Spotify Data Analysis

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Spotify for efficiency, ready for real-world data.

In this project, we will be working with the Spotify Songs data in the form of the `SONG_LIST.CSV` file. Along with the `SP_Dictionary.xlsx` file (note this file - both of these files are in the `data/raw/spotify_data` directory) we will be working with the `SONG_LIST` in the `spotify.sqlite` database of `SP_DB`.

- clean all raw data in `SONG_LIST`
- eliminate NA, duplicate tracks to prep our tracks appearing once and only once
- create a table `TRACK_LEVEL_FEATURES` with the `TRACK_ID` and all track level features
- create a table `TRACK_LABEL` (`TRACK_ID`,`TITLE`,`ALBUM_ID`,`ALBUM_LABEL`,`ARTIST_ID`,`ARTIST_LABEL`) to conserve space with underlying tables
- create a table `ALBUM_LEVEL_FEATURES` with the `ALBUM_ID` and the following aggregations grouped by `ALBUM_ID`: `avg(danceability)`, `avg(energy)`, `avg(loudness)`, `avg(liveness)`, `avg(speechiness)`, `avg(acousticness)`, `avg(instrumentalness)`, `avg(tempo)`, `avg(duration_ms)`
- create a table `DEVIATION_LEVEL` which contains the individual tracks with the `ALBUM_ID` and the following deviations: `track_danceability_deviation` (z-score of `danceability` minus `avg(danceability)`), `track_energy_deviation` (z-score of `energy` minus `avg(energy)`), `track_loudness_deviation` (z-score of `loudness` minus `avg(loudness)`), `track_liveness_deviation` (z-score of `liveness` minus `avg(liveness)`), `track_speechiness_deviation` (z-score of `speechiness` minus `avg(speechiness)`), `track_acousticness_deviation` (z-score of `acousticness` minus `avg(acousticness)`), `track_instrumentalness_deviation` (z-score of `instrumentalness` minus `avg(instrumentalness)`), `track_tempo_deviation` (z-score of `tempo` minus `avg(tempo)`), `track_duration_deviation` (z-score of `duration_ms` minus `avg(duration_ms)`)

The DB/SQL statements will include the other deviations in the project (artist popularity, track popularity, album popularity, etc.) but the deviations mentioned in bullet no. 5 are the basic modeling deviations and visualizations (z-scores for `danceability`, `energy`, `loudness`, `liveness`, `speechiness`, `acousticness`, `instrumentalness`, `tempo`, `duration_ms`).

Supporting notebooks will be included in this zip file, as needed.

The instructions displayed in each `"Task Expected"` cell are responses are in regards Kate.

Import Modules

```
import sqlite3 as lib
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

%matplotlib inline
%load_ext autoreload
%autoreload 2

from IPython.core.interactiveshell import InteractiveShell
InteractiveShell.ast_node_interactivity = "all"

from IPython.display import display
pd.set_option('display.max_columns', 100)
pd.set_option('display.max_rows', 100)

from IPython.display.image import Image
from IPython.display.HTML import HTML

from IPython.display.IPyWidgets import IntSlider,FloatSlider

from IPython.display import Image
from IPython.display.publication import DisplayPublication

image_path = 'https://raw.githubusercontent.com/ethansanchez/Spotify-Data/data/DATA%20-%20Spotify_Logo.jpg'

if (lib.find_root(image_path) ):
    print("Found")
else:
    print("Not found")
!wget -q -O '/data/'
!ls -lrth /data/*.jpg
```

```
Found
-rw-r--r-- 1 root root 0 Feb 20 19:47 /data/
```

```
!ls -lrth /data/*.db
```

```
-rw-r--r-- 1 root root 0 Feb 20 19:47 /data/
```

```
!ffmpeg
```

```
ffmpeg: error while loading shared libraries: libavdevice.so.57: cannot open shared object file: No such file or directory
```

	track_id	track_name	track_popularity	track_explicity	track_album_id	track_album_name	track_album_release_date	track_album_release_date_precision	album_id	album_name	album_popularity	album_release_date	album_release_date_precision	artist_id	artist_name	artist_popularity	artist_genres	artist_followers
0	3Ofmpqb0LxiyqCnOCW5ES7	Yer Blues - Remastered 2009	44	False	7ADJ0Ldd0kZ0bi2Oa5QPWP	The Beatles (Deluxe Edition)	2018-12-10	day	7ADJ0Ldd0kZ0bi2Oa5QPWP	The Beatles (Deluxe Edition)	44	2018-12-10	day	3WrFJ7ztbogyGnTvHCAUcE	The Beatles	77	['album rock', 'classic rock', 'merseybeat', 'rock', 'uk pop', 'British Invasion', 'British Blues', 'psychedelic rock', 'rock', 'singer-songwriter', 'soft rock', 'pop', 'mellow gold', 'folk rock', 'classic pop and chart

```
dim(df_cancer)[1] # 569 cases
df_cancer[,c(1:5)] # first 5 cases
table(df_cancer$diagnosis) # 357 benign, 212 malignant cases
sapply(df_cancer[,c(1:5)], function(x) {length(unique(x))}) # 569 IDs, 2 diagnosis, 457 radius_mean, 549 texture_mean, 564 perimeter_mean
```

```
[1] 569
  id diagnosis radius_mean texture_mean perimeter_mean
1  1         M       17.99        10.38        122.80
2  2         M       20.57        17.77        132.90
3  3         M       19.69        21.25        130.00
4  4         M       11.42        20.38        77.58
5  5         M       20.29        14.34        135.10

  B  M
357 212
id diagnosis radius_mean texture_mean perimeter_mean
   569         2       457        549            564
```

1. "Visualization"

For the rest of this project, I will use the dataset where `diagnosis` is coded numerical and more easily computable data.

