```
In [117]: import random
          import os
          import xgboost
          import shap
          import numpy
                                   as np
          import pandas
                                   as pd
          import matplotlib.pyplot as plt
          import seaborn
                                   as sns
          from sklearn.linear_model
                                        import LinearRegression
          from sklearn.ensemble
                                        import RandomForestRegressor
          from sklearn.metrics
                                        import mean absolute error
          from sklearn.model_selection import KFold
          from sklearn.model_selection import cross_val_score
          from sklearn.model selection import train test split
          from sklearn
                                        import metrics
          from sklearn.decomposition
                                        import PCA
          from sklearn.utils
                                        import resample
 In [2]: %run featimp
```

Feature Importance

May 9, Eileen Wang

Context

1. Intro

- What is Feature Importance?
- Dataset description and loading

2. Spearman's rank correlation coefficient

- Introduction and Implementation
- Visualization

3. Model-based Feature Importance

- Drop column importance
- Permutation importance

4. Comparing strategies on models

- Introduction and Implementation
- Visualization

5. Automatic feature selection algorithm

- Introduction and Implementation
- Visualization

6. Variance and empirical p-values for feature importances

- Variance Visualization
- · Empirical p-values

7. Summary

Intro

What is Feature Importance?

Imagine that you are dealing with a dataset with more than ten thousand features. Some features are just random noise, and some are highly relatived to each others, and some are super influential to your prediction, how can we weed out those unimportant features? Well, we always depend on numbers. So we have to find a way to quantize the importance of each feature and rank them by the number. As the result, there are some useful ways to do so and we will try them in this report.

Dataset description and loading

In order to focus on feature importance selection, I will use our old friend, Boston dataset, to do demonstrations since it's relatively simple that we can avoid complex data cleaning. Let's load it first!

```
In [177]: from sklearn.datasets import load_boston
X, y = load_boston(return_X_y=True)
```

We now have 13 features in this dataset.

```
In [165]: | column dict={}
           for index,col in enumerate(col names):
               column dict[index] = col
          column_dict
Out[165]: {0: 'CRIM',
            1: 'ZN',
            2: 'INDUS',
            3: 'CHAS',
            4: 'NOX',
            5: 'RM',
            6: 'AGE',
            7: 'DIS',
            8: 'RAD',
            9: 'TAX',
            10: 'PTRATIO',
            11: 'B',
            12: 'LSTAT'}
```

Spearman's rank correlation coefficient

Introduction and Implementation

The algorithm is pretty simple here. Just rank the features by its Spearman's rank correlation coefficient. However, this method suffers from codependent features. To deal with the issue, we use minimal-redundancy-maximal-relevance (mRMR), the idea behind this is that we rank our features not only by their relevance but also by their redundancy. The formula looks like:

of only by their relevance but also by their redundancy. The formula looks like:
$$J_{mRMR}(x_k) = I(x_k,y) - rac{1}{|S|} \sum_{x_j \in S} I(x_k,x_j)$$

The I function here is aim to get the mutual information from features. Here we will use Spearman's rank correlation coefficient to het such infomation.

```
In [7]: sfi = SpearFeatureImportance()
    sfi.fit(X,y)
    scores = sfi.score()

In [162]: df_spear = pd.DataFrame(list(zip(col_names, scores)),columns =['column', 's
    df_spear['score'] = df_spear['score'].apply(np.abs)
    df_spear['rank'] = df_spear['score'].rank(ascending=False)
```

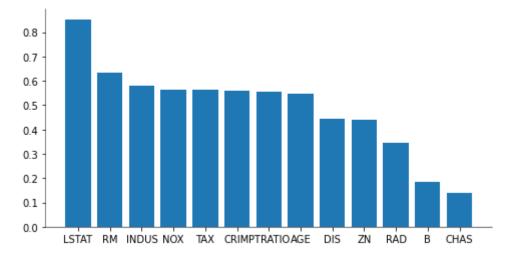
```
In [163]: df_spear = df_spear.sort_values('rank')
df_spear
```

Out[163]:

	column	score	rank
12	LSTAT	0.852914	1.0
5	RM	0.633576	2.0
2	INDUS	0.578255	3.0
4	NOX	0.562609	4.0
9	TAX	0.562411	5.0
0	CRIM	0.558891	6.0
10	PTRATIO	0.555905	7.0
6	AGE	0.547562	8.0
7	DIS	0.445857	9.0
1	ZN	0.438179	10.0
8	RAD	0.346776	11.0
11	В	0.185664	12.0
3	CHAS	0.140612	13.0

Visualization

The following graph shows the feature importances calculated by Spearman's rank correlation coefficient. We can see that LSTAT is the most relevant to our prediction and CHAS is more unimportant.



