Elements Of Data Science - F2022

Week 9: Dimensionality Reduction, Feature Selection and Feature Extraction

11/2/2022

TODOs

- Readings:
    - PML Chapter 6.1, Streamlining workflows with Pipelines
    - PML Chapter 8: Applying Machine Learning to Sentiment Analysis

- HW 2, Due **Fri Nov 4th, 11:59pm ET**
- Quiz 9, Due **Tues Nov 8th, 11:59pm ET**
- HW3 Out Friday, due Nov 18th

Quiz 7 Notes

- Be careful which dataset you're training/evaluating on: X_train vs X_test

Today

- **Joining Datasets**
- **Dimensionality Reduction**
    - **Feature Selection**
        - Linear Model with LASSO
        - Tree Based Models Feature Importance
        - Univariate Tests
        - Recursive Feature Selection
    - **Aside: Adjusted R^2**
    - **Feature Extraction**
        - PCA
- **Example: Image Recognition Using PCA**

Questions?

Environment Setup

Environment Setup

In [1]:
```
import numpy
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

from mlxtend.plotting import plot_decision_regions

sns.set_style('darkgrid')
%matplotlib inline
```

Joing Datasets

- often have two sets of data we need to join together

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- often have two sets of data we need to join together

```
In [3]: df_flower_name_orig = pd.DataFrame([[1001,'iris'],[1002,'rose']],
                                           columns=['flower_id','name'])

        df_flower_price_orig = pd.DataFrame([[1002,3.99],[1003,2.25]],
                                            columns=['flower_id','price'])
```

Joing Datasets

- often have two sets of data we need to join together

In [3]:
```
df_flower_name_orig = pd.DataFrame([[1001,'iris'],[1002,'rose']],
                                   columns=['flower_id','name'])

df_flower_price_orig = pd.DataFrame([[1002,3.99],[1003,2.25]],
                                    columns=['flower_id','price'])
```

In [4]:
```
display(df_flower_name_orig)
display(df_flower_price_orig)
```

	flower_id	name
0	1001	iris
1	1002	rose

	flower_id	price
0	1002	3.99
1	1003	2.25

Joing Datasets On Index

- easiest way to join Pandas DataFrames is on row index label
- may need to set the index from a column using `.set_index()`

In [5]:
```
df_flower_name_orig
```

Out[5]:

	flower_id	name
0	1001	iris
1	1002	rose

Joing Datasets On Index

- easiest way to join Pandas DataFrames is on row index label
- may need to set the index from a column using `.set_index()`

In [5]:
```
df_flower_name_orig
```

Out[5]:

	flower_id	name
0	1001	iris
1	1002	rose

In [6]:
```
df_flower_name = df_flower_name_orig.set_index('flower_id') # note: inplace=False, drop=True by default
df_flower_name
```

Out[6]:

	name
flower_id	
1001	iris
1002	rose

Joing Datasets On Index

- easiest way to join Pandas DataFrames is on row index label
- may need to set the index from a column using `.set_index()`

In [5]:
```
df_flower_name_orig
```

Out[5]:
```
   flower_id  name
0  1001       iris
1  1002       rose
```

In [6]:
```
df_flower_name = df_flower_name_orig.set_index('flower_id') # note: inplace=False, drop=True by default
df_flower_name
```

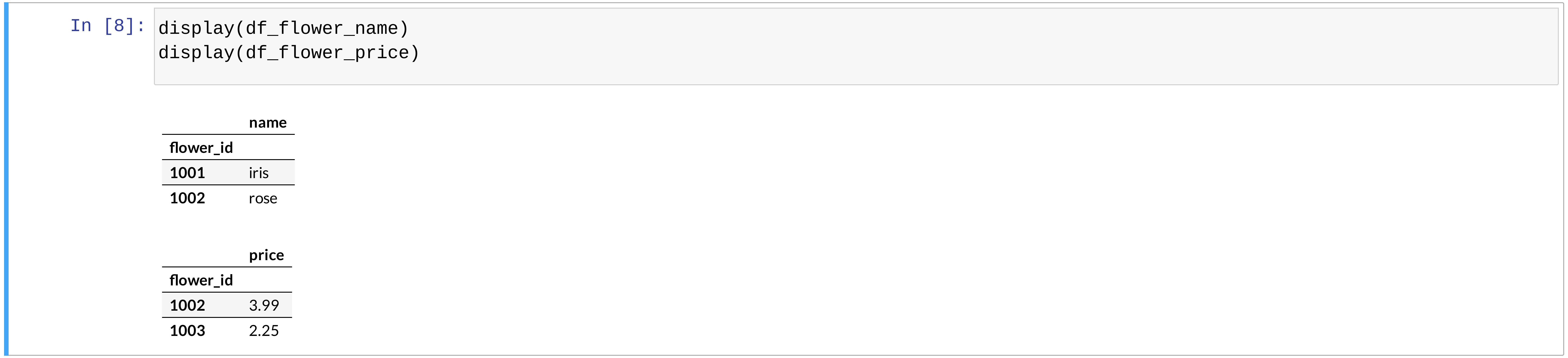
Out[6]:
```
           name
flower_id
1001       iris
1002       rose
```

In [7]:
```
df_flower_price = df_flower_price_orig.set_index('flower_id')
df_flower_price
```

Out[7]:
```
           price
flower_id
1002       3.99
1003       2.25
```

Joining Datasets in Pandas On Index Using `df.join()`

Joining Datasets in Pandas On Index Using `df.join()`

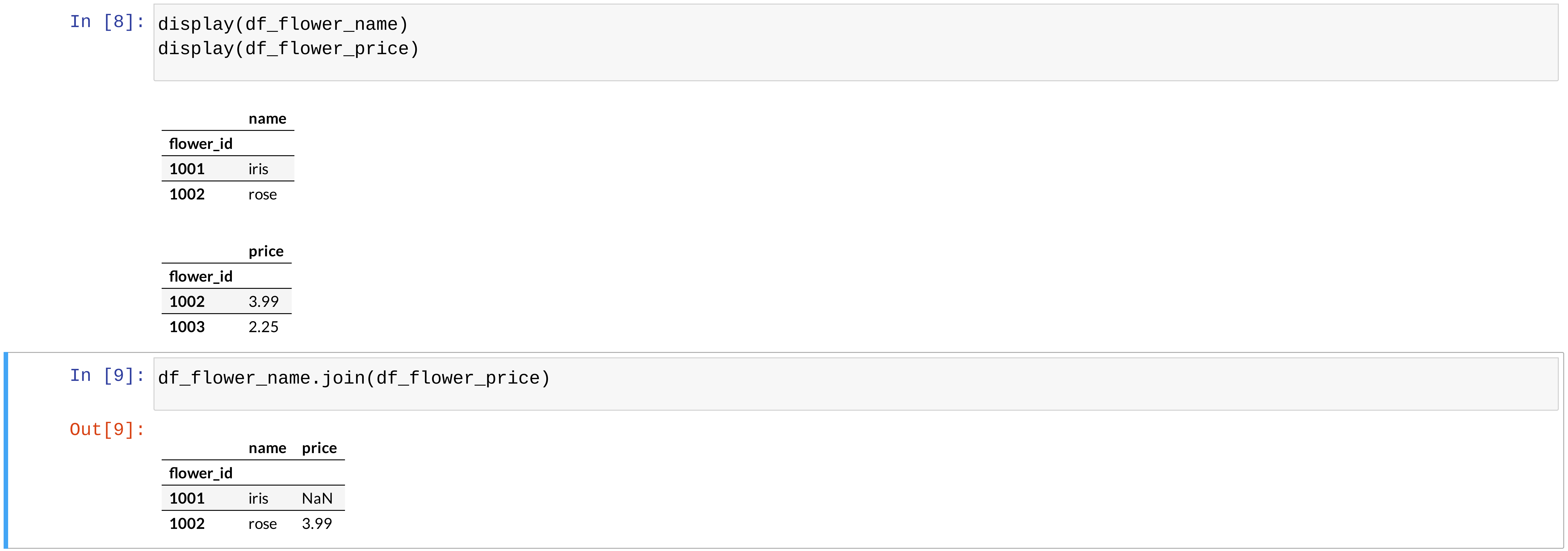


In [8]:
```
display(df_flower_name)
display(df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

	price
flower_id	
1002	3.99
1003	2.25

Joining Datasets in Pandas On Index Using `df.join()`



In [8]:

```
display(df_flower_name)
display(df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

	price
flower_id	
1002	3.99
1003	2.25

In [9]:

```
df_flower_name.join(df_flower_price)
```

Out[9]:

	name	price
flower_id		
1001	iris	NaN
1002	rose	3.99

Joining Datasets in Pandas On Index Using `df.join()`

In [8]:
```
display(df_flower_name)
display(df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

	price
flower_id	
1002	3.99
1003	2.25

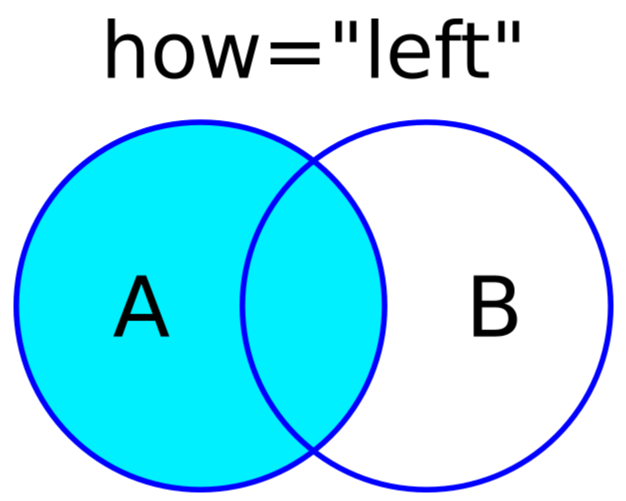
In [9]:
```
df_flower_name.join(df_flower_price)
```

Out[9]:

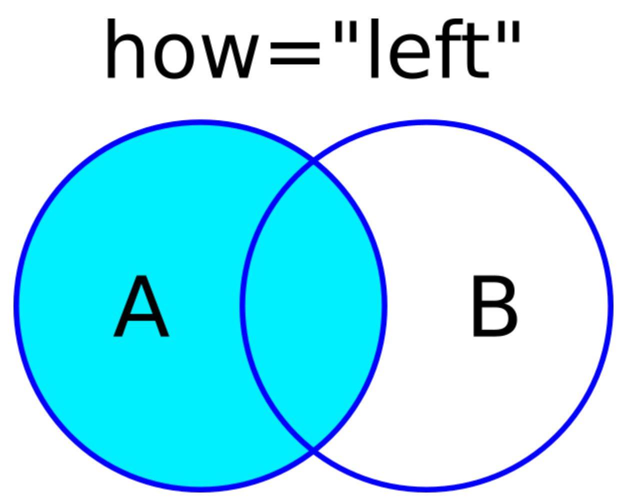
	name	price
flower_id		
1001	iris	NaN
1002	rose	3.99

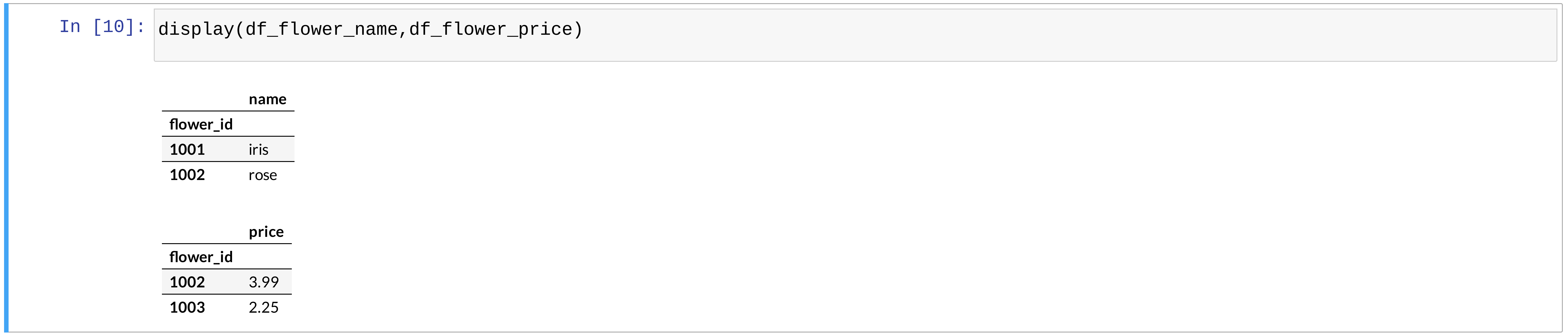
- by default, this is a 'Left Join'

Join Types: Left Join



Join Types: Left Join





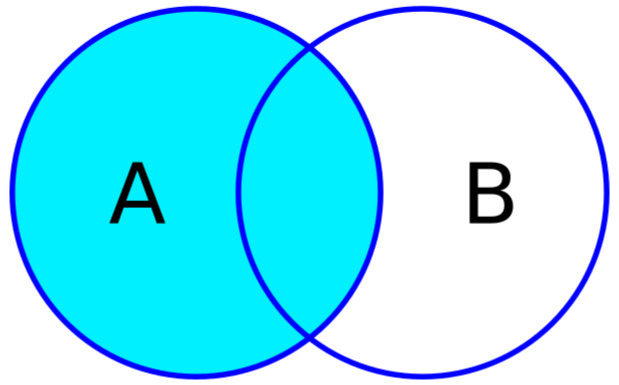
```
In [10]: display(df_flower_name,df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

	price
flower_id	
1002	3.99
1003	2.25

Join Types: Left Join

how="left"



```
In [10]: display(df_flower_name,df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

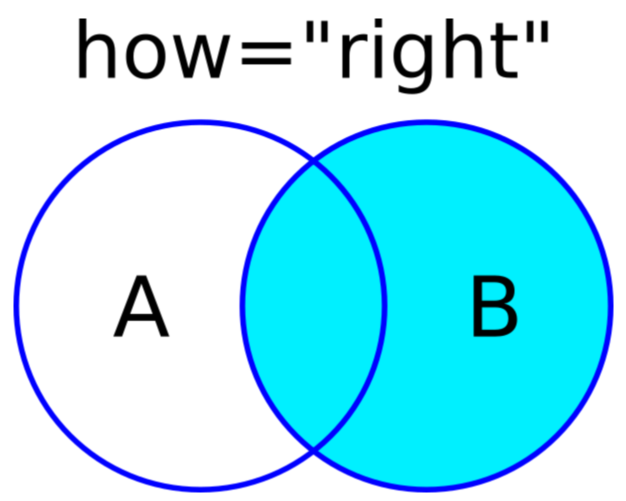
	price
flower_id	
1002	3.99
1003	2.25

```
In [11]: df_flower_name.join(df_flower_price,how="left") # default for df.join() is left join
```

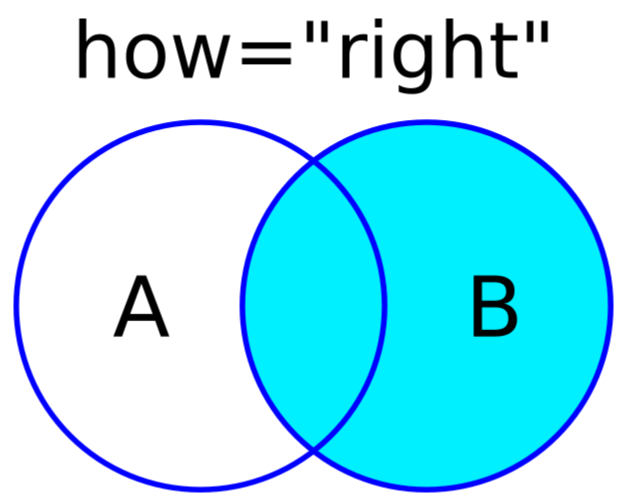
Out[11]:

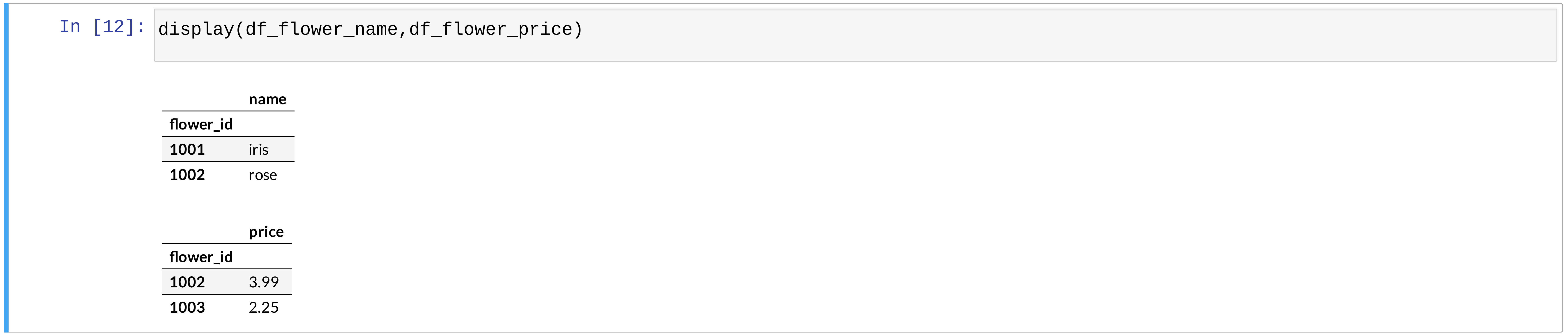
	name	price
flower_id		
1001	iris	NaN
1002	rose	3.99

Join Types: Right Join



Join Types: Right Join





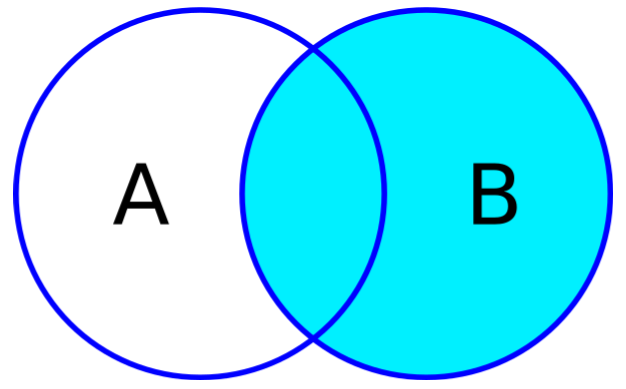
```
In [12]: display(df_flower_name,df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

	price
flower_id	
1002	3.99
1003	2.25

Join Types: Right Join

how="right"



```
In [12]: display(df_flower_name,df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

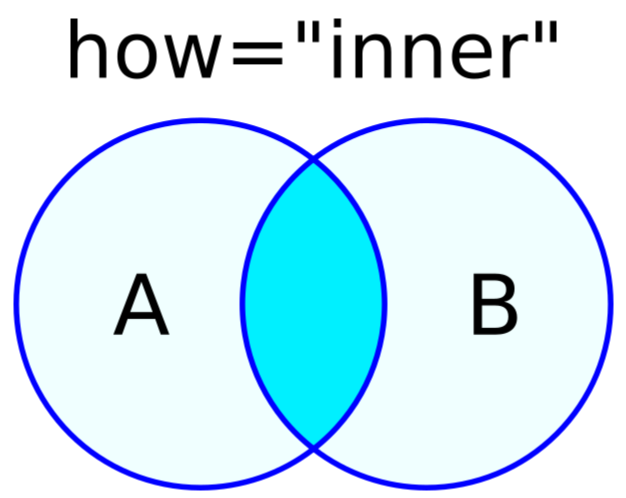
	price
flower_id	
1002	3.99
1003	2.25