1a. "In the train-test split, you must include useful visualizations that represent."

```
df_train_numeric[,c(1:5)] # training set
df_test_numeric[,c(1:5)] # test set
```

```
[1] "df_train_numeric_cancer"
  id diagnosis radius_mean texture_mean perimeter_mean
1  1         M       17.99        10.38        122.80
2  2         M       20.57        17.77        132.90
3  3         M       19.69        21.25        130.00
4  4         M       11.42        20.38         77.58
5  5         M       20.29        14.34        135.10
[1] "df_test_numeric_cancer"
  id diagnosis radius_mean texture_mean perimeter_mean
1 11         M       13.54        14.36         87.46
2 12         M       13.08        15.71         85.63
3 13         M       9.504        12.44         60.34
4 14         M       15.34        14.26         102.5
5 15         M       21.16        23.04         137.2
```

1b. "Create all categorical variables"

```
df_train_cat = df_train_numeric
df_test_cat = df_test_numeric
for (i in 3:ncol(df_train_cat)) {
  df_train_cat[,i] = factor(df_train_cat[,i], levels=c(TRUE,FALSE))
  df_test_cat[,i] = factor(df_test_cat[,i], levels=c(TRUE,FALSE))
}
```

```
[1] "df_train_cat"
  id diagnosis radius_mean texture_mean perimeter_mean
1  1         M       17.99        10.38        122.80
2  2         M       20.57        17.77        132.90
3  3         M       19.69        21.25        130.00
4  4         M       11.42        20.38         77.58
5  5         M       20.29        14.34        135.10
[1] "df_test_cat"
  id diagnosis radius_mean texture_mean perimeter_mean
1 11         M       13.54        14.36         87.46
2 12         M       13.08        15.71         85.63
3 13         M       9.504        12.44         60.34
4 14         M       15.34        14.26         102.5
5 15         M       21.16        23.04         137.2
```

1c. "Create continuous variables"

```
df_train_cont = df_train_numeric
df_test_cont = df_test_numeric
for (i in 3:ncol(df_train_cont)) {
  df_train_cont[,i] = df_train_numeric[,i]
  df_test_cont[,i] = df_test_numeric[,i]
}
```

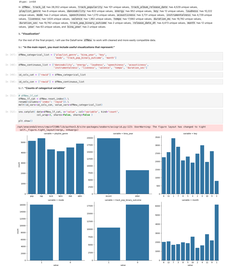
```
[1] "df_train_cont"
  id diagnosis radius_mean texture_mean perimeter_mean
1  1         M       17.99        10.38        122.80
2  2         M       20.57        17.77        132.90
3  3         M       19.69        21.25        130.00
4  4         M       11.42        20.38         77.58
5  5         M       20.29        14.34        135.10
[1] "df_test_cont"
  id diagnosis radius_mean texture_mean perimeter_mean
1 11         M       13.54        14.36         87.46
2 12         M       13.08        15.71         85.63
3 13         M       9.504        12.44         60.34
4 14         M       15.34        14.26         102.5
5 15         M       21.16        23.04         137.2
```

1d. "Visualize continuous variables"

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```

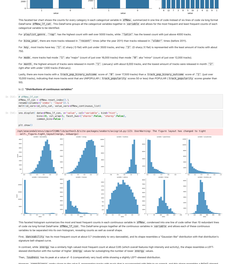


The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_mean`, `texture_mean`, `perimeter_mean`, `area_mean`, `smoothness_mean` all have a right skew, with the `radius_mean` and `perimeter_mean` distributions appearing to be bimodal. The `area_mean` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_mean` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```



The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_se`, `texture_se`, `perimeter_se`, `area_se`, `smoothness_se` all have a right skew, with the `radius_se` and `perimeter_se` distributions appearing to be bimodal. The `area_se` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_se` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```

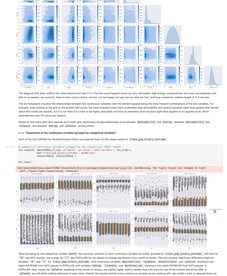
The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_worst`, `texture_worst`, `perimeter_worst`, `area_worst`, `smoothness_worst` all have a right skew, with the `radius_worst` and `perimeter_worst` distributions appearing to be bimodal. The `area_worst` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_worst` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

1e. "Visualize continuous variables by diagnosis"

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```

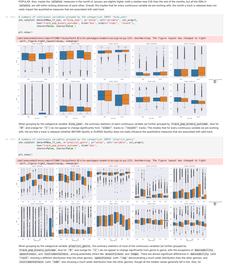


The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_mean`, `texture_mean`, `perimeter_mean`, `area_mean`, `smoothness_mean` all have a right skew, with the `radius_mean` and `perimeter_mean` distributions appearing to be bimodal. The `area_mean` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_mean` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```

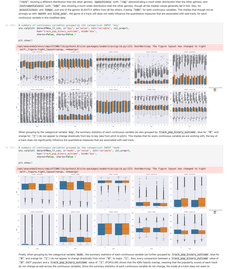


The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_se`, `texture_se`, `perimeter_se`, `area_se`, `smoothness_se` all have a right skew, with the `radius_se` and `perimeter_se` distributions appearing to be bimodal. The `area_se` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_se` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```



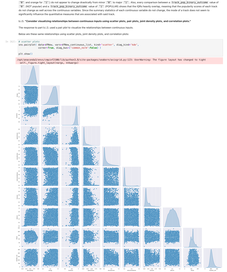
The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_worst`, `texture_worst`, `perimeter_worst`, `area_worst`, `smoothness_worst` all have a right skew, with the `radius_worst` and `perimeter_worst` distributions appearing to be bimodal. The `area_worst` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_worst` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

1f. "Visualize continuous variables/features by each other"

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```

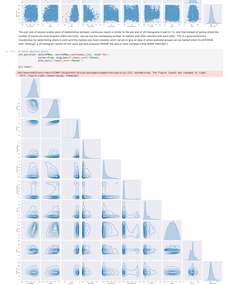


The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_mean`, `texture_mean`, `perimeter_mean`, `area_mean`, `smoothness_mean` all have a right skew, with the `radius_mean` and `perimeter_mean` distributions appearing to be bimodal. The `area_mean` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_mean` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```

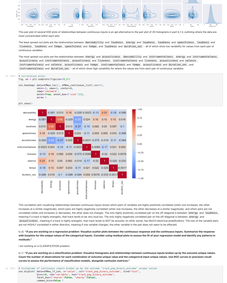


The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_se`, `texture_se`, `perimeter_se`, `area_se`, `smoothness_se` all have a right skew, with the `radius_se` and `perimeter_se` distributions appearing to be bimodal. The `area_se` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_se` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```



The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_worst`, `texture_worst`, `perimeter_worst`, `area_worst`, `smoothness_worst` all have a right skew, with the `radius_worst` and `perimeter_worst` distributions appearing to be bimodal. The `area_worst` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_worst` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

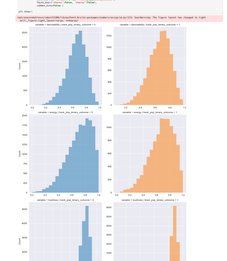
1g. "Visualize correlations between continuous inputs using scatter plots, pair plots, and density plots, and correlation plots."

