Comparison of Three Boosting Models on Parkinsons Prediction

Context:

Parkinson's disease (PD) is a disabling brain disorder that affects movements, cognition, sleep, and other normal functions. Unfortunately, there is no current cure—and the disease worsens over time. It's estimated that by 2037, 1.6 million people in the U.S. will have Parkinson's disease, at an economic cost approaching \$80 billion. Research indicates that protein or peptide abnormalities play a key role in the onset and worsening of this disease [1].

Overview:

Three tree based ensemble models are compared for predicting the categorical UPDR rating of Parkinsons symptoms. The models compared are XGBoost, LightGBM, and CatBoost. Additionally, the data is filtered to the first 12 months of visits for improved performance and a few engineered features are added. The target shows a significant imbalance in classes and so SMOTE (Synthetic Minority Oversampling Technique) is used to balance the target for training. Model hyperparameter tuning is performed using the hyperopt package which uses Bayesian optimization for exploring the search space of hyperparameters. Lastly, the information of whether the patient was on medication during the clinical visit is compared for model performance. The medication information has many missing values but shows predictive improvement in UPDRS 1 and UPDRS 3. AUC-ROC is used as the main comparison metric between models. The categorical threshold for the probability classification is fine-tuned to optimize in favor of Recall while also looking at the highest F1 score. Recall is favored over Precision to minimize False Negatives, which could cause patients to not seek treatment sooner. While False Positives have a negative impact on a patient, because they will likely have more frequent doctors visits, it is not as negatively impactful as a "likely" Parkinson's patient misdiagnosed as being "not at risk."

The default model parameters with no SMOTE and no medication data gave AUC-ROC aroun 0.59. The best performance for UPDRS 1 is AUC-ROC of 0.796 from a CatBoost Classifier using the Hyperopt hyperparameters and the data with SMOTE applied. The best performance for UPDRS 2 is AUC-ROC of 0.881 from a CatBoost Classifier using the Hyperopt hyperparameters, with the data medication data, and with SMOTE applied. The best performance for UPDRS 3 is AUC-ROC of 0.729 from a LightGBM Classifier using the Hyperopt hyperparameters, with the data medication data, and with SMOTE applied.

Summary of Best Performance Models

UPDRS 1 Prediction on Test Data

- CatBoost Hyperopt SMOTE model:
- AUC: 0.796

UPDRS 2 Prediction on Test Data

- CatBoost Hyperopt SMOTE Medication model:
- AUC: 0.881

UPDRS 3 Prediction on Test Data

- LGBoost Hyperopt SMOTE Medication model:
- AUC: 0.729

Data:

All of the data are from a Kaggle competition that began on February 16, 2023 and ended on May 18, 2023. The core of the dataset consists of protein abundance values derived from mass spectrometry readings of cerebrospinal fluid (CSF) samples gathered from several hundred patients [2]. As well, there is a column indicating whether the patient was taking any medication during the UPDRS assessment. This can affect motor function scores and is represented in the column "upd23b_clinical_state_on_medication."

Dimensional Columns:

- patient_id: a unique identifier for each patient
- visit_month: relative to the first visit, the number of months later for the current visit
- **visit_id:** a combination of the patient_id and the visit_month. Join key for protein and patient data.

All protein only mass spectrometry data is signified by the column having only the UniProt label for the protein with the column values being the protein abundance.

All peptide mass spectrometry data is signified by the protein UniProt labeled concatenated to peptide sequence with an underscore as the separator.

Metric Columns:

- **protein UniProt label:** contains the mass spectrometry protein abundance
- **UniProt_peptide label:** contains the mass spectrometry for the peptide abundance
- Upd23b_clinical_state_on_medication: whether the patient was on medication during the visit.
 - o Values can be "On", "Off", or NaN if unknown.

