

Winning @ WiDS Kaggle Datathon

Dan Ofer



Datathon
In
Numbers

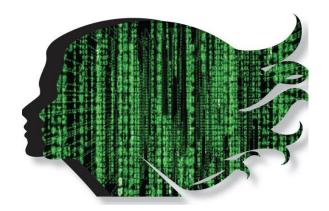
1479 Competitors

951 Teams

2 Months work

12,644 Entries

1 Winner

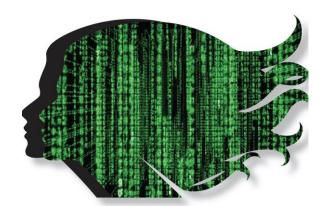


Women in Data Science (WiDS)

Aims to inspire and educate data scientists worldwide, regardless of gender, and to support women in the field.

The <u>Datathon challenge</u> is an annual, international competition, hosted on Kaggle

>= 50% Females per team



Women in Data Science (WiDS) Datathon 2020

OBJECTIVES:

- ✓ Predict patient survival/death in hospital intensive care units (ICU) from their first 24 hours medical records
- ✓ More than 130,000 hospital Intensive Care Unit (ICU) visits from patients, from > 200 hospitals in different countries
- ✓ Also a research paper tract!

OUR TEAM - WOMAN POWER

Noa Dagan

MD - Head of AI Driven Medicine at Clalit (HMO) Research Institute

Nurit Cohen Inger

Data scientist



Dan Ofer

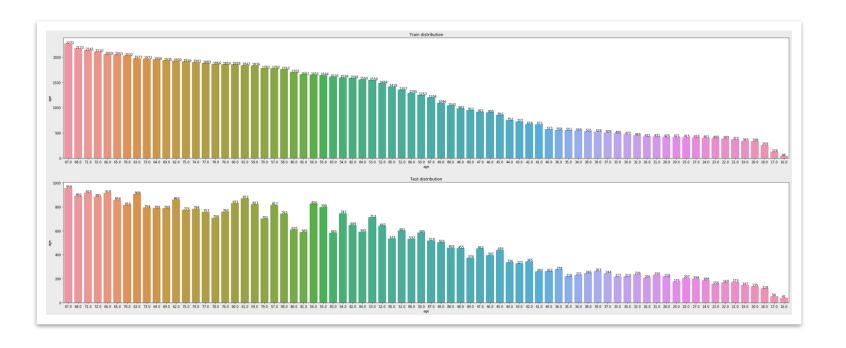
SparkBeyond senior DS, Bioinformatician, led previous healthcare/AI projects

Seffi Cohen

Kaggle Master BGU PhD student



The Dataset



THE DATASET

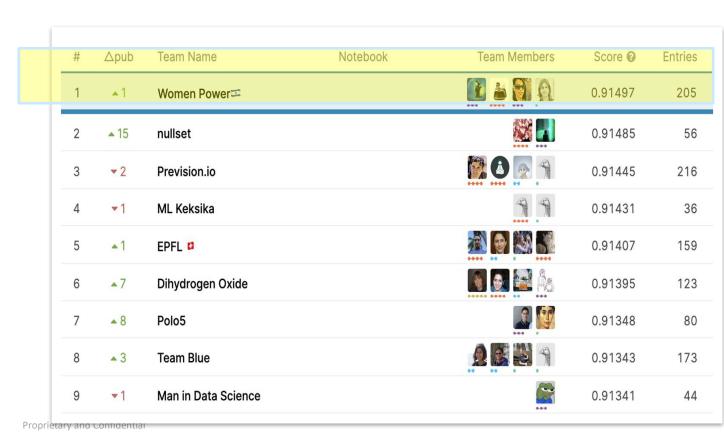
- Very "flat" data no time series, repeat visits, real world entities or free text
- 130,000 samples, 186 columns
- LOTS of missing variables, many missing not at random.
- Heterogenous mix of continuous, categorical, semi structured (medical codes)
- Many domain-specific, expert selected top features e.g. APACHE risk scores, aggregated lab tests results etc'