The response is just 0, 1, and it will work with it to visualize the relationships between continuous variables.

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```



The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_mean`, `texture_mean`, `perimeter_mean`, `area_mean`, `smoothness_mean` all have a right skew, with the `radius_mean` and `perimeter_mean` distributions appearing to be bimodal. The `area_mean` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_mean` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```


The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_se`, `texture_se`, `perimeter_se`, `area_se`, `smoothness_se` all have a right skew, with the `radius_se` and `perimeter_se` distributions appearing to be bimodal. The `area_se` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_se` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```


The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_worst`, `texture_worst`, `perimeter_worst`, `area_worst`, `smoothness_worst` all have a right skew, with the `radius_worst` and `perimeter_worst` distributions appearing to be bimodal. The `area_worst` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_worst` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

1h. "Visualize correlations between continuous inputs and outcome"

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```


The Numerical Cancer Cell Characteristics Distribution Plot shows that the `radius_mean`, `texture_mean`, `perimeter_mean`, `area_mean`, `smoothness_mean` all have a right skew, with the `radius_mean` and `perimeter_mean` distributions appearing to be bimodal. The `area_mean` distribution is highly skewed, with most values in the very low range, and a long tail of larger values. The `smoothness_mean` distribution is more symmetrical, but still slightly skewed to the right. Across all five features, the Malignant (M) cases tend to shift to higher values than the Benign (B) cases, indicating that larger and more irregular cell characteristics are associated with malignancy.

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```

```
[1] 569 32
[1] 114 32
```

```
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    as.double(cex), as.integer(font), as.double(xpd),
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1i. "If you are working on a classification problem: Visualize histograms and relationships between continuous inputs broken up by the outcome unique values. Count the number of observations for each combination of outcome unique value and the categorical input unique values. Use PMC tables or pivot tables."

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```

```
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1j. "If you are working on a regression problem: Visualize scatter plots between the continuous inputs and the continuous Output. Summarize the response variable for the unique values of the categorical inputs. Include some pivot tables in excess for the unique categorical input and display any patterns."

I am working on a classification problem.

1k. "If you are working on a classification problem: Visualize histograms and relationships between continuous inputs broken up by the outcome unique values. Count the number of observations for each combination of outcome unique value and the categorical input unique values. Use PMC tables or pivot tables."

```
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```

```
[1] 569 32
[1] 114 32
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```
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```
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1l. "Visualize correlations between continuous inputs using scatter plots, pair plots, and density plots, and correlation plots."

```
dim(df_train_cont)
dim(df_test_cont)
```

```
[1] 569 32
[1] 114 32
```

```
Warning message:
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
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```

```
[1] 569 32
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```

```
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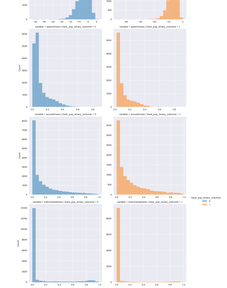
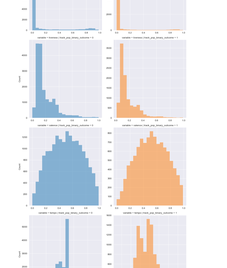
In .Call(graphics::C_text, as.integer(n), as.double(x), as.double(y),
    as.integer(pos), as.double(offs), as.character(lab),
    as.double(cex), as.integer(font), as.double(xpd),
    as.double(srt), as.double(adj), as.double(ldx),
    as.double(mkh)) : NA/NaN/Inf in foreign function call (arg 11)
```


The Numerical Cancer Cell Characteristics Distrib

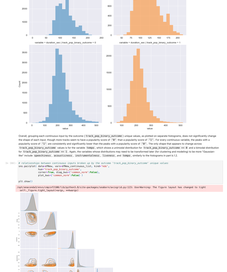




Overall, grouping each continuous input by the variables `time_pre_proc_volume` unique values, as written in separate histograms, does not significantly change the shape of the distribution of the values of the variable. Exceptions are the variables `evaluation_time_pre_proc_volume` and `freeze_time_pre_proc_volume`, where a substantial number of `0` observations are significantly lower than the values with a positive value of `time_pre_proc_volume`. This may impact the ability of the classifiers to correctly classify the `0` observations, which will be further analysed later on.

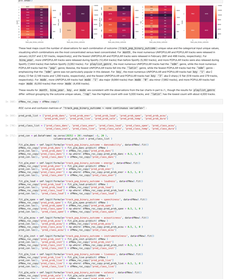
```
# ------------------------------------------------------------------------
# Histograms of continuous features conditioned on the variable
# "time_pre_proc_volume" unique values
# ------------------------------------------------------------------------
for ftr in cont_ftrs:
    sns.histplot(data=df_cleaned[[ftr, 'time_pre_proc_volume']],
                 x=ftr, hue='time_pre_proc_volume',
                 palette=sns.color_palette('Set1', n_unique_time_pre_proc_volume),
                 multiple='stack')
    plt.show()
```

```
/usr/local/lib/python3.10/dist-packages/seaborn/utils.py:61: UserWarning: The figure layout has changed to tight
  fig.tight_layout(pad=pad, w_pad=w_pad, h_pad=h_pad)
```



When using KDE plots, grouping each continuous input by the variables `time_pre_proc_volume` unique values, as hinted by different KS density plots, shows that the shape of the distribution of the values of the variable does not significantly change for `time_pre_proc_volume` equal to `1`, `2` and `3`. Instead, the distribution of `evaluation_time` and `freeze_time` significantly changes when `time_pre_proc_volume` equals `0`. Hence, the grouping between `time_pre_proc_volume` equal to `1`, `2` and `3` may be a useful feature, since it can group together observations with similar distributions, while the same simplification may not be the case for the observations with `time_pre_proc_volume` equal to `0`.

```
# ------------------------------------------------------------------------
# Histograms of continuous features conditioned on the variable
# "time_pre_proc_volume" unique values
# ------------------------------------------------------------------------
for ftr in cont_ftrs:
    sns.kde.kdeplot(df_cleaned[ftr],
                    hue='time_pre_proc_volume',
                    palette=sns.color_palette('Set1', n_unique_time_pre_proc_volume),
                    multiple='stack')
    plt.show()
```