```
In [13]: df_flower_name.join(df_flower_price,how='right')
```

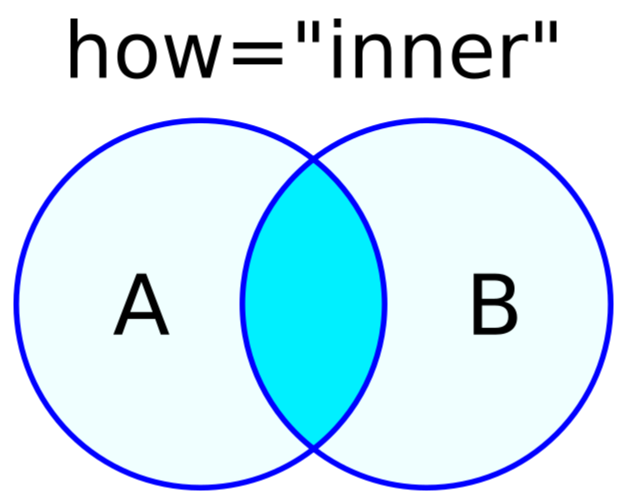
Out[13]:

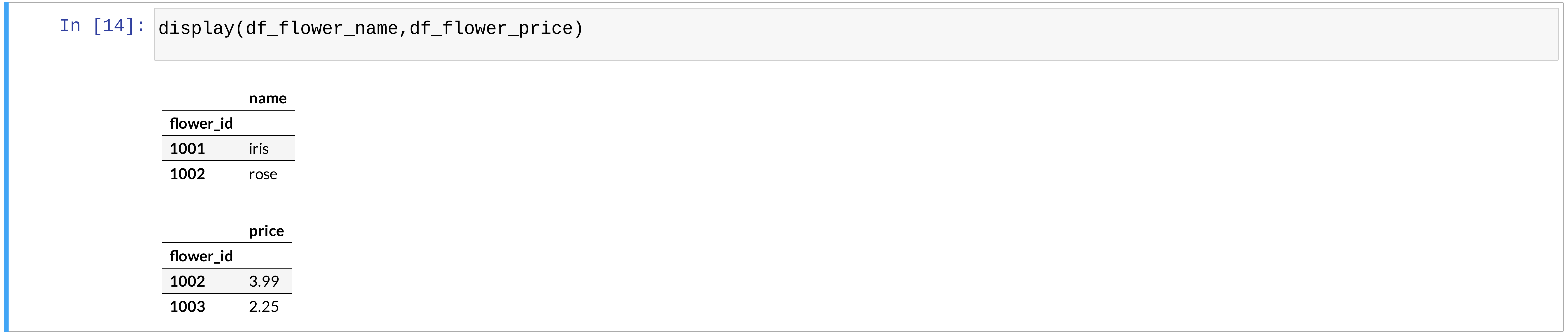
	name	price
flower_id		
1002	rose	3.99
1003	NaN	2.25

Join Types: Inner Join



Join Types: Inner Join



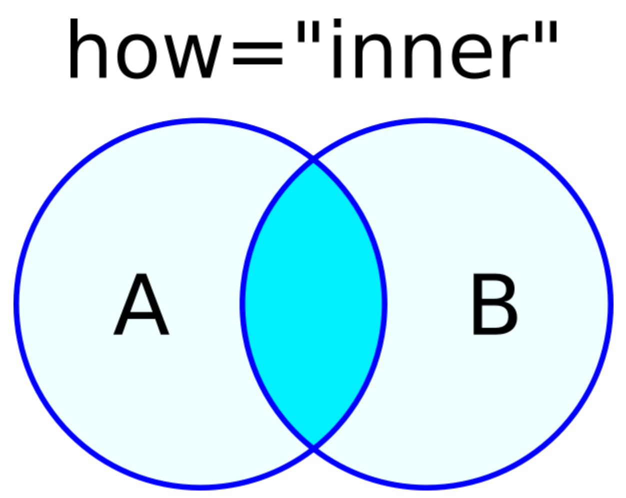


```
In [14]: display(df_flower_name,df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

	price
flower_id	
1002	3.99
1003	2.25

Join Types: Inner Join



```
In [14]: display(df_flower_name,df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

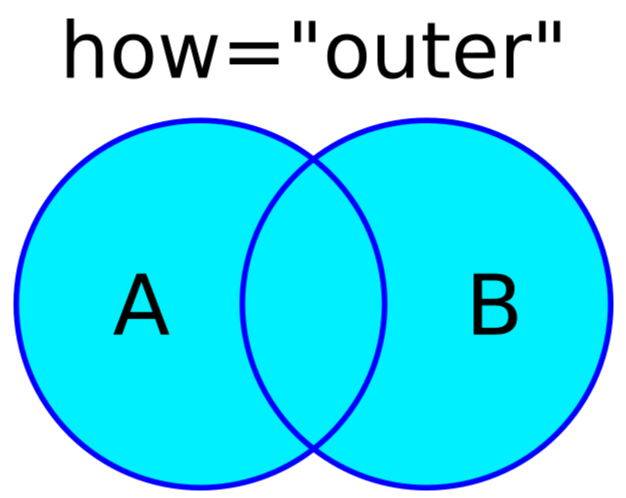
	price
flower_id	
1002	3.99
1003	2.25

```
In [15]: df_flower_name.join(df_flower_price,how='inner')
```

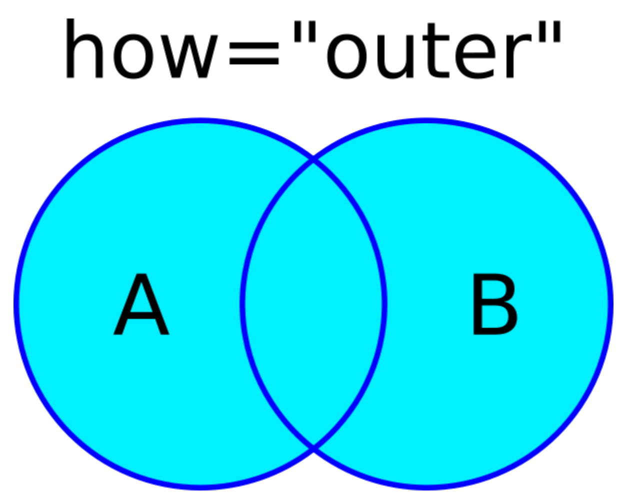
Out[15]:

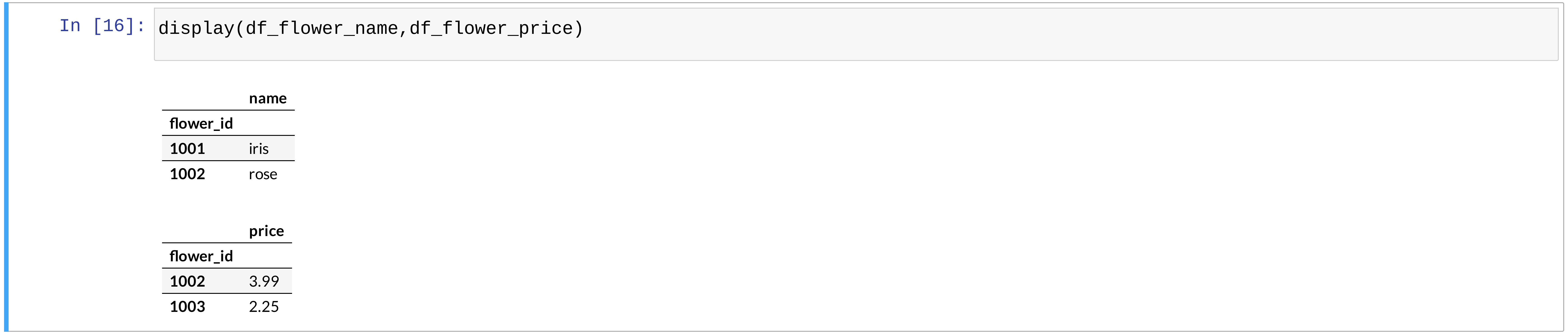
	name	price
flower_id		
1002	rose	3.99

Join Types: Outer Join



Join Types: Outer Join



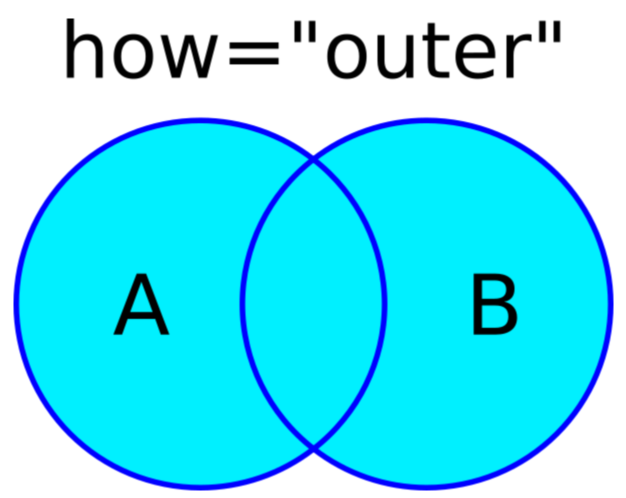


```
In [16]: display(df_flower_name,df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

	price
flower_id	
1002	3.99
1003	2.25

Join Types: Outer Join



```
In [16]: display(df_flower_name,df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

	price
flower_id	
1002	3.99
1003	2.25

```
In [17]: df_flower_name.join(df_flower_price,how='outer')
```

Out[17]:

	name	price
flower_id		
1001	iris	NaN
1002	rose	3.99
1003	NaN	2.25

Setting the Index When Reading in Data

- instead of using `.set_index()`, can specify `index_col=`on `.read` functions

Setting the Index When Reading in Data

- instead of using `.set_index()`, can specify `index_col=` on `.read` functions

```
In [18]: # this csv has column for purchase_id
         pd.read_csv('../data/flowershop_data_with_dups.csv'
                    ).head(2)
```

Out[18]:

	purchase_id	lastname	purchase_date	stars	price	favorite_flower
0	1000	PERKINS	2017-04-08	5	19.599886	iris
1	1001	ROBINSON	2017-01-01	5	37.983904	NaN

Setting the Index When Reading in Data

- instead of using `.set_index()`, can specify `index_col=` on `.read` functions

```
In [18]: # this csv has column for purchase_id
         pd.read_csv('../data/flowershop_data_with_dups.csv'
                    ).head(2)
```

Out[18]:

	purchase_id	lastname	purchase_date	stars	price	favorite_flower
0	1000	PERKINS	2017-04-08	5	19.599886	iris
1	1001	ROBINSON	2017-01-01	5	37.983904	NaN

```
In [19]: # can set the index when reading in the csv
         pd.read_csv('../data/flowershop_data_with_dups.csv',
                     index_col='purchase_id'                  # set the index column when reading/loading data
                    ).head(2)
```

Out[19]:

	lastname	purchase_date	stars	price	favorite_flower
purchase_id					
1000	PERKINS	2017-04-08	5	19.599886	iris
1001	ROBINSON	2017-01-01	5	37.983904	NaN

Joining on the Index using `.join()`

Joining on the Index using `.join()`

```
In [20]: # imagine that 'name' is a categorical variable
         df_flower_name[['name']]
```

Out[20]:

	name
flower_id	
1001	iris
1002	rose

Joining on the Index using `.join()`

In [20]:
```
# imagine that 'name' is a categorical variable
df_flower_name[['name']]
```

Out[20]:

	name
flower_id	
1001	iris
1002	rose

In [21]:
```
# converting categorical to one-hot using get_dummies
pd.get_dummies(df_flower_name['name'],prefix='flower_name')
```

Out[21]:

	flower_name_iris	flower_name_rose
flower_id		
1001	1	0
1002	0	1

Joining on the Index using `.join()`

In [20]:
```
# imagine that 'name' is a categorical variable
df_flower_name[['name']]
```

Out[20]:

	name
flower_id	
1001	iris
1002	rose

In [21]:
```
# converting categorical to one-hot using get_dummies
pd.get_dummies(df_flower_name['name'],prefix='flower_name')
```

Out[21]:

	flower_name_iris	flower_name_rose
flower_id		
1001	1	0
1002	0	1

In [22]:
```
# can join back using the default index
df_flower_name[['name']].join(pd.get_dummies(df_flower_name['name'],prefix='flower_name'))
```

Out[22]:

	name	flower_name_iris	flower_name_rose
flower_id			
1001	iris	1	0
1002	rose	0	1

Join on Columns Instead of Index using `pd.merge()`

- to do more complicated joins, use `pd.merge()`

Join on Columns Instead of Index using `pd.merge()`

- to do more complicated joins, use `pd.merge()`

```
In [23]: # using the dataframes before setting index using .set_index()
         pd.merge(df_flower_name_orig,
                  df_flower_price_orig,
                  left_on='flower_id',
                  right_on='flower_id') # what is the default join for merge?
```

Out[23]:

	flower_id	name	price
0	1002	rose	3.99

Join on Columns Instead of Index using `pd.merge()`

- to do more complicated joins, use `pd.merge()`

```
In [23]: # using the dataframes before setting index using .set_index()
         pd.merge(df_flower_name_orig,
                  df_flower_price_orig,
                  left_on='flower_id',
                  right_on='flower_id') # what is the default join for merge?
```

Out[23]:

	flower_id	name	price
0	1002	rose	3.99

```
In [24]: # if both id columns have the same name, can just use "on="
         pd.merge(df_flower_name_orig,
                  df_flower_price_orig,
                  on='flower_id',
                  how='outer')
```

Out[24]:

	flower_id	name	price
0	1001	iris	NaN
1	1002	rose	3.99
2	1003	NaN	2.25

Joining Datasets Review

- Use `.join()` when you can, joining on Pandas DataFrame row index labels
- May need to set the dataframe row index labels
    - `index_col=` when creating the DataFrame or
    - `.set_index()` after DataFrame creation
- Know the different general join types: Left, Right, Inner, Outer
- Use `pd.merge()` when you need something more complex than joining on row index

Questions about joining datasets?

Dimensionality Reduction

Recall: Methods for Avoiding Overfitting

- Collect additional examples
- Use a simple model
- Regularization
- **Reduce the dimensions of our data: Dimensionality Reduction**

Dimensionality Reduction

- Reasons to reduce the number of features:
  - improve *model performance* (reduce complexity to reduce chance of overfitting)
  - improve *speed performance* (reduce number of calculations)
  - *interpretation* (which features are most important?)

- **Feature Selection**
  - choose a subset of original features

- **Feature Extraction**
  - combine/transform features to generate a new feature space

Load Binary Wine Classification

Load Binary Wine Classification

```
In [25]: from sklearn.datasets import load_wine
         from sklearn.model_selection import train_test_split

         wine = load_wine()

         X_wine = pd.DataFrame(wine.data,columns=wine.feature_names)
         y_wine = wine.target

         # reduce to binary classification
         X_wine = X_wine.iloc[y_wine < 2]
         y_wine = y_wine[y_wine < 2]

         X_train,X_test,y_train,y_test = train_test_split(X_wine,y_wine,stratify=y_wine,random_state=0)

         wine_feature_names = X_wine.columns.values
         wine_feature_names
```

```
Out[25]: array(['alcohol', 'malic_acid', 'ash', 'alcalinity_of_ash', 'magnesium',
                'total_phenols', 'flavanoids', 'nonflavanoid_phenols',
                'proanthocyanins', 'color_intensity', 'hue',
                'od280/od315_of_diluted_wines', 'proline'], dtype=object)
```

Load Binary Wine Classification

In [25]:
```python
from sklearn.datasets import load_wine
from sklearn.model_selection import train_test_split

wine = load_wine()