Data Description:

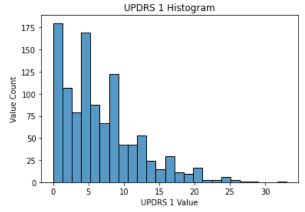
248 Patients

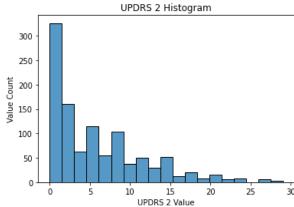
968 Unique Peptides

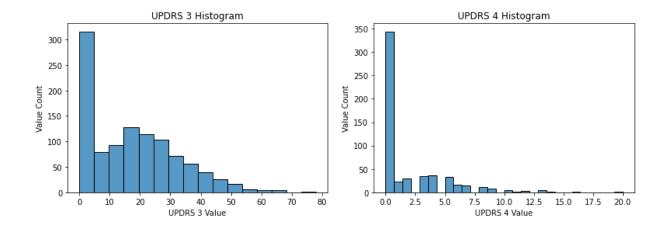
227 Unique Proteins

UPDRS Max and Min Values:

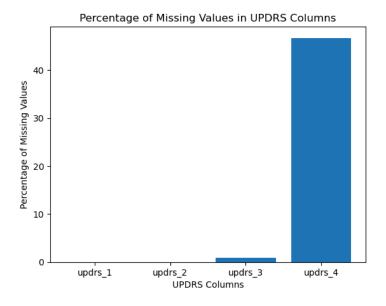
UPDRS 1: 0 to 33
UDPRS 2: 0 to 29
UDPRS 3: 0 to 78
UPDRS 4: 0 to 20







For each UPDRS there are many more for the value 0, and this is extremely the case for UPDRS 4.



Remove UPDRS 4 from the Experiment

Looking at the missing values for each UPDRS, roughly 45% of the values are missing for UPDRS 4 which concludes me to remove this target from the prediction. It is primarily 0's and has almost half of the values missing, thus it will not be a good target to learn from and predict.

Convert the Target from a Regression value to a Catgorical value

Use the range of values given from Wikipedia [3]

UPDRS 1 (Range: 0 – 52)

Mild: 0 - 10
 Moderate: 11 - 21
 Severe: 22 - 52

UPDRS 2 (Range: 0 – 52)

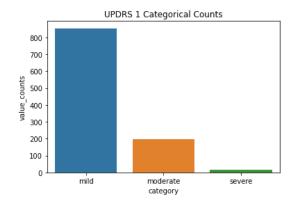
Mild: 0 - 12
 Moderate: 13 - 29
 Severe: 30 - 52

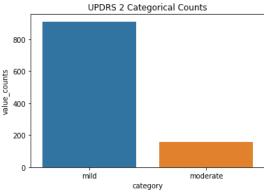
UPDRS 3 (Range: 0 – 132)

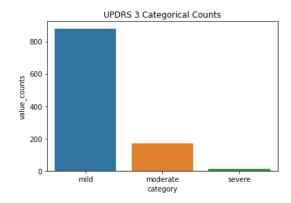
Mild: 0 - 32Moderate: 33 - 58Severe: 59 - 132

Combine the Moderate and Severe Categories

After converting the targets into categories, there is significant class imbalance of the targets. The category "severe" is barely represented and will not perform well in a ML model. In order to adjust for this issue, **moderate and severe will be combined into a single category**. This will mean the model will now be determining whether a user will have mild vs non-mild symptoms (moderate/severe).







Feature Engineering

- Number of Visits:

Since a patient who is experiencing more symptoms may be visiting the doctor more frequently, the number of visits was added as a feature.

Number of proteins with value > 0:

Perhaps the number of proteins expressed has an effect on the parkinson's symptoms

- Number of peptides with value > 0:

Perhaps the number of peptides expressed has an effect on the parkinson's symptoms

- Number of proteins and peptides with value > 0:

Perhaps the number of proteins expressed has an effect on the parkinson's symptoms

Protein X Protein was implemented on the data. Because this grew the number of features exponentially, it meant the training time for the model was far too long for any benefit. The correlation values of the protein x protein columns to the UPDRS values were not showing that there was a benefit to using the engineered feature. As well, the data explodes to 51,302 protein x protein combinations.

Boosting Models

With the high number of features (proteins and peptides) and low correlation of the features to the target, a decision tree based model seemed to be a good option. Decision tree based models do not require feature selection preprocessing. Using a Random Forest with boosting

typically provides the best performance. The Random Forest is an ensemble model of Decision Trees which typically generalizes well when the trees are low depth. The boosting helps the Random Forest learn from the samples that it got wrong in the previous trees.

Three boosting models were tried for this project.

