ex-fi-sol

May 23, 2023

```
[]: 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.model_selection import train_test_split
  from sklearn.metrics import mean_squared_error
  %matplotlib inline
  sns.set_style('whitegrid')
```

1 Exercise 1: Permutation Feature Importance Exercise

1.0.1 a)

Permutation Feature Importance compares the performance of the model on the original data with the performance on perturbed data, where the dependence of the variable of interest (let's call it x_j) with the target Y variable is broken.

In order to break the dependence of x_j with $y, \, x_j$ is replaced with a permuted version \tilde{x}_j which is independent of the target.

However, by permuting the variable we do not only break the dependence with y, but also with all other covariates. As such, we may create unrealistic observations.

For example, time of the year may be dependent with the highest temperature on a day. If we resample the variable time of the year independently of the temperature high, we may create observations where time of the year is winter and temperature high is 40 degrees celsius.

1.0.2 b)

If a feature anyway independent of its covarites $(x_j \perp x_{-j})$, then PFI does not extrapolate to unseen regions.

Intuitively, the reason is that no dependence with the covariates is broken, since there were not dependencies between x_i and the remaining variables x_{-i} to begin with..

We discuss the theoretical background of the issue in more detail in the in-class exercise.

1.0.3 c)

```
[]: df = pd.read_csv('extrapolation.csv', index_col=0)

X, y = df[df.columns[df.columns != 'y']], df['y']
X_train, X_test, y_train, y_test = train_test_split(X, y, train_size=0.7)

model = LinearRegression()
model.fit(X_train, y_train)

print('MSE: {}'.format(mean_squared_error(model.predict(X_test), y_test)))
```

MSE: 0.008937939178929953

1.1 d)

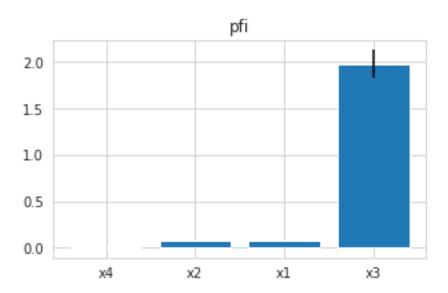
First, we implement PFI. Here we implement the methods generically, such that the perturbation mechanism can easily be replaced. Therefore, we make use of *args and **kwargs.

```
[]: def pfi_fname(fname, predict, score, X_test, y_test, *args):
         """Function that returns the pfi for a single feature.
         Arqs:
             fname: feature of interest name
             predict: prediciton function
             score: performance metric
             X_test: data for the evaluation
             y_test: respective labels
             *args: further arguments (which are ignored)
         Returns:
             performance: performance metric
         X_test_perturbed = X_test.copy(deep=True)
         X_test_perturbed[fname] = np.random.permutation(X_test_perturbed[fname])
         performance = score(y_test, predict(X_test_perturbed)) - score(y_test,_u
      →predict(X_test))
         return performance
     def fi_naive(fi_fname, predict, score, X_test, y_test, *args, **kwargs):
         """Naive feature importance implementation.
         Args:
             perf_pert: function that returns performance for some perturbation.
             predict: prediction function
             score: performance metric
             X_test: test data for the evaluation
             y_test: respective labels
```

```
*args: further arguments, e.g. training data (can be ignored here)
    Returns:
        results: relevance for each feature (in the order of X test.columns)
    # compute performance under perturbation
    results = []
    for fname in X_test.columns:
        imp = fi_fname(fname, predict, score, X_test, y_test, *args, **kwargs)
        results.append(imp)
    # compute pfi scores
    results = np.array(results)
    return results
import multiprocess as mp
def n_times(n, method, *args, return_raw=False, **kwargs):
    """Parallelized implementation for the repeated evaluation of fi.
    Arqs:
        n: number of repetitions
        method: feature importance method.
        args: all further arguments that are required for the method
        return\_raw: Whether only the aggregation (mean, stdd) or also the raw_{\!\perp}
 \hookrightarrow results are returned
    Returns:
       mean_fi, std_fi, (raw results)
    pool = mp.Pool(mp.cpu_count())
    with pool: # a simple for loop would be ok as well
        results = [pool.apply(method, args=args, kwds=kwargs) for _ in range(n)]
    results = np.array(results)
    if return_raw:
        return np.mean(results, axis=0), np.std(results, axis=0), results
    else:
        return np.mean(results, axis=0), np.std(results, axis=0)
```

Now we apply the method to our model and dataset.

plt.bar(X_test.columns[ordering], fis_mean[ordering], yerr=fis_std[ordering])
plt.show()



1.1.1 e)

 X_3 is the most important feature, with X_1 and X_2 sharing the second place. PFI considers X_4 to be irrelevant.

According to the PFI interpretation rules, without further assumptions about the data, we know that

- X_1, X_2, X_3 are used by the model for it's prediction
- X_1, X_2, X_3 are dependent with Y and/or dependent with the covariates
- X_4 may be independent of Y and covariates and/or not used by the model. We only know that it is not both dependent and used by the model.