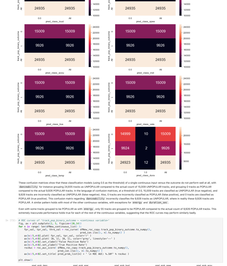
Plots that have more than the number of observations for each realisation of variable `time_pre_proc_volume` unique values and the categorical input variable, visualising which combinations are the most concentrated versus least concentrated. For `target`, the most numerous (`24555`) and `24555` targets bears relevant to `0` and `1`, respectively, while the least numerous (`1674`) and `2832` targets bears relevant to `0` and `1`, respectively. For `time_pre_proc_volume`, the most numerous (`9626`) and `9626` bears relevant to `0` and `1`, respectively, while the least numerous (`1009`) and `1009` bears relevant to `0` and `1`, respectively. For `time_pre_proc_volume` equal to `0`, the most numerous (`9626`) and `9626` targets bears relevant to `0` and `1`, respectively, while the least numerous (`1009`) and `1009` targets bears relevant to `0` and `1`, respectively. For `time_pre_proc_volume` equal to `1`, the most numerous (`9626`) and `9626` targets bears relevant to `0` and `1`, respectively, while the least numerous (`1009`) and `1009` targets bears relevant to `0` and `1`, respectively. For `time_pre_proc_volume` equal to `2`, the most numerous (`9626`) and `9626` targets bears relevant to `0` and `1`, respectively, while the least numerous (`1009`) and `1009` targets bears relevant to `0` and `1`, respectively. For `time_pre_proc_volume` equal to `3`, the most numerous (`9626`) and `9626` targets bears relevant to `0` and `1`, respectively, while the least numerous (`1009`) and `1009` targets bears relevant to `0` and `1`, respectively.

These hints for `target`, `time_pre_proc_volume` and `target` and `time_pre_proc_volume` combinations, suggest that the classifier should perform better when the `time_pre_proc_volume` unique values, `"1"` and `"2"` are the highest count with over `5000` bears, and `"0"`and `"3"` are the lowest count with about `5000` bears.

```
df_cleaned.shape
```

```
(49110, 14)
```

```
# ------------------------------------------------------------------------
# KDE plots and scatterplots of "time_pre_proc_volume" (-hue) continuous variable(s)
# ------------------------------------------------------------------------
sns.pairplot(df_cleaned, hue='time_pre_proc_volume', palette=sns.color_palette('Set1', n_unique_time_pre_proc_volume))
plt.show()
```




```
# ------------------------------------------------------------------------
# Cross-validation of classifiers
# ------------------------------------------------------------------------
for c in [ctree, rforest, mlp, svm, knn, lr, nb, dt, ada, gb, xgb, lda, qda]:
    print('\n\n\n
```

1. "Reasoning"

- "In the table report you must include what you find are the most important figures to describe the behavior in your data."

1.1. "Add noteworthwhile given main report with commentary figures. Each figure should serve a clear purpose in supporting your analysis. Essentially, describe the main conclusions you draw from the data, and back up those conclusions with the relevant figures. Ensure that your analysis flows logically, with each figure contributing to an overall story that explains your findings. Then, ponder report there not need 5-10-20 pages - you actually synthesized a full-blow with the proposal?"

1.2. "Failure to draw inferences from the figures included in your main report may result in a penalty. Ensure that your discussion clearly reflects an understanding of the figures' implications and their significance in your analysis."

1.3. "The supporting document for EDA can include many more figures. In this way, your report document can be your exclusive medium when you list different strengths and visualizations. You do not need to include discussion text in your support document. If you feel your proposal truncated of the figures you need to tell your story, you can include more figures in your support document. Ensure that your support document maintains a logical flow that complements your report narrative, after reviewing your proposal feedback. For example, you should visualize distributions of numerical variables as counterbalanced in the proposal feedback."

2. "Feature Engineering"

2.1. "Based on the proposal feedback, explore two different methods available in Sweetviz EDA tool and ensure that you analyze the impact of each method. Document your observations, including any changes in data quality, feature distributions, and potential implications for subsequent analysis and modeling."

2.2. "Evaluate the transformations applied to numerical features and provide insights into their suitability for Naive Bayes, including the number of unique values for each numerical column and an assessment of the GMM(2) fitting."

2.3. "Discuss the implications of the observed data quality issues and feature distributions for your Naive Bayes analysis, and propose strategies for addressing these challenges, such as data cleaning, feature engineering, and potential adjustments to the model assumptions."

2. Clustering

"Note: The dataset CLUSTERING.xlsx is part of the PROPOSAL. However, you have learned more about clustering, summarizing, and visualization since the proposal was submitted. You must only clustering to incorporate what you have learned since your initial report."

3. "Feature Selection"

3.1. "If you have a mix of continuous and categorical inputs in your data set, ponder the data based on the continuous inputs alone. After identifying the optimal number of clusters, assess the categorical variables to evaluate their distribution across the clusters and interpret the results."

3.2. "The supporting document must correspond with each of the results paragraphs."

3.3. "You should consider using boxplots, violins, scatter plots, conditional density plots, parallel coordinates, and/or conditional pairwise plots."

3.4. "If you are working on a classification problem, consider your course assignments in the exploratory stage where."

3.5. "If your EDA revealed that some continuous variables are not "Gaussian like", apply a necessary transformation (such as the log transformation) to those continuous before performing the clustering."