X_wine = pd.DataFrame(wine.data,columns=wine.feature_names)
y_wine = wine.target

# reduce to binary classification
X_wine = X_wine.iloc[y_wine < 2]
y_wine = y_wine[y_wine < 2]

X_train,X_test,y_train,y_test = train_test_split(X_wine,y_wine,stratify=y_wine,random_state=0)

wine_feature_names = X_wine.columns.values
wine_feature_names
```

Out[25]:
```
array(['alcohol', 'malic_acid', 'ash', 'alcalinity_of_ash', 'magnesium',
       'total_phenols', 'flavanoids', 'nonflavanoid_phenols',
       'proanthocyanins', 'color_intensity', 'hue',
       'od280/od315_of_diluted_wines', 'proline'], dtype=object)
```

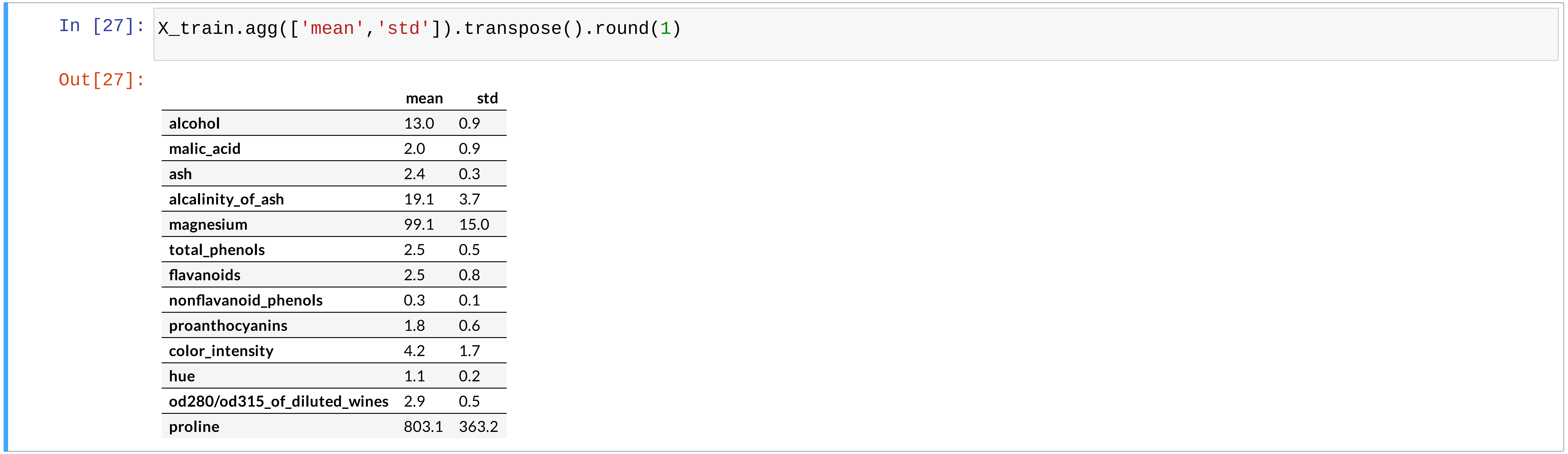
In [26]:
```python
X_train.head(3)
```

Out[26]:

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phenols	flavanoids	nonflavanoid_phenols	proanthocyanins	color_intensity	hue	od280/od315_of_diluted_wines	pro
86	12.16	1.61	2.31	22.8	90.0	1.78	1.69	0.43	1.56	2.45	1.33	2.26	49
121	11.56	2.05	3.23	28.5	119.0	3.18	5.08	0.47	1.87	6.00	0.93	3.69	46
30	13.73	1.50	2.70	22.5	101.0	3.00	3.25	0.29	2.38	5.70	1.19	2.71	12

Need to Standardize Features

Need to Standardize Features



In [27]:
```
X_train.agg(['mean','std']).transpose().round(1)
```

Out[27]:

	mean	std
alcohol	13.0	0.9
malic_acid	2.0	0.9
ash	2.4	0.3
alcalinity_of_ash	19.1	3.7
magnesium	99.1	15.0
total_phenols	2.5	0.5
flavanoids	2.5	0.8
nonflavanoid_phenols	0.3	0.1
proanthocyanins	1.8	0.6
color_intensity	4.2	1.7
hue	1.1	0.2
od280/od315_of_diluted_wines	2.9	0.5
proline	803.1	363.2

Standardize Features

Standardize Features

In [28]:

```
from sklearn.preprocessing import StandardScaler

ss = StandardScaler()
X_train_zscore = ss.fit_transform(X_train)
X_train_zscore = pd.DataFrame(X_train_zscore, columns=wine_feature_names)

X_test_zscore = ss.transform(X_test)
```

Standardize Features

In [28]:
```python
from sklearn.preprocessing import StandardScaler

ss = StandardScaler()
X_train_zscore = ss.fit_transform(X_train)
X_train_zscore = pd.DataFrame(X_train_zscore, columns=wine_feature_names)

X_test_zscore = ss.transform(X_test)
```

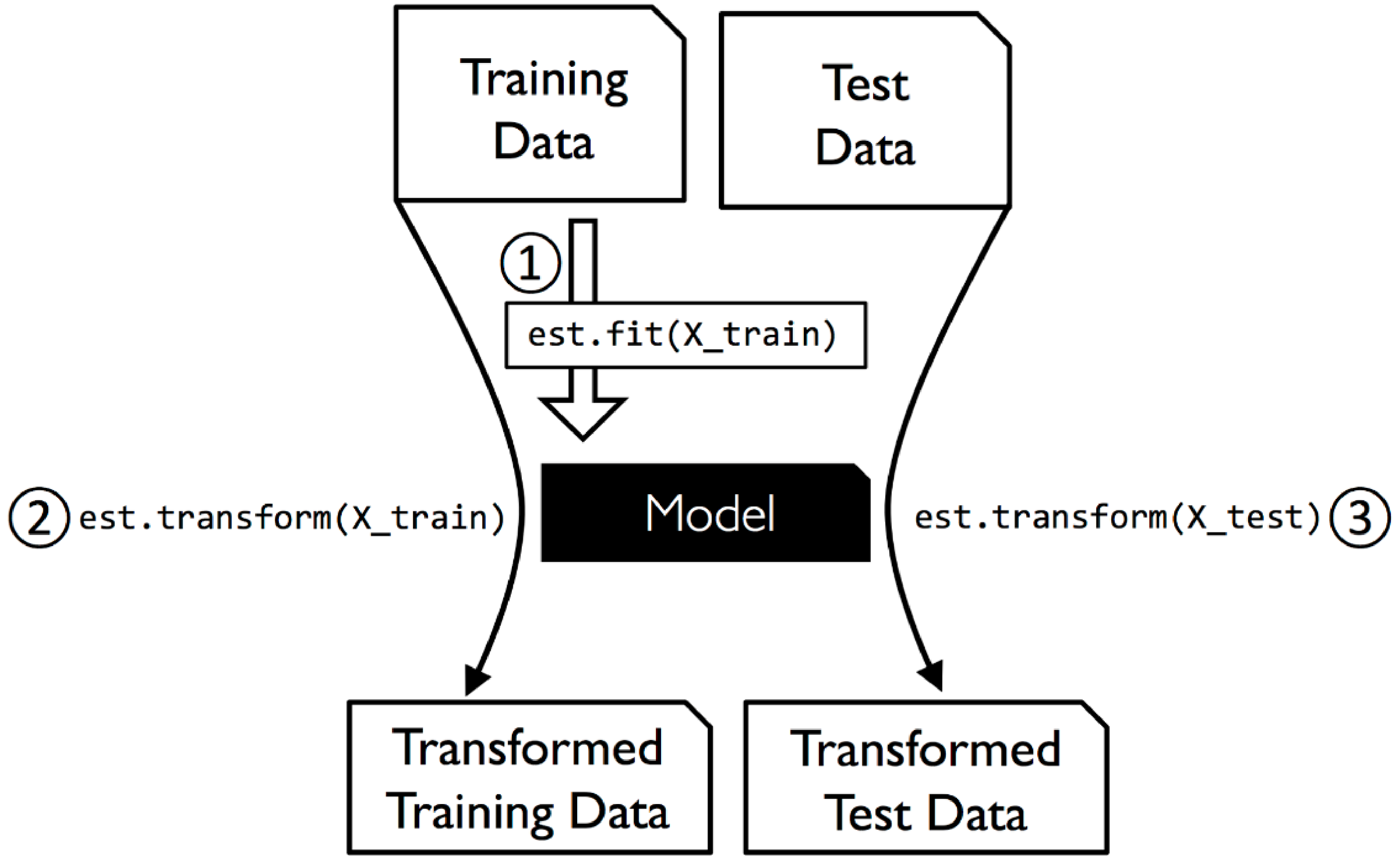
In [29]:
```python
X_train_zscore.agg(['mean','std']).T.round(1)
```

Out[29]:

	mean	std
alcohol	-0.0	1.0
malic_acid	-0.0	1.0
ash	0.0	1.0
alcalinity_of_ash	-0.0	1.0
magnesium	0.0	1.0
total_phenols	0.0	1.0
flavanoids	0.0	1.0
nonflavanoid_phenols	-0.0	1.0
proanthocyanins	0.0	1.0
color_intensity	0.0	1.0
hue	-0.0	1.0
od280/od315_of_diluted_wines	-0.0	1.0
proline	-0.0	1.0

Recall: Predicting vs Transforming with Train/Test Split

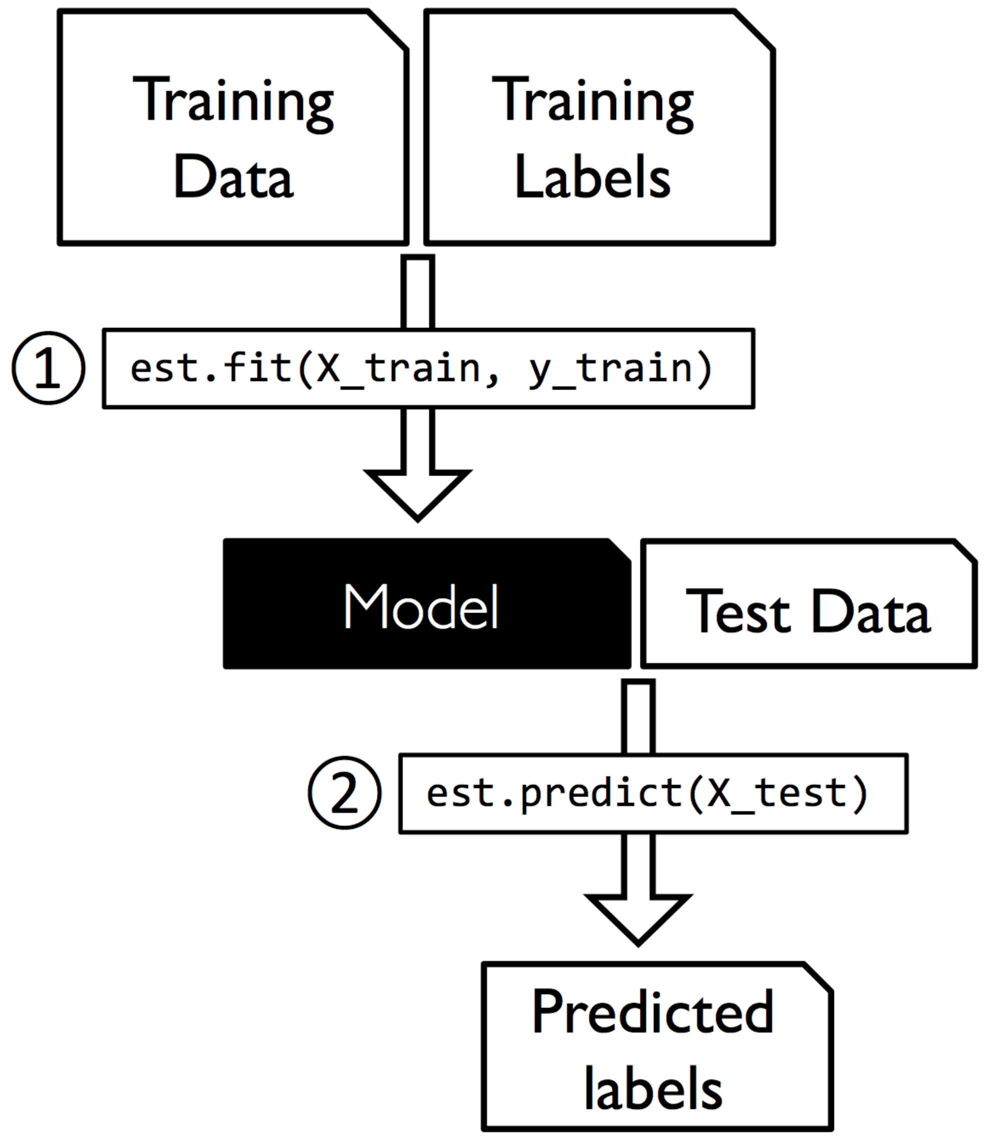
- When transforming data, fit on the training set, transform both train and test



From PML

Recall: Predicting vs Transforming with Train/Test Split

- When performing prediction, train on the training set, evaluate on the test set



From PML

Feature Selection

- Select a subset of features
- Based on how much they contribute to predicting the target 'y'

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- From a Model
    - Linear Model with LASSO Regularization
    - Tree Based Models Feature Importance
- Univariate Tests
- Recursive Feature Selection

Feature Selection: LASSO (L1)

- LASSO or ℓ_1 or `l1` regularization drives the coefficient of uninformative features to 0

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In [30]: from sklearn.linear_model import LogisticRegression

         # First, without regularization
         #   C is the inverse regularization strength: higher means less regularization
         logr = LogisticRegression(penalty="none", solver="lbfgs", random_state=0)
         logr.fit(X_train_zscore, y_train)
         logr.coef_[0].round(2)
```

```
Out[30]: array([ -8.14,  -4.41,  -8.11,  11.54,  -2.72,   2.24,  -3.52,   1.05,
                  0.91,  -1.55,   0.2 ,  -3.87, -14.43])
```

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                  0.91,  -1.55,   0.2 ,  -3.87, -14.43])
```

```
In [31]: pd.Series(logr.coef_[0],index=wine_feature_names).sort_values(ascending=False).round(2)

Out[31]: alcalinity_of_ash               11.54
         total_phenols                    2.24
         nonflavanoid_phenols             1.05
         proanthocyanins                  0.91
         hue                              0.20
         color_intensity                 -1.55
         magnesium                       -2.72
         flavanoids                      -3.52
         od280/od315_of_diluted_wines    -3.87
         malic_acid                      -4.41
         ash                             -8.11
         alcohol                         -8.14
         proline                        -14.43
         dtype: float64
```

Feature Selection: LASSO (L1) Cont.

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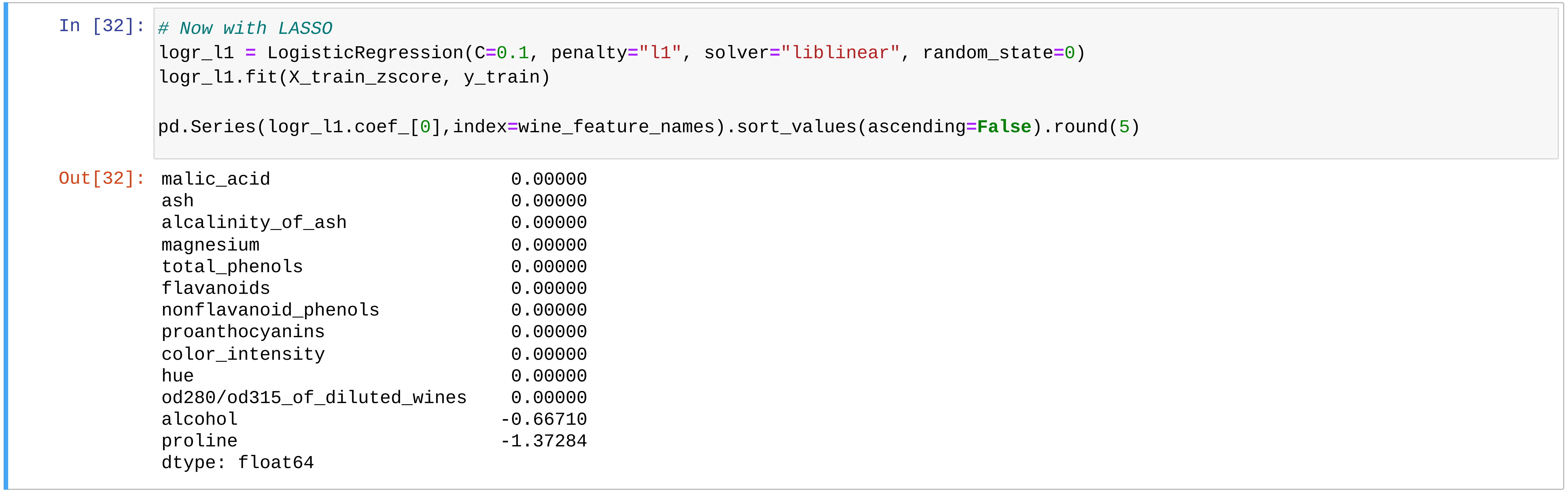
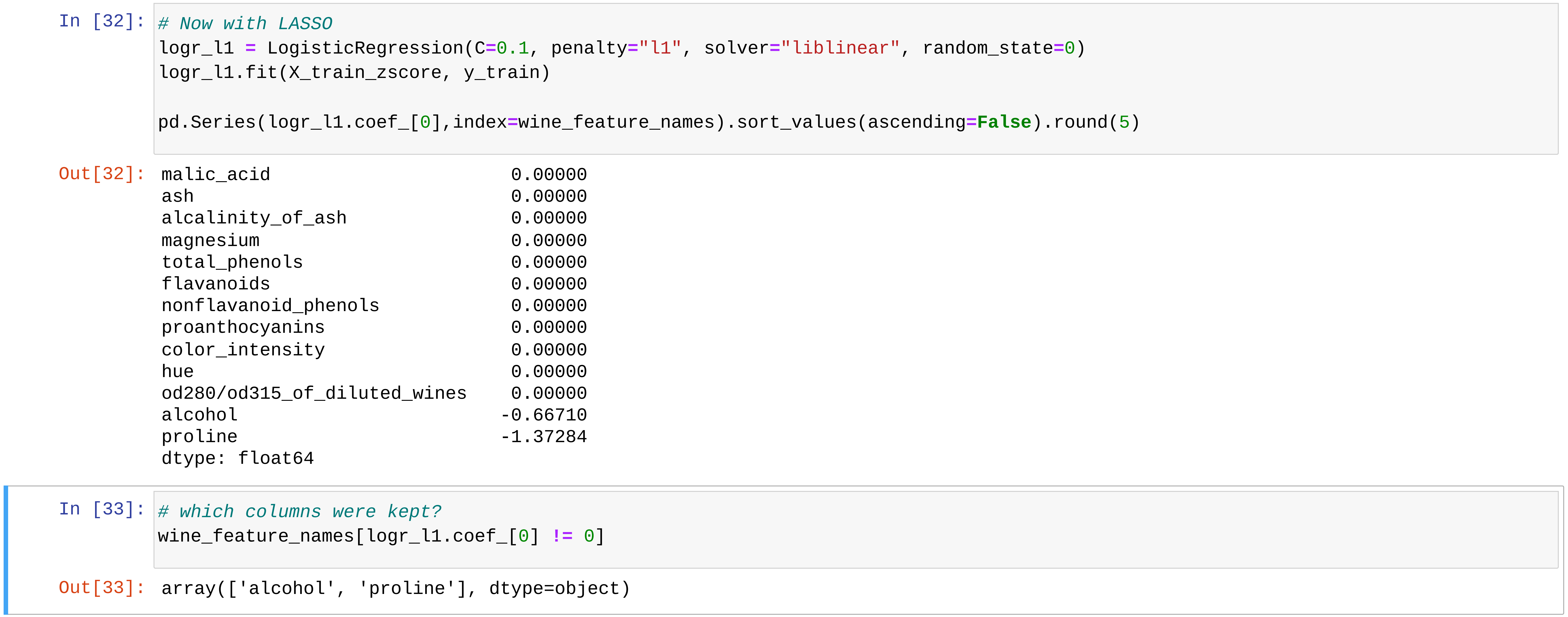


