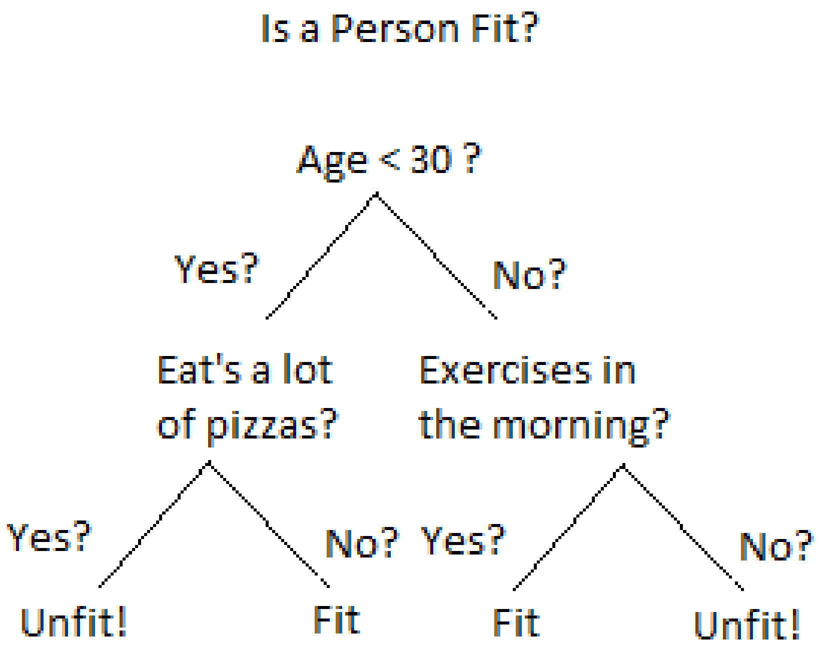
Assessing Feature Importance

Importance of an Attribute

Let's think again about the structure of DT models



- Every node is associated to an attribute
- ...And leads to an impurity reduction at training time

Intuitively, the attribute is responsible for the reduction

Importance of an Attribute

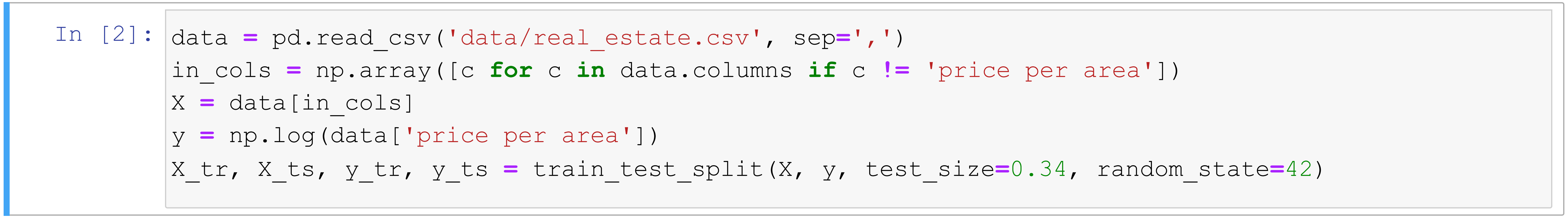
By summing the reductions on a whole tree

...We can compute attribute importance scores

- These typically normalized so as to sum up to 1
- Hence, if an attribute j has importance 0.3
- ...Then 30% of the impurity reduction was due to that attribute

In scikit-learn, this computation is done by default at training time

To see that in action, let's start by loading the housing dataset

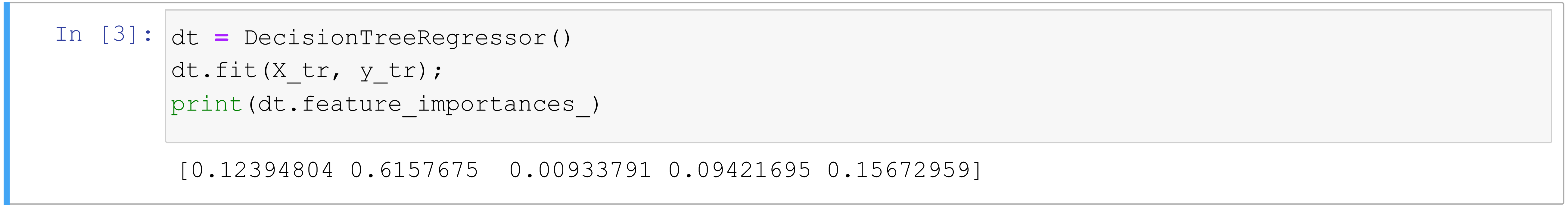


In [2]:

```
data = pd.read_csv('data/real_estate.csv', sep=',')
in_cols = np.array([c for c in data.columns if c != 'price per area'])
X = data[in_cols]
y = np.log(data['price per area'])
X_tr, X_ts, y_tr, y_ts = train_test_split(X, y, test_size=0.34, random_state=42)
```