Next, we move on to deal with codependence. Let's check the heatmap of Spearman's rank correlation coefficient among our features. Some features have relatively high coefficient like AGE and NOX.

```
In [159]: boston_df = pd.DataFrame(X,columns =col_names)
    corr = boston_df.corr(method = 'spearman')
    plt.figure(figsize=(10, 8))
    sns.heatmap(corr, annot = True)
    plt.show()
```



```
In [166]: features, X_s = sfi.mRMR(13)
           feature_col =[]
           for index in features:
               feature_col.append(column_dict[index])
In [167]: feature_col
Out[167]: ['RM',
            'B',
            'DIS',
            'PTRATIO',
            'ZN',
            'CHAS',
            'RAD',
            'CRIM',
            'INDUS',
            'NOX',
            'AGE',
            'TAX',
            'LSTAT']
```

After mRMR, we got a list of final choice.

Model-based Feature Importance

If we already selected a model, we can get feature importances by fitting the model. The idea is that we drop or permute the target column to see the difference in out metric, and take this as its feature importance. To keep things simple, we use linear regression and mean absolute error(MSE) as out model and metric here.

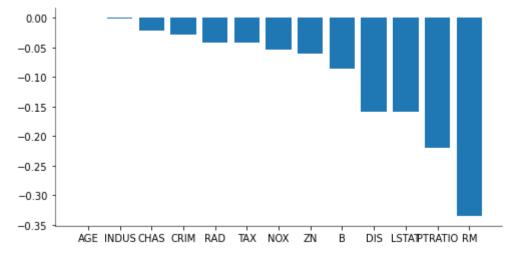
Drop column importance

The brute-force way is dropping target column directly.

```
In [19]: lr = LinearRegression()
   metric = mean_absolute_error
   X = pd.DataFrame(X)
```

Out[36]:

	column	score	rank
6	AGE	0.000231	1.0
2	INDUS	-0.001387	2.0
3	CHAS	-0.020696	3.0
0	CRIM	-0.028138	4.0
8	RAD	-0.041385	5.0
9	TAX	-0.042306	6.0
4	NOX	-0.053274	7.0
1	ZN	-0.059844	8.0
11	В	-0.085443	9.0
7	DIS	-0.158841	10.0
12	LSTAT	-0.159272	11.0
10	PTRATIO	-0.219717	12.0
5	RM	-0.335068	13.0



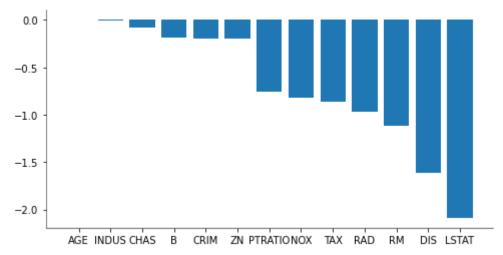
As we can see, drop any columns in our dataset will do negetive impact on our model. This method is easy, simple and direct but it has a drawback that we have to fit the model every time which is very computation expensive.

Permutation importance

There is a more smart way than dropping the column -- we permute it. To illustrate, we break the relationship between target column and other columns but keep the distribution. By doing so, we can get similar result as dropping it but save the computation time on refitting models.

Out[37]:

	column	score	rank
6	AGE	0.001164	1.0
2	INDUS	-0.006160	2.0
3	CHAS	-0.077577	3.0
11	В	-0.183113	4.0
0	CRIM	-0.192629	5.0
1	ZN	-0.199838	6.0
10	PTRATIO	-0.754291	7.0
4	NOX	-0.822739	8.0
9	TAX	-0.861189	9.0
8	RAD	-0.965287	10.0
5	RM	-1.115558	11.0
7	DIS	-1.613015	12.0
12	LSTAT	-2.087886	13.0



