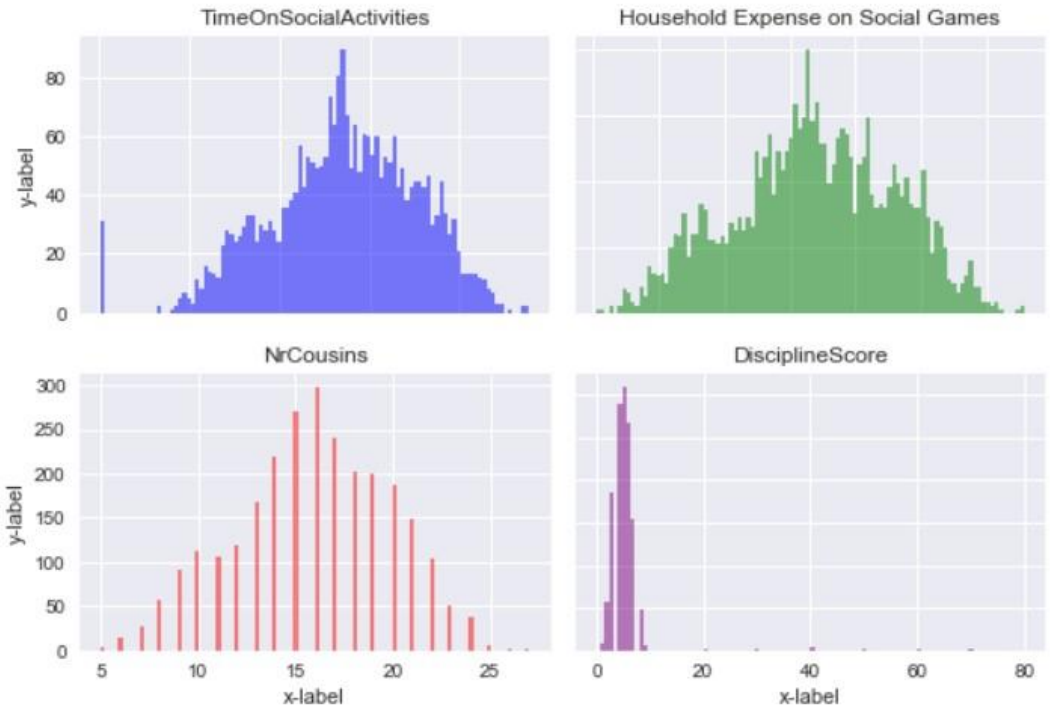
Feature Extraction Analysis

Some of the features have anomalies that skew the results greatly and therefore we truncated these features.

For example :



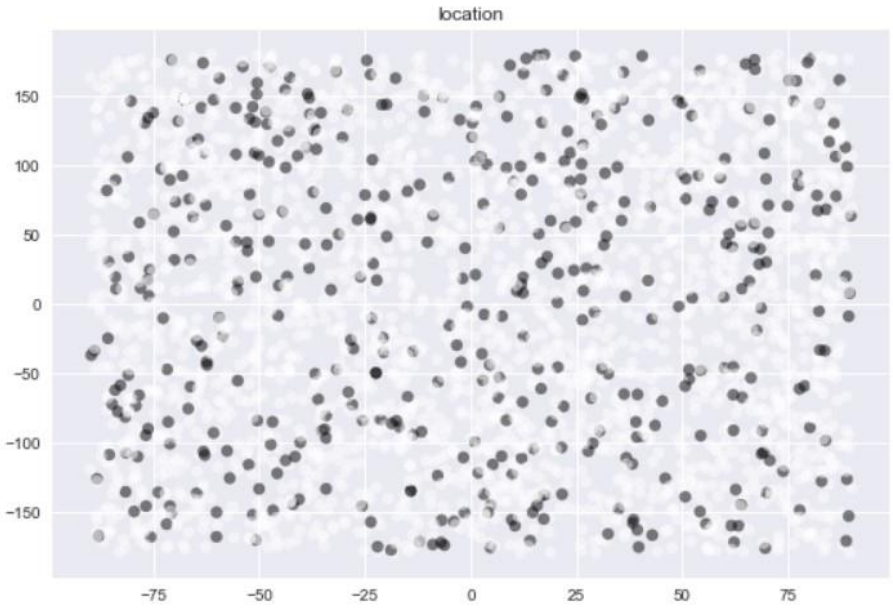
Time on Social Media and Discipline Score have major outliers so those were truncated.