Attribute Importance in scikit-learn

After training, the importances are available in a class attribute



In [3]:

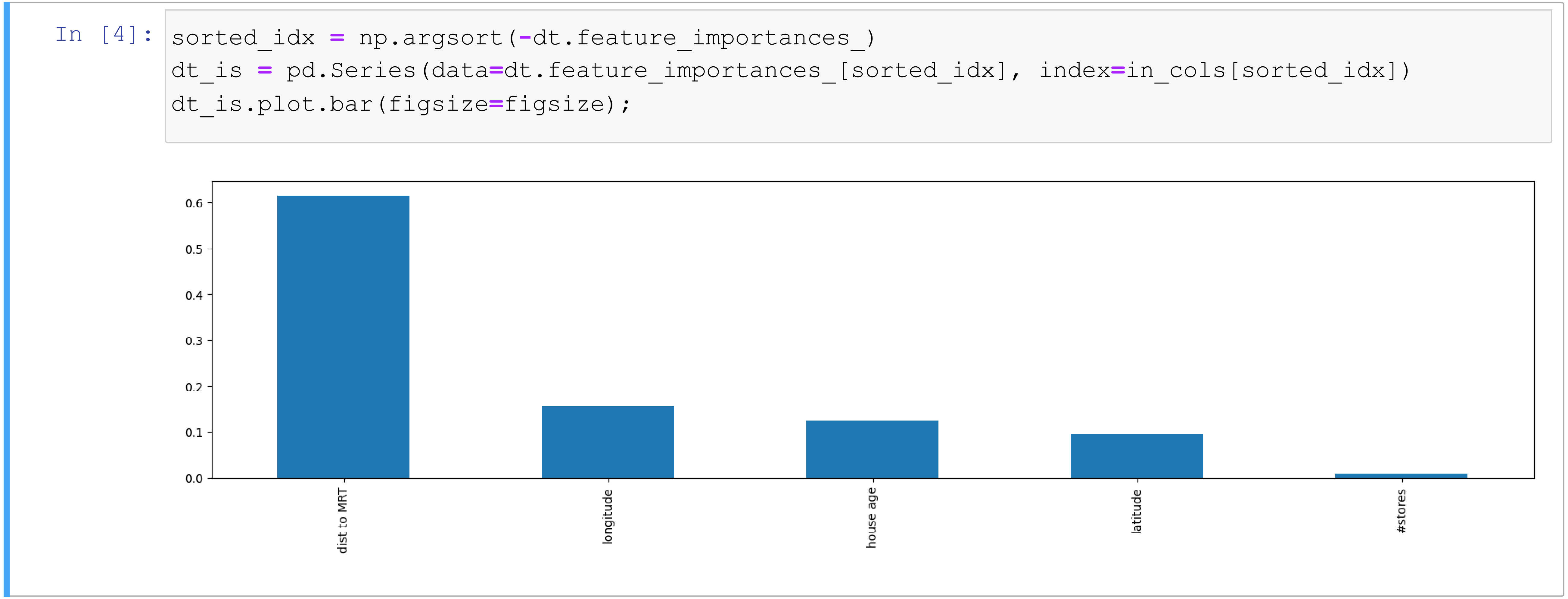
```python
dt = DecisionTreeRegressor()
dt.fit(X_tr, y_tr);
print(dt.feature_importances_)
```

```
[0.12394804 0.6157675  0.00933791 0.09421695 0.15672959]
```

- Due to how the scores are computed, there is no need for standardization
  - Range differences are not a problem with DTs
- Since DTs are non-linear, the score can account for non-linear relations
- ...But for the same reason they lack sign information
  - We do not get to know the "direction" of the impact of an attribute

