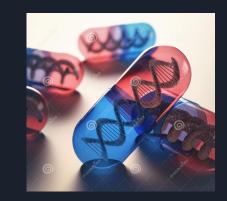
# Final Presentation: MoA Prediction

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# Introduction



#### Drug discovery

Scientists seek to identify a protein target associated with a disease and develop a molecule that can modulate that protein target. As a shorthand to describe the biological activity of a given molecule, scientists assign a label referred to as mechanism-of-action or MoA for short.

Our data from the Kaggle: MoA prediction competition <a href="https://www.kaggle.com/c/lish-moa">https://www.kaggle.com/c/lish-moa</a>

# Project Aims

**Aim**: analyze the cellular responses with algorithms that search for similarity to known patterns in genomic database with known MoAs.

Predicting multiple targets of the MoA responses of different samples based on the gene expression, cell viability, treatment duration and treatment dose data.

- Example of MoA targets

NFKB\_inhibitor, Serotonin\_receptor\_antagonist, DNA\_inhibitor, Dopamine\_receptor\_antagonist, Cyclooxygenase\_inhibitor, Proteasome\_inhibitor, Calcium\_channel\_blocker, ...

# Data Statistics

**Train\_data:** 23,814 samples **Test\_data:** 3,982 samples

Sig\_ids: Uniquely identify each sample

**Features**: [23,814 X 875]-training [3,982 X 875]-testing

	А	В	С	D	Е	F	G
1	sig_id	cp_type	cp_time	cp_dose	g-0	g-1	g-2
2	id_000644l	trt_cp	24	D1	1.062	0.5577	-0.2479
3	id_000779l	trt_cp	72	D1	0.0743	0.4087	0.2991
4	id_000a626	trt_cp	48	D1	0.628	0.5817	1.554
5	id_0015fd3	trt_cp	48	D1	-0.5138	-0.2491	-0.2656
6	id_001626l	trt_cp	72	D2	-0.3254	-0.4009	0.97
7	id_001762a	trt_cp	24	D1	-0.6111	0.2941	-0.9901

cp\_type: samples treated with a compound(trt\_cp) or a control perturbation(ctl\_vehicle)

cp\_time: treatment duration (24, 48 and 72 hours)

cp\_dose: treatment dose (high or low)

g-: 772 gene expressions (g-0 to g-771) c-: 100 cell viability (c-0 to c-99)

**Targets:** [23,814 X 206]

Probability of having MoA labels (totally 206)

Arithmetic data

Α	В	С	D	Е	F
sig_id	5-alpha_re	11-beta-hs	acat_inhibi	acetylcholi	acetylcholi
id_000644l	0	0	0	0	0
id_000779l	0	0	0	0	0
id_000a626	0	0	0	0	0
id_0015fd3	0	0	0	0	0
id_001626l	0	0	0	0	0
id_001762a	0	0	0	0	0
	sig_id id_000644l id_000779l id_000a626 id_0015fd3 id_001626l		sig_id 5-alpha_re 11-beta-hs   id_000644! 0 0   id_000779! 0 0   id_000a626 0 0   id_0015fd3 0 0   id_001626! 0 0	sig_id 5-alpha_re 11-beta-hs acat_inhibi   id_000644! 0 0 0   id_000779! 0 0 0   id_000a62! 0 0 0   id_0015fd3 0 0 0   id_001626! 0 0 0	sig_id 5-alpha_re 11-beta-hs acat_inhibi acetylcholi   id_000644k 0 0 0 0   id_000779k 0 0 0 0 0   id_000a62k 0 0 0 0 0   id_0015fd3 0 0 0 0 0   id_001626k 0 0 0 0 0

### Evaluation

Every sig\_id(sample) will be predicting the probability that the sample had a positive response for each MoA target.

The Log Loss Function (From the competition)

N(sig\_id) rows and M(MoA targets) columns

 $\widehat{oldsymbol{\mathcal{Y}}}_{i,m}$  is the predicted probability of a positive MoA response for a sig\_id

 $y_{i,m}$  is the ground truth, 1 for a positive response, 0 otherwise

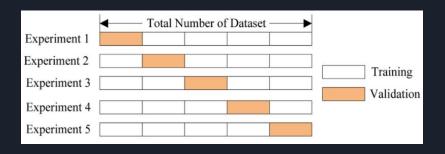
Score is the average validation loss of all experiments (7 folds)

$$LogLoss = -\frac{1}{M} \sum_{m=1}^{M} \frac{1}{N} \sum_{i=1}^{N} (y_{i,m} \log(\hat{y}_{i,m}) + (1 - y_{i,m}) \log(1 - \hat{y}_{i,m}))$$

#### K-Fold Cross-Validation

Split the dataset into k groups: folds

For each fold:



Take this fold as validation set and the remaining k-1 folds as training set

Fit a model on the training set and evaluate it on the validation set

We set k=7 for this dataset (7-fold Cross-validation)

Reason: There are 23,814 training samples: It is divided by 7.

To reduce time for running

# Plans after the Midterm Presentation



# Methods

Find some baselines for the MoA prediction.