| training_v2.csv (61.75 MB) 20 of 100 columns ▼ Views ✓ Ш □ | | | | | | | | | |
|---|------------|-------|-------|------------|-------------|----------|----------|-------------------------|---------------------------------|
| hospital | # hospital | A age | A bmi | # elective | A ethnicity | A gender | A height | A hospital | A icu_ad |
| 118 | 0 | 68 | 22.73 | 0 | Caucasian | М | 180.3 | Floor | Floor |
| 81 | 0 | 77 | 27.42 | 0 | Caucasian | F | 160 | Floor | Floor |
| 118 | 0 | 25 | 31.95 | 0 | Caucasian | F | 172.7 | Emergency Department | Accident Emergency |
| 118 | 0 | 81 | 22.64 | 1 | Caucasian | F | 165.1 | Operating Room | Operating Room / Recovery |
| 33 | 0 | 19 | NA | 0 | Caucasian | М | 188 | | Accident Emergency |



A TOUGH BASELINE

- APACHE death prob feature as baseline: 85 AUC
- My baseline gradient boosting (Catboost) kernel got ~ 90.2 AUC
- A SparkBeyond (~AutoML) model with expert tricks and xgboost got ~ 90.4 AUC
- Our winning model ensemble:
 91.497 AUC
- Tiny spread! And strong baseline features!



OUR PIPELINE



1st place writeup: https://www.kaggle.com/c/widsdatathon2020/discussion/133189



FEATURE ENGINEERING, SELECTION, IMPUTATION



MISSING VALUES IMPUTATION

Many "missing not at random" variables - NOT doing a lab test can be more informative than the test itself!

Default Catboost/tree models worked very well (built-in support for missing values)

- BUT! Imputing missing values by domain knowledge (e.g. BMI: Body-mass index = ht/wt^2) or predictive models important and improved final model.
- Other models can't work with missing values necessitating imputation

Very laborious work - 186 columns!

- Clear boost to model performance.
- Outperformed default model imputations

Hard to say if worthwhile in the "real world"...

Except for easily imputable demographic variables such as BMI, age.. which ARE worthwhile!

Imputation

Smart imputations of features

- By frequency
- By Median
- By Iterative imputations
- 4) By ML model

FEATURE ENGINEERING: 1. Domain knowledge

Golden feature: should_be_dead

Grouped insights from different biological measurements that are not compatible with life

= Benefits of having a Md. on the team;)



FEATURE ENGINEERING: 1. Domain knowledge

- ✓ Many aggregated features e.g. counting how many multiple chronic conditions or subgroups of chronic conditions a patient had, the total number of tests performed, summation of tests or diagnostics with missing values...
- ✓ Bucketing continuous variables into discrete bins, based on medical knowledge
- ✓ Grouping of related measures to a final score (e.g. Glasgow Coma Scale)
- Computing kidney function based on relevant lab test and diagnostic codes
- Computing pulse pressure variables by subtracting the systolic and diastolic Blood Pressure measures
- ✓ Deltas/Diff Variables for a variable per hour +- per day
- ✓ Grouping medical diagnoses codes into semantic categories based on the hierarchical nature of the medical coding system
 - ✓ The codes were semistructured, similar to ICD codes.
 - e.g. 123 = kidney cancer, 12 = cancer, etc'

And many many more!



FEATURE ENGINEERING: 2. Universal tricks

- ✓ Row level (or columns' subset) aggregations: count nans, zeroes, max/min
- Count transformation (replace value with the # times it appeared)
- ✓ Measures of anomalousness Isolation forest derived anomaly score
- ✓ Hash on subset of columns to create similar profiles (e.g. binned age, weight, gender, lifelong chronic diseases)
- ✓ Add aggregate features by these hashes. e.g. mean risk of death for age+weight profile
- ✓ Feature interactions restricted to subset of columns and functions (x,÷,max, min, value range/diff).
- ✓ Used SparkBeyond feature selection for this initially, to generate candidates e.g. "max Blood Pressure in first hour divided by max BP over first day"



FEATURE ENGINEERING: 3. SB augmented tricks

- ✓ Not actually used, but "cool"
- ✓ I extracted from an external PDF lexicon descriptions of the APACHE medical codes diagnosis.
 I then ran SB/world knowledge to get semantic concepts
- ✓ Features were insightful but did not improve model, presumably due to low cardinality (1k<) of the structured codes</p>
- Concepts associated with higher risk of death included: intensive care medicine, respiration & lungs, infectious diseases (e.g. sepsis, infections)
- Concepts with a lower risk of death included: coronary artery bypass (e.g. open heart surgery), medical specialties (e.g. surgeons), drugs (e.g. overdose or drug withdrawals) & crime

FEATURE SELECTION (FS)

We used multiple feature selection techniques. We checked these techniques separately and experimented whilst iteratively dropping features in a fast <u>LightGBM</u> pipeline, according to what improved the local validation or Leaderboard score.