Attribute Importance in scikit-learn

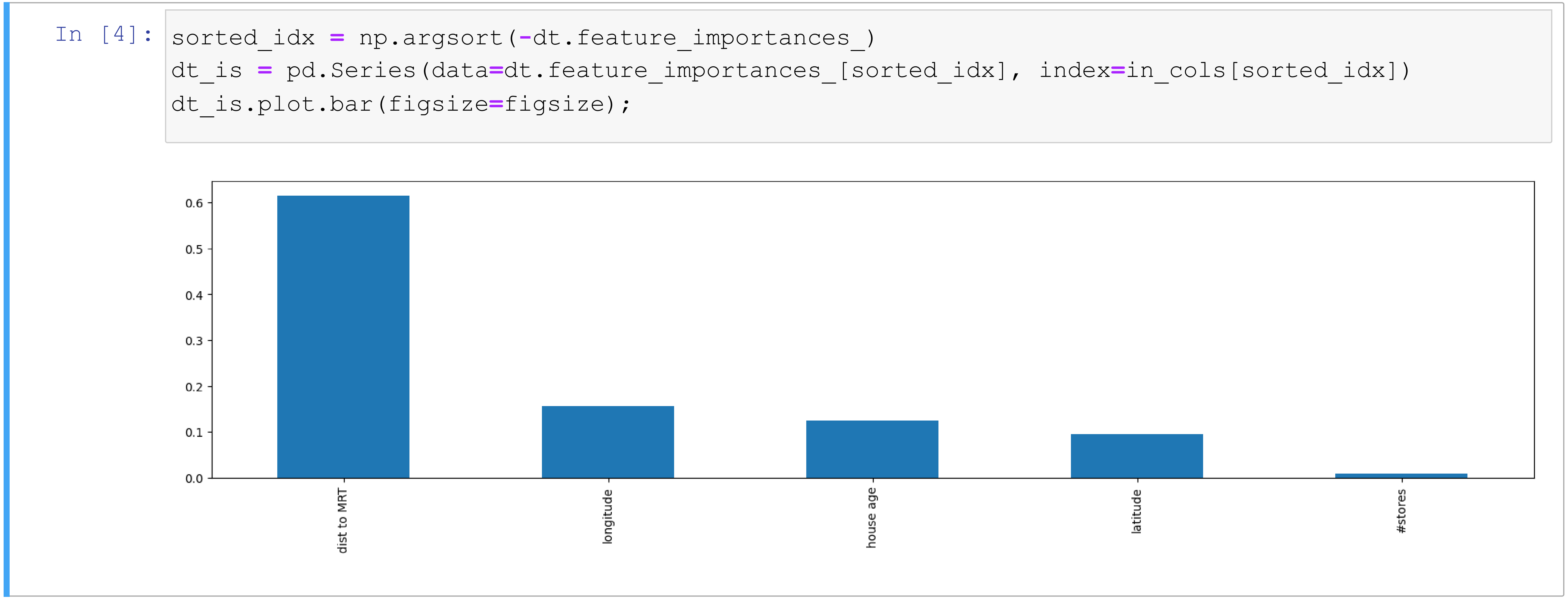
Let's plot the importances



```
In [4]: sorted_idx = np.argsort(-dt.feature_importances_)
        dt_is = pd.Series(data=dt.feature_importances_[sorted_idx], index=in_cols[sorted_idx])
        dt_is.plot.bar(figsize=figsize);
```

Attribute Importance in scikit-learn

Let's plot the importances



```
In [4]: sorted_idx = np.argsort(-dt.feature_importances_)
        dt_is = pd.Series(data=dt.feature_importances_[sorted_idx], index=in_cols[sorted_idx])
        dt_is.plot.bar(figsize=figsize);
```

