

Final Project

Majorz

```
library(tidyverse)
library(tidymodels)
library(glmnet)
library(Stat2Data)
library(ggcorrplot)
spotify <- read_csv("data/tf_mini.csv")

spotify_mode <- spotify |>
  mutate(new_mode = if_else(mode == "major", 1, 0),
         new_mode = as.numeric(new_mode))

spotify_mode |> drop_na(new_mode)
```

```
# A tibble: 50,704 x 31
  track_id      durat~1 relea~2 us_po~3 acous~4 beat_~5 bounc~6 dance~7 dyn_r~8
  <chr>         <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
1 t_a540e552-1~  110.    1950    100.    0.458    0.519    0.505    0.400    7.51
2 t_67965da0-1~  188.    1950    100.    0.916    0.419    0.546    0.491    9.10
3 t_0614ecd3-a~  161.    1951    99.6    0.813    0.426    0.508    0.492    8.37
4 t_070a63a0-7~  175.    1951    99.7    0.397    0.401    0.360    0.552    5.97
5 t_d6990e17-9~  370.    1951    100.    0.729    0.371    0.335    0.483    5.80
6 t_fcb90952-0~  178.    1951    100.    0.186    0.549    0.579    0.744    8.67
7 t_20675f8a-3~  166.    1952    100.    0.519    0.592    0.640    0.741    9.53
8 t_7577ca53-5~  198.    1952    99.5    0.787    0.472    0.448    0.427    6.91
9 t_8a461a4e-6~  215.    1954    100.    0.155    0.526    0.566    0.523    8.63
10 t_ae523005-8~  281.    1954    97.4    0.941    0.233    0.209    0.242    4.83
# ... with 50,694 more rows, 22 more variables: energy <dbl>, flatness <dbl>,
#   instrumentalness <dbl>, key <dbl>, liveness <dbl>, loudness <dbl>,
#   mechanism <dbl>, mode <chr>, organism <dbl>, speechiness <dbl>,
#   tempo <dbl>, time_signature <dbl>, valence <dbl>, acoustic_vector_0 <dbl>,
```

```
# acoustic_vector_1 <dbl>, acoustic_vector_2 <dbl>, acoustic_vector_3 <dbl>,
# acoustic_vector_4 <dbl>, acoustic_vector_5 <dbl>, acoustic_vector_6 <dbl>,
# acoustic_vector_7 <dbl>, new_mode <dbl>, and abbreviated variable names ...
```

```
glm_all_mode <- glm(new_mode ~ us_popularity_estimate + duration + release_year + acousticness +
  beat_strength + bounciness + danceability + dyn_range_mean + energy +
  flatness + instrumentalness + key + liveness + loudness + mechanism +
  organism + speechiness + tempo + time_signature + valence,
  data = spotify_mode,
  family = "binomial")
summary(glm_all_mode)
```

Call:

```
glm(formula = new_mode ~ us_popularity_estimate + duration +
  release_year + acousticness + beat_strength + bounciness +
  danceability + dyn_range_mean + energy + flatness + instrumentalness +
  key + liveness + loudness + mechanism + organism + speechiness +
  tempo + time_signature + valence, family = "binomial", data = spotify_mode)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.3569	-1.2543	0.7625	0.9493	1.8185

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	32.2683808	2.3096693	13.971	< 2e-16 ***
us_popularity_estimate	-0.0112941	0.0085642	-1.319	0.187249
duration	-0.0008868	0.0001370	-6.472	9.68e-11 ***
release_year	-0.0145826	0.0010562	-13.807	< 2e-16 ***
acousticness	0.4800550	0.1339125	3.585	0.000337 ***
beat_strength	2.3227249	0.3798220	6.115	9.64e-10 ***
bounciness	-4.2116774	0.5087117	-8.279	< 2e-16 ***
danceability	0.2508033	0.1611182	1.557	0.119556
dyn_range_mean	0.1188409	0.0200062	5.940	2.85e-09 ***
energy	-0.5804580	0.1072094	-5.414	6.15e-08 ***
flatness	0.7082200	0.3348900	2.115	0.034448 *
instrumentalness	-0.3421403	0.0522757	-6.545	5.95e-11 ***
key	-0.0930592	0.0026793	-34.733	< 2e-16 ***
liveness	0.3261005	0.0588139	5.545	2.95e-08 ***
loudness	0.0223914	0.0043966	5.093	3.53e-07 ***

```

mechanism          -0.8263282  0.2122943  -3.892  9.93e-05 ***
organism           -0.3927748  0.3168700  -1.240  0.215144
speechiness        -1.0627013  0.0967583 -10.983  < 2e-16 ***
tempo              0.0027563  0.0004504   6.120  9.37e-10 ***
time_signature     -0.2081995  0.0260103  -8.005  1.20e-15 ***
valence            0.5394631  0.0506272  10.656  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