Comparing strategies on models

Introduction and Implementation

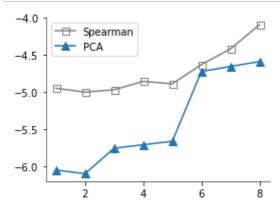
In this part, we will use three different models and two feature importances technics -- Spearman's rank correlation coefficient and PCA (from scikit learn library) -- to find out how many features do we need. only thing we need to do here is calculate the average validation score on models fitted by k features.

```
In [78]: def plot comparing(model, top k):
             result spear=[]
             result_pca=[]
             for k in range(1,top_k+1):
                 clf = model
                 X_top_k = X[list(df_spear[df_spear['rank'] <=k]['column'])]</pre>
                 score_list = cross_val_score(clf, X_top_k, y, cv=5, scoring='neg_me
                 avg score = score list.sum()/len(score list)
                 result_spear.append(avg_score)
                 pca = PCA(n_components=k)
                 X_top_k_PCA = pca.fit_transform(X)
                 score_list = cross_val_score(clf, X_top_k PCA, y, cv=5, scoring='ne
                 avg score = score list.sum()/len(score list)
                 result_pca.append(avg_score)
             fig, ax = plt.subplots(figsize=(4,3))
             ax.plot(range(1,top_k+1),result_spear,'s-',markersize=7, c='grey',fills
             ax.plot(range(1,top k+1),result pca,'^-',markersize=8,label="PCA",lw=1.
             ax.spines['top'].set_visible(False)
             ax.spines['right'].set_visible(False)
             ax.spines['left'].set_linewidth(.5)
             ax.spines['bottom'].set_linewidth(.5)
             plt.legend()
             plt.show()
```

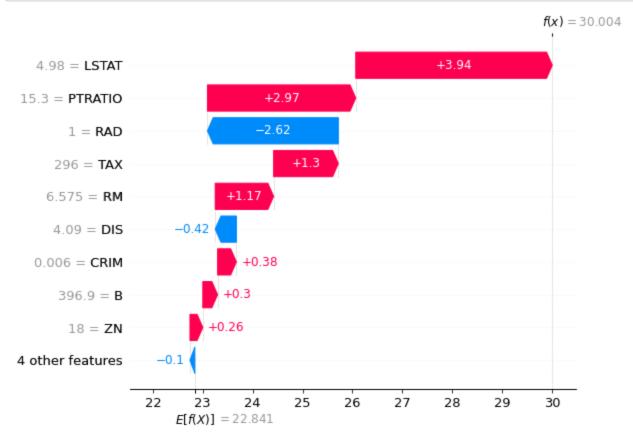
Visualization

The following line plots show the fact that as we put more and more features to our model, the performance gets better, which is consistent to what we got on model-based feature importance selection process. Then we will compare the result to shapley values byt utilizing SHAP library.

```
In [79]: lr = LinearRegression()
plot_comparing(lr, 8)
```

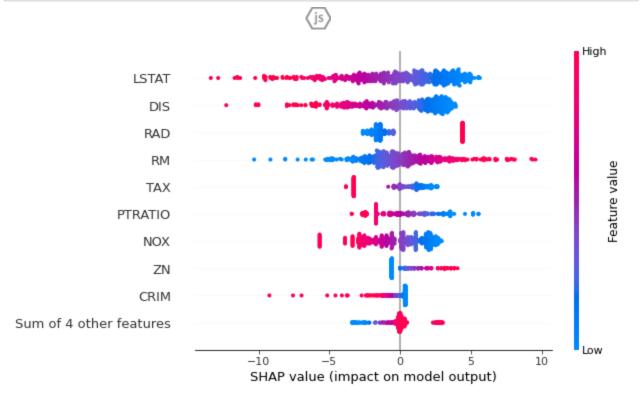


```
In [197]: model = LinearRegression().fit(X, y)
    X100 = shap.utils.sample(X, 100)
    explainer = shap.Explainer(model.predict, X100)
    shap_values = explainer(X)
    shap.plots.waterfall(shap_values[0])
```