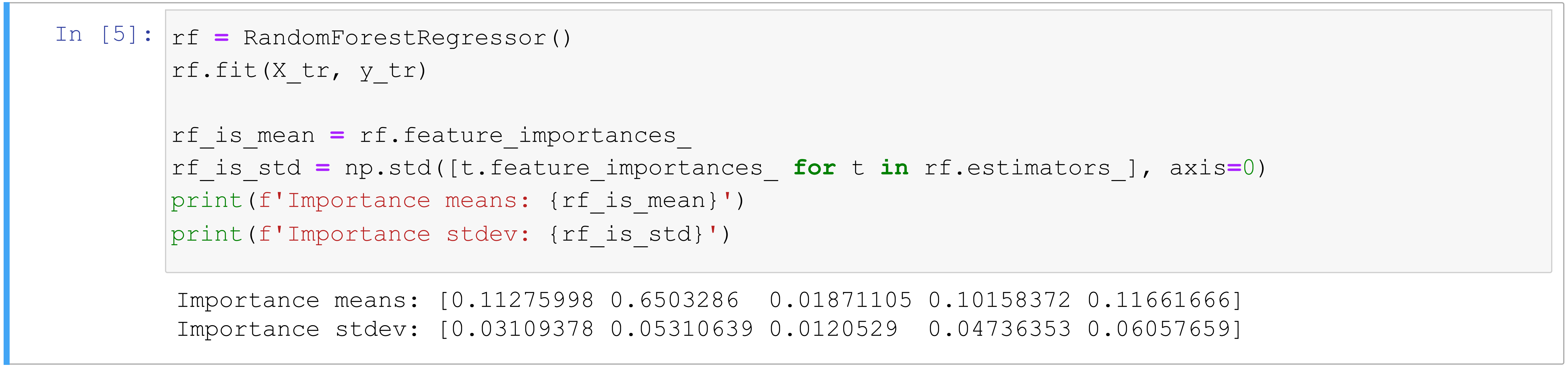
- Our tree is (finally) making some use of the longitude attribute!

Attribute Importance in Random Forest

A similar approach can be applied to Random Forests

...Except that with RF we get one importance vector per tree

- From this we can obtain means (automatically computed by scikit-learn)
- ...But also standard deviations



```
In [5]: rf = RandomForestRegressor()
        rf.fit(X_tr, y_tr)

        rf_is_mean = rf.feature_importances_
        rf_is_std = np.std([t.feature_importances_ for t in rf.estimators_], axis=0)
        print(f'Importance means: {rf_is_mean}')
        print(f'Importance stdev: {rf_is_std}')
```

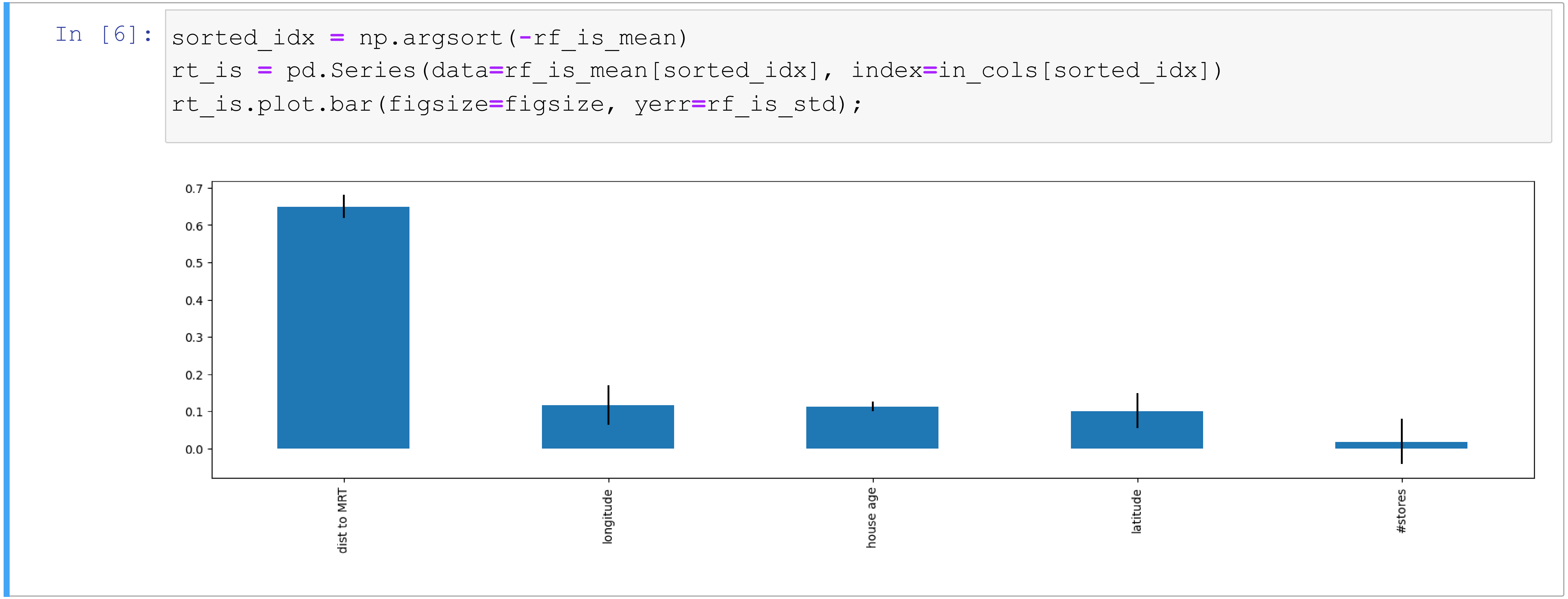
```
Importance means: [0.11275998 0.6503286  0.01871105 0.10158372 0.11661666]
Importance stdev: [0.03109378 0.05310639 0.0120529  0.04736353 0.06057659]
```