<u>Shapley</u> values helped for high level interpretation

We dropped features using a mix of the following methods:

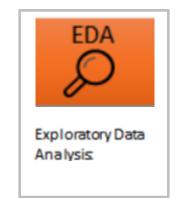
- Features with a high percentage of missing values (80% and up)
- Collinear (highly correlated) features with threshold above 0.99
- Feature with zero standard deviation (contains just 1 unique value 'readmission_status')
- Features ranked by <u>Recursive Feature Elimination</u> with a linear regression model (e.g. 'paco2_for_ph_apache')
- Features with zero importance according to permutation FS in <u>ELI5</u> (e.g. 'hepatic_failure')
- We dropped our top features, the existing APACHE death risk scores
 ('apache_4a_hospital_death_prob', 'apache_4a_icu_death_prob', and derived features). We found this
 improved our validation score, possibly due to bias in how the score is calculated by humans, leading to model
 overfitting
- Features with a different train test distribution, or no test set coverage according to adversarial validation models ('icu id', 'hospital id'..)



ADVERSARIAL VALIDATION

Set train/test split as target label Useful for:

- Feature selection
- Identifying leaks
- Concept drift
- Datapoint selection:
 - From train set, select points most like test set and use those as local validation set



SparkBeyond was good for this! - rapid iterations

Statistical (K-S) approach didn't work as well - too easy to distinguish train from test

i ----→

Based on this - we identified that train/test was mostly partitioned on hospital wards.

We dropped related columns (which had been top features), as they wouldn't generalize to the test set



FEATURES

| ↑ Rank ① | Feature | Direction (1) | Score ① | Train 🕤 | Train Support | Feature Missing Values | Histogram ① |
|----------|---|-----------------------------|---------|---------|------------------|---------------------------|---------------|
| 1 | gcs_motor_apache < 5.759 | x2.43 for hospital_death: 1 | 0.081 | 0.081 | 11737 (23%) | | |
| 2 | d1_lactate_min_div_diasbp_min ≥ 0.066 | x5.07 for hospital_death: 1 | 0.059 | 0.080 | 2518 (5%) | 74.83% (78.21% of | $\overline{}$ |
| 3 | bun_apache ≥ 26.915 | x1.79 for hospital_death: 1 | 0.035 | 0.049 | 17557 (34%) | | |
| 4 | d1_sysbp_min < 80.5 | x2.41 for hospital_death: 1 | 0.034 | 0.065 | 10274 (20%) | 0.15% (0.80% of True) | |
| 5 | d1_arterial_ph_min < 7.242 | x4.06 for hospital_death: 1 | 0.030 | 0.065 | 3228 (6%) | 66.03% (70.37% of | |
| 6 | ventilated_apache ≥ 0.5 | x2.05 for hospital_death: 1 | 0.029 | 0.078 | 16562 (32%) | | |
| 7 | left_average_spo2 < 92.5 | x3.36 for hospital_death: 1 | 0.028 | 0.046 | 3607 (7%) | 0.28% (4.18% of True) | |
| 8 | apache_2_diagnosis inRange (112.5 to 115.5) | x2.47 for hospital_death: 1 | 0.027 | 0.050 | 7973 (15%) | | |
| 9 | should_be_dead ≥ 1 | x6.73 for hospital_death: 1 | 0.027 | 0.061 | 1133 (2%) | | |
| 10 | d1_temp_min < 35.685 | x2.55 for hospital_death: 1 | 0.027 | 0.044 | 6661 (13%) | 2.55% (20.66% of True) | |