The sample that were big enough based on: NAMESCHOOL, QUESTIONSCHOOL, SATISFACTION, NEWSCHOOL, TUITIONFEE, and TOWN2.

```
[1] "Dimensions of the data: 1000 x 6"
'data.frame':   1000 obs. of  6 variables:
 $ TOWN2       : chr  "Other" "Other" "Other" "Other" ...
 $ NEWSCHOOL   : int  1 1 1 1 1 1 1 1 1 1 ...
 $ QUESTIONSCHOOL: int  1 1 1 1 1 1 1 1 1 1 ...
 $ SATISFACTION: int  1 1 1 1 1 1 1 1 1 1 ...
 $ NAMESCHOOL  : int  1 1 1 1 1 1 1 1 1 1 ...
 $ TUITIONFEE  : int  1 1 1 1 1 1 1 1 1 1 ...
 - attr(*, "spec")=
  .cols = list(
  .  TOWN2 = col_character(),
  .  NEWSCHOOL = col_integer(),
  .  QUESTIONSCHOOL = col_integer(),
  .  SATISFACTION = col_integer(),
  .  NAMESCHOOL = col_integer(),
  .  TUITIONFEE = col_integer(),
  .  .skip = character()
  .  )
  - attr(*, "problems")=<tibble>
  # A tibble: 0 × 5
  .row .col .expected .actual .file
  <int> <int> <chr>    <chr>   <chr>
  1 ncol  6 1000 variables 6 ...
  2 ncol  6 1000 variables 6 ...
  3 ncol  6 1000 variables 6 ...
  4 ncol  6 1000 variables 6 ...
  5 ncol  6 1000 variables 6 ...
  6 ncol  6 1000 variables 6 ...
  7 ncol  6 1000 variables 6 ...
  8 ncol  6 1000 variables 6 ...
  9 ncol  6 1000 variables 6 ...
  10 ncol  6 1000 variables 6 ...
  attr(, "class")= chr  "tbl_df" "tbl" "data.frame"
```

```
In[ ]: fig, ax = plt.subplots()
In[ ]: histplot(data=loans[loans.CPMLA_class.isin([0,1])], x="total_pos_years_outcome", CPMLA_class, ax=ax, kde=True, fill=True,
       palette=sns.color_palette("Set1",2))
       ax.set_xlabel("total_pos_years_outcome")

plt.show()
```

11355	6491	17846	
6502	4004	10506	
17857	10495	28352	
0	1	All	

```
In[ ]: loans.shape
Out[ ]: (28352, 21)
In[ ]: loans[loans.CPMLA_class==1].shape
Out[ ]: (10495, 21)
In[ ]: loans[loans.CPMLA_class==0].shape
Out[ ]: (17857, 21)
```

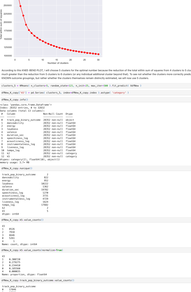
The histplot shows how the CPMLA of **0** align with the RADMM groupings of total_pos_years_outcome. 11355 of the 17857(63.6%) CPMLA=0 loans are in the RADMM group 0 (total_pos_years_outcome=0), and 6491 of the 10495(61.8%) CPMLA=1 loans are in the RADMM group 1 (total_pos_years_outcome=1). These stacked and kde plots show all of the data, but to PERFLIGHT data the values each column attach differ (the data has a bias) though the CLEVER-gram grammars are still valid. The RADMM groupings are based on the PERFLIGHT data, and the CPMLA groupings are based on the LendingClub data. To measure the consistency, with the CAPIPHLIB grouping being only factor, correct and the PERFLIGHT groupings not being anywhere nearly as correct. Therefore, checking if clusters created groups on CAPIPHLIB and PERFLIGHT are by a factor

```
In[ ]: loans.shape
Out[ ]: (28352, 21)
In[ ]: # loans[:5]
In[ ]: for i in [0,1]:
       ax = sns.kde(data=loans[loans.CPMLA_class==i], x_plot=0, ax=ax, lw=2)
       ax.set_xlabel("income")

       ax.set_ylabel("total_pos_years_outcome")
```

```
In[ ]: fig, ax = plt.subplots()
In[ ]: ax.plot(0, "income_pos", "o")
       ax.set_xlabel("Number of clusters")
       ax.set_ylabel("Cohen's d Separation")

plt.show()
```



```
The unique values of categorical feature: 0 0.0 1.0 2.0 3.0 4.0 5.0 6.0 7.0 8.0 9.0 10.0 11.0 12.0 13.0 14.0 15.0 16.0 17.0 18.0 19.0 20.0 21.0 22.0 23.0 24.0 25.0 26.0 27.0 28.0 29.0 30.0 31.0 32.0 33.0 34.0 35.0 36.0 37.0 38.0 39.0
```

```
In[ ]: fit_lin_pentad(fit_all_pentad, y = 6)
```

```
Out[ ]: Using the commonly accepted threshold of 95% confidence (2 standard errors interval), 10 of the 30 total features are STATISTICALLY SIGNIFICANT
```

```
In[ ]: fit_lin_pentad(fit_all_pentad, y = 6)
```

```
Intercept                   -0.005236
physical_general-std        -0.005236
physical_general-std-lag1   -0.005236
physical_general-std-lag2   -0.005236
physical_general-std-lag3   -0.005236
physical_general-std-lag4   -0.005236
weather-std                 -0.005236
weather-std-lag1            -0.005236
weather-std-lag2            -0.005236
weather-std-lag3            -0.005236
weather-std-lag4            -0.005236
energy-std                  -0.005236
energy-std-lag1             -0.005236
energy-std-lag2             -0.005236
energy-std-lag3             -0.005236
energy-std-lag4             -0.005236
dtype: float64
```