Bonus: If we would additionally analyze the data we find out that X_1, X_2 are dependent but X_3 is independent of all covariates.

As such, we could further conclude that X_3 is dependent with Y (but do not know for X_1, X_2 without looking into the data).

1.1.2 f)

```
[]: print(model.coef_, model.intercept_)
```

 $[-0.20295108 \quad 0.20318676 \quad 1.00971948 \quad 0.00611803] \quad 0.0025435035702275517$

```
[]: from scipy.stats import pearsonr
rho = df.corr()
pval = df.corr(method=lambda x, y: pearsonr(x, y)[1]) - np.eye(*rho.shape)
```

```
p = pval.applymap(lambda x: ''.join(['*' for t in [0.01,0.05,0.1] if x<=t]))
rho.round(2).astype(str) + p</pre>
```

```
[]:
                                xЗ
              x1
                       x2
                                          x4
                                                    у
          1.0***
                   1.0***
                              0.03
                                      -0.05
     x1
                                                0.02
          1.0***
                   1.0***
     x2
                              0.03
                                      -0.05
                                                0.02
     x3
            0.03
                     0.03
                            1.0***
                                       -0.0
                                              1.0***
                    -0.05
                                     1.0***
     x4
           -0.05
                              -0.0
                                                  0.0
            0.02
                     0.02
                            1.0***
                                        0.0
                                              1.0***
     У
```

Our interpretation was correct.

$1.1.3 \, \mathrm{g}$

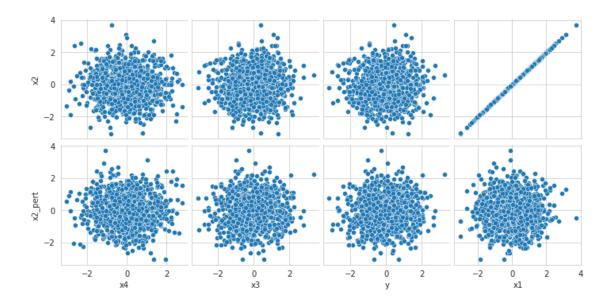
If we know the dependence structure of the covariates we can infer whether or not the PFI value is nonzero due to a dependence with the covariates or not. In our example we now know that x_3 is independent of its covariates, so we hypothesize that x_3 is actually dependent with y (and would perform importance tests as a consequence). Since x_1, x_2 are dependent, for those variables we cannot infer anything about the dependence with y with the covariates dependence structure and PFI alone.

1.2 h)

We use the extrapolation.csv dataset. We create a pairplot showing the pairwise scatterplot of the original feature as well as the corresponding perturbed variable with all remaining feature variables (and potentially y).

```
def pairplot_comparison(data, fname):
    data.loc[:, fname+'_pert'] = np.random.permutation(data.loc[:, fname])
    data = data[sorted(data.columns)]
    all_except_fname = list(set(data.columns) - set([fname, fname + '_pert']))
    sns.pairplot(data, y_vars=[fname, fname+'_pert'], x_vars=all_except_fname)

pairplot_comparison(df, 'x2')
```



We can see that the strong correlation of x_2 with x_1 (top row) is broken after permutation (bottom row). All other pairwise (in)dependencies are unchanged. Note: We only assess pairwise, unconditional dependencies. Without assumptions about the data, we cannot know whether further conditional depencies with the remaining covariates were broken.

2 Exercise 2: Feature Importance without Extrapolation

2.0.1 a)

An efficient, pytorch based implementation is given in a separate file (utils.py).

In order to keep things clean, we only provide a small wrapper function here.

/shared-libs/python3.7/py/lib/python3.7/site-packages/tqdm/auto.py:22:
TqdmWarning: IProgress not found. Please update jupyter and ipywidgets. See
https://ipywidgets.readthedocs.io/en/stable/user_install.html
from .autonotebook import tqdm as notebook_tqdm

```
[]: J = ['x1', 'x3']
C = ['x2', 'x4']
sample = sample_cond(J, C, X_train, X_test, num_samples=10)
sample.head()
```

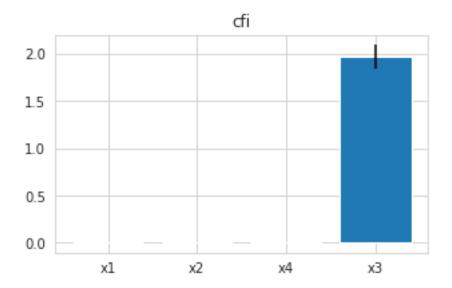
```
[]: x1 x3
i sample
653 0 0.545276 0.081977
1 0.511839 -0.691888
2 0.521899 -1.500667
3 0.522237 -0.686662
4 0.503619 -0.536446
```

2.1 b)

We implement conditional feature importance (CFI).

```
def cfi_fname(fname, predict, score, X_test, y_test, X_train, *args):
    """conditional feature importance for a feature fname"""
    X_test_perturbed = X_test.copy(deep=True)
    C = sorted(X_test.columns[X_test.columns != fname])
    sample = sample_cond([fname], C, X_train, X_test)
    X_test_perturbed[fname] = sample.to_numpy()
    performance = score(y_test, predict(X_test_perturbed)) - score(y_test, u)
    predict(X_test))
    return performance
```

2.2 c)



Now, only X_3 is considered relevant. We knnw that

- X_3 is conditionally dependent with $Y(X_3 \perp Y | X_1, X_2, X_4)$ and it is used by the model
- without further assumtions, we cannot make conclusions about the remaining variables. We only know that they are not at the same time conditionally dependent with Y and used by the model for it's prediction.