The bmi score had data that was anomalous because it was physically impossible because bmi = weight/ (height)^2. Therefore, any bmi above 45 was truncated.

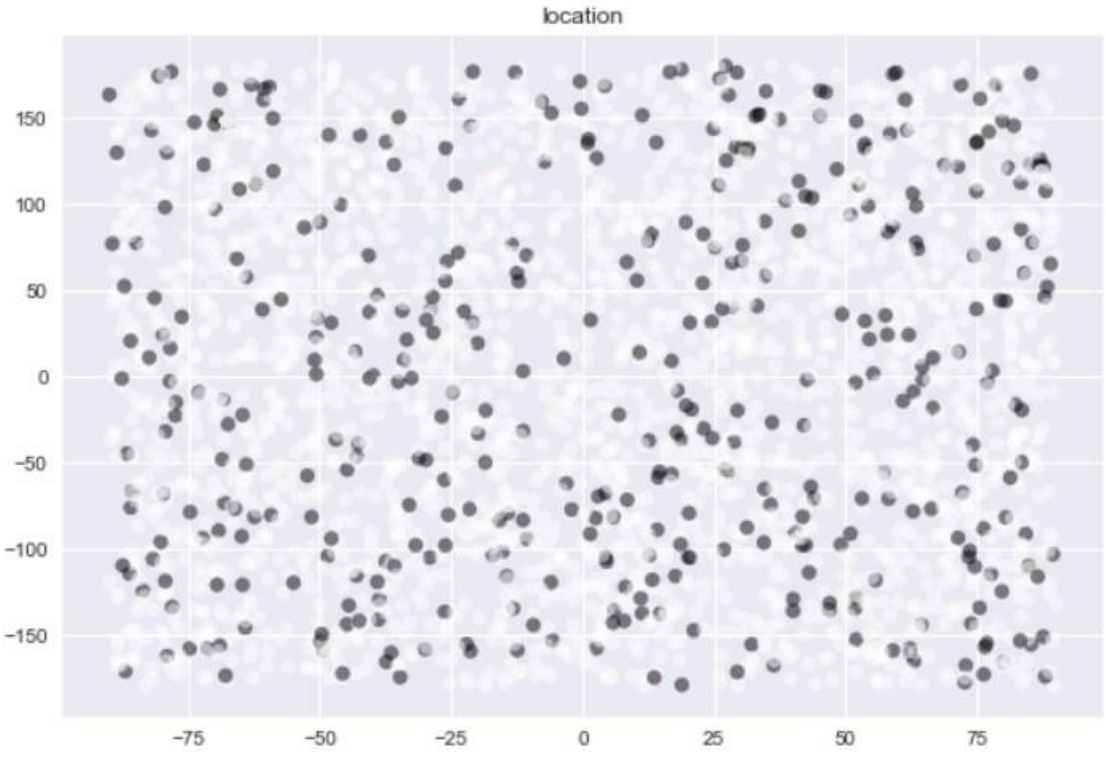
We changed the classification to multi label with labels for risk, type of disease, and whether the person spreads the disease. This is important because some features like Syndrome Class indicate whether a person spreads or doesn't but isn't informative about the other labels.

We observed the location to check whether it can give any reliable information about the type of disease. Maybe if people are congregated closely to each other then there is an outbreak. Yet observing the data there isn't a clear case of that:

Cases of Flue are in black and white not-flue:



Cases of covid in black and non-covid in white:



Graphs of other diseases are similar and show no specific area or zones of outbreak. Therefore the location feature is redundant.

Also, the likelihood of spread or risk are related to the location of the person, rather to physiological, behavioral traits.

From general knowledge, the address, patient ID, date of test, number of cousins are redundant as well. Also, the professions have too many types in the dataset and from human knowledge are irrelevant.

For scaling we tried to use Quantile Transformer from sklearn but because it truncated too much of the data the results were flawed. Eventually we used standard scaling of (x- (avg))/(std. deviation).

