

# 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 (significance level of 0.05). However, it is critical to improve this baseline model in the following ways:

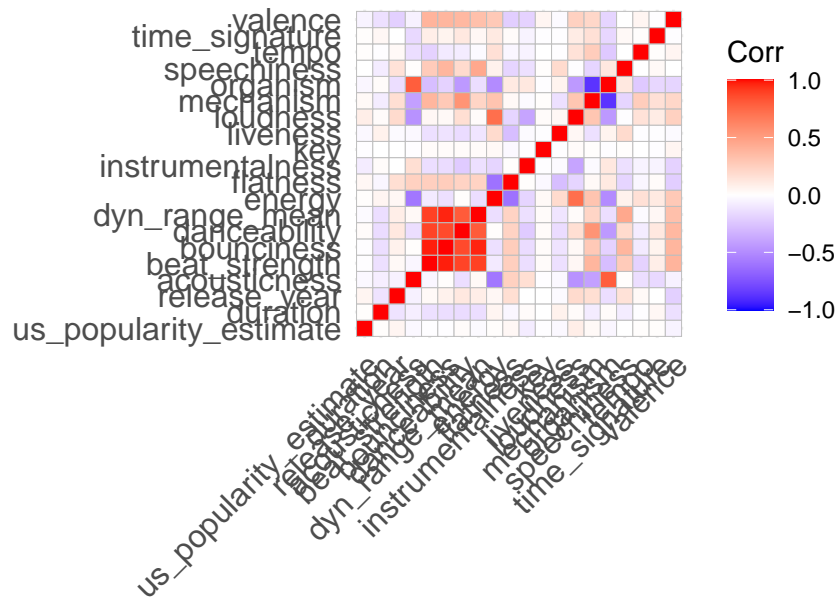
- 1) Confirm that there are not instances of multicollinearity (or model overfitting)
- 2) Ensure that the variables included are meaningfully contributing to the model
- 3) Optimize the model and determine if interactions or changes are appropriate

```
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 = "Correlation of Spotify Data Variables")
```

## Correlation of Spotify Data Variables



#Source [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.

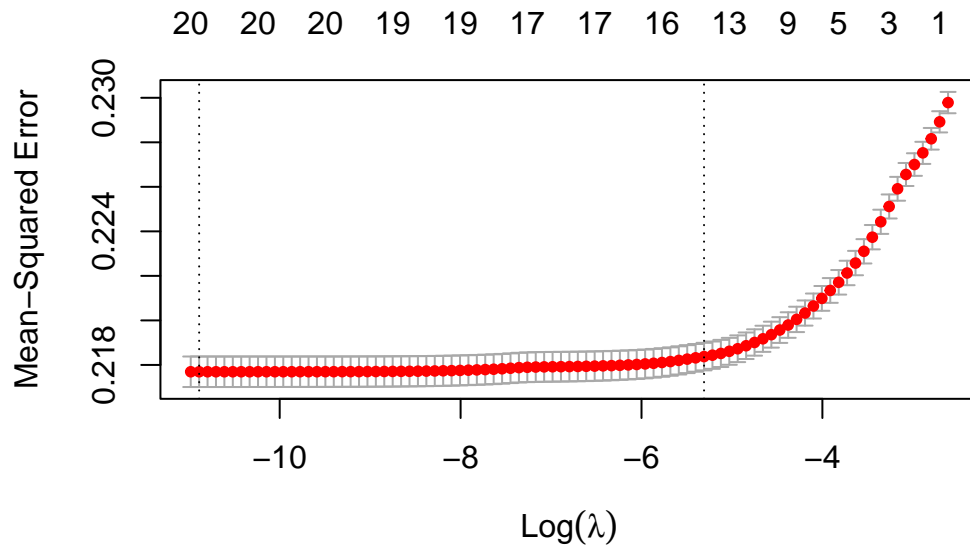
```
y <- spotify_mode$new_mode
x <- model.matrix(new_mode ~ us_popularity_estimate + duration + release_year +
  acoustictness + beat_strength + bounciness + danceability +
  dyn_range_mean + energy + flatness + instrumentalness + key +
  liveness + loudness + mechanism + organism + speechiness +
  tempo + time_signature + valence,
  data = spotify_mode, family = "binomial")
lasso_sc <- cv.glmnet(x, y, alpha = 1)
best_lambda <- lasso_sc$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 -0.0023679722
duration           -0.0001815326
release_year       -0.0027552856
acoustictness       0.0812649420
beat_strength       0.4395871374
bounciness          -0.8228417626
danceability        0.0540884815
dyn_range_mean      0.0228099401
energy              -0.1261583504
flatness            0.1277800576
instrumentalness    -0.0765283096
key                 -0.0204720118
liveness            0.0689359419
loudness            0.0046767651
mechanism           -0.1463426787
organism            -0.0386700035
speechiness         -0.2428939108
tempo               0.0005691694
time_signature      -0.0409648214
valence             0.1198943315
```

LASSO kept all of the predictors.

```
plot(lasso_sc)
```



not sure if this is needed or not<sup>^</sup>

## Introduction and Data

### Methodology

Evaluating assumptions:

figure out to make this smaller or how to get charts to show<sup>^</sup>

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**