Our method:

Multi-layer neural network with permutation importance

Compared method:

- 1. Kernel logistic regression
- 2. TabNet

# Compared method 1: Kernel Logistic Regression

This method uses the Kernel Ridge Regression with RBF kernel and

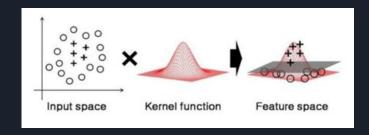
Platt scaling for the calibration (Logistic Regression)

Hyperparameter Setting (C: 1 and gamma: 100)

Use Nystroem Approximation (To reduce the computational costs)

Score: 0.0189

$$K_{RBF}(x, x') = \exp(-\gamma ||x - x'||^2)$$
  $\gamma = \frac{1}{2\sigma^2}$ 

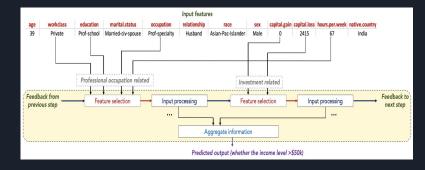


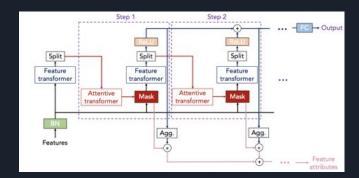
# Compared method 2: TabNet

### Tree-like deep method

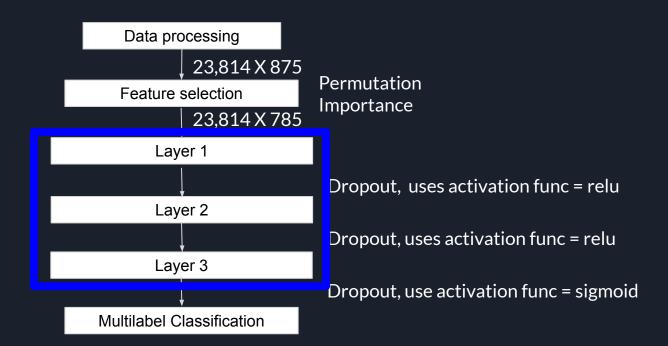
- a. It does feature selection automatically using attention mechanisms
- b. Similar to decision tree, it makes the decision in a sequential manner

Score: 0.1553





# Multilayer Neural Network with feature selection



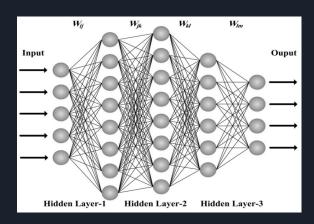
# Multi-Layer Neural Network

It's implemented using tensorflow

First hidden layer with 2,048 neurons

Second hidden layers with 1,024 neurons

Use Adam as the optimizer of the neural network



Set up a learning rate scheduler with ReduceLROnPlateau.

# Multilayer Neural Network with feature selection

Permutation importance: Finds important features In this method, important features are collected & used

sig_id	cp_type	cp_time	cp_dose	g-0	g-1	g-2	g-3	g-4	g-5	g-6	g-7	g-8	g-9
id_000644	trt_cp	24	D1	1.062	0.5577	-0.2479	-0.6208	-0.1944	-1.012	-1.022	-0.0326	0.5548	-0.0921
id_000779	trt_cp	72	D1	0.0743	0.4087	0.2991	0.0604	1.019	0.5207	0.2341	0.3372	-0.4047	0.8507
id_000a62	trt_cp	48	D1	0.628	0.5817	1.554	-0.0764	-0.0323	1.239	0.1715	0.2155	0.0065	1.23
id_0015fd3	trt_cp	48	D1	-0.5138	-0.2491	-0.2656	0.5288	4.062	-0.8095	-1.959	0.1792	-0.1321	-1.06
id_001626	trt_cp	72	D2	-0.3254	-0.4009	0.97	0.6919	1.418	-0.8244	-0.28	-0.1498	-0.8789	0.863

Features: 875

Samples : 23814

# Multilayer Neural Network with feature selection

Permutation importance: Finds important features In this method, important features are gathered & used

Shuffles data of each column and compare the result

Decrease: important Increase: not important

sig_id	cp_type	cp_time	cp_dose	g-0	g-1	g-2	g-3	g-4	g-5	g-6	g-7	g-8	g-9
id_000644	trt_cp	24	D1	1.062	0.5577	-0.2479	-0.6208	-0.1944	-1.012	-1.022	-0.0326	0.5548	-0.0921
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id_0015fd3	trt_cp	48	D1	-0.5138	-0/2491	-0.2656	0.5288	4.062	-0.8095	-1.959	0.1792	-0.1321	-1.06
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Features:

Samples : 23814

Scores: 0.0161

# Scores of each method

Method	Log Loss
Kernel Logistic Regression	0.0189
TabNet	0.1553
Multi-Layer Neural Network with Permutation Importance	0.0161



#### Results

#### **Ablation Study:**

- Multi-Layer Neural Network with Permutation Importance: 0.0161
- Multi-Layer Neural Network: 0.0163

#### Parameter Study:

- 1-Layer Neural Network: 0.0170
- 2-Layer Neural Network: 0.0164
- 4-Layer Neural Network: 0.0169
- 5-Layer Neural Network: 0.0169
- 6-Layer Neural Network: 0.0177

# Improvement

Use tanh activation: 0.0165

More hidden units in each layer: 0.0163

Less hidden units in each layer: 0.0168

Using PCA for dimension reduction: 0.0166

Using PCA and variance threshold: 0.0166

# Additional...

#### **Label Smoothing**

- regularization technique for the overconfident problem
  - decrease the gap among logits (i.e., output before the softmax)
  - make the learning process more smooth
- formula
  - $\circ$  y\_ls = (1-a) \* y + a/k

# Conclusion&Issue

#### Conclusions:

Simple model could work better than fancy models

Hyperparameters are important

#### Issues:

Hard to improve the performance

Lack of computational resource

# Thank you!