We used PCA, filter algorithm , on the pcrResults mainly because they were they had correlation among them. Then we also used Sequential Backward Selection with the data from the PCA, and we implemented by ourselves the SBS , with k-nearest neighbors' classifier as scoring function

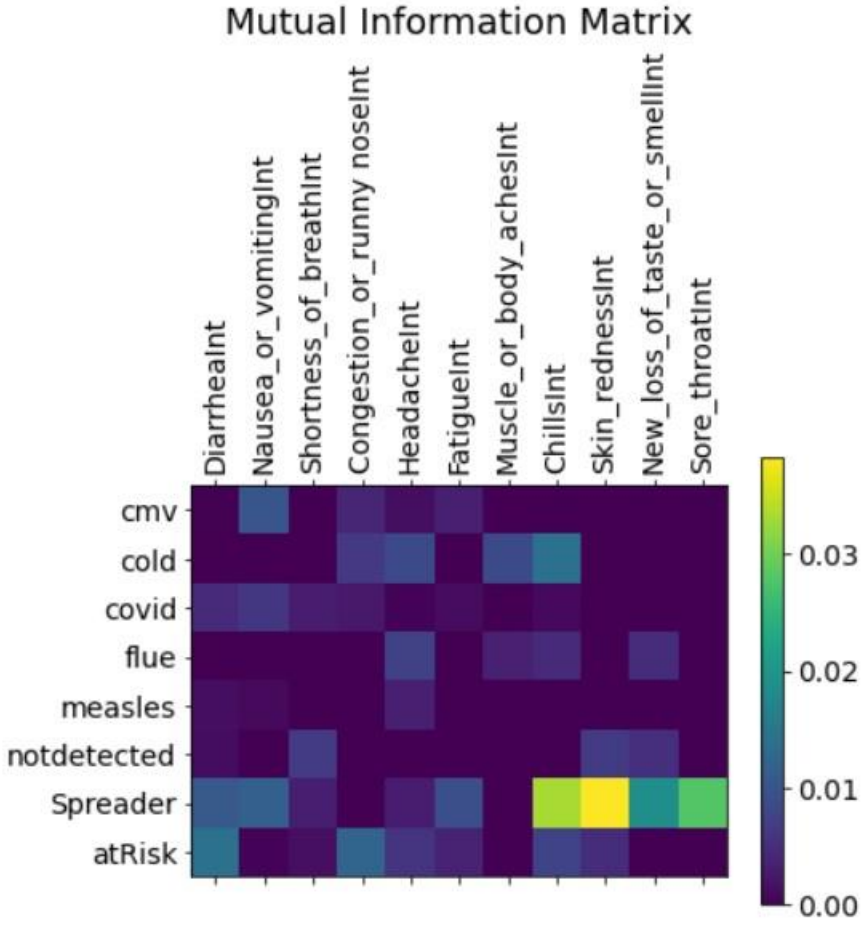
Plotting SyndromeClass vs. the features before with the 24 categories we observed the following:

Where the right-hand side is the categories and the top side are the syndrome classes and we saw that non-spreading people mostly didn't exhibit syndromes 1 and 4. Then we chose to keep the feature.

We chose to remove AvgHouseholdExpenseOnPresents, `AvgHouseholdExpenseOnSocialGames, AvgHouseholdExpenseParkingTicketsPerYear, AvgMinSportsPerDay, AvgTimeOnSocialMedia and AvgTimeOnStuding.`

By Occam's razor principle the learning will be more efficient excluding them, because they are immaterial to communicable diseases, because they focus on the household and activities that don't pose much risk to catch diseases.

We used Mutual Information to assess SelfDeclarationOfIllnessForm and the occurrence of diseases. We found very low mutual information correlation between a syndrome reported and one of the diseases in the t est results, but there was some correlation if the person was spreading. as seen :


Mutual Information Matrix
DiarrheaInt
Nausea_or_vomitingInt
Shortness_of_breathInt
Congestion_or_runny noseInt
HeadacheInt
FatigueInt
Muscle_or_body_achesInt
ChillsInt
Skin_rednessInt
New_loss_of_taste_or_smellInt
Sore_throatInt
cmv
cold
covid
flue
measles
notdetected
Spreader
atRisk
0.03
0.02
0.01
0.00