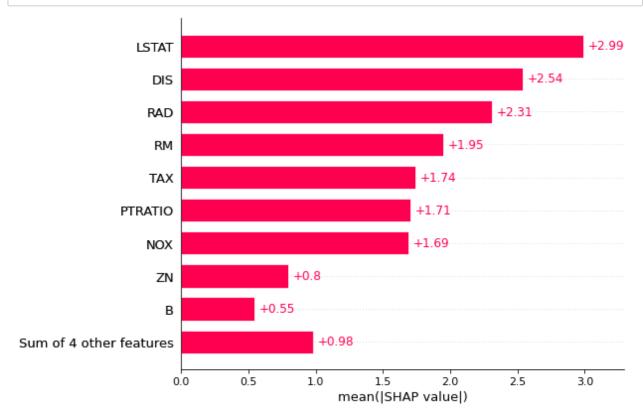


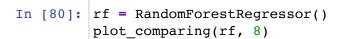


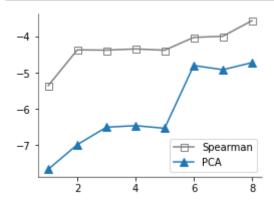
In [199]: shap.initjs()
shap.plots.beeswarm(shap_values)



In [200]: shap.plots.bar(shap_values)

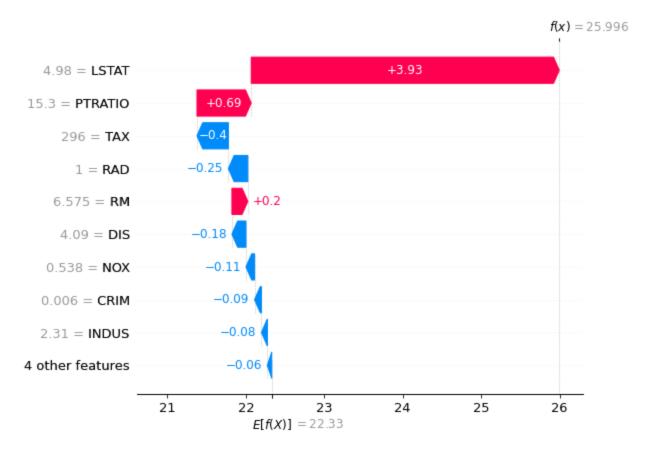




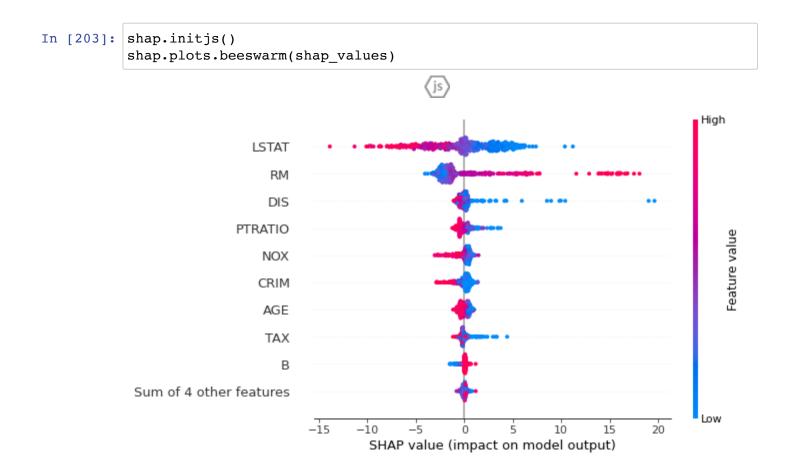


```
In [201]: model = RandomForestRegressor().fit(X, y)
    X100 = shap.utils.sample(X, 100)
    explainer = shap.Explainer(model.predict, X100)
    shap_values = explainer(X)
    shap.plots.waterfall(shap_values[0])
```

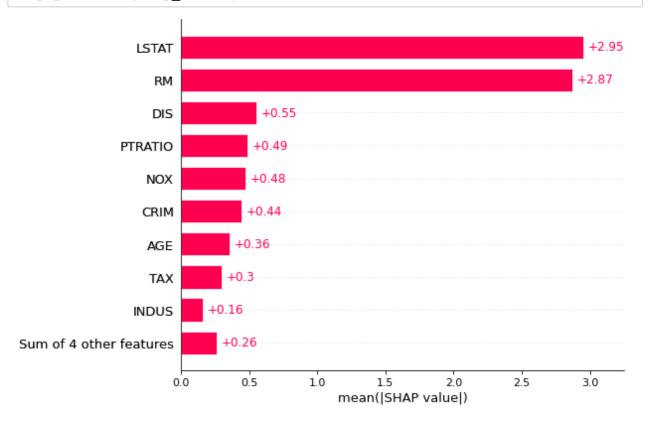
Permutation explainer: 507it [01:46, 4.33it/s]