(Dispersion parameter for binomial family taken to be 1)

```

Null deviance: 66141  on 50703  degrees of freedom
Residual deviance: 63327  on 50683  degrees of freedom
AIC: 63369

```

Number of Fisher Scoring iterations: 4

As demonstrated by the regression model above, there are many predictors that are statistically significant, using the significance level of $\alpha = 0.5$. However, it is critical to improve this baseline model in the following ways:

- 1) Confirm that there are not instances of multicollinearity (or model overfitting)
- 2) Ensure that the variables included are meaningfully contributing to the model
- 3) Optimize the model and determine if interactions or changes are appropriate

```

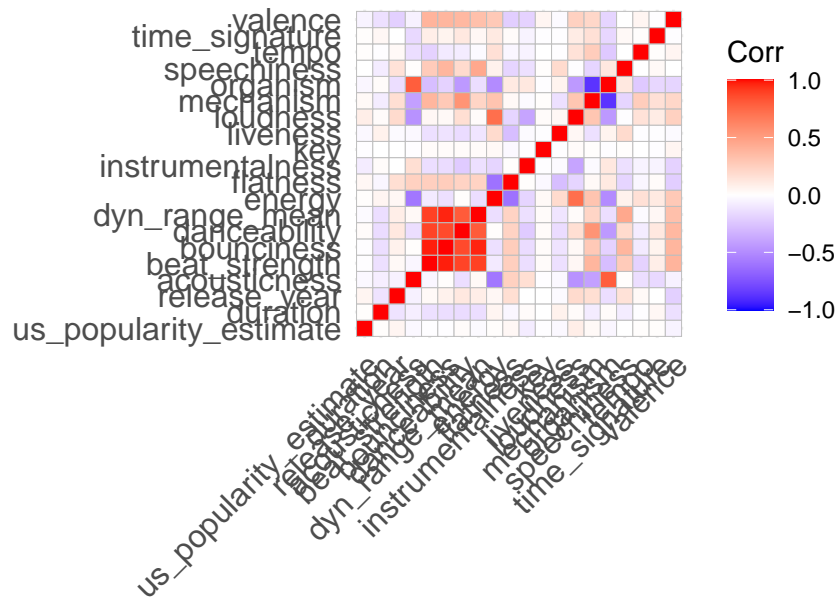
spotify_cor <- spotify_model|>
  select(us_popularity_estimate, duration, release_year, acousticness,
    beat_strength, bounciness, danceability, dyn_range_mean, energy,
    flatness, instrumentalness, key, liveness, loudness, mechanism,
    organism, speechiness, tempo, time_signature, valence)

cor_spotify <- cor(spotify_cor)

ggcorrplot(cor_spotify)+
  labs(title = "Corrleation of Spotify Data Variables")

```

Correlation of Spotify Data Variables



Source used: [http://www.sthda.com/english/wiki/ggcorrplot-visualization-of-a-correlation-matrix-using-ggplot2#:~:text=The%20easiest%20way%20to%20visualize,ggcorr\(\)%20in%20ggally%20package](http://www.sthda.com/english/wiki/ggcorrplot-visualization-of-a-correlation-matrix-using-ggplot2#:~:text=The%20easiest%20way%20to%20visualize,ggcorr()%20in%20ggally%20package)

Examining the correlation plot above, it appears there are variables that have a high positive correlation with each other. This causes great concern with multicollinearity as the model may be overfitted. For example,

- beat_strength is highly correlated with
 - dyn_range_mean
 - danceability
 - bounciness

Therefore, to prevent overfitting in our regression model, the following variables should be removed:

- 1) beat_strength
- 2) dyn_range_mean
- 3) danceability
- 4) bounciness

In addition to removing variables due to extremely high correlations, it is also important to select variables that make an impact on the model. For example, some variables may be replicated or not meaningful by nature to the outcome of interest; therefore, removal is essential. In this analysis, we decided to use a LASSO model to select variables that are essential to the model.