FEATURES

| Rank 🛈 | · • · | Feature | Direction of Effect | Score 🕕 | Train ① RIG | Train Support | Feature Missing | Histogram ① |
|--------|-------|---|-----------------------------|---------|----------------|------------------|--------------------|-------------|
| 9 | * | should_be_dead ≥ 1 | x6.73 for hospital_death: 1 | 0.027 | 0.061 | 1133 (2%) | | |
| 16 | * | diasbp_invasive_started_after_firstHour | x2.95 for hospital_death: 1 | 0.017 | 0.036 | 3879 (8%) | | |
| 18 | * | not isNaN(arterial_po2_d1_value_range) | x1.87 for hospital_death: | 0.017 | 0.064 | 18240 (35%) | | |
| 19 | * | min(d1_mbp_min, d1_mbp_invasive_min) < 46.5 | x3.69 for hospital_death: 1 | 0.017 | 0.042 | 2685 (5%) | 74.18% | |
| 20 | * | row_zero_count ≥ 35 | x1.05 for hospital_death: | 0.017 | 0.054 | 25328 (49%) | | |
| 22 | * | fio2_cat = "high" | x3.37 for hospital_death: 1 | 0.016 | 0.045 | 3455 (7%) | | |
| 26 | * | d1_temp_max notInRange (36.61 to 38.02) | x1.75 for hospital_death: 1 | 0.013 | 0.028 | 12936 (25%) | 2.55% (| |
| 47 | * | high_lectate | x8.81 for hospital_death: 1 | 0.009 | 0.045 | 496 (0.963%) | | |
| 127 | * | ph_cat = "low" | x8.76 for hospital_death: 1 | 0.002 | 0.007 | 84 (0.163%) | | |
| 246 | * | low_heartrate2 | x5.78 for hospital_death: 1 | 0.001 | 0.023 | 585 (1%) | | |

Models



XGboost LightGBM Catboost Random Forest Deep Learning (FastAI)



Robust ensemble of 20+ models with diverse results Using Test Time Augmentation for tabular data – a novel approach

Modeling

- Gradient Boosting trees (Catboost, Xgboost, LightGBM, H2O GBM)
- Scikit learn (KNN, Logistic Regression, Random Forest, Extremely Randomized Trees, Histogram-Based Gradient Boosting)
- Deep learning models (Pytorch and Tensorflow) - weaker results (~88 AUC) but diverse and contributed to the final ensemble

Ensembled with **Pystacknet** (Python stacknet port) = Automated stacked, boosting, CrossValidated ensembles

Pseudolabelling

Take high confidence predictions on test set, and add them to training set

Ensembling methods

- Diverse data sets imputation techniques, features, and data generation
- Stacking the models using 3 layers stacknet.
- Normalized the models probabilities.
- Test Time Augmentation (TTA)
 TTA is a novel technique that aims to increase accuracy and decrease unfair bias. It works by by generating new similar test sets with mild changes. For example, the age, gender, and ethnic values. Then we ensemble them together.

FINALLY... WE WON!

| # | △pub | Team Name | Notebook | Team Members | Score ? | Entries |
|---|-------------|--------------|----------|--------------|---------|---------|
| 1 | - 1 | Women Power≖ | | | 0.91497 | 205 |
| 2 | ▲ 15 | nullset | | | 0.91485 | 56 |
| 3 | ▼ 2 | Prevision.io | | | 0.91445 | 216 |
| 4 | ▼ 1 | ML Keksika | | | 0.91431 | 36 |
| 5 | 1 | EPFL D | | | 0.91407 | 159 |



Results on the private leaderboard:

https://www.kaggle.com/c/widsdatathon2020/leaderboard

Detail writeup of our approach:

https://www.kaggle.com/c/widsdatathon2020/discussion/133189



INSIGHTS

- Tabular data in a complex domain important to get *deep* involvement of a domain expert, e.g. a medical doctor
 - Also helpful during data cleaning & imputation
- Ensemble methods always work Double entendre: "modelwise" and "peoplewise"/"featurewise"
- The existing APACHE risk scores underperform compared to ML models trained on the data, with said models generalizing surprisingly well across to different hospitals/ICU wards
- Even with a relatively large and clean dataset, manual feature engineering is valuable
- Winning a kaggle competition depends on the right team and accurate teamwork, along with a healthy dose of hard work and luck:)
- Our 1st place detailed write up: <u>https://www.kaggle.com/c/widsdatathon2020/discussion/133189</u>



THANK YOU!

Questions