```
In [32]: # Now with LASSO
         logr_l1 = LogisticRegression(C=0.1, penalty="l1", solver="liblinear", random_state=0)
         logr_l1.fit(X_train_zscore, y_train)

         pd.Series(logr_l1.coef_[0],index=wine_feature_names).sort_values(ascending=False).round(5)
```

```
Out[32]: malic_acid                      0.00000
         ash                             0.00000
         alcalinity_of_ash               0.00000
         magnesium                       0.00000
         total_phenols                   0.00000
         flavanoids                      0.00000
         nonflavanoid_phenols            0.00000
         proanthocyanins                 0.00000
         color_intensity                 0.00000
         hue                             0.00000
         od280/od315_of_diluted_wines    0.00000
         alcohol                        -0.66710
         proline                        -1.37284
         dtype: float64
```

Feature Selection: LASSO (L1) Cont.



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Out[32]: malic_acid                      0.00000
         ash                             0.00000
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         color_intensity                 0.00000
         hue                             0.00000
         od280/od315_of_diluted_wines    0.00000
         alcohol                        -0.66710
         proline                        -1.37284
         dtype: float64
```

```
In [33]: # which columns were kept?
         wine_feature_names[logr_l1.coef_[0] != 0]

Out[33]: array(['alcohol', 'proline'], dtype=object)
```

Feature Selection: Tree Based Model Feature Importance

- Trees choose questions based on removing impurity
- We can rank the feature based on how much impurity they remove

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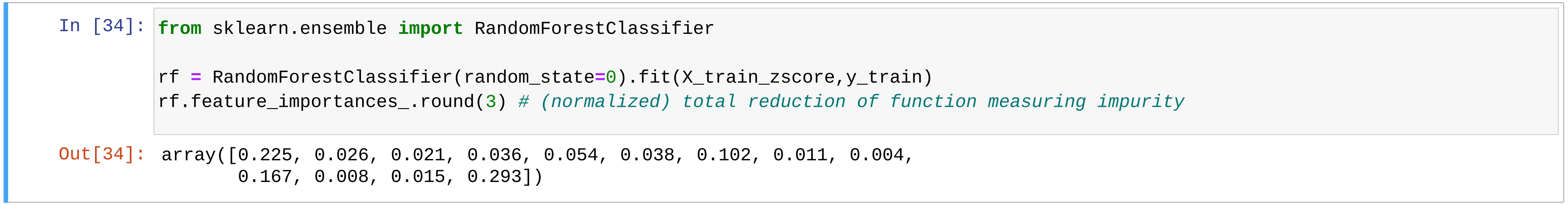

```
In [34]: from sklearn.ensemble import RandomForestClassifier

         rf = RandomForestClassifier(random_state=0).fit(X_train_zscore,y_train)
         rf.feature_importances_.round(3) # (normalized) total reduction of function measuring impurity

Out[34]: array([0.225, 0.026, 0.021, 0.036, 0.054, 0.038, 0.102, 0.011, 0.004,
                0.167, 0.008, 0.015, 0.293])
```

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- Trees choose questions based on removing impurity
- We can rank the feature based on how much impurity they remove

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       0.167, 0.008, 0.015, 0.293])
```

In [35]:
```
rf_feature_importances = pd.Series(rf.feature_importances_,index=wine_feature_names)
rf_feature_importances.sort_values(ascending=False).round(3)
```

Out[35]:
```
proline                         0.293
alcohol                         0.225
color_intensity                 0.167
flavanoids                      0.102
magnesium                       0.054
total_phenols                   0.038
alcalinity_of_ash               0.036
malic_acid                      0.026
ash                             0.021
od280/od315_of_diluted_wines    0.015
nonflavanoid_phenols            0.011
hue                             0.008
proanthocyanins                 0.004
dtype: float64
```

Feature Selection: Tree Based Model Feature Importance

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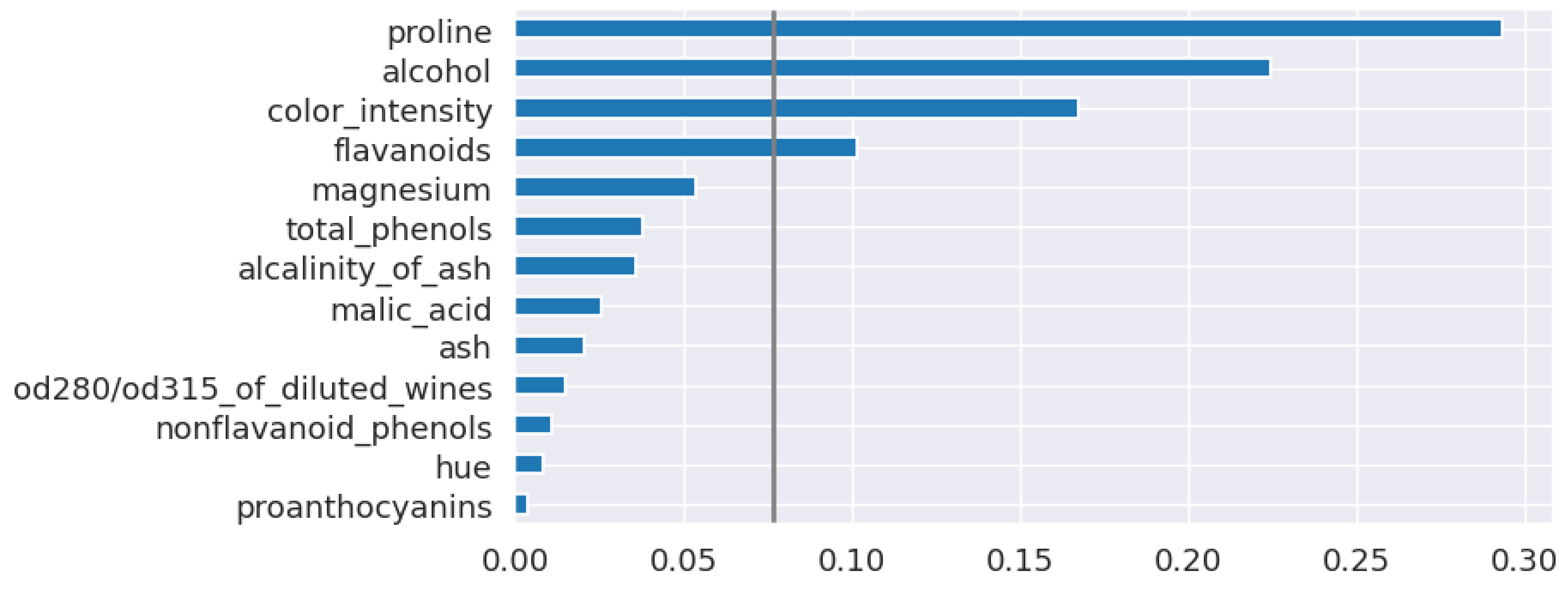
In [36]:
```
fig,ax = plt.subplots(1,1,figsize=(6,3),dpi=130)
rf_feature_importances.sort_values().plot.barh(ax=ax);
ax.axvline(rf_feature_importances.mean(),color='gray');
```



Feature Selection: Tree Based Model Feature Importance

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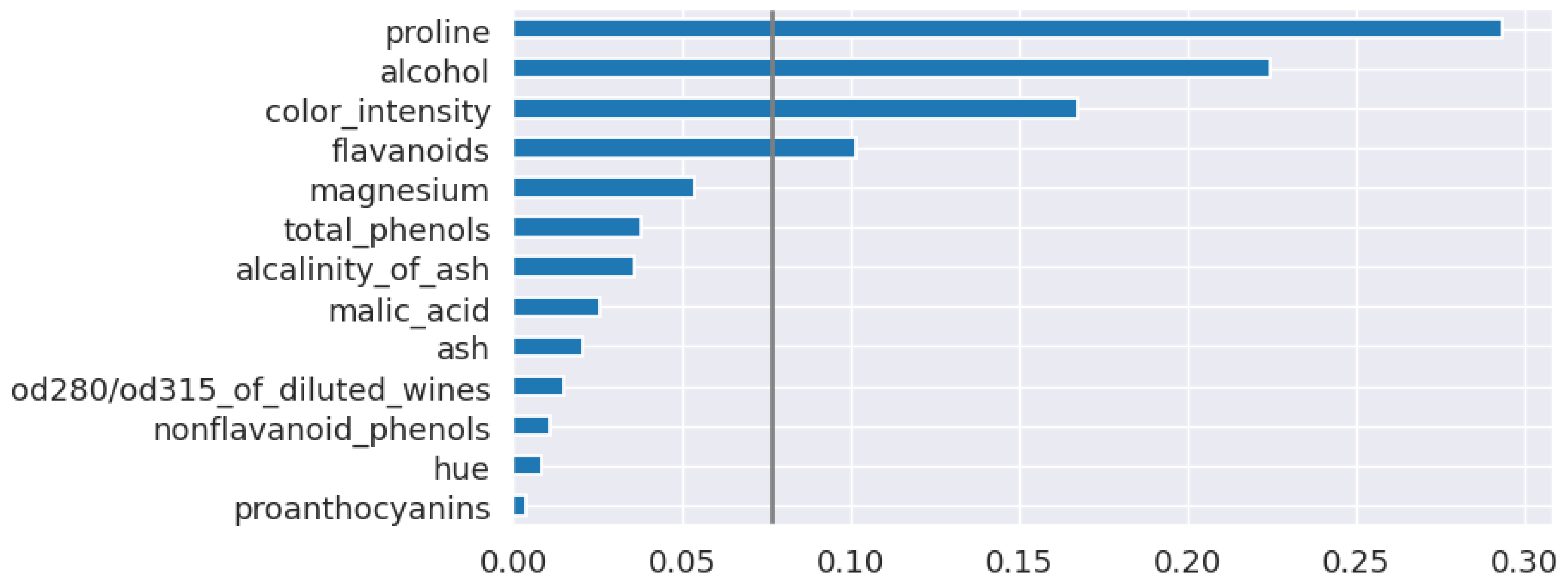

- Which of these features should we keep?
    - Elbow method
    - Threshold at mean

Feature Selection: SelectFromModel

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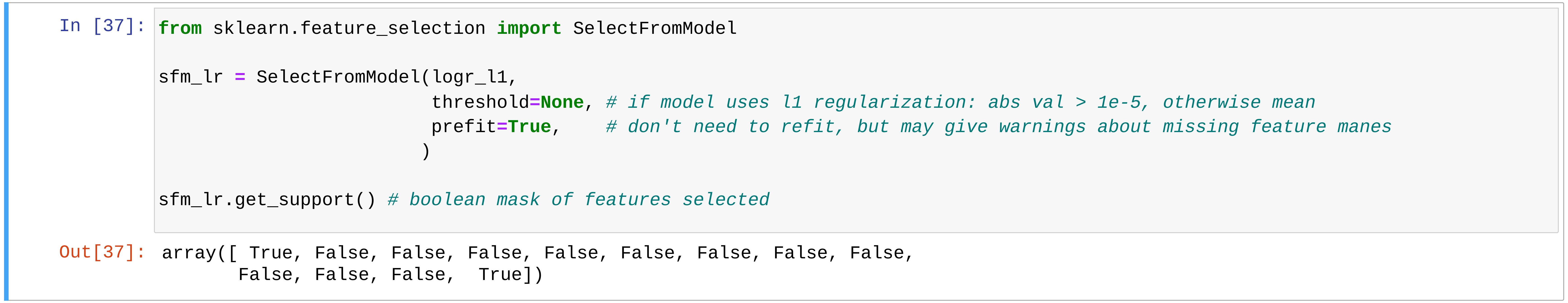

In [37]:

```
from sklearn.feature_selection import SelectFromModel

sfm_lr = SelectFromModel(logr_l1,
                         threshold=None, # if model uses l1 regularization: abs val > 1e-5, otherwise mean
                         prefit=True,    # don't need to refit, but may give warnings about missing feature manes
                        )

sfm_lr.get_support() # boolean mask of features selected
```

Out[37]:

```
array([ True, False, False, False, False, False, False, False, False,
       False, False, False,  True])
```

Feature Selection: SelectFromModel

```
In [37]: from sklearn.feature_selection import SelectFromModel

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Out[37]: array([ True, False, False, False, False, False, False, False, False,
                False, False, False,  True])
```

```
In [38]: wine_feature_names[sfm_lr.get_support()]
```

```
Out[38]: array(['alcohol', 'proline'], dtype=object)
```

Feature Selection: SelectFromModel

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In [37]: from sklearn.feature_selection import SelectFromModel

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```
In [39]: X_train_subset = sfm_lr.transform(X_train_zscore)
         X_train_subset.shape

         /home/bgibson/anaconda3/envs/eods-f22/lib/python3.10/site-packages/sklearn/base.py:443: UserWarning: X has feature names, but S
         electFromModel was fitted without feature names
           warnings.warn(

Out[39]: (97, 2)
```

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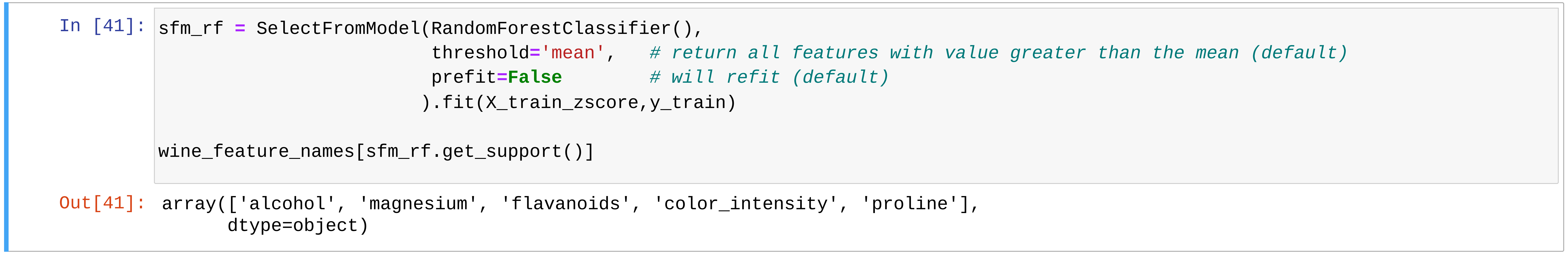
Out[39]: (97, 2)
```

```
In [40]: X_train_subset[:3].round(3) # note that this is no longer a dataframe

Out[40]: array([[-0.903, -0.853],
                [-1.58 , -0.936],
                [ 0.871,  1.334]])
```

Feature Selection: SelectFromModel Cont.

Feature Selection: SelectFromModel Cont.



In [41]:
```
sfm_rf = SelectFromModel(RandomForestClassifier(),
                         threshold='mean',   # return all features with value greater than the mean (default)
                         prefit=False        # will refit (default)
                        ).fit(X_train_zscore,y_train)

wine_feature_names[sfm_rf.get_support()]
```

Out[41]:
```
array(['alcohol', 'magnesium', 'flavanoids', 'color_intensity', 'proline'],
      dtype=object)
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Feature Selection: SelectFromModel Cont.