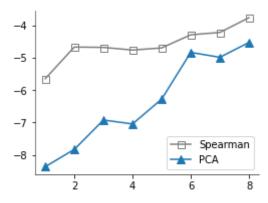


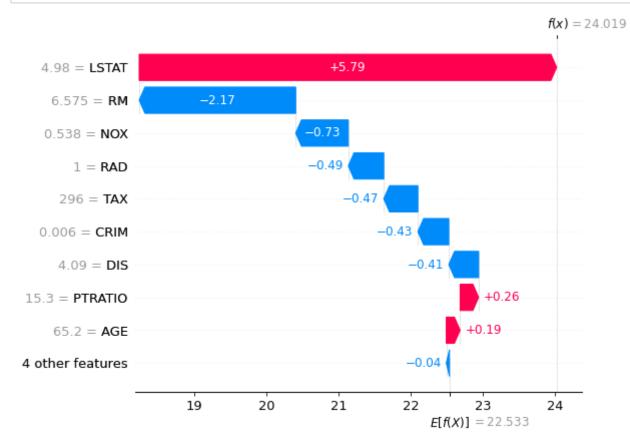


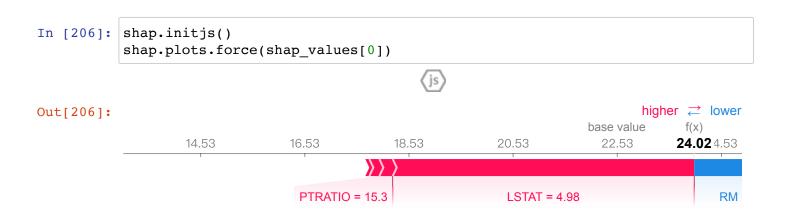
In [204]: shap.plots.bar(shap_values)



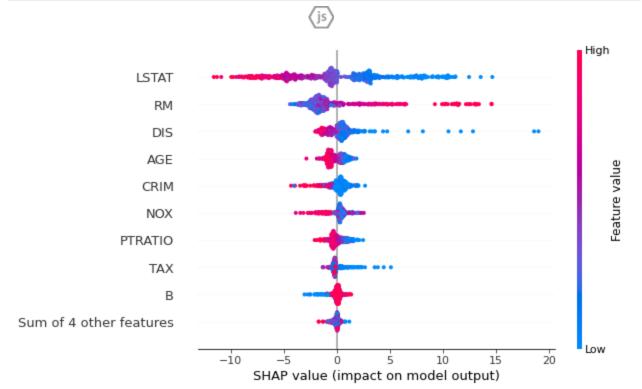


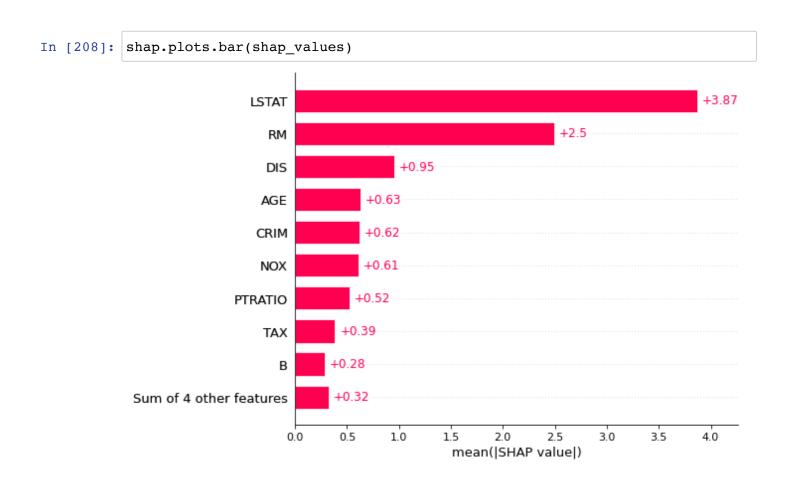












Automatic feature selection algorithm

Introduction and Implementation

Now we want to try another way to find best fit for our model. The algorithm here is as following:

- 1. calculate validation error on the whole dataset as the baseline
- 2. drop the least important features and calculate validation error again
- 3. if the error get worse, stop and take the columns in previous step as the best fit.

