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Background Information & Kaggle About our Data Submissions on Kaggle Findings Moving Forward





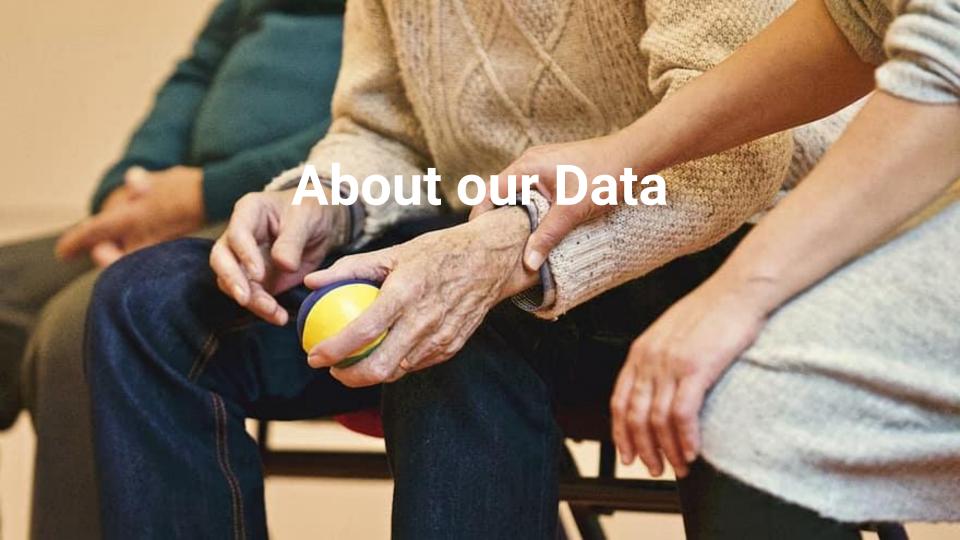
AMP-PD

"Parkinson's disease (PD) is a chronic and progressive neurological disease that is marked by tremors in the resting muscles, rigidity, slowness of movement, impaired balance and a shuffling gait, In addition, many people with PD develop non-motor symptoms such as behavioral changes and cognitive impairment."

Currently there is no cure, however there are treatments to relieve symptoms.



- Competitions are hosted on Kaggle.com
- Anyone can host a competition, in our case AMP-PD is hosting ours
- The goal is to make predictions using models
- Predictions must be formatted in specific ways
- Scores are graded by host
- Kaggle updates a live leaderboard with the the entries while the competition is ongoing



About our Competition

Hosted by Accelerating Medicines Partnership® Parkinson's Disease (AMP®PD)

- Public-Private partnership made to help study Parkinson's Disease
- Goal is predict the severity of one Parkinson's throughout its progression
- Uses real-world data from thousands of patients



About our Competition

Hosted by AMP-PD

• Teams: 1,225

Competitors: 1,347

• Entries: 17,745

Max team size is 5

Limited to 5 submissions per day

Variables

- **Updrs** Rating scale for Parkinson's Disease symptoms, range 1-4, 4 being worst
- Peptide Sequence of amino acids within the peptide
- PeptideAbundance Frequency of the amino acid in the sample
- UniProt The UniProt ID code for the associated protein
- NPX Normalized protein expression
- upd23b_clinica_state_on_medication Was the patient taking medication
- visit_month month patient came on visit

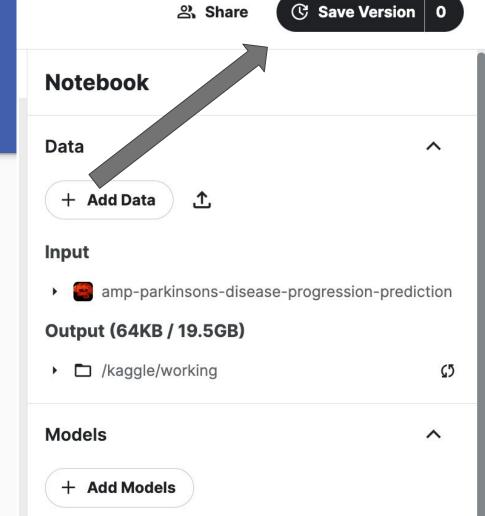


	▲ prediction =	# rating =	# group_key =
Submitting findings	3342_0_updrs_1_ plus_0_months	0	0
	3342_0_updrs_1_ plus_6_months	0	0
	3342_0_updrs_1_ plus_12_months	0	0
 Each competition has a different way of submitting findings need to estimate both their UPDRS scores for that visit and predict their scores for any potential visits 6, 12, and 24 months later 	3342_0_updrs_1_ plus_24_months	0	0
	3342_0_updrs_2_ plus_0_months	0	0
	3342_0_updrs_2_ plus_6_months	0	0
	3342_0_updrs_2_ plus_12_months	0	0
	3342_0_updrs_2_ plus_24_months	0	0
	3342_0_updrs_3_ plus_0_months	0	0
	3342_0_updrs_3_ plus_6_months	0	0