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In [41]: sfm_rf = SelectFromModel(RandomForestClassifier(),
                                  threshold='mean',   # return all features with value greater than the mean (default)
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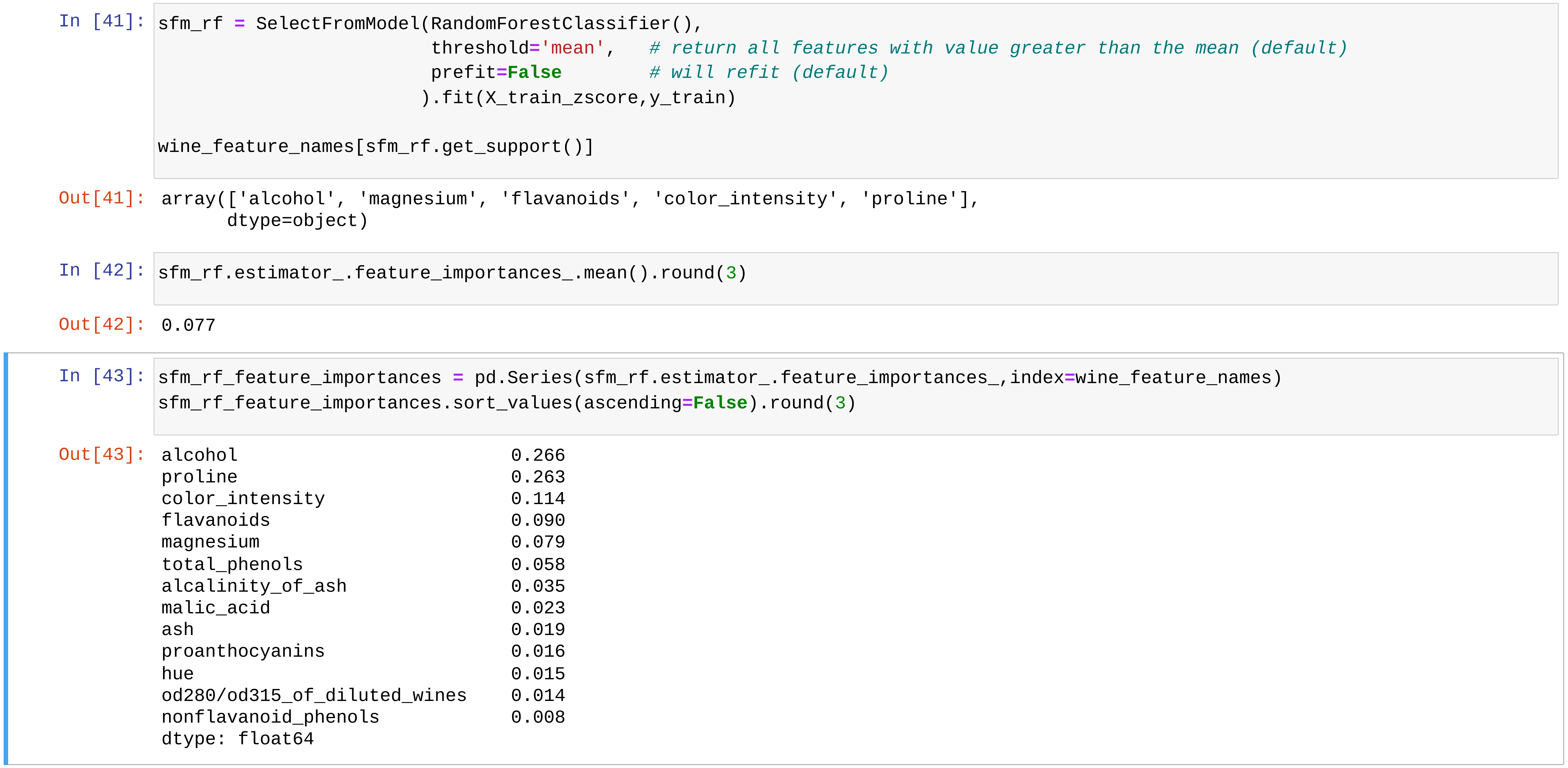
         wine_feature_names[sfm_rf.get_support()]
```

```
Out[41]: array(['alcohol', 'magnesium', 'flavanoids', 'color_intensity', 'proline'],
               dtype=object)
```

```
In [42]: sfm_rf.estimator_.feature_importances_.mean().round(3)
```

```
Out[42]: 0.077
```

Feature Selection: SelectFromModel Cont.



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```
In [42]: sfm_rf.estimator_.feature_importances_.mean().round(3)
```

```
Out[42]: 0.077
```

```
In [43]: sfm_rf_feature_importances = pd.Series(sfm_rf.estimator_.feature_importances_,index=wine_feature_names)
         sfm_rf_feature_importances.sort_values(ascending=False).round(3)
```

```
Out[43]: alcohol                         0.266
         proline                         0.263
         color_intensity                 0.114
         flavanoids                      0.090
         magnesium                       0.079
         total_phenols                   0.058
         alcalinity_of_ash               0.035
         malic_acid                      0.023
         ash                             0.019
         proanthocyanins                 0.016
         hue                             0.015
         od280/od315_of_diluted_wines    0.014
         nonflavanoid_phenols            0.008
         dtype: float64
```

Feature Selection: Univariate Tests

- Perform statistical test on each feature **independent of all others**
    - Rank and select top k features
    - sklearn: `SelectKBest`
    - requires a scoring function
- Example: `f_classif`
    - F-test
    - estimates the degree of linear dependency between feature x and target y

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  - sklearn: `SelectKBest`
  - requires a scoring function
- Example: `f_classif`
  - F-test
  - estimates the degree of linear dependency between feature x and target y

```
In [44]: from sklearn.feature_selection import SelectKBest, f_classif

         # select 2 best features
         kbest = SelectKBest(score_func=f_classif, # default,
                             k=3                   # how many features to keep
                            ).fit(X_train, y_train)
         wine_feature_names[kbest.get_support()]

Out[44]: array(['alcohol', 'color_intensity', 'proline'], dtype=object)
```

Feature Selection: Recursive Feature Elimination

- Would like to test all possible combinations of features
- Likely prohibitively expensive/time-consuming
- Instead recursively select smaller subsets of features
- Requires a model that assigns weights or importance to features

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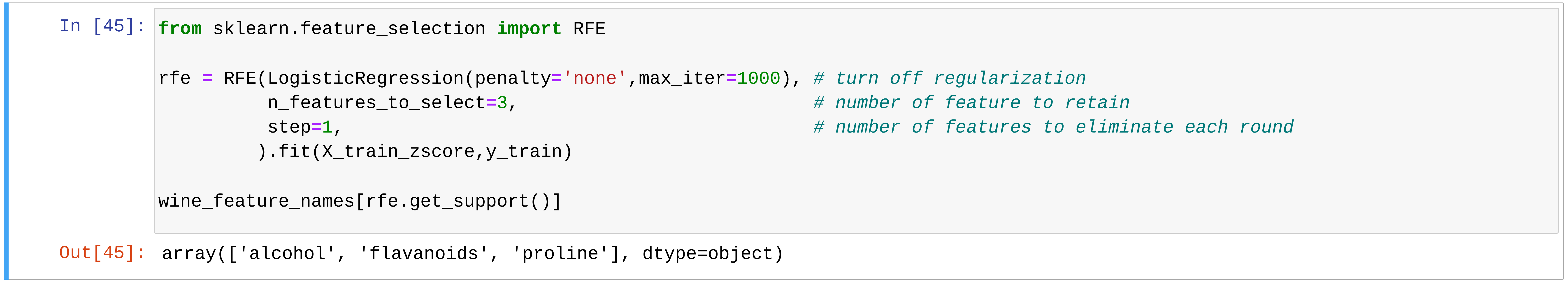

```
In [45]: from sklearn.feature_selection import RFE

         rfe = RFE(LogisticRegression(penalty='none',max_iter=1000), # turn off regularization
                   n_features_to_select=3,                           # number of feature to retain
                   step=1,                                           # number of features to eliminate each round
                  ).fit(X_train_zscore,y_train)

         wine_feature_names[rfe.get_support()]

Out[45]: array(['alcohol', 'flavanoids', 'proline'], dtype=object)
```

Feature Selection: Other Methods

- by **Variance**
    - eliminate columns where all rows have the same (or almost all the same) value
- **Sequential Feature Selection**
    - greedy algorithm similar to Recursive Feature Elimination
    - uses performance metric (eg accuracy) instead of weights, importances
    - via `mlxtend`
- **Exaustive Feature Selection**
    - evaluate all possible feature combinations
    - uses performance metric (eg accuracy) instead of weights, importances
    - via `mlxtend`
- Other **Univariate tests**
    - `f_regression`, F-test for regression task
    - `mutual_info_classif` and `_regression`
    - `chi2`, for classification, requires non-negative values

Questions on Feature Selection?

When changing number of features: Use Adjusted R^2

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- Adding features guarantees an increase in R^2
- R^2 describes the proportion of explained variance
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- where n is the number of observations, m is the number of features

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- where n is the number of observations, m is the number of features

```
In [46]: def adj_r2(model,X,y):
             n,m = X.shape
             return 1-(1-model.score(X,y))*(n-1)/(n-m-1)
```

Changing number of features: Use Adjusted R^2 Cont.

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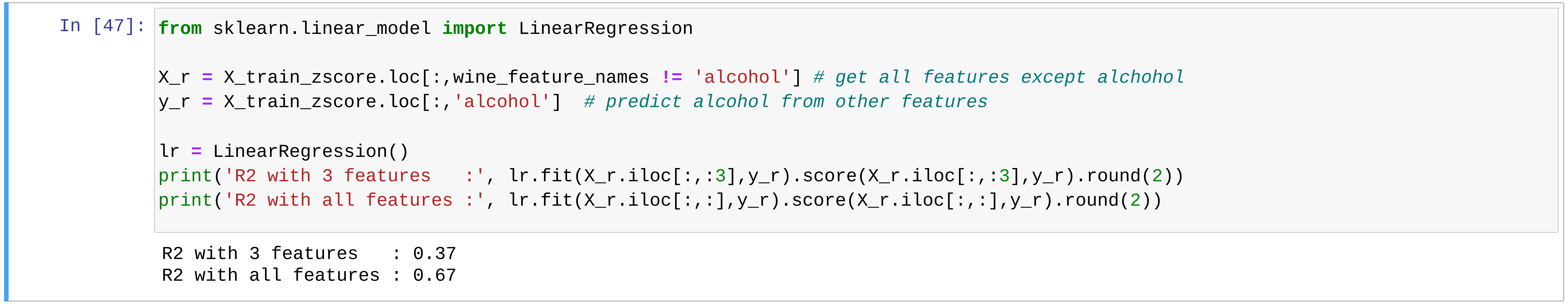


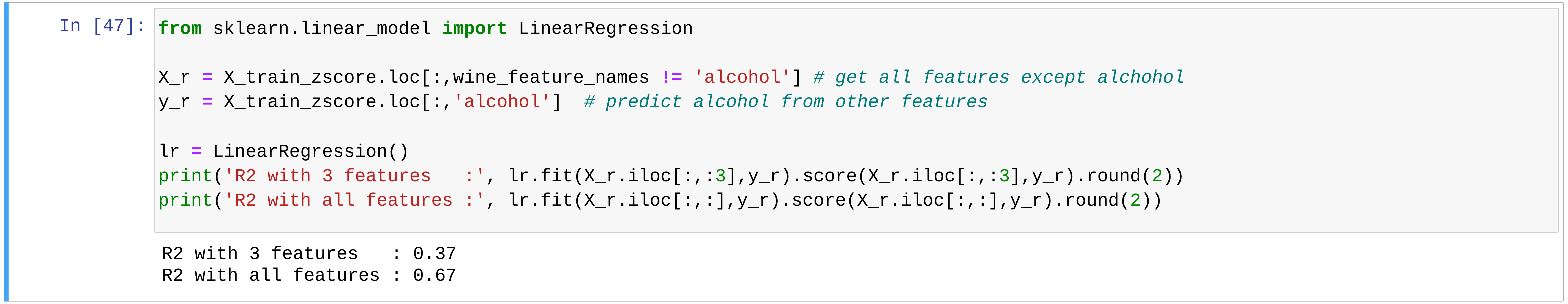
```
In [47]: from sklearn.linear_model import LinearRegression

         X_r = X_train_zscore.loc[:,wine_feature_names != 'alcohol'] # get all features except alchohol
         y_r = X_train_zscore.loc[:,'alcohol']  # predict alcohol from other features

         lr = LinearRegression()
         print('R2 with 3 features   :', lr.fit(X_r.iloc[:,:3],y_r).score(X_r.iloc[:,:3],y_r).round(2))
         print('R2 with all features :', lr.fit(X_r.iloc[:,:],y_r).score(X_r.iloc[:,:],y_r).round(2))
```

```
R2 with 3 features   : 0.37
R2 with all features : 0.67
```

Changing number of features: Use Adjusted R^2 Cont.



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R2 with 3 features   : 0.37
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Is this due to a better model or just adding features?

In [48]:
```
print('Adj R2 with 3 features   :',adj_r2(lr.fit(X_r.iloc[:,:3],y_r),X_r.iloc[:,:3],y_r).round(2))
print('Adj R2 with all features :',adj_r2(lr.fit(X_r.iloc[:,:],y_r),X_r.iloc[:,:],y_r).round(2))
```

```
Adj R2 with 3 features   : 0.35
Adj R2 with all features : 0.62
```

Changing number of features: Use Adjusted R^2 Cont.

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R2 with 3 features   : 0.37
R2 with all features : 0.67
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```

```
Adj R2 with 3 features   : 0.35
Adj R2 with all features : 0.62
```

- Now we know the increase is due to a better model and not just adding features

Changing number of features: Use Adjusted R^2 Cont.

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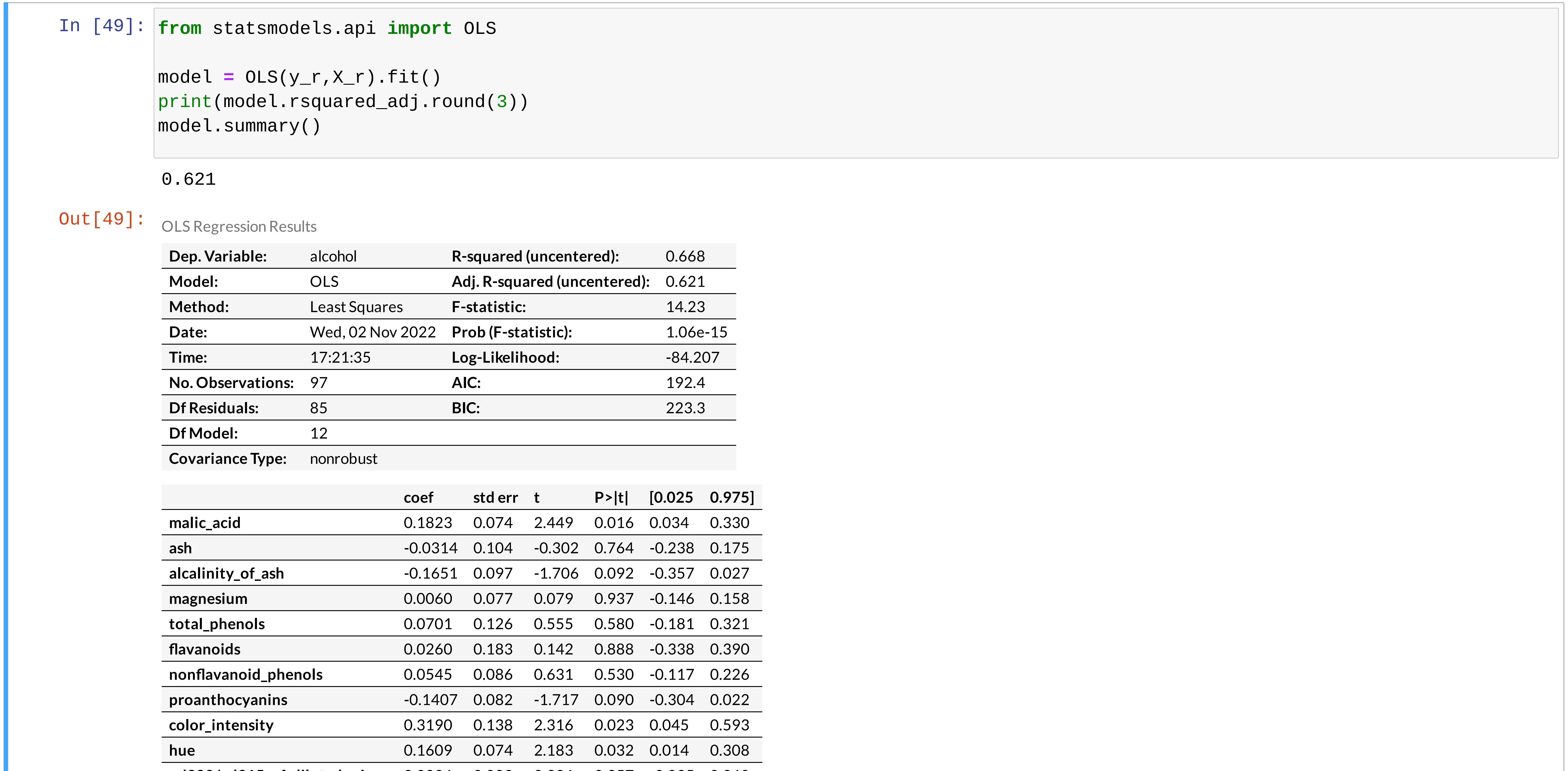


In [49]:

```python
from statsmodels.api import OLS

model = OLS(y_r,X_r).fit()
print(model.rsquared_adj.round(3))
model.summary()
```

```
0.621
```

Out[49]:

OLS Regression Results

Dep. Variable:	alcohol	**R-squared (uncentered):**	0.668
Model:	OLS	**Adj. R-squared (uncentered):**	0.621
Method:	Least Squares	**F-statistic:**	14.23
Date:	Wed, 02 Nov 2022	**Prob (F-statistic):**	1.06e-15
Time:	17:21:35	**Log-Likelihood:**	-84.207
No. Observations:	97	**AIC:**	192.4
Df Residuals:	85	**BIC:**	223.3
Df Model:	12		
Covariance Type:	nonrobust		

	coef	std err	t	P>|t|	[0.025	0.975]
malic_acid	0.1823	0.074	2.449	0.016	0.034	0.330
ash	-0.0314	0.104	-0.302	0.764	-0.238	0.175
alcalinity_of_ash	-0.1651	0.097	-1.706	0.092	-0.357	0.027
magnesium	0.0060	0.077	0.079	0.937	-0.146	0.158
total_phenols	0.0701	0.126	0.555	0.580	-0.181	0.321
flavanoids	0.0260	0.183	0.142	0.888	-0.338	0.390
nonflavanoid_phenols	0.0545	0.086	0.631	0.530	-0.117	0.226
proanthocyanins	-0.1407	0.082	-1.717	0.090	-0.304	0.022
color_intensity	0.3190	0.138	2.316	0.023	0.045	0.593
hue	0.1609	0.074	2.183	0.032	0.014	0.308

Questions re Adjusted R^2?

Feature Extraction

- Transform original features into new feature space
- Can be thought of as compression while maintaining relevant information
- Often used for:
    - visualization (multi-dimensional to 2-D)
    - compression (storage)
    - dimensionality reduction
- Popular methods:
    - **Principal Component Analysis:** Unsupervised data compression
    - Linear Discriminant Analysis: Supervised method to maximize class separation
    - Kernel PCA, etc.