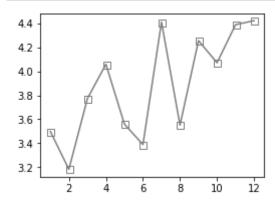
```
In [182]: | lr = LinearRegression()
          metric = mean absolute error
          X train, X val, y train, y val = train test split(X, y, test size=0.2)
          lr.fit(X_train,y_train)
          validation error = metric(y val, lr.predict(X val))
          for i in range(len(X.columns),1,-1):
              lr = LinearRegression()
              X_drop = X[list(df_spear[df_spear['rank'] < i]['column'])]</pre>
              X train, X val, y train, y val = train test split(X drop, y, test size=
              lr.fit(X_train,y_train)
              new_validation_error = metric(y_val, lr.predict(X_val))
              if new validation error > validation error:
                  result = list(df spear[df spear['rank'] < i+1]['column'])</pre>
                  break
              else:
                  validation error = new validation error
          print(result)
          ['LSTAT', 'RM', 'INDUS', 'NOX', 'TAX', 'CRIM', 'PTRATIO', 'AGE', 'DIS',
```

```
'ZN', 'RAD', 'B', 'CHAS']
```

In this case, we got worse score at the first drop so it suggest us to keep every features.

Visualization

```
In [185]: | lr = LinearRegression()
          metric = mean absolute error
          X train, X val, y train, y val = train test split(X, y, test size=0.2)
          lr.fit(X_train,y_train)
          validation_error = metric(y_val, lr.predict(X_val))
          val err=[]
          for i in range(len(X.columns),1,-1):
              lr = LinearRegression()
              X_drop = X[list(df_spear[df_spear['rank'] < i]['column'])]</pre>
              X_train, X_val, y_train, y_val = train_test_split(X_drop, y, test_size=
              lr.fit(X_train,y_train)
              new_validation_error = metric(y_val, lr.predict(X_val))
              val err.append(new validation error)
          fig, ax = plt.subplots(figsize=(4,3))
          ax.plot(range(1,len(val_err)+1),val_err,'s-',markersize=7, c='grey',fillsty
          plt.show()
```



Variance and empirical p-values for feature importances

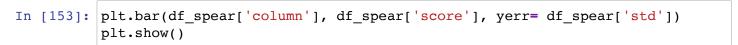
Now we want to know to what degree our feature importance is reliable. In order to answer that, calculating the variance or standard deviation and p-value is useful. In this part, we use bootstrapping method on our dataset to get standard deviation.

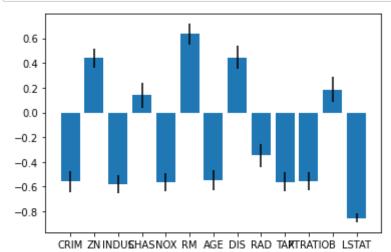
```
In [144]: result=[]
for _ in range(1000):
    data = X
    data['y'] = y
    boot = resample(data, replace=True, n_samples=len(data)//5)
    boot_X = np.array(boot.drop(columns=['y'], axis=1))
    boot_y = np.array(boot['y'])
    sfi = SpearFeatureImportance()
    sfi.fit(boot_X, boot_y)
    scores = sfi.score()
    result.append(scores)
```

```
In [149]: std = np.std(np.array(result), axis=0)
```

Out[150]:

	column	score	rank	std
0	CRIM	-0.558891	9.0	0.081765
1	ZN	0.438179	3.0	0.077604
2	INDUS	-0.578255	12.0	0.075246
3	CHAS	0.140612	5.0	0.100605
4	NOX	-0.562609	11.0	0.074067
5	RM	0.633576	1.0	0.082331
6	AGE	-0.547562	7.0	0.078061
7	DIS	0.445857	2.0	0.092741
8	RAD	-0.346776	6.0	0.091992
9	TAX	-0.562411	10.0	0.077830
10	PTRATIO	-0.555905	8.0	0.075377
11	В	0.185664	4.0	0.104087
12	LSTAT	-0.852914	13.0	0.034403