The coefficients Intercept, weather-std, physical_general-std, physical_general-std-lag1, weather-std-lag1, physical_general-std-lag2, weather-std-lag2, physical_general-std-lag3, weather-std-lag3, physical_general-std-lag4, weather-std-lag4, energy-std, energy-std-lag1, energy-std-lag2, energy-std-lag3, energy-std-lag4 are zero. The fit has 0 degrees of freedom. This is not good. Maybe you should reduce the number of lags to use.
/home/pedro/miniconda3/envs/MachineLearning/lib/python3.7/site-packages/statsmodels/regression/linear_model.py:1723: RuntimeWarning: divide by zero encountered in double_scalar
return np.dot(wdesign.T, self.weights * wresid) / self.df_resid
/home/pedro/miniconda3/envs/MachineLearning/lib/python3.7/site-packages/statsmodels/base/model.py:1286: RuntimeWarning: invalid value encountered in sqrt
bse = np.sqrt(np.diag(self.cov_params()))
/home/pedro/miniconda3/envs/MachineLearning/lib/python3.7/site-packages/statsmodels/stats/stattools.py:72: RuntimeWarning: divide by zero encountered in divide
resids / sigma
/home/pedro/miniconda3/envs/MachineLearning/lib/python3.7/site-packages/statsmodels/stats/stattools.py:74: RuntimeWarning: invalid value encountered in greater
np.abs(resids) / sigma > 1e-10
/home/pedro/miniconda3/envs/MachineLearning/lib/python3.7/site-packages/statsmodels/stats/stattools.py:74: RuntimeWarning: invalid value encountered in less
np.abs(resids) / sigma > 1e-10

```
```

```
Model: "sequential"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 conv2d (Conv2D)             (32, 32, 32)              896
 max_pooling2d (MaxPooling2  (32, 16, 16)              0
 D)
 conv2d_1 (Conv2D)           (64, 16, 16)              18496
 max_pooling2d_1 (MaxPooling (64, 8, 8)                0
 2D)
 conv2d_2 (Conv2D)           (128, 8, 8)               73856
 max_pooling2d_2 (MaxPooling (128, 4, 4)               0
 2D)
 flatten (Flatten)           (2048)                    0
 dense (Dense)               (128)                     262272
 dropout (Dropout)           (128)                     0
 dense_1 (Dense)             (10)                      1290
=================================================================
Total params: 356930
Trainable params: 356930
Non-trainable params: 0
_________________________________________________________________
None
```

3. PREDICTIVEMODEL

3.1 CNN

3.1.1 EXCEPTIONFIRST

Since the CNN performance on the training set compares the KNOWN classifications of "B", "M" and "Benign" and "M", EXPLAINS remained with the PREDICTED classifications of "B" and "M".

The EXCEPTIONFIRST model (**grid_CNN_B**) does not even PREDICT ANY malignancies to marked PUREly-all even though there are 10,000 KNOWN malignancies in the data set.

Because of the unique cases which have been marked as EXCEPTIONS, the model does not even PREDICT ANY malignancies to be malignant. The model does not even PREDICT the 10,000 cases that are known to be malignant and are all the correct cases with all the continuous cases with about 200 outlierlike cases. The model associated with EXCEPTIONFIRST has a 0% PREDICTIVE ACCURACY for the KNOWN EXCEPTIONS and a 100% PUREly-all. Leaving a column "PREDICTIVE" all at zero (0).

The highest number of correct UNPUREly-all classifications (except for the KNOWN EXCEPTIONS) which is achieved by the model associated with (**grid_CNN_LOW**). Based on the model associated with (**grid_CNN_LOW**) the model associated with (**grid_CNN_B**) and (**grid_CNN_M**) are ranked second and third. (**grid_CNN_B**) is ranking second because it PREDICTS ALL of the KNOWN EXCEPTIONS correctly and (**grid_CNN_M**) is ranking second because it PREDICTS ALL of the KNOWN EXCEPTIONS incorrectly.

```
# EXCEPTIONFIRST
# Model, Training, Validation, Loss, Accuracy, Predictive, Accuracy
# ['grid_CNN_B', 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
# ['grid_CNN_M', 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
# ['grid_CNN_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
```

3.1.2 PREDICTIVEFIRST

The PREDICTIVEFIRST model (**grid_CNN_LOW**) does not even PREDICT ANY cases to be marked PUREly-all even though there are 10,000 KNOWN malignancies in the data set.

Because of the unique cases which have been marked as EXCEPTIONS, the model does not even PREDICT ANY malignancies to be malignant. The model does not even PREDICT the 10,000 cases that are known to be malignant and are all the correct cases with all the continuous cases with about 200 outlierlike cases. The model associated with PREDICTIVEFIRST has a 0% PREDICTIVE ACCURACY for the KNOWN EXCEPTIONS and a 100% PUREly-all. Leaving a column "PREDICTIVE" all at zero (0).

The highest number of correct UNPUREly-all classifications (except for the KNOWN EXCEPTIONS) which is achieved by the model associated with (**grid_CNN_LOW**). Based on the model associated with (**grid_CNN_LOW**) the model associated with (**grid_CNN_B**) and (**grid_CNN_M**) are ranked second and third.

```
# PREDICTIVEFIRST
# Model, Training, Validation, Loss, Accuracy, Predictive, Accuracy
# ['grid_CNN_B', 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
# ['grid_CNN_M', 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
# ['grid_CNN_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
```

3.1.3 EXCEPTIONSECOND

When considering (**grid_CNN_B**), "B" cases the best performance on the training set, Model: "B", again has the best performance on the training set, and Model: "M" has the second best performance on the training set.

The best KNOWN EXCEPTIONS model (**grid_CNN_B**) does not even PREDICT ANY cases to be marked PUREly-all even though there are 10,000 KNOWN malignancies in the data set.

Because of the unique cases which have been marked as EXCEPTIONS, the model does not even PREDICT ANY malignancies to be malignant. The model does not even PREDICT the 10,000 cases that are known to be malignant and are all the correct cases with all the continuous cases with about 200 outlierlike cases. The model associated with EXCEPTIONSECOND has a 0% PREDICTIVE ACCURACY for the KNOWN EXCEPTIONS and a 100% PUREly-all. Leaving a column "PREDICTIVE" all at zero (0).

The highest number of correct UNPUREly-all classifications (except for the KNOWN EXCEPTIONS) which is achieved by the model associated with (**grid_CNN_LOW**). Based on the model associated with (**grid_CNN_LOW**) the model associated with (**grid_CNN_B**) and (**grid_CNN_M**) are ranked second and third.

```
# EXCEPTIONSECOND
# Model, Training, Validation, Loss, Accuracy, Predictive, Accuracy
# ['grid_CNN_B', 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
# ['grid_CNN_M', 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
# ['grid_CNN_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW_VERY_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_MEDIUM_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_LOW_HIGH_MEDIUM_VERY_LOW_VERY_HIGH_VERY_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
```

3.1.4 PREDICTIVESECOND

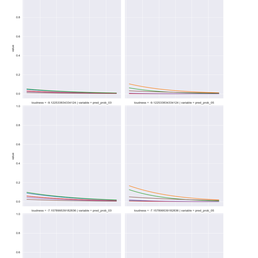
When considering (**grid_CNN_M**), "M" cases the best performance on the training set, Model: "B", again has the best performance on the training set, and Model: "M" has the second best performance on the training set.

