## q 0.20538725 1.427512 1.015657 0.846198
## s 0.28004522 1.427512 1.015657 0.846198
## t 3.74395601 1.427512 1.015657 0.846198
## u 0.10458156 1.427512 1.015657 0.846198
pcaData$m3Fit = predict(m3, type="response")
iData = filter(pcaData, label==1)
nData = filter(pcaData, label==0)
m3Plot1 = scatter3D(pcaData$PC1, pcaData$PC2, pcaData$PC3, phi = 0, theta = 0, bty="g",
                   colvar=pcaData$m3Fit, col=ramp.col(c("green", "blue")),
                   main = "Probability of predicting Ironic Label by First Three PCs",
                   xlab = "PC1", ylab = "PC2", zlab = "PC3")
```

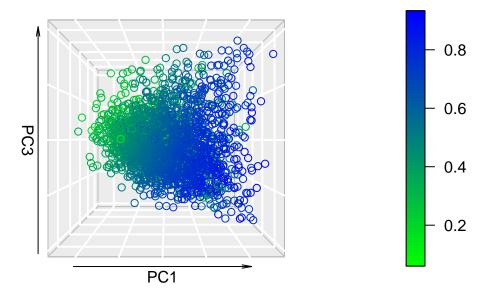


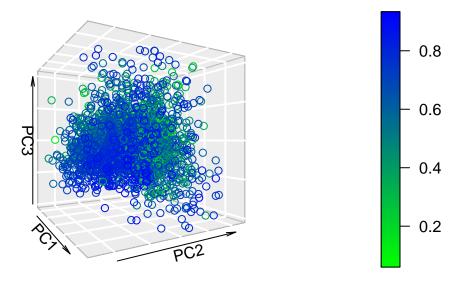


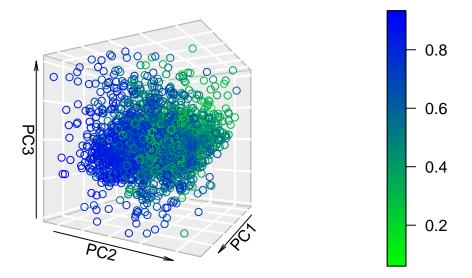


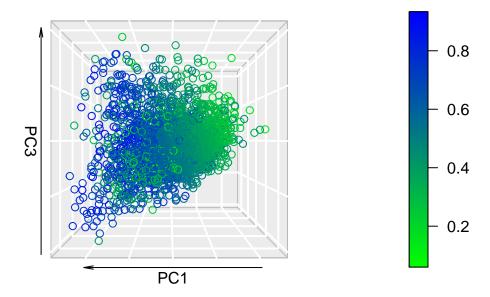


#Plotting only ironic samples

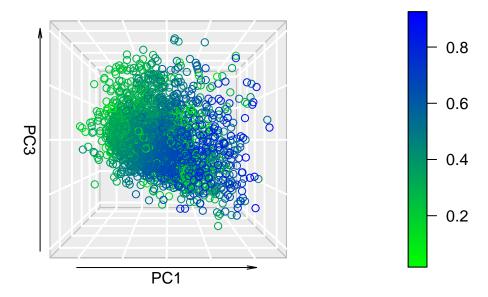


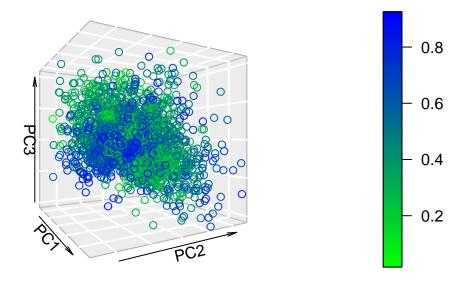


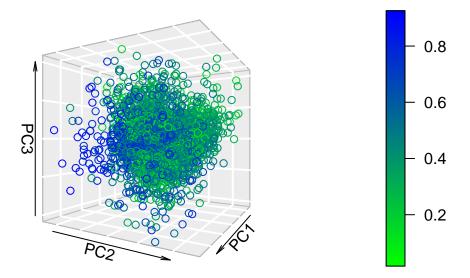


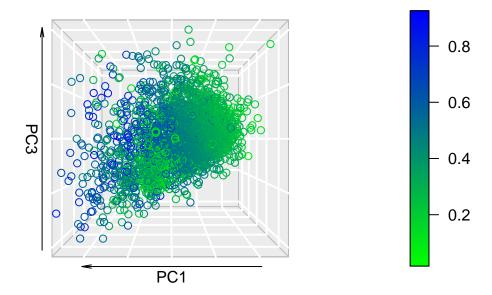


Plotting only non-ironic samples









Fresh model trained on 80% of the data and tested on 20% to get ROC curve Remove model predictions from original data

```
pcaData = select(pcaData, -m3Fit)
```

Train/test split

```
smp_size = floor(0.80 * nrow(pcaData))
set.seed(6)
train_ind = sample(seq_len(nrow(pcaData)), size = smp_size)
trainData = pcaData[train_ind, ]
testData = pcaData[-train_ind, ]
```

Train fresh model on training data

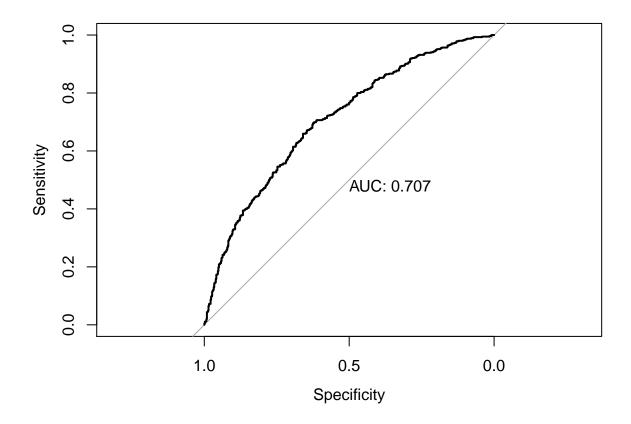
Calculate predictions from test data

```
testData$m4pred = predict(m4, testData, type="response")

test_roc = roc(testData$label ~ testData$m4pred, plot = TRUE, print.auc = TRUE)

## Setting levels: control = 0, case = 1

## Setting direction: controls < cases</pre>
```



```
'Balanced Accur~ Accuracy
##
                                 F1 Sensitivity Specificity 'Pos Pred Value'
##
                <dbl>
                         <dbl> <dbl>
                                           <dbl>
                                                       <dbl>
                                                                        <dbl>
                0.651
                        0.651 0.638
                                           0.614
                                                       0.688
                                                                        0.663
## # ... with 13 more variables: 'Neg Pred Value' <dbl>, AUC <dbl>, 'Lower
## # CI' <dbl>, 'Upper CI' <dbl>, Kappa <dbl>, MCC <dbl>, 'Detection
```

```
## # Rate' <dbl>, 'Detection Prevalence' <dbl>, Prevalence <dbl>,
## # Predictions <list>, ROC <named list>, 'Confusion Matrix' <list>,
## # Process <list>
```

#### plot\_confusion\_matrix(cm)

## Warning in plot\_confusion\_matrix(cm): 'ggimage' is missing. Will not plot arrows
## and zero-shading.

## Warning in plot\_confusion\_matrix(cm): 'rsvg' is missing. Will not plot arrows
## and zero-shading.