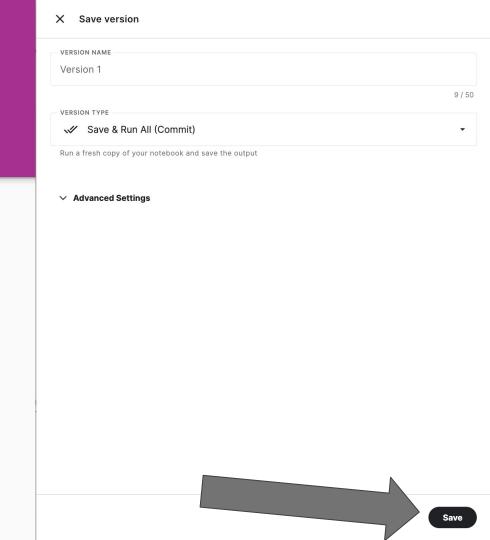
```
count = 0
for (test, test_peptides, test_proteins, sample_submission) in iter_test:
    targets = sample_submission.prediction_id.str.split('_').str[2:4].apply(lambda x: '_'.join(x))
    if count == 0:
        print (targets)
    print (10*'---sample submission ---')
    print (sample_submission.head())
    print (10*'----')
    sample_submission['rating'] = targets.map(mean_dict)
    env.predict(sample_submission)
    count += 1
```

How that data frame is formatted

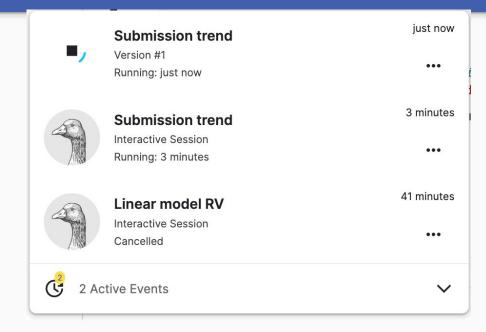
- First step after code is done
- Click save version

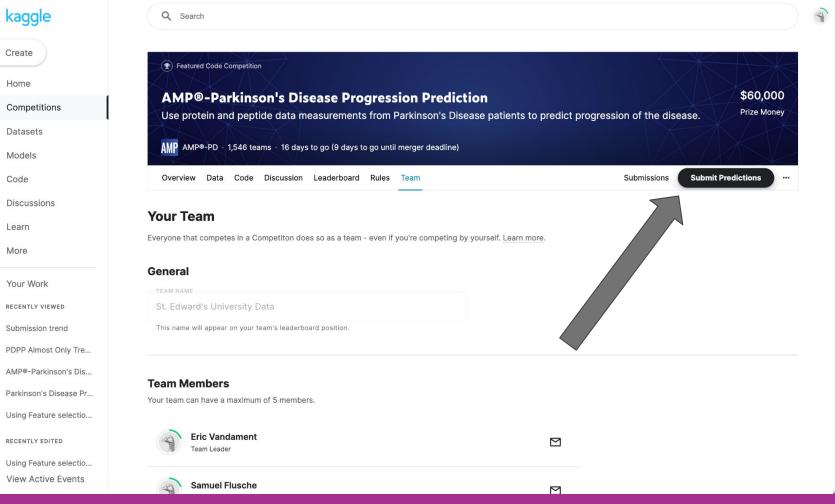


- Change name
- Save or save and commit
- Advance settings allow you to pick how you want to run the code
- Saving output