This information can be used for statistical consideration

- E.g. for discarding features based on a p-value

Attribute Importance in Random Forest

Let's plot the RF importances



In [6]:

```
sorted_idx = np.argsort(-rf_is_mean)
rt_is = pd.Series(data=rf_is_mean[sorted_idx], index=in_cols[sorted_idx])
rt_is.plot.bar(figsize=figsize, yerr=rf_is_std);
```

- Both "house age" and "longitude" have an unsually large error bar
- "#stores" should arguably be discarded

Limitations of Impurity Importances

These scores are sometimes called impurity based importance

They have several advantages:

- They are very cheap to compute
- They account for non-linear effects
- They come with statistical information (for RFs)

However, they also have some limitations

- They are only as reliable as the model that is making the predictions
  - Never trust importances for an inaccurate model!
- They may give an unfair advantage to attributes with many values
  - If an attribute has many distinct values
  - ...Accidental correlation with the target becomes more likely

Permutation Importance

Let's consider again our current issue

- Attributes with certain distributions (e.g. many values, roughly uniformly spread)
- ...Tend to be favored by impurity-based importance

How can we address this?

For example we could compare the performance of two variants of a model:

- One trained on the original data
- ...And one trained on a modified dataset, where:
  - The correlation between an attribute j and the target has been destroyed
  - ...But the distribution of attribute j is intact

The gap in model accuracy will be a measure of the importance of j

Permutation Importance

We can achieve this by permuting the values of an attribute j

By doing so:

- Any correlation between j and the target becomes statistically unlikely
- ...But the distribution of j stays exacly the same

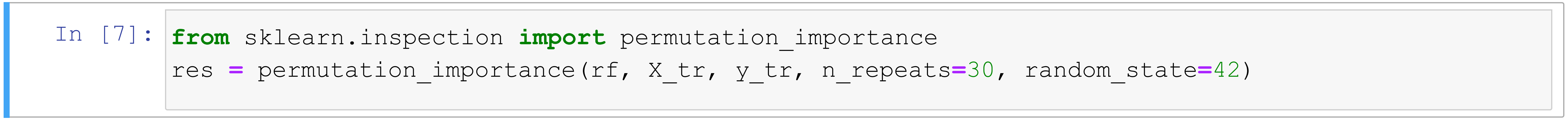
Then we can proceed as planned

- We train variants of the model
- We compute the values of a chosen quality metric (e.g. MSE, accuracy)
- We repeat for all attributes
- ...And finally we can normalize like for the impurity-based importances

This type of score is known as permutation importance

Permutation Importance

The approach is pre-implemented in scikit-learn

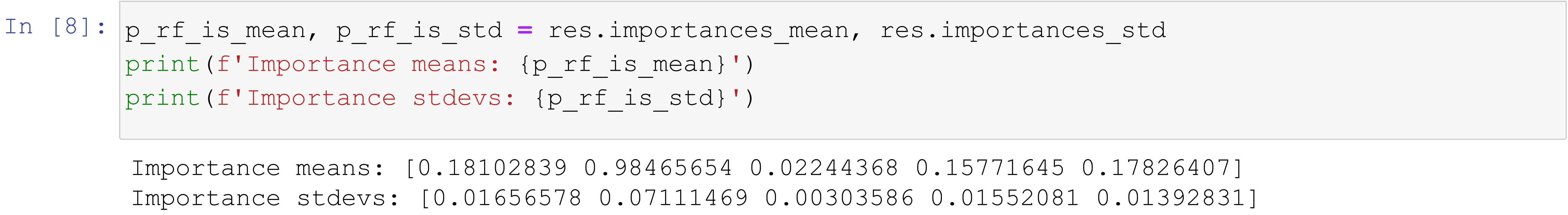


In [7]:
```
from sklearn.inspection import permutation_importance
res = permutation_importance(rf, X_tr, y_tr, n_repeats=30, random_state=42)
```