Principal Component Analysis (PCA)

- Unsupervised Learning method (ignores label)
- Idea:
    - Directions of high variance in the data contain important information
    - Colinear features can be combined
    - Find directions of maximum variance
    - Project onto subspace with same or fewer dimensions

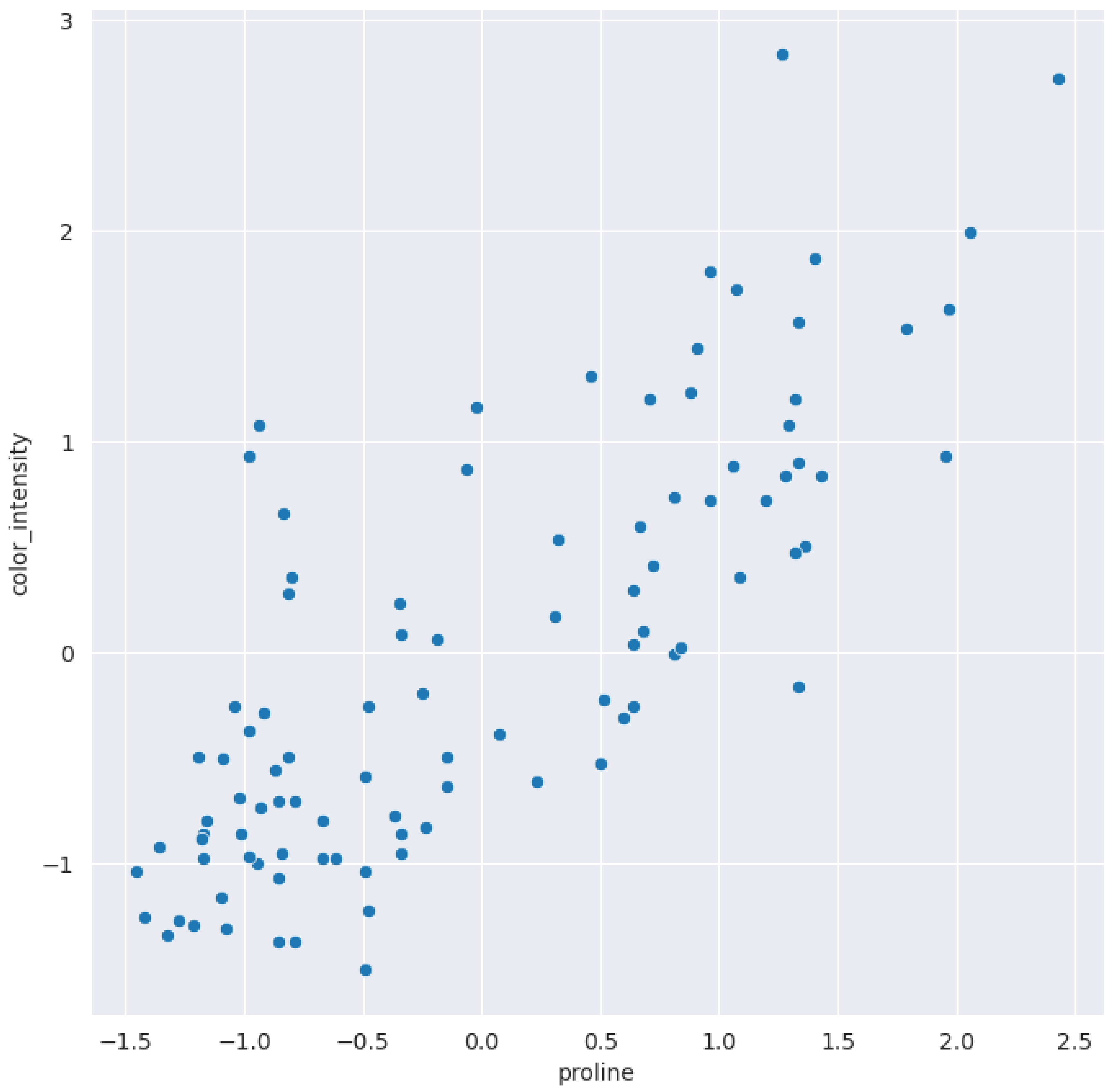
Principal Component Analysis (PCA)

- How it works:
    0. first center the data (subtract the means)
    1. extract first component:
        - direction (combination of features)
        - explains maximum variance
    2. extract next component:
        - direction, orthogonal to the first (linearly independent)
        - explains max remaining variance
    3. repeat:
        - max number of possible components equals number of original dimensions

PCA Example

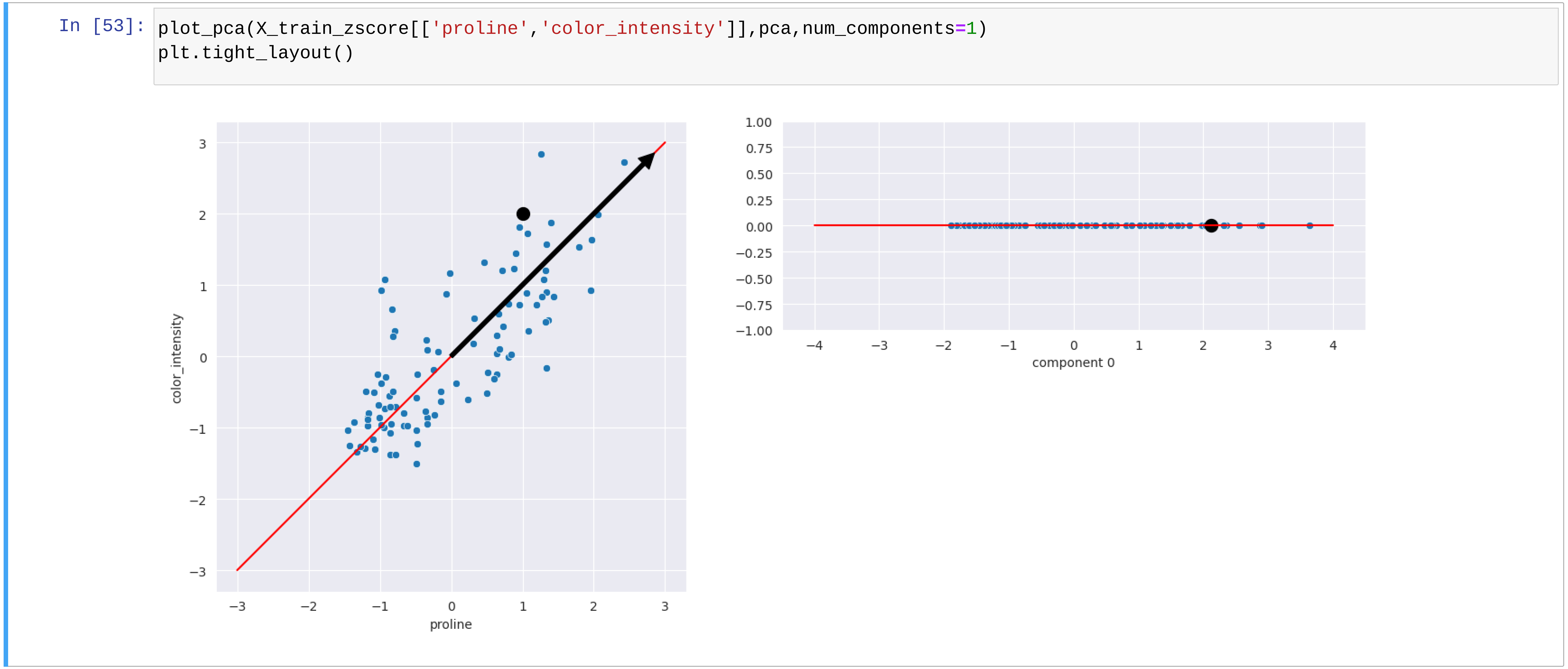
PCA Example

```
In [51]: fig,ax = plt.subplots(1,1,figsize=(8,8))
         sns.scatterplot(x='proline',y='color_intensity',data=X_train_zscore,ax=ax);
```

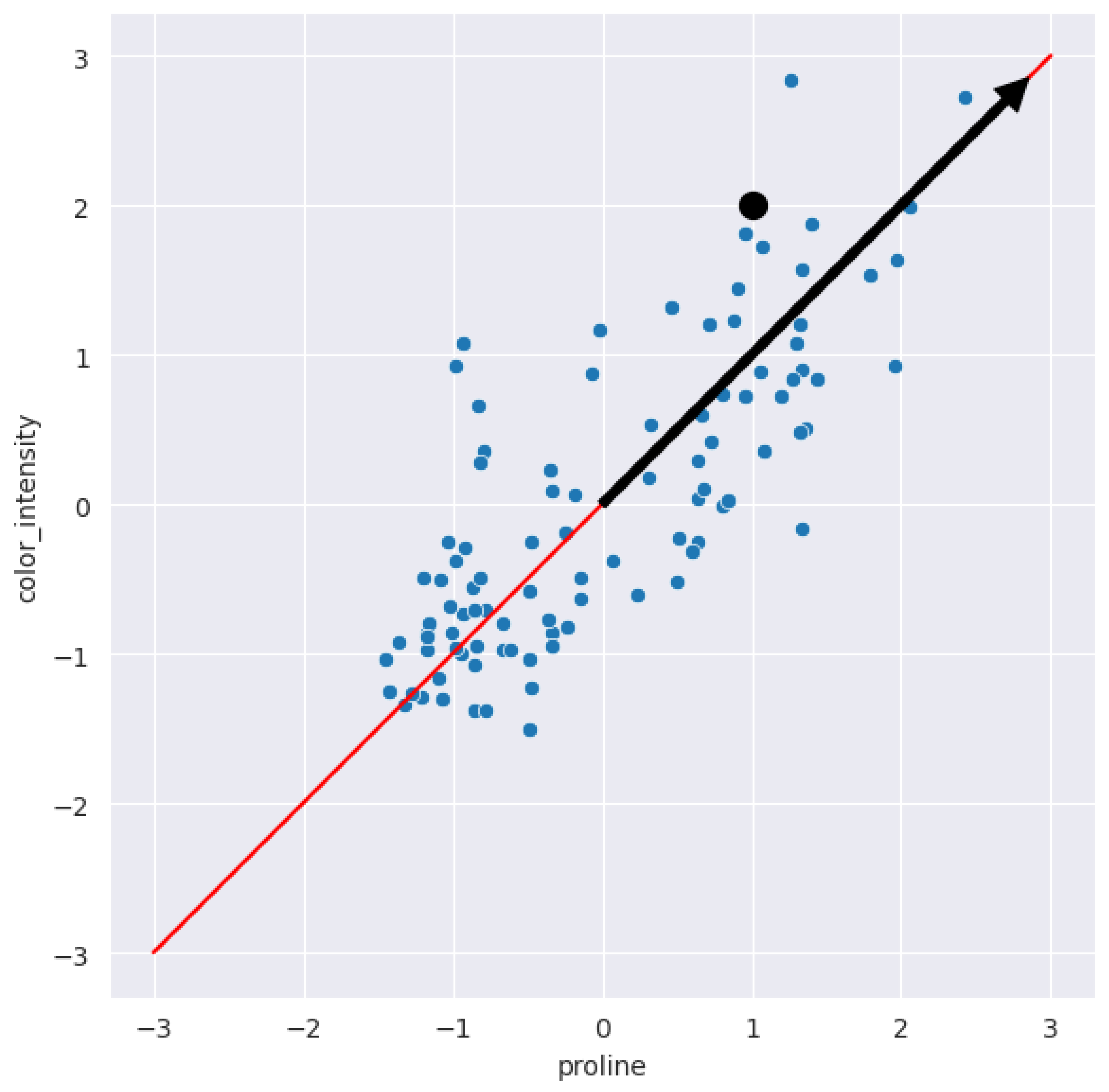


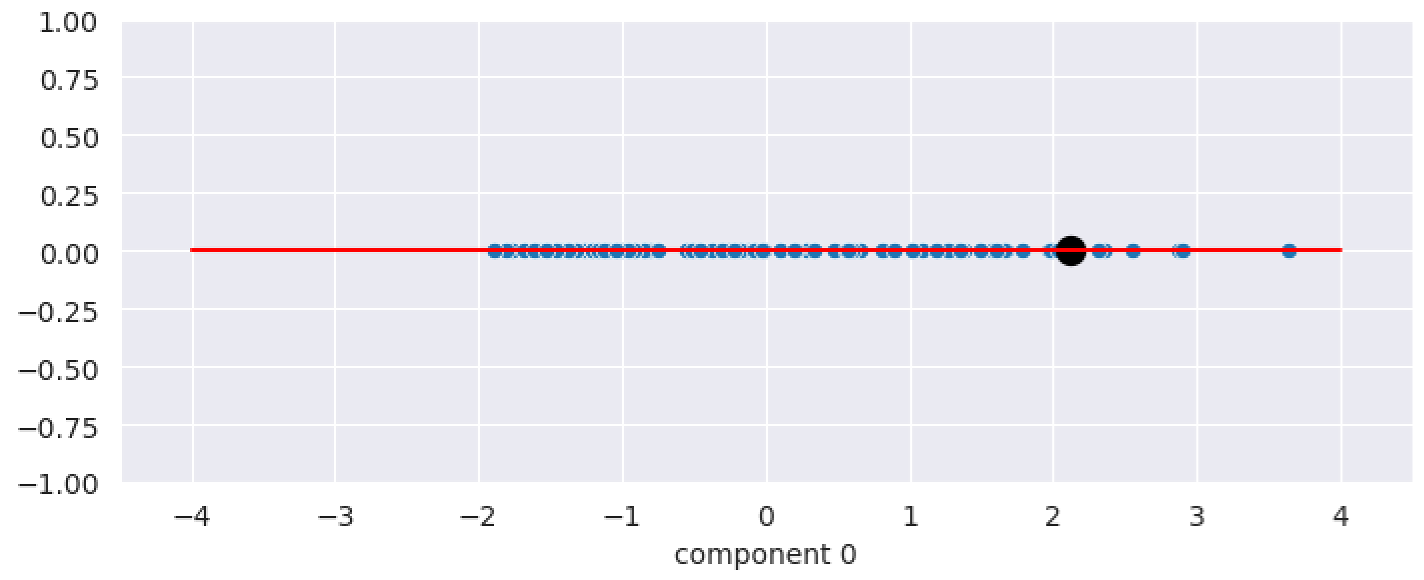
PCA Example Cont.

PCA Example Cont.



```
In [53]: plot_pca(X_train_zscore[['proline','color_intensity']],pca,num_components=1)
         plt.tight_layout()
```

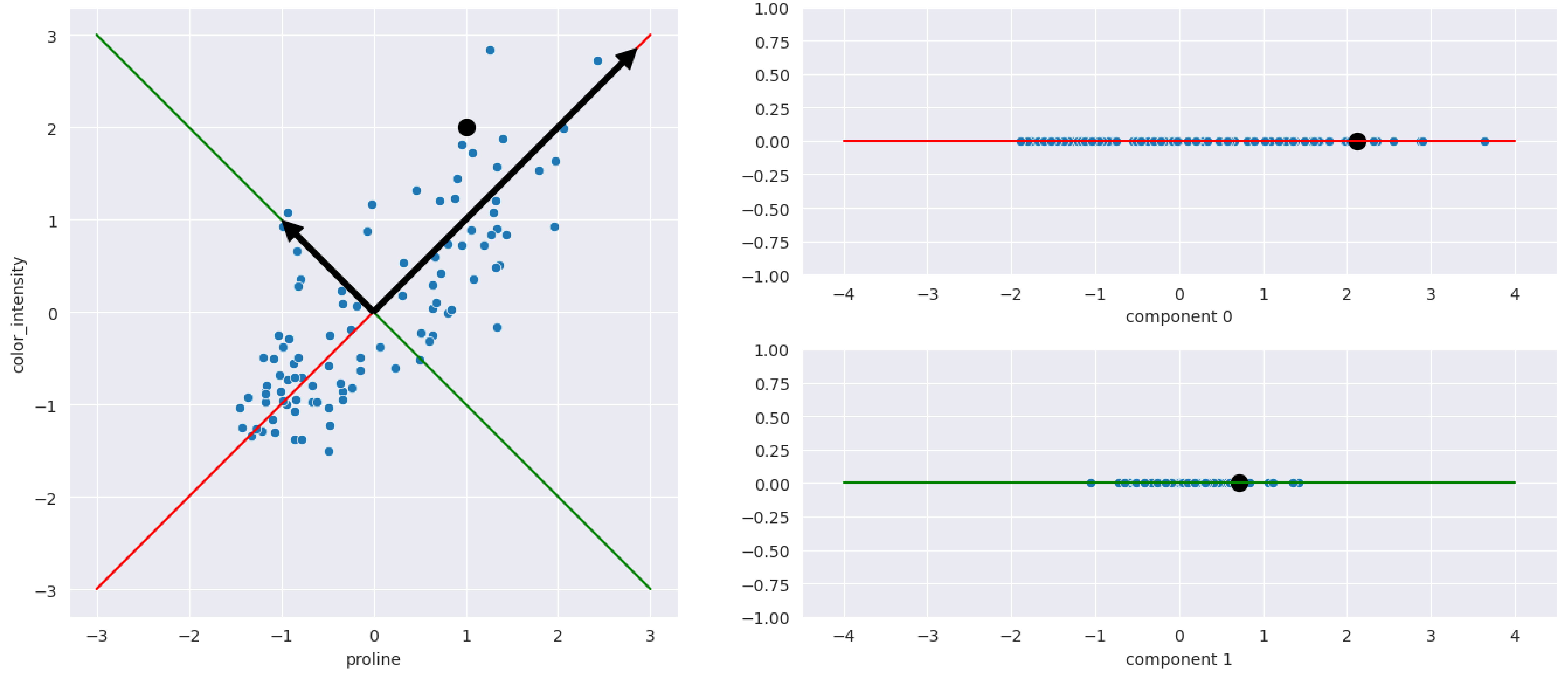




PCA Example Cont.