LightGBM

A gradient boosting ensemble model that grows leaf-wise, meaning only a single leaf is split when considering the gain. Leafwise growth can lead to overfitting and is best controlled by tuning the max tree depth. LightGBM uses histogram binning of data for determining splits. This can be controlled by parameters max_bin and min_data_in_bin. One key feature of LightGBM is the speed of training a model [4]. This performance comes mainly from exclusive feature bundling. The gradient boosting is expressed in the GOSS (Gradient One-Sided Sampling) which gives higher weights to the data points with larger gradients [5].

XGBoost

XGBoost or extreme gradient boosting uses depth wise growth for its trees. It uses CART (classification and regression trees) to score each leaf [6]. Sampling is simple bootstrap sampling with no weights used in splitting.

CatBoost

A gradient boosting ensemble model that has specific benefits for categorical features. It does not require the user to preprocess the categorical features. The CatBoost model grows the Decision Trees symmetrically, meaning that at every depth level all of the nodes use the same split condition [7]. For splitting, the model uses Minimal Variance Sampling, which is performed at the tree level and optimizes the split scoring accuracy [8].

Model Performance

Objective: Predict the categorical value of the UPDRS for the current visit.

Model Default Hyperparameters

Using 5 fold Cross Validation and taking the mean results of each the 5 holdout sets for default hyperparameters for each model.

UPDRS 1

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.598	0.825	0.705	0.220	0.335
LigthtGBM	0.582	0.822	0.736	0.181	0.290
CatBoost	0.542	0.813	0.793	0.090	0.159

UPDRS 2

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.576	0.869	0.825	0.159	0.266
LigthtGBM	0.580	0.872	0.847	0.165	0.276
CatBoost	0.543	0.863	0.850	0.088	0.160

UPDRS 3

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.590	0.854	0.750	0.193	0.307
LigthtGBM	0.593	0.858	0.839	0.193	0.314
CatBoost	0.557	0.847	0.834	0.119	0.208

Hyperparameter Optimization Using Hyperopt

Using 5 fold Cross Validation and taking the mean results of each the 5 holdout sets for best hyperparameters from the tuning package hyperopt for each model.

UPDRS 1

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.623	0.803	0.516	0.323	0.397
LigthtGBM	0.566	0.797	0.485	0.180	0.263
CatBoost	0.566	0.815	0.685	0.150	0.246

UPDRS 2

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.617	0.864	0.599	0.266	0.368
LigthtGBM	0.569	0.851	0.518	0.169	0.255
CatBoost	0.583	0.861	0.610	0.186	0.285

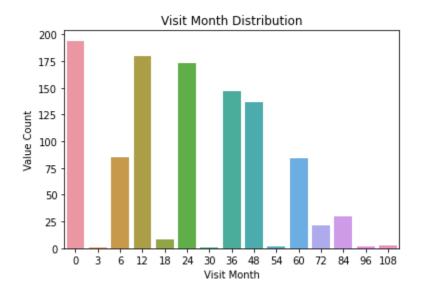
UPDRS 3

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.619	0.859	0.728	0.257	0.380
LigthtGBM	0.617	0.854	0.666	0.260	0.374
CatBoost	0.586	0.836	0.524	0.208	0.298

Hyperopt Conclusion: The hyperparameter optimization showed an improvement mainly for XGBoost across each UPDRS.

Using Only Data from the First 12 Months

The distribution of visit months is most high in the 0 to 24 range. Perhaps the later visit months are actually only adding noise because the protein changes have already happened and may have a delayed effect on the symptoms.



UPDRS Categorical Max Values in the First 12 Months

For **UPDRS 1**, **84.84**% of patients hit their max category in the first twelve months

For UPDRS 2, 86.48% of patients hit their max category in the first twelve months

For **UPDRS 3**, **82.38%** of patients hit their max category in the first twelve months

This shows that the first 12 months may give more valuable data in terms of the categorical target.

Approximately 50% of the patients who get Parkinson's diagnosis get it within the first 12 months of visits.