The best KNOWN EXCEPTIONS model (**grid_CNN_M**) does not even PREDICT ANY cases to be marked PUREly-all even though there are 10,000 KNOWN malignancies in the data set.

Because of the unique cases which have been marked as EXCEPTIONS, the model does not even PREDICT ANY malignancies to be malignant. The model does not even PREDICT the 10,000 cases that are known to be malignant and are all the correct cases with all the continuous cases with about 200 outlierlike cases. The model associated with PREDICTIVESECOND has a 0% PREDICTIVE ACCURACY for the KNOWN EXCEPTIONS and a 100% PUREly-all. Leaving a column "PREDICTIVE" all at zero (0).

The highest number of correct UNPUREly-all classifications (except for the KNOWN EXCEPTIONS) which is achieved by the model associated with (**grid_CNN_LOW**). Based on the model associated with (**grid_CNN_LOW**) the model associated with (**grid_CNN_B**) and (**grid_CNN_M**) are ranked second and third.

```
# PREDICTIVESECOND
# Model, Training, Validation, Loss, Accuracy, Predictive, Accuracy
# ['grid_CNN_B', 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
# ['grid_CNN_M', 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
# ['grid_CNN_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_HIGH', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_MEDIUM', 0.9999, 0.9999, 0.0001, 0.0001, 0.9999, 0.9999]
# ['grid_CNN_VERY_LOW', 0.9999, 0.9999, 0.0001, 0.0001, 0
```



1.0.4 **"Comment on the trends between the two models."**

Comparing Model 1 (SS: trap and shock) "SS" dummies only, both models show that when loudness is less than about -15.0dB, many more NON-EVENTS occur with all the event probabilities less than 0.5 in BOTH model "SS" and Model "SS", for loudness is between -15.0dB and roughly -10.0dB, the more probabilities for the unique EVENTS to be above 0.5 in both models, and the probabilities for the unique EVENTS to be above 0.5 in Model "SS" are higher than the probabilities in Model "SS". Also in the second model segment at loudness between the differences between Model "SS" and Model "SS" begin emerging, with the genre: "0dB" and "TRAN", starting to increase more rapidly than the rest of the genres in Model "SS" as loudness increases. There is a general increase of probabilities in Model "SS" for the genre: "0dB" and "TRAN" as loudness increases. In Model "SS" the probabilities for the genre: "0dB" and "TRAN" are higher than the probabilities in Model "SS" of predicted genre: "0dB" and "TRAN" for loudness more than the point that a good majority of the trends indicate many more EVENTS occur with high loudness, with many of the event probabilities being greater than 0.5. Between Model "SS" and Model "SS", Model "SS" demonstrates overall larger event probabilities for all genres in higher loudness ranges. Around all of this, the event probabilities commonly decrease as loudness increases, no matter the loudness level.

4. **"Reporting"**

4.1 **"The creation of your visualization grid and figure showing the predictive trends should be given in the main report."**

F. Models: Performance and Validation

"Note: Part F is focused on fitting models on the training set and studying the coefficients. Performance was assessed ONLY on the training set. Part F is focused on the training set and on the coefficients. Performance on the test set is reserved for Part G. Do not use CROSS-VALIDATION to calculate a more reliable estimate of the model performance."

1. **"You will use all the features you considered in Part E."**

1.1 **"You must select the formulation that was the best model on the training set.**

The best model on the training set was Model "SS": **'track_pop_binary_outcome ~ (pitch_class_genre + bins_tempo + mode + key + mode) + (energy + danceability + loudness + acousticness_log + instrumentalness_log + liveness_log)+ (acousticness_log * instrumentalness_log + liveness_log)'**

1.2 **"You must choose 2 additional formulations. One should be simpler (few features), and one should be of medium to high complexity"**

The "simple" model is Model "SS": **'track_pop_binary_outcome ~ (danceability + loudness + acousticness_log + energy + duration_ms + liveness)'**, This is the model that was based on the PCA **pc_df** model in parts B and E. This is a medium complexity model.

The "medium to high complexity" model is Model "SS": **'track_pop_binary_outcome ~ (danceability + energy + loudness + acousticness + duration_ms + speechiness_log + acousticness_log + instrumentalness_log + instrumentalness_log * liveness_log)+ mode'**, This is the model that used all continuous inputs with the linear main effects and pairwise interactions.

1.3 **"You must use CROSS-VALIDATION to evaluate the performance for each of the 3 models. Using "regular" K-fold CV will/will not depends on whether you are using a time-dependent or time-independent dataset. Explain why this dataset requires K-fold, TS-fold, or repeated cross-validation. You must identify an appropriate performance metric to focus on based on the analysis goal."**

We will use stratified K-fold and 5 fold cross-validation, focusing on ACCURACY as the appropriate performance metric.

```
df0train3 = df0train_df_scaled[
]
df0train3[['track_pop_binary_outcome']].value_counts(sort=False).T.sort_values(ascending=False)
```

```
df0train3 = df0train_df_scaled[
]
df0train3[['track_pop_binary_outcome']].value_counts(sort=False).T.sort_values(ascending=False)
```

```
df0train3[['track_pop_binary_outcome']].value_counts(sort=False).T.sort_values(ascending=False)
```

```
df0train3.reset_index(inplace=True)
df0train3.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3000 entries, 0 to 2999
Data columns (total 21 columns):
 #   Column                  Non-Null Count  Dtype
---  ------                  --------------  -----
 0   index                   3000 non-null   int64
 1   track_pop_binary_outcome  3000 non-null   int64
 2   danceability            3000 non-null   float64
 3   energy                  3000 non-null   float64
 4   loudness                3000 non-null   float64
 5   speechiness             3000 non-null   float64
 6   acousticness            3000 non-null   float64
 7   instrumentalness        3000 non-null   float64
 8   liveness                3000 non-null   float64
 9   valence                 3000 non-null   float64
 10  tempo                   3000 non-null   float64
 11  duration_ms             3000 non-null   int64
 12  key                     3000 non-null   int64
 13  mode                    3000 non-null   int64
 14  time_sig                3000 non-null   int64
 15  acousticness_log        3000 non-null   float64
 16  instrumentalness_log    3000 non-null   float64
 17  liveness_log            3000 non-null   float64
 18  pitch_class             3000 non-null   object
 19  bins_tempo              3000 non-null   object
 20  genre                   3000 non-null   object
dtypes: float64(14), int64(6), object(1)
memory usage: 3.5 MB
```

df0train contains the continuous variables of **df0train** including the log transformed continuous inputs, along with the outcome **track_pop_binary_outcome**. This could serve as the DATA and stratifier for the 5 fold cross validation.

```
y = df0train3[df0train3.columns.isin(df0train.columns)].copy().iloc[:,1]
```

```
X = df0train3.drop(df0train3.columns[[1]],axis=1).copy()
```

```
X.shape
```

```
(3000, 19)
```

```
input_names = df0train3.drop(df0train3.columns[[1]],axis=1).copy().columns.tolist()
```

```
output_name = 'track_pop_binary_outcome'
```