PCA Example Cont.

```
In [54]: plot_pca(X_train_zscore[['proline','color_intensity']],pca,num_components=2)
         plt.tight_layout()
```



PCA in sklearn

PCA in sklearn

```
In [55]: from sklearn.decomposition import PCA

         pca = PCA().fit(X_train_zscore)

         print(f'num input features: {X_train_zscore.shape[1]}')
         print(f'num pca components: {pca.n_components_}')

          num input features: 13
          num pca components: 13
```

```
In [56]: pca.components_[0].round(2)

Out[56]: array([ 0.35, -0.05,  0.16, -0.18,  0.23,  0.38,  0.4 , -0.22,  0.24,
                 0.38,  0.12,  0.21,  0.39])
```

PCA in sklearn

```
In [55]: from sklearn.decomposition import PCA

         pca = PCA().fit(X_train_zscore)

         print(f'num input features: {X_train_zscore.shape[1]}')
         print(f'num pca components: {pca.n_components_}')

         num input features: 13
         num pca components: 13
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```
In [56]: pca.components_[0].round(2)

Out[56]: array([ 0.35, -0.05,  0.16, -0.18,  0.23,  0.38,  0.4 , -0.22,  0.24,
                 0.38,  0.12,  0.21,  0.39])
```

```
In [57]: print(' + \n'.join([f'{w: 0.2f}*{f}' for f,w in zip(wine_feature_names,pca.components_[0])]))

          0.35*alcohol +
         -0.05*malic_acid +
          0.16*ash +
         -0.18*alcalinity_of_ash +
          0.23*magnesium +
          0.38*total_phenols +
          0.40*flavanoids +
         -0.22*nonflavanoid_phenols +
          0.24*proanthocyanins +
          0.38*color_intensity +
          0.12*hue +
          0.21*od280/od315_of_diluted_wines +
          0.39*proline
```

PCA: Explained Variance

- How much of the variance in the dataset is explained by each component?

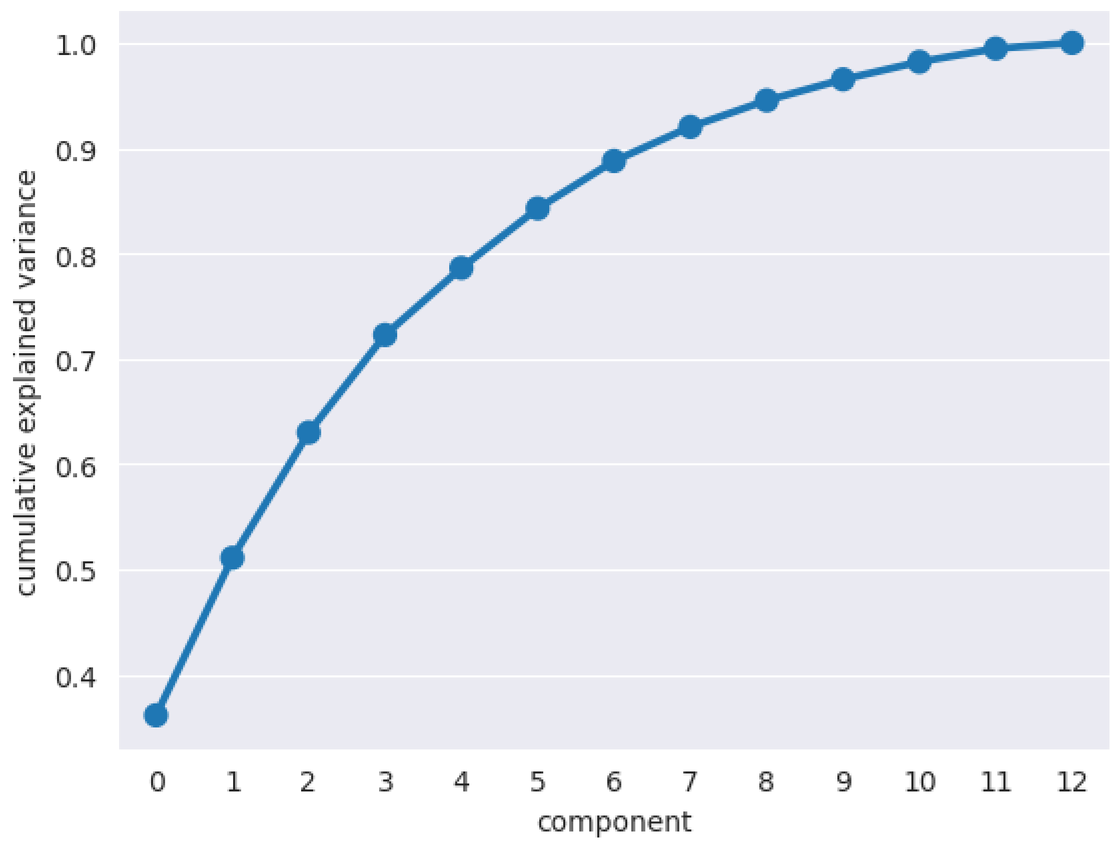
PCA: Explained Variance

- How much of the variance in the dataset is explained by each component?

```
In [58]: pca = PCA().fit(X_train_zscore)

         print(f'explained_variance            : {pca.explained_variance_.round(2)}')
         print(f'explained_variance_ratio_     : {pca.explained_variance_ratio_.round(2)}')
         print(f'cumulative explained variance : {pca.explained_variance_ratio_.cumsum().round(2)}')
         df_var = pd.DataFrame({'component':range(pca.n_components_),
                                'cumulative explained variance':pca.explained_variance_ratio_.cumsum()})
         sns.pointplot(x='component',y='cumulative explained variance',data=df_var);
```

```
explained_variance            : [4.75 1.96 1.56 1.22 0.84 0.74 0.59 0.42 0.33 0.26 0.22 0.17 0.07]
explained_variance_ratio_     : [0.36 0.15 0.12 0.09 0.06 0.06 0.05 0.03 0.03 0.02 0.02 0.01 0.01]
cumulative explained variance : [0.36 0.51 0.63 0.72 0.79 0.84 0.89 0.92 0.95 0.97 0.98 0.99 1.  ]
```



Dimensionality Reduction with PCA

Dimensionality Reduction with PCA

In [59]:
```
pca_2d = PCA(n_components=2)
X_pca = pca_2d.fit_transform(X_train_zscore)
X_pca = pd.DataFrame(X_pca,columns=['component0','component1'])

fig,ax=plt.subplots(1,2,figsize=(14,6))
sns.scatterplot(x='proline',y='color_intensity',data=X_train_zscore,ax=ax[0]);
sns.scatterplot(x='component0',y='component1',data=X_pca,ax=ax[1]);
ax[0].axis('equal');ax[1].axis('equal');
```

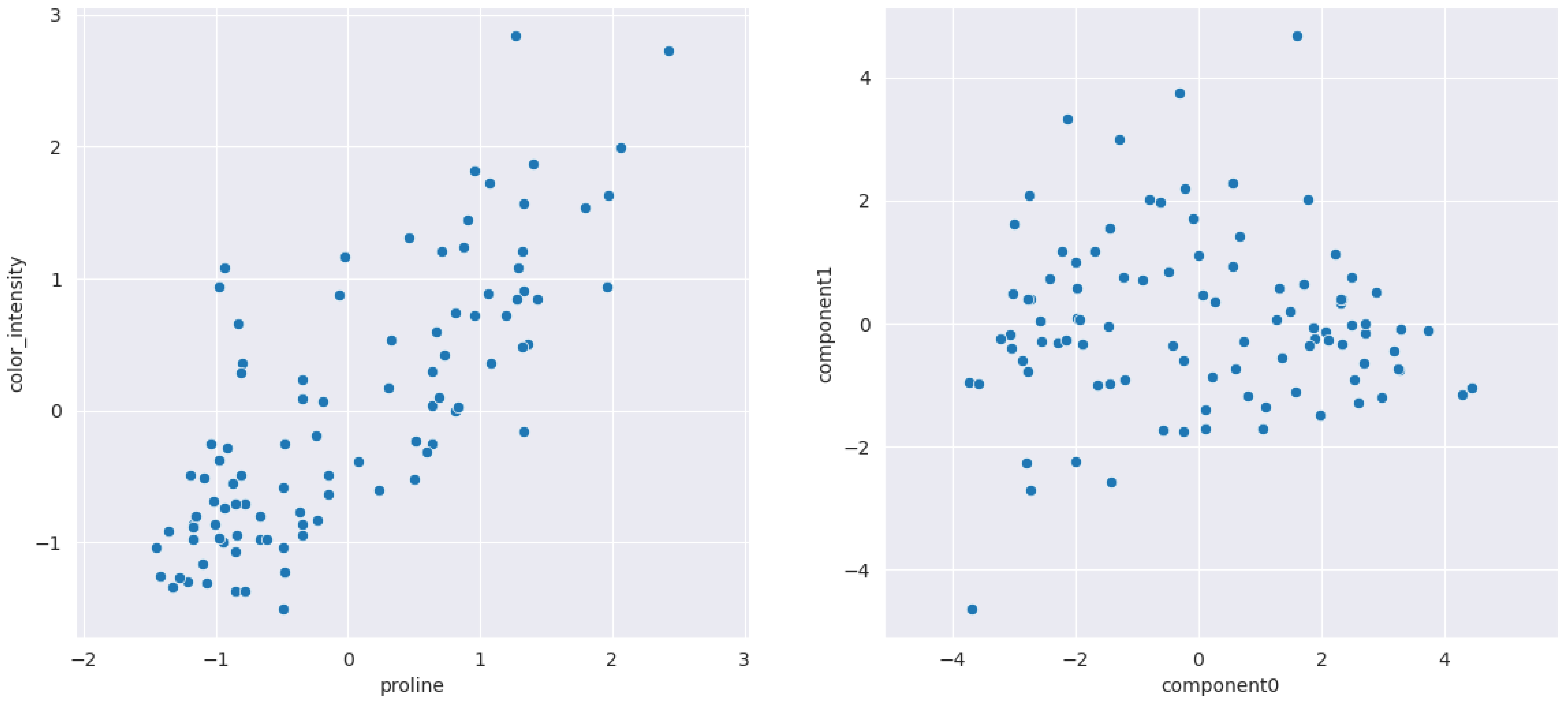


Image Recognition Example

PCA and Image Recognition

- Generally, an image is represented by a grid of pixels
- Each pixel is a square that takes a value representing a shade (usually a value between 0 and 255)
- 1024 x 1024 pixels = 1,048,576 pixels = 1 megapixel
- iPhone X11 Pro : 12 megapixels
- Color images contain three layers: red, green, blue
- ~36 million pixel values
- A very high dimensional space!

- Image classification using PCA?
    - Example based on Faces recognition example using eigenfaces and SVMs

Example Dataset: Labeled Faces in th Wild (LFW)

Labeled Faces in the Wild

Example Dataset: Labeled Faces in th Wild (LFW)

Labeled Faces in the Wild

```
In [60]: from sklearn.datasets import fetch_lfw_people

         lfw_people = fetch_lfw_people(min_faces_per_person=70, resize=0.6)
```

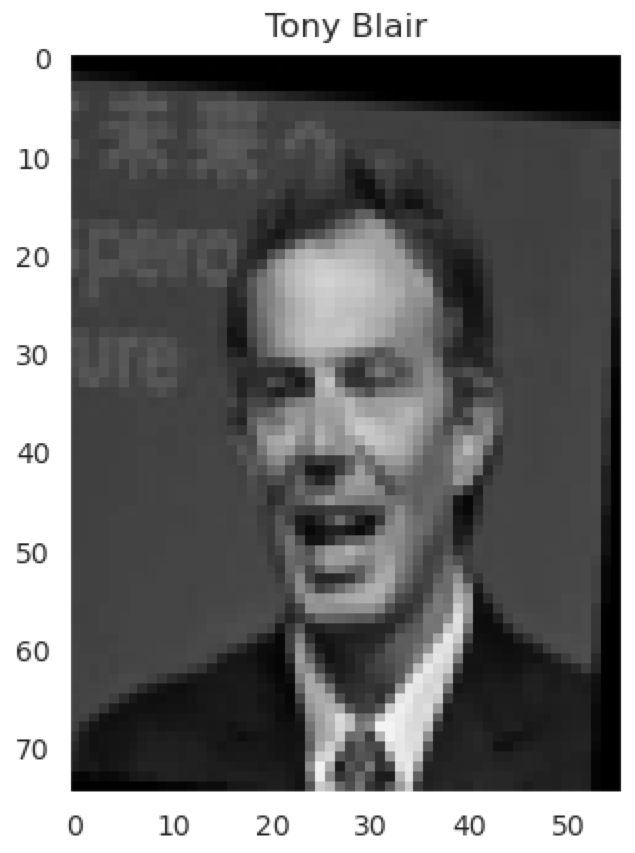
Example Dataset: Labeled Faces in th Wild (LFW)

Labeled Faces in the Wild

In [60]:
```
from sklearn.datasets import fetch_lfw_people

lfw_people = fetch_lfw_people(min_faces_per_person=70, resize=0.6)
```

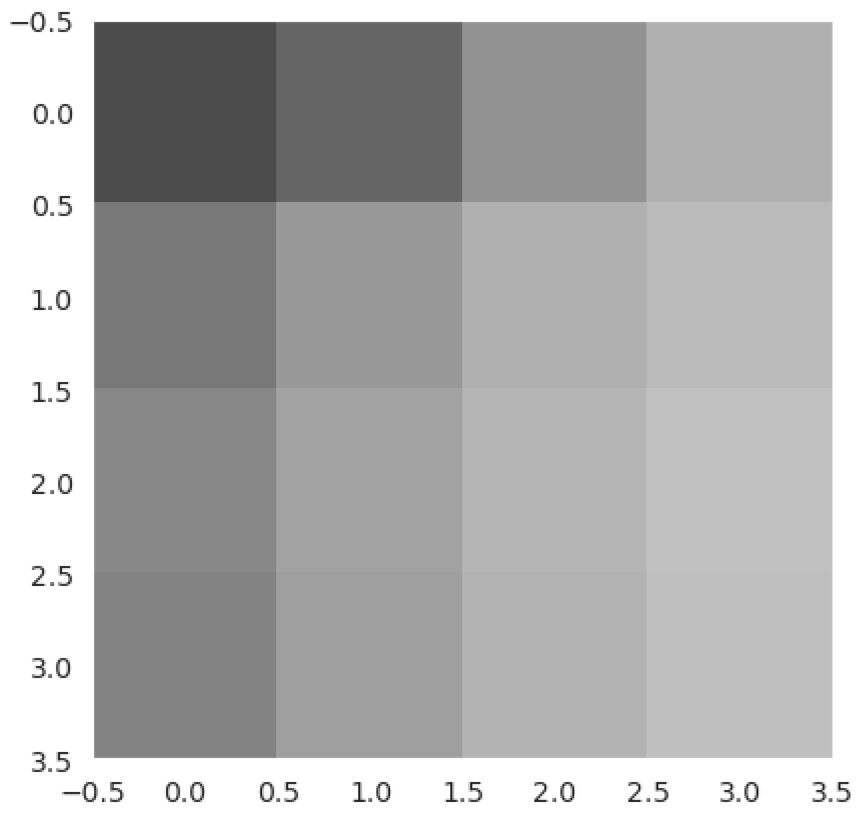
In [61]:
```
sns.set_style('dark')
plt.imshow(lfw_people.images[1], cmap=plt.cm.gray, vmin=0, vmax=1)
plt.title(lfw_people.target_names[lfw_people.target[1]], size=12);
```



Example Pixel Values

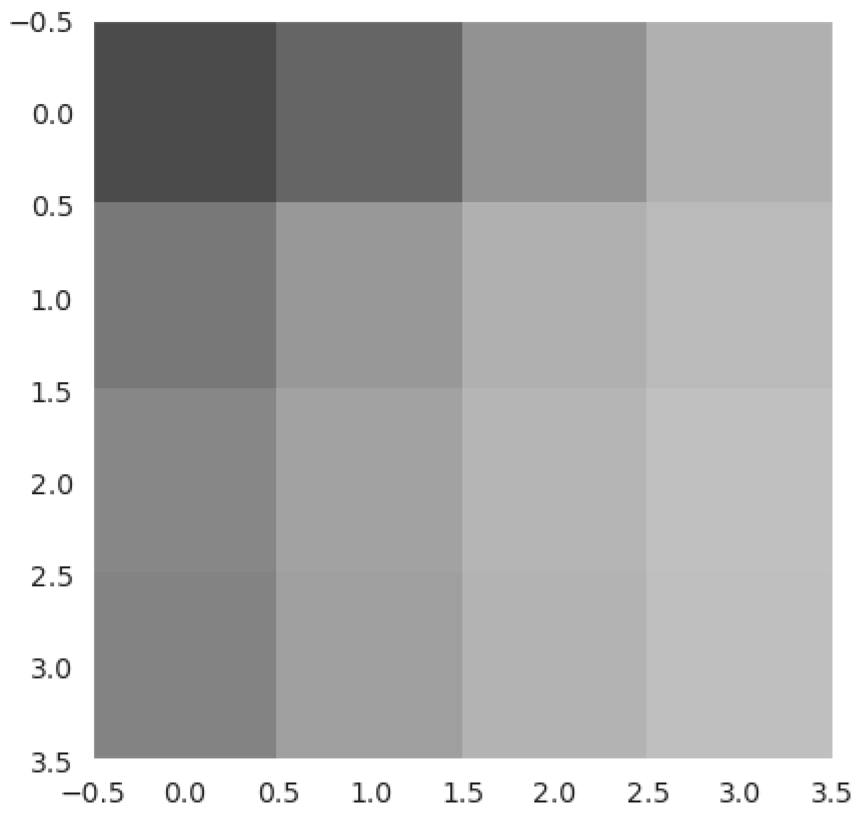
Example Pixel Values

In [62]:
```
# sample of 3x3 set of pixels
plt.imshow(lfw_people.images[1][20:24,20:24],cmap=plt.cm.gray,vmin=0, vmax=1);
```



Example Pixel Values

```
In [62]: # sample of 3x3 set of pixels
         plt.imshow(lfw_people.images[1][20:24,20:24],cmap=plt.cm.gray,vmin=0, vmax=1);
```



```
In [63]: lfw_people.images[1][13:16,13:16].round(2)

Out[63]: array([[0.25, 0.24, 0.29],
                [0.25, 0.25, 0.25],
                [0.25, 0.25, 0.25]], dtype=float32)
```

Representing each Image: Flatten

- Grid as a fixed length feature vector?