UPDRS 1: 58.9% of the patients with max diagnosis of Parkinson's get it in 12 months

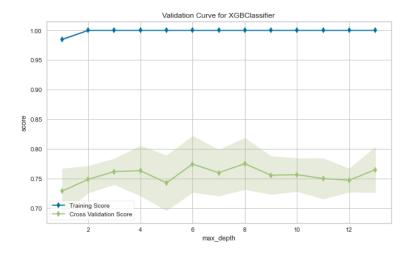
UPDRS 2: 50% of the patients with max diagnosis of Parkinson's get it in 12 months

UPDRS 3: 47% of the patients with max diagnosis of Parkinson's get it in 12 months

Prediction of Max Categorical Value using 12 Month Data

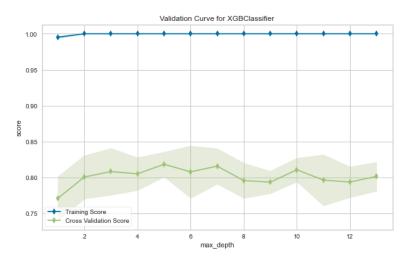
Validation curves for the hyperparameters Max Depth and Subsample were tried for finding the optimal values of the hyperparameters. These two hyperparameters tend to have a large impact on the performance, so testing them manually gives more intuition on their effect. The validation curve was measured using the metric AUC-ROC .

UPDRS 1 - Max Depth Validation Curve



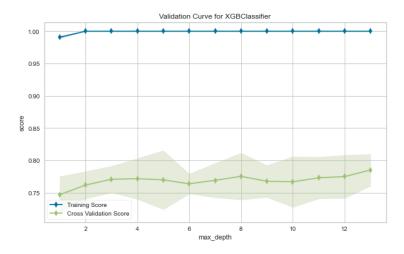
The UPDRS 1 AUC score for the validation curve for Max Depth showed a high value at max_depth = 6 and 8, Since 6 is lower and should be better for generalization, the Max Depth used was 6.

UPDRS 2 - Max Depth Validation Curve



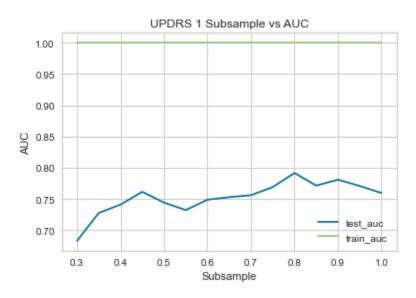
The UPDRS 2 AUC score for the validation curve for Max Depth showed a high value at $max_depth = 5$

UPDRS 3 - Max Depth Validation Curve

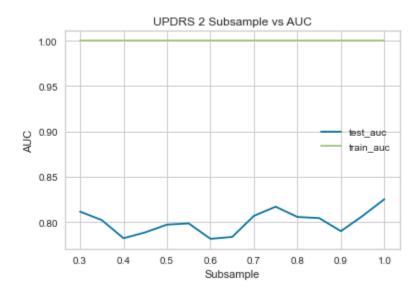


The UPDRS 3 AUC score for Max Depth the value of max_depth = 4 will be used even though the best AUC was max_depth = 8. But since the AUC values are close and max depth 4 will be better at generalizing, it will be used.

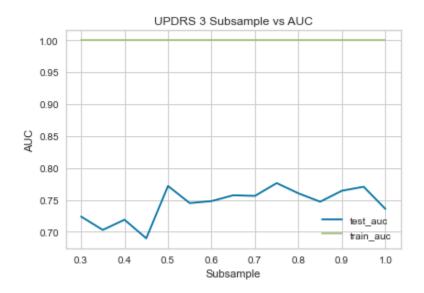
UPDRS 1 - Subsample Validation Curve



UPDRS 2 - Subsample Validation Curve



UPDRS 3 – Subsample Validation Curve



Fine Tuned Hyperparameter Comparison for XGBoost

UPDRS 1

	AUC	Accuracy	Precision	Recall	F1
Default	0.696	0.727	0.707	0.532	0.607
Max Depth	0.696	0.727	0.707	0.530	0.605
Scale Pos Wt	0.693	0.725	0.706	0.529	0.604
Subsample	0.670	0.702	0.671	0.503	0.575

UPDRS 2

	AUC	Accuracy	Precision	Recall	F1
Default	0.671	0.764	0.694	0.424	0.526
Max Depth	0.663	0.765	0.718	0.396	0.510
Scale Pos Wt	0.716	0.791	0.730	0.518	0.606
Subsample	0.716	0.791	0.730	0.518	0.606

UPDRS 3

	AUC	Accuracy	Precision	Recall	
Default	0.670	0.710	0.698	0.485	0.572
Max Depth	0.656	0.859	0.728	0.257	0.380
Scale Pos Wt	0.669	0.702	0.657	0.515	0.577
Subsample	0.677	0.705	0.649	0.544	0.592

By using only the 12 months of data to forecast for the max UPDRS value, the default hyperparameters for XGBoost show a significant improvement compared to using all of the visit months data.