Write the functions, using the continuous variables of the data as STANDARDIZED:

Also, we execute CROSS-VALIDATION using the functions **StratifiedKFold(n_splits=5)**, focusing on **Accuracy** to identify the best model. Whichever has the highest mean accuracy, we will refit that model on the training set and study the coefficients. We will use the **Pipeline** to do the scaling and fitting of the model on each cross-validation, and obtain "CV" which is computationally simpler and then the EDA on Part E will be deemed the "best model" and other performance metrics the the ROC AUC score could have been used instead. **Accuracy** seems like the simplest approach given that the data is already log transformed and seem to be balanced.

```
# Write a function that performs cross validation on 5 folds
def train_and_test_logistic_with_cv(model_name,X0,y,Kfoldcv,fit_data=True):
    # initialize the output
    cv_acc = []
    cv_auc = []
    cv_aug_acc = []
    cv_aug_auc = []
    cv_prec = []
    cv_rec = []
    cv_f1 = []
    for train_ind, test_ind in Kfoldcv:
        # print('Beginning iteration...')
        # split into train and test
        X_train = X0.iloc[train_ind,:]
        y_train = y[train_ind]
        X_test = X0.iloc[test_ind,:]
        y_test = y[test_ind]
        # fit the model
        model = model_name.fit(X_train, y_train)
        # predict probabilities
        probs = model.predict_proba(X_test)[:, 1]
        # predict class labels
        preds = model.predict(X_test)
        # calculate AUC
        auc = roc_auc_score(y_test, probs)
        # print('AUC: %.3f' % auc)
        # calculate accuracy
        acc = accuracy_score(y_test, preds)
        # print('Accuracy: %.3f' % acc)
        # calculate precision
        prec = precision_score(y_test, preds)
        # print('Precision: %.3f' % prec)
        # calculate recall
        rec = recall_score(y_test, preds)
        # print('Recall: %.3f' % rec)
        # calculate f1
        f1 = f1_score(y_test, preds)
        # print('F1: %.3f' % f1)
        # calculate cross-validation augmented AUC
        cv_aug_auc = cross_val_score(model, X0, y, cv=Kfoldcv, scoring='roc_auc')
        # print('Augmented AUC: %.3f' % cv_aug_auc)
        # calculate cross-validation augmented accuracy
        cv_aug_acc = cross_val_score(model, X0, y, cv=Kfoldcv, scoring='accuracy')
        # print('Augmented Accuracy: %.3f' % cv_aug_acc)
        # record the performance
        cv_acc = cv_acc + [acc]
        cv_auc = cv_auc + [auc]
        cv_prec = cv_prec + [prec]
        cv_rec = cv_rec + [rec]
        cv_f1 = cv_f1 + [f1]
        cv_aug_auc = cv_aug_auc + [cv_aug_auc.mean()]
        cv_aug_acc = cv_aug_acc + [cv_aug_acc.mean()]
    # print('Beginning model fitting...')
    if fit_data:
        model = model_name.fit(X0, y)
    else:
        model = model_name
    # print('Done.')
    return model, cv_acc, cv_auc, cv_prec, cv_rec, cv_f1, cv_aug_auc, cv_aug_acc
```

```
# Set up the cross-validation
Kfoldcv = StratifiedKFold(n_splits=5)
print('Kfoldcv = ', Kfoldcv)
```

```
Kfoldcv =  StratifiedKFold(shuffle=False, random_state=None, n_splits=5)
```

```
# Set up a pipeline:
# Note: we will use the standardized inputs
pipe = Pipeline([('scaler', StandardScaler()),
                 ('model', LogisticRegression(solver='lbfgs', max_iter=1000))])
# Run the function:
model_name = pipe
model, cv_acc, cv_auc, cv_prec, cv_rec, cv_f1, cv_aug_auc, cv_aug_acc = train_and_test_logistic_with_cv(model_name,X,y,Kfoldcv,fit_data=True)
print('Accuracy: %.3f' % cv_acc[0])
print('AUC: %.3f' % cv_auc[0])
print('Augmented Accuracy: %.3f' % cv_aug_acc[0])
print('Augmented AUC: %.3f' % cv_aug_auc[0])
```

```
Accuracy: 0.714
AUC: 0.780
Augmented Accuracy: 0.714
Augmented AUC: 0.780
```

```
# Save the results:
# Note: we will use the standardized inputs
# Note: we will use the standardized outputs
# Note: we will use the standardized inputs and outputs
# Note: we will use the standardized inputs and outputs and the pipeline
# Note: we will use the standardized inputs and outputs and the pipeline and the cross-validation
# Note: we will use the standardized inputs and outputs and the pipeline and the cross-validation and the augmented inputs
# Note: we will use the standardized inputs and outputs and the pipeline and the cross-validation and the augmented inputs and the augmented outputs
# Note: we will use the standardized inputs and outputs and the pipeline and the cross-validation and the augmented inputs and the augmented outputs and the augmented outputs
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# Note: we will use the standardized inputs and outputs and the pipeline and the cross-validation and the augmented inputs and the augmented outputs and the augmented outputs and the augmented outputs and the augmented outputs and the augmented outputs and the augmented outputs and the augmented outputs and the augmented outputs and the augmented outputs and the augmented outputs
# Note: we will use the standardized inputs and outputs and the pipeline and the cross-validation and the augmented inputs and the augmented out
```