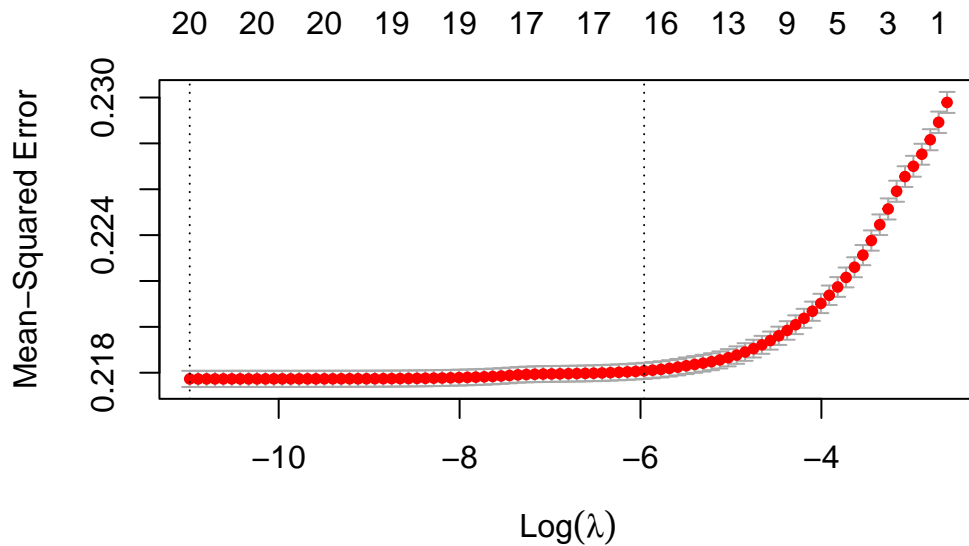
```
y <- spotify_mode$new_mode
x <- model.matrix(new_mode ~ us_popularity_estimate + duration + release_year +
                  acoustictness + beat_strength + bounciness + danceability +
                  dyn_range_mean + energy + flatness + instrumentalness + key +
                  liveness + loudness + mechanism + organism + speechiness +
                  tempo + time_signature + valence,
                  data = spotify_mode, family = "binomial")
lasso_sc <- cv.glmnet(x, y, alpha = 1)
best_lambda <- lasso_sc$lambda.min
lasso_final <- glmnet(x, y, alpha = 1, lambda = best_lambda)
lasso_final$beta
```

21 x 1 sparse Matrix of class "dgCMatrix"

```
              s0
(Intercept)      .
us_popularity_estimate -0.0023697882
duration            -0.0001815571
release_year        -0.0027550965
acoustictness         0.0815694288
beat_strength         0.4406993904
bounciness           -0.8245052957
danceability          0.0543096770
dyn_range_mean        0.0228553572
energy               -0.1261488336
flatness              0.1279289732
instrumentalness      -0.0765082818
key                  -0.0204724936
liveness              0.0689480595
loudness              0.0046781996
mechanism            -0.1469295172
organism              -0.0394018658
speechiness           -0.2428625066
tempo                 0.0005698640
time_signature        -0.0409603010
valence               0.1199079212
```

LASSO kept all of the predictors.

```
plot(lasso_sc)
```



not sure if this is needed or not[^]

Introduction and Data

Methodology

Evaluating assumptions:

figure out to make this smaller or how to get charts to show[^]

There had to be less data points for some of the predictors because there was only so many different values and enough of them to be able to get the empirical logits. For example, with key there is only 12 unique values, but not all of them had enough values to be calculated, so we did 10 groups. I eliminated the titles to make the plots more clear and because they were repetitive. In summary, we concluded that linearity is met for _____ because there is no major pattern in empirical logits. Linearity was not met for _____ because _____.

```

glm_aug <- glm_aug |>
  mutate(prob = exp(.fitted)/(1 + exp(.fitted)),
         pred_mode = ifelse(prob > 0.5, "Major", "Minor")) |>
  select(.fitted, prob, pred_mode, new_mode)

table(glm_aug$pred_mode, glm_aug$new_mode)

```

Using our logistic regression model as a classifier for any infection by using a threshold of 0.5 predicted probability, we are able to calculate the following values:

Prevalence:

Sensitivity:

Specificity:

Positive predicted value:

Negative predicted value:

This implies that _____

```

glm_aug |>
  roc_auc(truth = as.factor(new_mode),
         prob,
         event_level = "second") |>
  autoplot()

glm_aug |>
  roc_auc(truth = as.factor(new_mode),
         prob,
         event_level = "second")

```

Results

HOW to pick which predictors are the best???

One predictor that makes sense to interpret is key because key has changes in whole numbers while many of the other predictors are within tenths of differences of each other amongst observations. Holding all other predictors constant, for every one (unit) increase in key, we expect the log-odds of a song being major rather than minor to increase by approximately 0.0931. So, when holding all other predictors constant, we for every one number increase in key (find what this means), the odds of the patient getting any infection is predicted to be multiplied by $e^{0.0931} = 1.0976$. For an example, while holding all other predictors constant,

the relative odds of a song being major rather than minor comparing a song with key 10 vs a song with key 2 is $e^{8*0.0931}$ is 2.106.

to be continued

Discussion