The default hyperparameters perform quite well for XGBoost. When trying to optimize some of the hyperparameters manually, there is not much improvement except in the UPDRS 2. This mainly came from using the scale pos weight to balance out the target values.

Hyperopt Hyperparameter Tuning

Hyperopt is a python package for hyperparameter tuning that uses the algorithm Tree-based Parzen Estimators (TPE) to explore a search space of hyperparameter values and minimize a function, such as AUC score [8][9]. This hyperparameter tuning package allows for a faster way to cover combinations of hyperparameters that should improve performance.

XGBoost Hyperparameters to Tune [11]

max_depth: the maximum depth of a tree. Deep trees can lead to overfitting while shallow trees may not predict as well. Tuning to find the minimum depth, meaning low variance, but with good performance on the evaluation metric.

min_child_weight: the minimum sum of instance weight in a child. If the weight is larger, then the model will generalize better.

subsample: ratio of data sampled for each decision tree. Where 0.5 means, half the training data will be sampled prior to creating the decision tree.

colsample_bytree: the ratio of columns sampled for each decision tree. The default is 1, which means that all columns are used. By adjusting this ratio, it can create more weak learner trees by randomly excluding some of the columns on each tree.

reg_alpha: L1 (Lasso) regularization on the terms. A higher alpha means a more generalized model.

reg_lambda: L2 (Ridge) regularization on the terms. A higher lambda means a more generalized model.

gamma: the minimum loss reduction needed to make a partition on a leaf node. The larger gamma is the more shallow a tree will be and the more generalized the model.

learning_rate: step wise shrinkage of the feature weights at each of the boosting steps. This prevents overfitting by decreasing the variance of the model. The default value is 0.3

max_delta_step: the maximum delta step each leaf is allowed. This can help when there is class imbalance in the data.

LightGBM Hyperparameters to Tune [12]

max_depth: default is -1, which means no limit.

min_data_in_leaf: default is 20. Minimum number of data in a leaf. This can reduce overfitting on the training data.

bagging_freq: default is 0, which means no bagging. Values greater than 0 are the number of iterations before a new sample with the bagging fraction of the total data is taken.

bagging_fraction: default is 1.0. This is similar to feature fraction but will randomly select part of data without resampling. This can be used to speed up training and reduce overfitting.

tree_learner: default is serial, which is a single machine tree learner. The options are serial, feature, data, voting.

is_unbalance: set to true if the training data is unbalanced. Default is false.

boosting: gbdt, rf, and dart. Default is gbdt.

lambda_l1: L1 (Lasso) regularization.

lamdba_l2: L2 (Ridge) regularization.

feature fraction: the ratio of features to use on each tree. Default is 1.0.

learning rate: default is 0.1. This is the shrinkage rate.

max_delta_step: default is 0.0. The final max output of leaves is learning_rate * max_delta_step. Used to limit the output of leaves.

CatBoost Hyperparameters to Tune:

depth: the max depth of a tree. The default is 6.

learning_rate: shrinkage used in updates. The default value is selected automatically for binary classification with other parameters set to default. In all other cases default is 0.03

bagging_temperature: The higher the value the more aggressive the bagging is. Default is None.

min_data_in_leaf: the minimum data required in a leaf node for a split. Default is None.

I2_leaf_reg: L2 (Ridge) regularization. Default is None

Hyperopt Hyperparameter Tuning Results

UPDRS 1

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.701	0.728	0.691	0.563	0.620
LigthtGBM	0.673	0.696	0.628	0.561	0.593
CatBoost	0.566	0.815	0.685	0.150	0.246

UPDRS 2

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.723	0.752	0.712	0.549	0.620
LigthtGBM	0.666	0.700	0.528	0.577	0.551
CatBoost	0.583	0.861	0.610	0.186	0.295

UPDRS 3

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.702	0.746	0.702	0.560	0.623
LigthtGBM	0.697	0.724	0.674	0.576	0.621
CatBoost	0.586	0.836	0.524	0.208	0.298

Apply SMOTE for Class Imbalance

By using Synthetic Minority Oversampling on the UPDRS values for the training data, the predictive ability was improved significantly. As well, by fine-tuning the threshold cutoff for the classification, the recall and precision can be optimized.