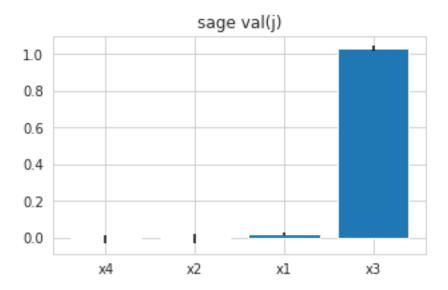
2.2.1 d)

```
[]: import pandas as pd
    idx = pd.IndexSlice
    def repeat_df(df, n):
         """function that repeats dataframe with multiindex"""
        ix 1 = df.index
        multindex = pd.MultiIndex.from_product([list(ix_1), list(range(n))],__
      →names=['i', 'sample'])
        df_new = pd.DataFrame([], columns=df.columns, index=multindex)
        for ii in range(n):
            df_new.loc[idx[:, ii], df.columns] = df[df.columns].to_numpy()
        return df_new
    def c_value_func_partial(J, predict, score, X_test, y_test, X_train,_
      """partial value function, i.e. performance given all features are
        reconstructed conditional on the set J, marginalization of the prediction
         over the remaining features
```

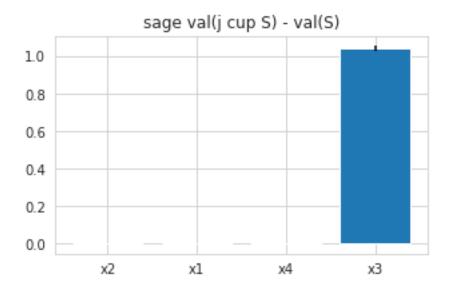
```
C = [f for f in X_test.columns if f not in J]
   if len(C) == 0:
       return score(predict(X_test), y_test)
    sample = sample_cond(C, J, X_train, X_test, num_samples=n marginalize)
   X_test_pert = repeat_df(X_test, n_marginalize)
   X_test_pert[C] = sample.loc[X_test_pert.index, C].to_numpy()
   X_test_pert['y_hat'] = predict(X_test_pert)
   y_hat_agg = X_test_pert['y_hat'].groupby('i', sort=False).mean().loc[X_test.
 →index]
   return score(y_hat_agg, y_test)
def c_value_func(J, S, *args, **kwargs):
    """conditional sage value function of variables j given coalition S"""
   return c_value_func_partial(S, *args, **kwargs) - c_value_func_partial(J +__
 ⇒S, *args, **kwargs)
def sage_val_empty(fname, predict, score, X_test, y_test, X_train,_
 """sage value given empty coalition"""
   return c_value_func([fname], [], predict, score, X_test, y_test, X_train,_
 →n_marginalize=n_marginalize)
def sage_val_remainder(fname, predict, score, X_test, y_test, X_train,_
 →n_marginalize=10):
    """sage value given full remainder as coaliation"""
   remainder = [f for f in X_test.columns if f != fname]
   return c_value_func([fname], remainder, predict, score, X_test, y_test,__

¬X_train, n_marginalize=n_marginalize)
```

2.2.2 e)



We can hypothesize that x_3 is pairwise dependent with y, while all other variables are pairwise independent with y. We learn that x_3 is used by the model. We do not know for the remaining variables.



We additionally learn that the contribution of x_3 is unaffected by knowing further covariables.

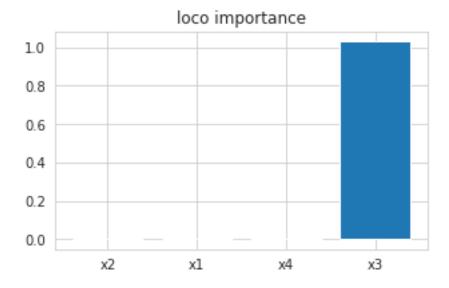
2.3 Exercise 3: Refitting based importance

2.3.1 a)

```
[]: from sklearn.base import clone

def loco(fname, predict, score, X_test, y_test, X_train, y_train, model):
    """loco importance for feature fname"""
    y_hat_pre = predict(X_test)
    model_new = clone(model)
    remainder = [f for f in X_train.columns if f != fname]
    model_new.fit(X_train[remainder], y_train)
    y_hat_post = model_new.predict(X_test[remainder])
    diff = score(y_hat_post, y_test) - score(y_hat_pre, y_test)
    return diff
```

2.3.2 b)



2.3.3 c)

Result is similar as for SAGE and CFI: only feature x_3 is considered relevant. We learn that x_3 provides more information than the remaining features combined, (while the other features do not contribute to the performance at all).

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