The function allows us to specify a number of repetitions

- Repeating is a good idea since we are relying on random permutations
- ...And allows us to obtain standard deviations

Both results can be accessed from the returned "result" object:

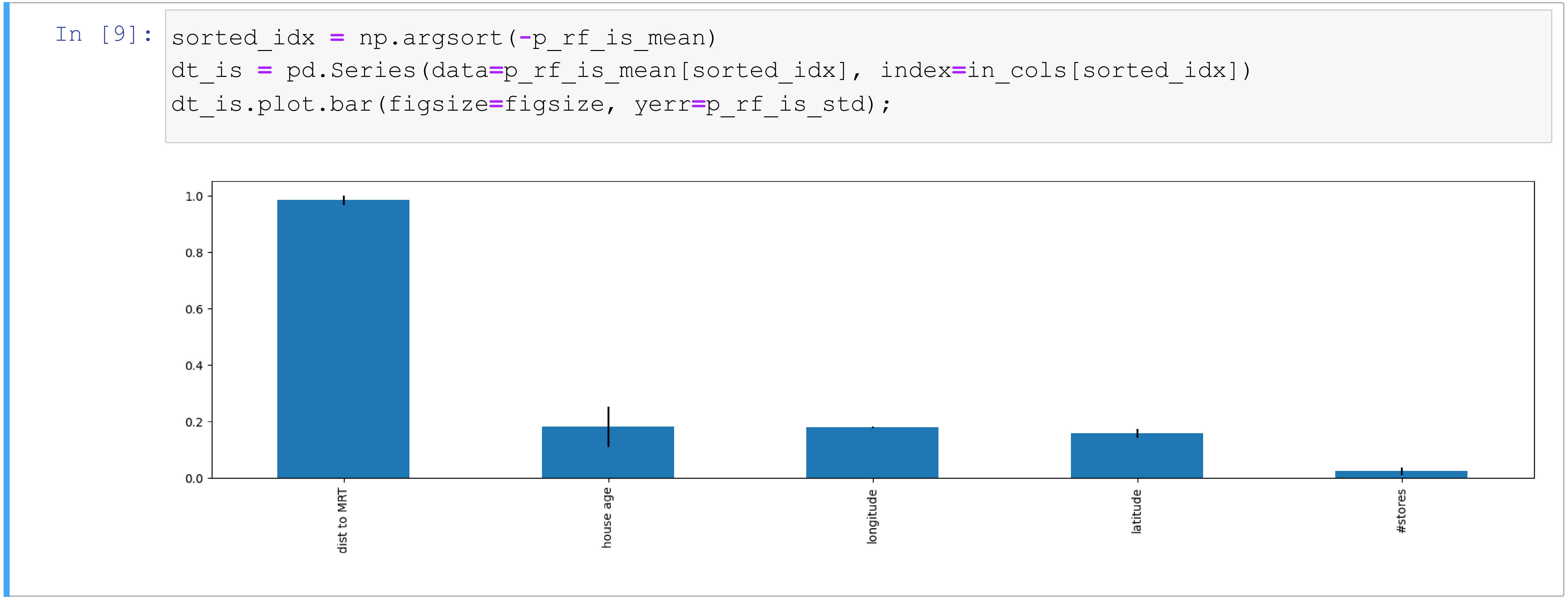


In [8]:
```
p_rf_is_mean, p_rf_is_std = res.importances_mean, res.importances_std
print(f'Importance means: {p_rf_is_mean}')
print(f'Importance stdevs: {p_rf_is_std}')
```

```
Importance means: [0.18102839 0.98465654 0.02244368 0.15771645 0.17826407]
Importance stdevs: [0.01656578 0.07111469 0.00303586 0.01552081 0.01392831]
```

Permutation Importance

We can plot the results as usual



In [9]:

```
sorted_idx = np.argsort(-p_rf_is_mean)
dt_is = pd.Series(data=p_rf_is_mean[sorted_idx], index=in_cols[sorted_idx])
dt_is.plot.bar(figsize=figsize, yerr=p_rf_is_std);
```

The new results are consistsent with the previous ones (and more reliable)

Some Final Consideration

Permutation importances have some strong advantave over impurity ones

- They can be computed for a wide range of estimators (not just tree)
- They are not biased towards certain attributes
- They naturally lend themselves to statistical analysis

As a main drawback, they are more expensive to compute

- They require to train multiple models
- ...And to repeat the process multiple times