UPDRS 1 Training data:

Class 0: 225 samplesClass 1: 225 samples

UPDRS 2 Training data:

Class 0: 255 samplesClass 1: 255 samples

UPDRS 3 Training data:

Class 0: 227 samplesClass 1: 227 samples

Overall SMOTE Results:

UPDRS 1

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.679	0.675	0.650	0.764	0.702
LigthtGBM	0.699	0.696	0.714	0.646	0.678
CatBoost	0.722	0.717	0.699	0.771	0.733

UPDRS 2

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.823	0.821	0.805	0.847	0.825
LigthtGBM	0.767	0.765	0.783	0.734	0.758
CatBoost	0.825	0.821	0.837	0.801	0.819

UPDRS 3

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.708	0.706	0.662	0.838	0.740
LigthtGBM	0.725	0.727	0.770	0.648	0.704
CatBoost	0.724	0.722	0.750	0.673	0.709

Fine-Tuning the Threshold for Classification Using Test Data

By adjusting the classification threshold cutoff for each of the models, the recall and precision can be optimized for the performance needs.

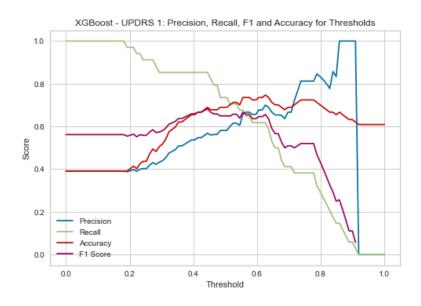
The test data is a stratified holdout fold of the 5 Fold CV labeling which did not have SMOTE performed on the data.

XGBoost UPDRS 1

AUC: 0.7497225305216426

Accuracy: 0.6551724137931034 Precision: 0.5370370370370371 Recall: 0.8529411764705882

Theshold: 0.4

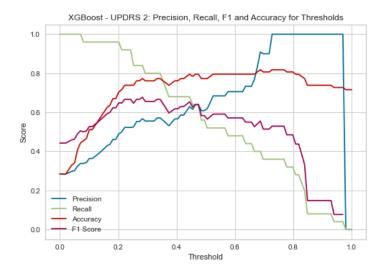


XGBoost UPDRS 2

AUC: 0.8596825396825396

Accuracy: 0.636363636363636364 Precision: 0.43636363636363634

Recall: 0.96 Theshold: 0.17

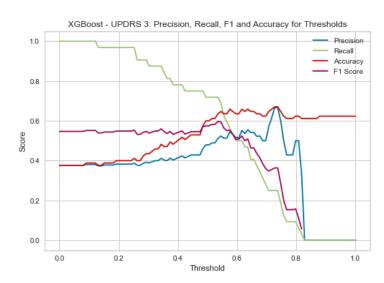


XGBoost UPDRS 3

AUC: 0.6432783018867925

Accuracy: 0.38823529411764707 Precision: 0.3780487804878049

Recall: 0.96875 Theshold: 0.15

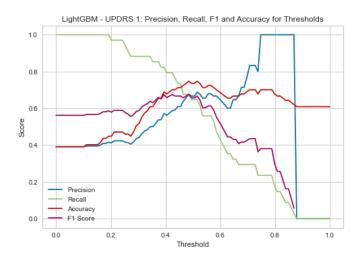


LightGBM UPDRS 1

AUC: 0.7591564927857937

Accuracy: 0.6896551724137931 Precision: 0.5714285714285714 Recall: 0.8235294117647058

Theshold: 0.4

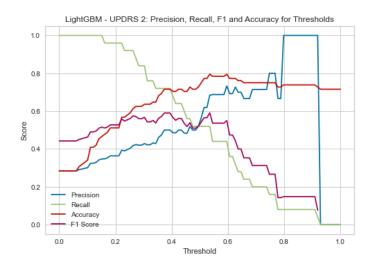


LightGBM UPDRS 2

AUC: 0.7853968253968254

Accuracy: 0.7159090909090909

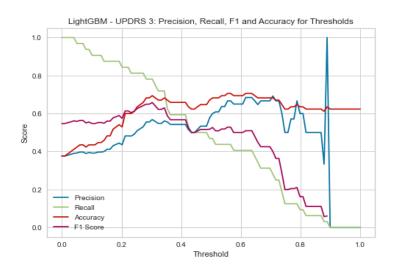
Precision: 0.5 Recall: 0.72 Theshold: 0.38