As for p-value, first thind we have to do is to create a null distribution, which means shuffling y and then compute the feature importances again. To do so, I want to borrow useful functions from a amazing <u>Kaggle notebook (https://www.kaggle.com/ogrellier/feature-selection-with-null-</u>

importances) and do some changes to fit my case.

```
In [224]: from sklearn.metrics import roc auc score
          import lightqbm as lqb
          def get_feature_importances(data, shuffle, seed=None):
              # Gather real features
              train features = [f for f in data if f not in ['y']]
              # Go over fold and keep track of CV score (train and valid) and feature
              # Shuffle target if required
              y = data['y'].copy()
              if shuffle:
                  # Here you could as well use a binomial distribution
                  y = data['y'].copy().sample(frac=1.0)
              sfi = SpearFeatureImportance()
              sfi.fit(np.array(data[train features]),np.array(y))
              # Get feature importances
              imp df = pd.DataFrame()
              imp df["feature"] = list(train features)
              imp df["importance gain"] = sfi.score()
              return imp df
```

```
In [225]: null_imp_df = pd.DataFrame()
          nb runs = 80
          import time
          start = time.time()
          dsp = ''
          data = X
          data['y'] = y
          for i in range(nb runs):
              # Get current run importances
              imp df = get feature importances(data=data, shuffle=True)
              imp_df['run'] = i + 1
              # Concat the latest importances with the old ones
              null imp df = pd.concat([null imp df, imp df], axis=0)
              # Erase previous message
              for 1 in range(len(dsp)):
                  print('\b', end='', flush=True)
              # Display current run and time used
              spent = (time.time() - start) / 60
              dsp = 'Done with %4d of %4d (Spent %5.1f min)' % (i + 1, nb_runs, spent
              print(dsp, end='', flush=True)
```

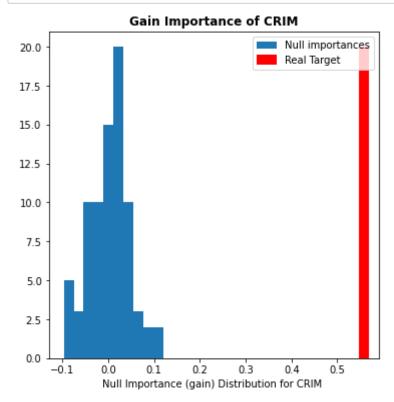
Done with 80 of 80 (Spent 0.1 min)

```
In [227]: null_imp_df.head()
```

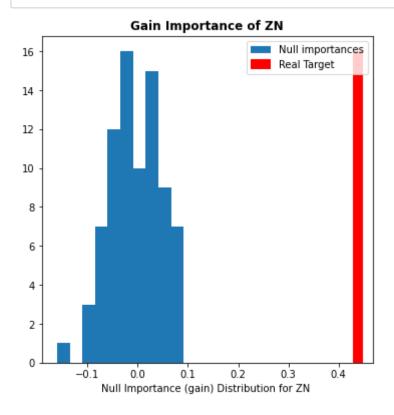
Out[227]:

	feature	importance_gain	run
0	CRIM	-0.080958	1
1	ZN	0.083073	1
2	INDUS	-0.066545	1
3	CHAS	-0.014717	1
4	NOX	-0.062999	1

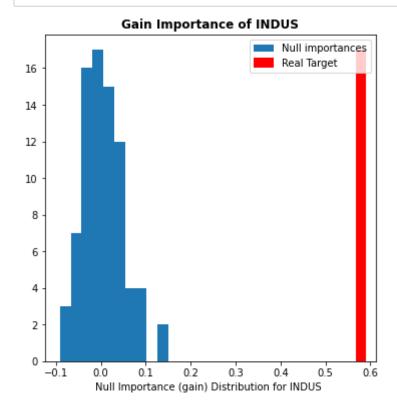
In [240]: display_distributions(actual_imp_df_=df_spear, null_imp_df_=null_imp_df, fe



In [241]: display_distributions(actual_imp_df_=df_spear, null_imp_df_=null_imp_df, fe



In [242]: display_distributions(actual_imp_df_=df_spear, null_imp_df_=null_imp_df, fe



I simply take three features ramdomly to see the p-value distribution. we can see that the p-value obviously far lower than 5%, which means it is significant.

Summary

Feature selecting process is crucial to model training. Unrelated features cause noise and bias to model and make the prediction unreliable. In this report, we used several different methods to calculate feature importance, including Spearman's rank correlation coefficient, PCA and model-based, and implemented strategy to get top features and reliability of our numbers.