- Submission will run on bottom left
- Wait until it finishes running





Come back to here

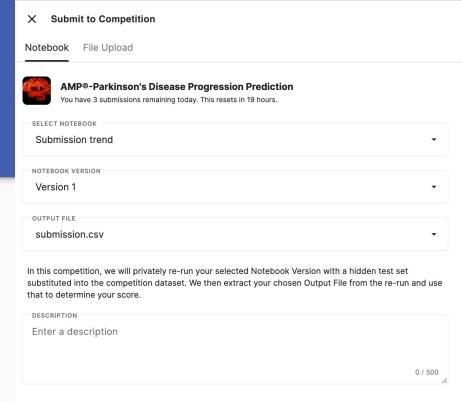
Home

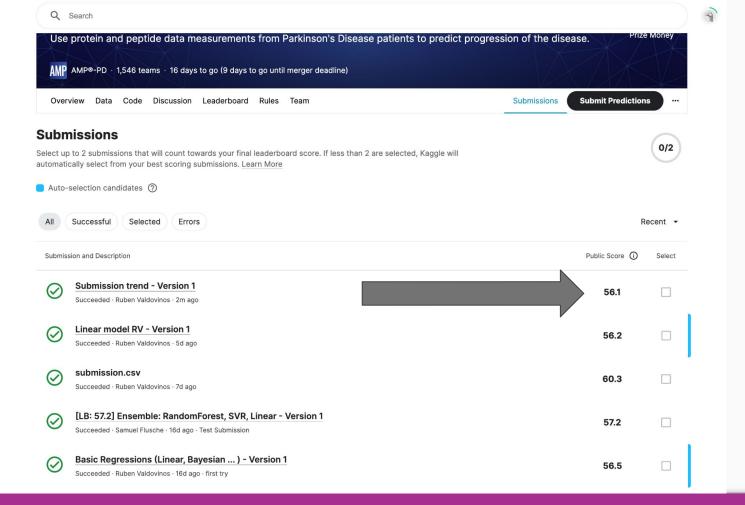
Learn

More

<> Code

- Choose which notebook
- Pick correct version
- Pick correct output file





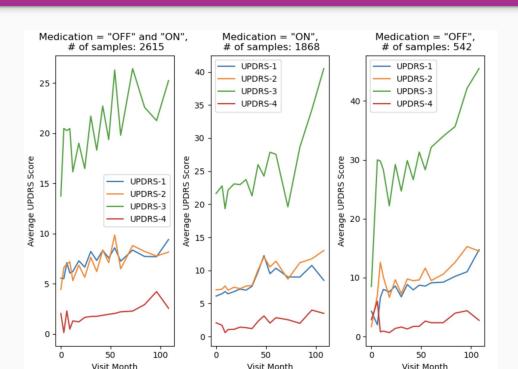
This is what the final submission will look like



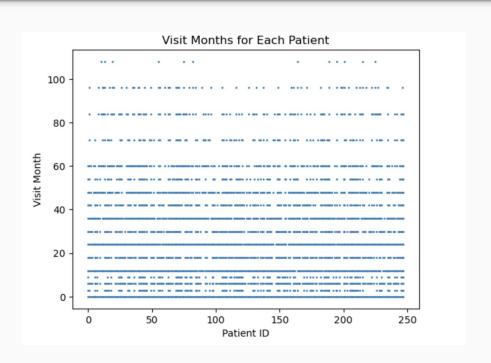
Analysis of Others

- Top scorers have not made their scores public
- Successful models we found almost 'cheat'
- Many of the public models don't even touch the protein and peptide data
- This means that a lot of the data focus exclusively on the typical trends of parkinson's progression and not the corresponding medical factors of the patient.

Our Analysis



Our Analysis



Our Analysis

- Wanted to try to utilize the protein and peptide data in models
- A few ways to do this, always involves combining all dataframes
- We combined protein and peptide data into the dataframe and ran the same regression,
 - o Gave a score of 56.9
- Experimented with ensembling, only lowered the score

Analysis Challenges and Aids

- Failed submissions still count as submissions
- Complicated models can be hard to submit correctly

 Data prep is easy, most of what you need is already out there

Our Results

Our Best Score: 56.1 (from SGD regressor code)

Place: 244

Overall Best Score: 53.6

- Top 22% of entries
- Tied with 143 other people
- Top 25 only ones below score of 56.0

244

St. Edward's University Data







56.1



Your Best Entry!

Your submission scored, which is not an improvement of your previous score. Keep trying!



Improving Models

- Successfully utilizing protein/peptide will require more complicated models
- Some people have started creating deep learning models or models better utilizing the time series
- The best models usually have a combination of different techniques

Thank you