LightGBM UPDRS 3

AUC: 0.7034198113207548 Accuracy: 0.6941176470588235 Precision: 0.5681818181818182

Recall: 0.78125 Threshold: 0.3

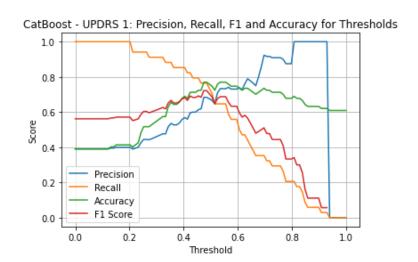


CatBoost UPDRS 1

AUC: 0.7957824639289677

Accuracy: 0.7701149425287356 Precision: 0.6842105263157895 Recall: 0.7647058823529411

Threshold: 0.48

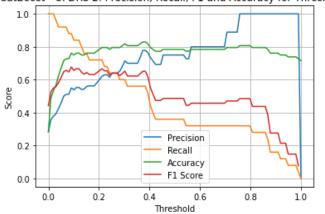


CatBoost UPDRS 2

AUC: 0.8647619047619048 Accuracy: 0.79545454545454 Precision: 0.6206896551724138

Recall: 0.72 Threshold: 0.21





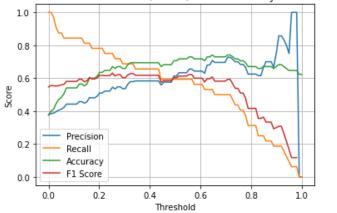
CatBoost UPDRS 3

AUC: 0.7175707547169811

Accuracy: 0.6588235294117647 Precision: 0.5333333333333333

Recall: 0.75 Threshold: 0.25

CatBoost - UPDRS 3: Precision, Recall, F1 and Accuracy for Thresholds



Use Patient Med Data along with Hyperopt Params and SMOTE

There is data on whether the patient was on medication during the clinical visit. This can affect the value of the UPDRS score.

Overall Results with medication data included:

UPDRS 1

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.727	0.721	0.692	0.804	0.744
LigthtGBM	0.737	0.734	0.761	0.680	0.718
CatBoost	0.767	0.764	0.771	0.756	0.763

UPDRS 2

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.823	0.819	0.805	0.845	0.825
LigthtGBM	0.808	0.807	0.828	0.768	0.797
CatBoost	0.848	0.845	0.854	0.832	0.843

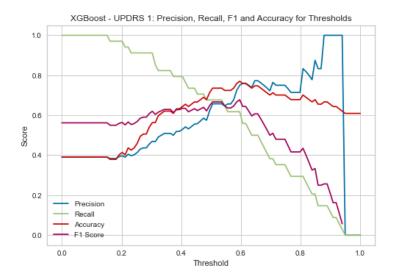
UPDRS 3

	AUC	Accuracy	Precision	Recall	F1
XGBoost	0.712	0.711	0.667	0.834	0.741
LigthtGBM	0.725	0.726	0.776	0.648	0.706
CatBoost	0.717	0.715	0.739	0.678	0.707

XGBoost UPDRS 1

ROC-AUC: 0.7502774694783573 Accuracy: 0.7241379310344828 Precision: 0.63888888888888 Recall: 0.6764705882352942

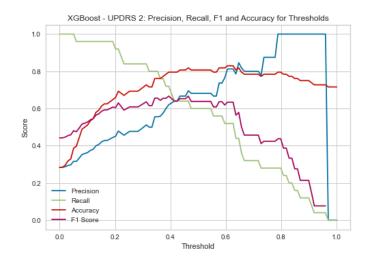
Threshold: 0.5



XGBoost UPDRS 2

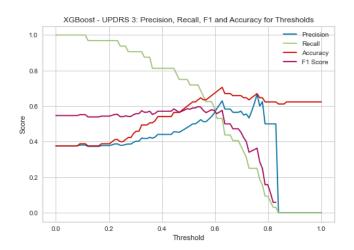
ROC-AUC: 0.8526984126984127 Accuracy: 0.7159090909090909

Precision: 0.5 Recall: 0.8 Threshold: 0.33



XGBoost UPDRS 3

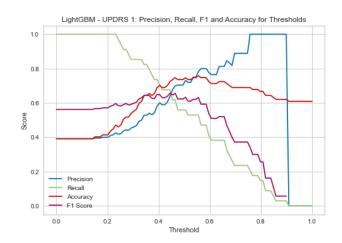
ROC-AUC: 0.6762971698113207 Accuracy: 0.6235294117647059 Precision: 0.5 Recall: 0.71875 Threshold: 0.52



LightGBM UPDRS 1

ROC-AUC: 0.7680355160932297 Accuracy: 0.6436781609195402 Precision: 0.5283018867924528 Recall: 0.8235294117647058

Threshold: 0.35

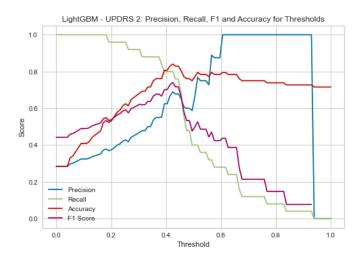


LightGBM UPDRS 2

ROC-AUC: 0.8558730158730159

Accuracy: 0.8295454545454546 Precision: 0.66666666666666

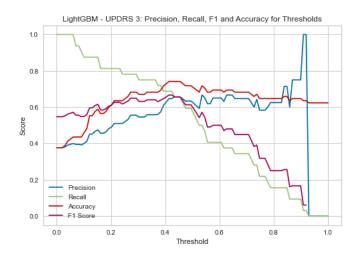
Recall: 0.8 Threshold: 0.42



LightGBM UPDRS 3

ROC-AUC: 0.7287735849056605 Accuracy: 0.6823529411764706 Precision: 0.555555555555556

Recall: 0.78125 Threshold: 0.28



CatBoost UPDRS 1

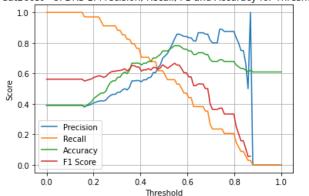
ROC-AUC: 0.7691453940066593 Accuracy: 0.6551724137931034

Precision: 0.54

Recall: 0.7941176470588235

Threshold: 0.36

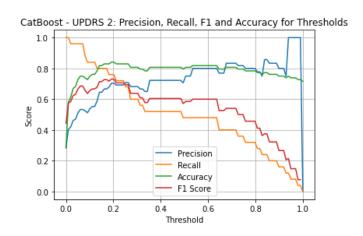




CatBoost UPDRS 2

ROC-AUC: 0.8806349206349207 Accuracy: 0.82954545454546 Precision: 0.6923076923076923

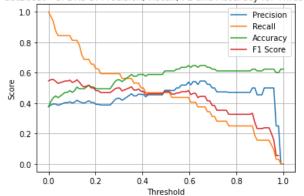
Recall: 0.72 Threshold: 0.22



CatBoost UPDRS 3

ROC-AUC: 0.5866745283018868 Accuracy: 0.49411764705882355 Precision: 0.4098360655737705

Recall: 0.78125 Threshold: 0.13 CatBoost - UPDRS 3: Precision, Recall, F1 and Accuracy for Thresholds



Summary of Best Performance Models

UPDRS 1 Prediction on Test Data

- CatBoost Hyperopt SMOTE model:

- AUC: 0.796

UPDRS 2 Prediction on Test Data

CatBoost Hyperopt SMOTE Medication model:

- AUC: 0.881

UPDRS 3 Prediction on Test Data

LGBoost Hyperopt SMOTE Medication model:

- AUC: 0.729

Footnotes:

- 1. https://www.kaggle.com/competitions/amp-parkinsons-disease-progression-prediction
- 2. https://www.kaggle.com/competitions/amp-parkinsons-disease-progression-prediction/data
- 3. https://en.wikipedia.org/wiki/Unified Parkinson%27s disease rating scale
- 4. https://www.microsoft.com/en-us/research/wp-content/uploads/2017/11/lightgbm.pdf
- 5. https://pro.arcgis.com/en/pro-app/latest/tool-reference/geoai/how-lightgbm-works.ht m
- 6. https://xgboost.readthedocs.io/en/stable/tutorials/model.html
- 7. https://pro.arcgis.com/en/pro-app/latest/tool-reference/geoai/how-catboost-works.htm
- 8. https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0262895
- 9. https://hyperopt.github.io/hyperopt/

- 10. https://towardsdatascience.com/hyperopt-demystified-3e14006eb6fa
- 11. https://xgboost.readthedocs.io/en/latest/parameter.html
- 12. https://lightgbm.readthedocs.io/en/latest/Parameters.html