Representing each Image: Flatten

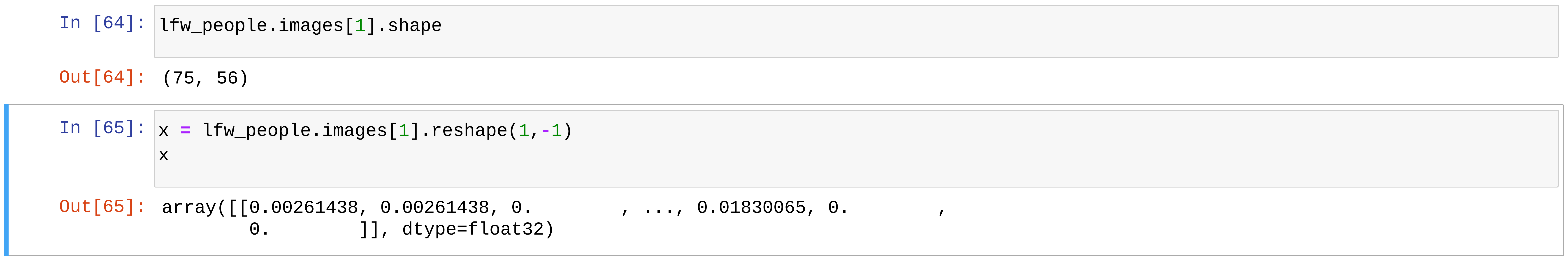
- Grid as a fixed length feature vector?

```
In [64]: lfw_people.images[1].shape

Out[64]: (75, 56)
```

Representing each Image: Flatten

- Grid as a fixed length feature vector?



```
In [64]: lfw_people.images[1].shape

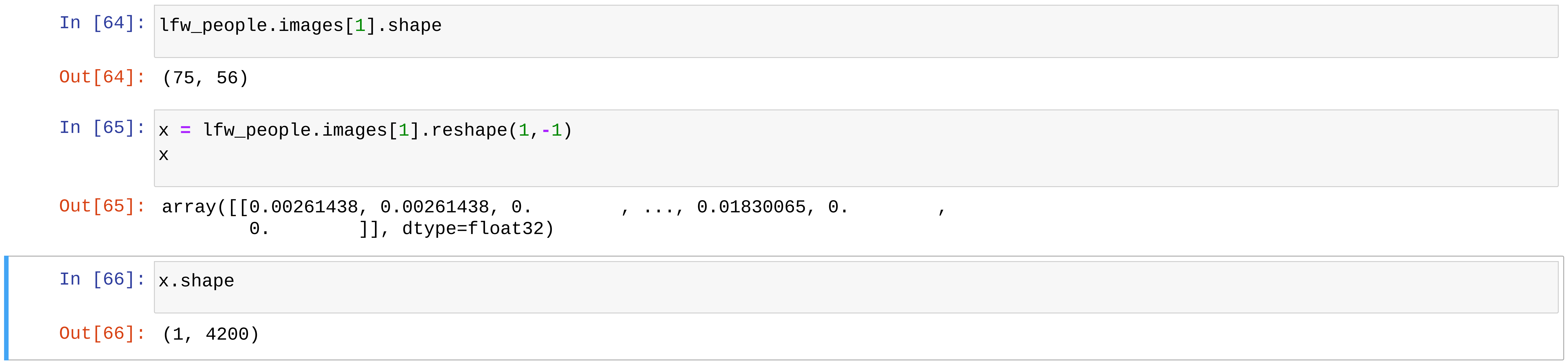
Out[64]: (75, 56)

In [65]: x = lfw_people.images[1].reshape(1,-1)
         x

Out[65]: array([[0.00261438, 0.00261438, 0.        , ..., 0.01830065, 0.        ,
                 0.        ]], dtype=float32)
```

Representing each Image: Flatten

- Grid as a fixed length feature vector?



```
In [64]: lfw_people.images[1].shape

Out[64]: (75, 56)

In [65]: x = lfw_people.images[1].reshape(1,-1)
         x

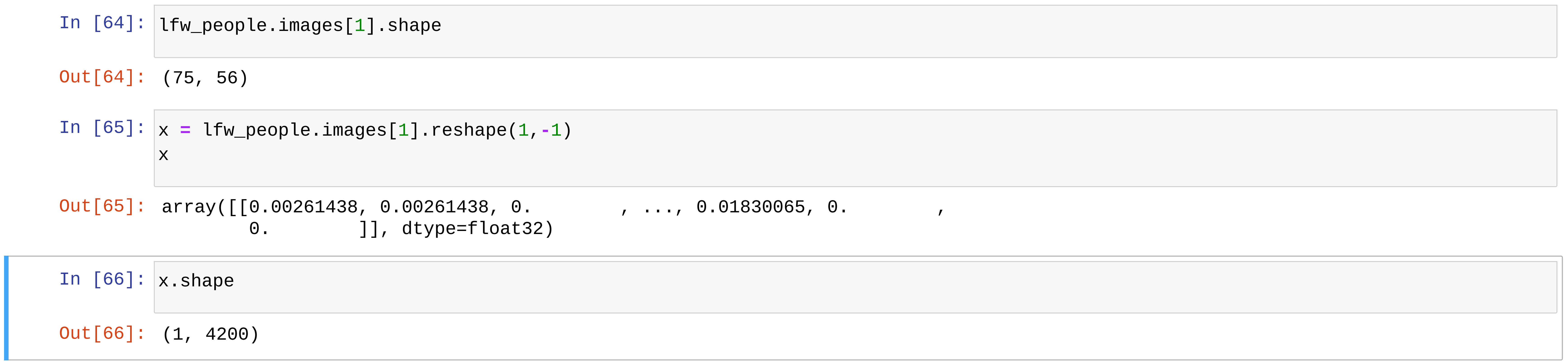
Out[65]: array([[0.00261438, 0.00261438, 0.        , ..., 0.01830065, 0.        ,
                 0.        ]], dtype=float32)

In [66]: x.shape

Out[66]: (1, 4200)
```

Representing each Image: Flatten

- Grid as a fixed length feature vector?



```
In [64]: lfw_people.images[1].shape

Out[64]: (75, 56)

In [65]: x = lfw_people.images[1].reshape(1,-1)
         x

Out[65]: array([[0.00261438, 0.00261438, 0.        , ..., 0.01830065, 0.        ,
                 0.        ]], dtype=float32)

In [66]: x.shape

Out[66]: (1, 4200)
```

What information do we lose when we do this?

Create a Dataset

Create a Dataset

In [67]:

```python
# get the shape of images for plotting the
n_samples, h, w = lfw_people.images.shape

# use actual pixel values, ignoring relative position
X_faces = lfw_people.data
n_features = X_faces.shape[1]

# the label to predict is the id of the person
y_faces = lfw_people.target
target_names = lfw_people.target_names
n_classes = target_names.shape[0]

# create train/test split
X_train_faces, X_test_faces, y_train_faces, y_test_faces = train_test_split(X_faces, y_faces,
                                                                            test_size=0.25,
                                                                            stratify=y_faces,
                                                                            random_state=0)

print(f"image_size: {h}x{w}")
print("n_features: %d" % n_features)
print("n_classes : %d" % n_classes)
print(f"n_train   : {len(X_train_faces)}")
print(f"n_test    : {len(X_test_faces)}")
```

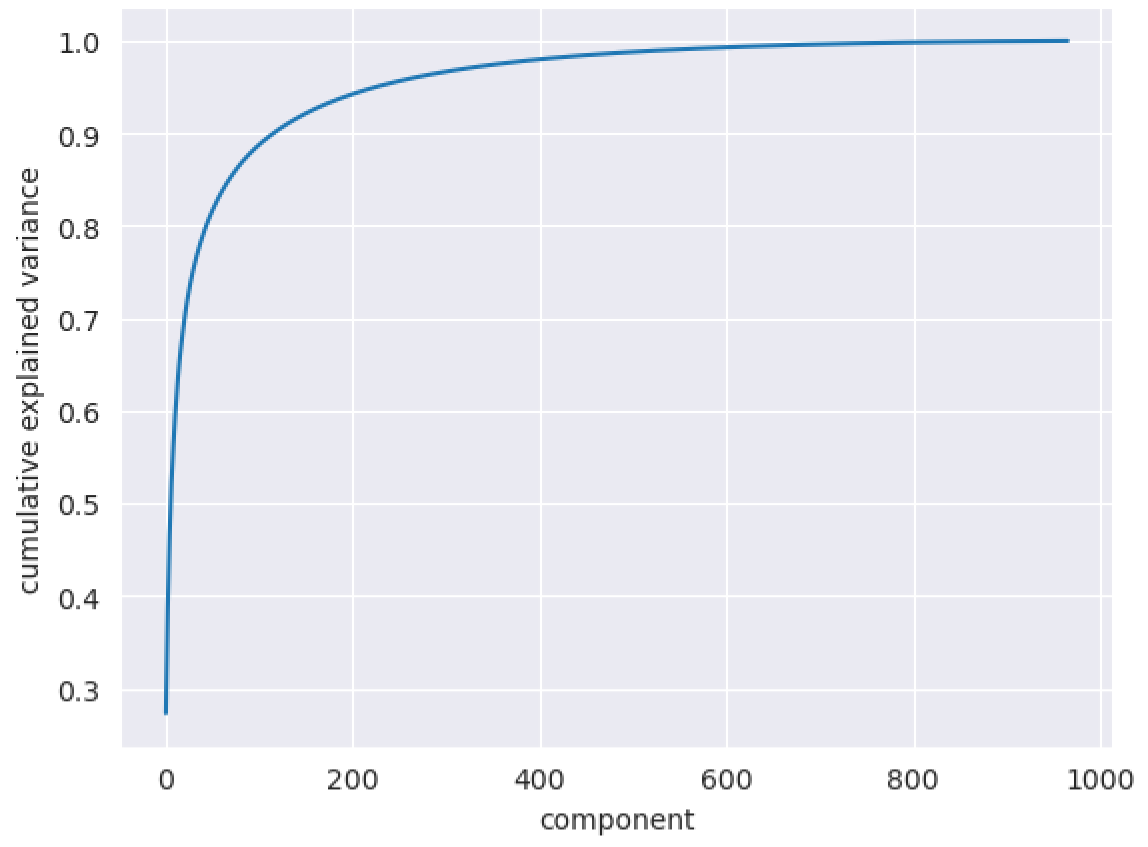
```
image_size: 75x56
n_features: 4200
n_classes : 7
n_train   : 966
n_test    : 322
```

Variance explained by PCA

Variance explained by PCA

```
In [68]: pca_faces = PCA().fit(X_train_faces)

         df_var_faces = pd.DataFrame({'component':range(pca_faces.n_components_),
                                      'cumulative explained variance':pca_faces.explained_variance_ratio_.cumsum()})
         # using lineplot here instead of pointplot because of the large number of components
         with sns.axes_style('darkgrid'):
             sns.lineplot(x='component',y='cumulative explained variance',data=df_var_faces);
```



Compute PCA and Transform

Compute PCA and Transform

In [69]:
```
# set the number of dimensions we want to retain
n_components = 200

# instantiate and fit on X_train
pca_faces = PCA(n_components=n_components,
                svd_solver='randomized',
                whiten=True).fit(X_train_faces)

# extract and reshape components into eigenfaces for plotting
eigenfaces = pca_faces.components_.reshape((n_components, h, w))

# transform the training and test set for classification
X_train_faces_pca = pca_faces.transform(X_train_faces)
X_test_faces_pca = pca_faces.transform(X_test_faces)
```

Compute PCA and Transform

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```
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eigenfaces = pca_faces.components_.reshape((n_components, h, w))

# transform the training and test set for classification
X_train_faces_pca = pca_faces.transform(X_train_faces)
X_test_faces_pca = pca_faces.transform(X_test_faces)
```

In [70]:
```
pca_faces.components_[0].round(2)
```

Out[70]:
```
array([0.01, 0.01, 0.01, ..., 0.  , 0.  , 0.  ], dtype=float32)
```

Compute PCA and Transform

In [69]:
```python
# set the number of dimensions we want to retain
n_components = 200

# instantiate and fit on X_train
pca_faces = PCA(n_components=n_components,
                svd_solver='randomized',
                whiten=True).fit(X_train_faces)

# extract and reshape components into eigenfaces for plotting
eigenfaces = pca_faces.components_.reshape((n_components, h, w))

# transform the training and test set for classification
X_train_faces_pca = pca_faces.transform(X_train_faces)
X_test_faces_pca = pca_faces.transform(X_test_faces)
```

In [70]:
```python
pca_faces.components_[0].round(2)
```

Out[70]:
```
array([0.01, 0.01, 0.01, ..., 0.  , 0.  , 0.  ], dtype=float32)
```

In [71]:
```python
pca_faces.singular_values_.round(2)
```

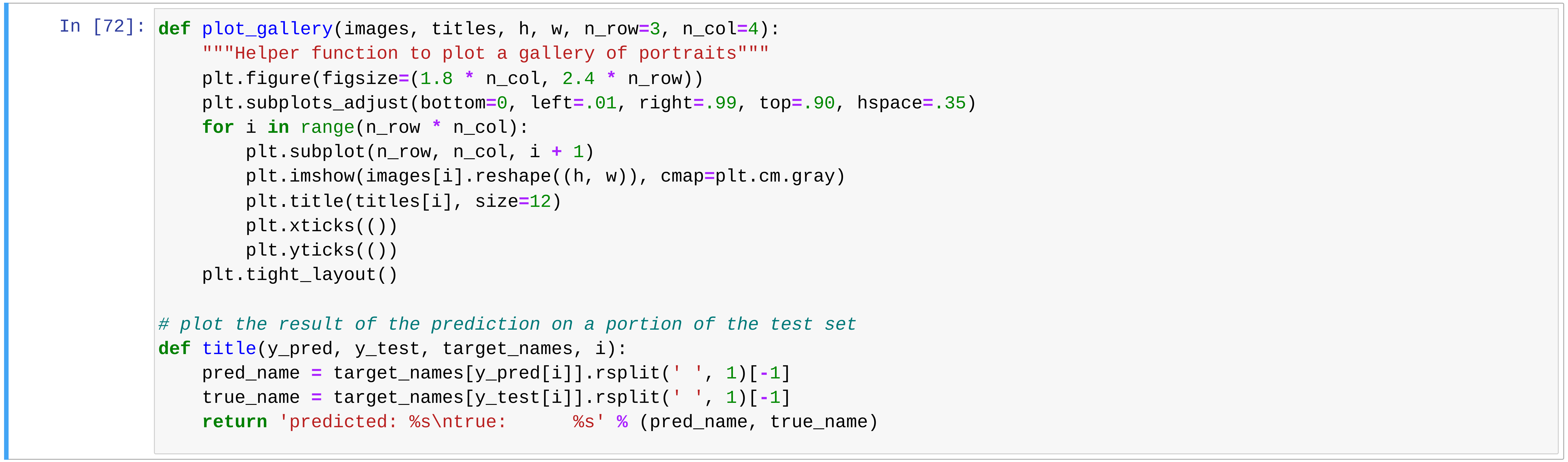
Out[71]:
```
array([255.19, 117.42, 115.07, 102.78,  91.69,  84.31,  79.27,  70.63,
        66.71,  65.5 ,  61.31,  58.95,  56.8 ,  54.46,  52.38,  49.04,
        46.8 ,  45.43,  44.75,  44.01,  42.64,  41.01,  40.44,  38.07,
        37.74,  35.97,  35.33,  34.61,  33.79,  32.88,  32.09,  31.6 ,
        31.08,  30.14,  29.7 ,  29.02,  28.72,  28.21,  27.53,  27.3 ,
        26.96,  26.69,  26.44,  25.95,  25.12,  24.88,  24.59,  24.34,
        23.93,  23.57,  23.37,  22.91,  22.77,  22.53,  22.44,  22.16,
        21.83,  21.69,  21.26,  21.01,  20.87,  20.6 ,  20.48,  20.2 ,
        19.92,  19.8 ,  19.59,  19.23,  19.12,  18.93,  18.78,  18.67,
        18.51,  18.24,  18.16,  18.05,  17.9 ,  17.74,  17.57,  17.47,
        17.33,  17.03,  16.83,  16.61,  16.52,  16.32,  16.26,  16.15,
        16.05,  15.84,  15.68,  15.67,  15.52,  15.45,  15.28,  15.13,
```

Eigenfaces

- What if we plot the top 12 components (eigenfaces) using .reshape(h,w)?

Eigenfaces

- What if we plot the top 12 components (eigenfaces) using .reshape(h,w)?



```
In [72]: def plot_gallery(images, titles, h, w, n_row=3, n_col=4):
             """Helper function to plot a gallery of portraits"""
             plt.figure(figsize=(1.8 * n_col, 2.4 * n_row))
             plt.subplots_adjust(bottom=0, left=.01, right=.99, top=.90, hspace=.35)
             for i in range(n_row * n_col):
                 plt.subplot(n_row, n_col, i + 1)
                 plt.imshow(images[i].reshape((h, w)), cmap=plt.cm.gray)
                 plt.title(titles[i], size=12)
                 plt.xticks(())
                 plt.yticks(())
             plt.tight_layout()

         # plot the result of the prediction on a portion of the test set
         def title(y_pred, y_test, target_names, i):
             pred_name = target_names[y_pred[i]].rsplit(' ', 1)[-1]
             true_name = target_names[y_test[i]].rsplit(' ', 1)[-1]
             return 'predicted: %s\ntrue:      %s' % (pred_name, true_name)
```

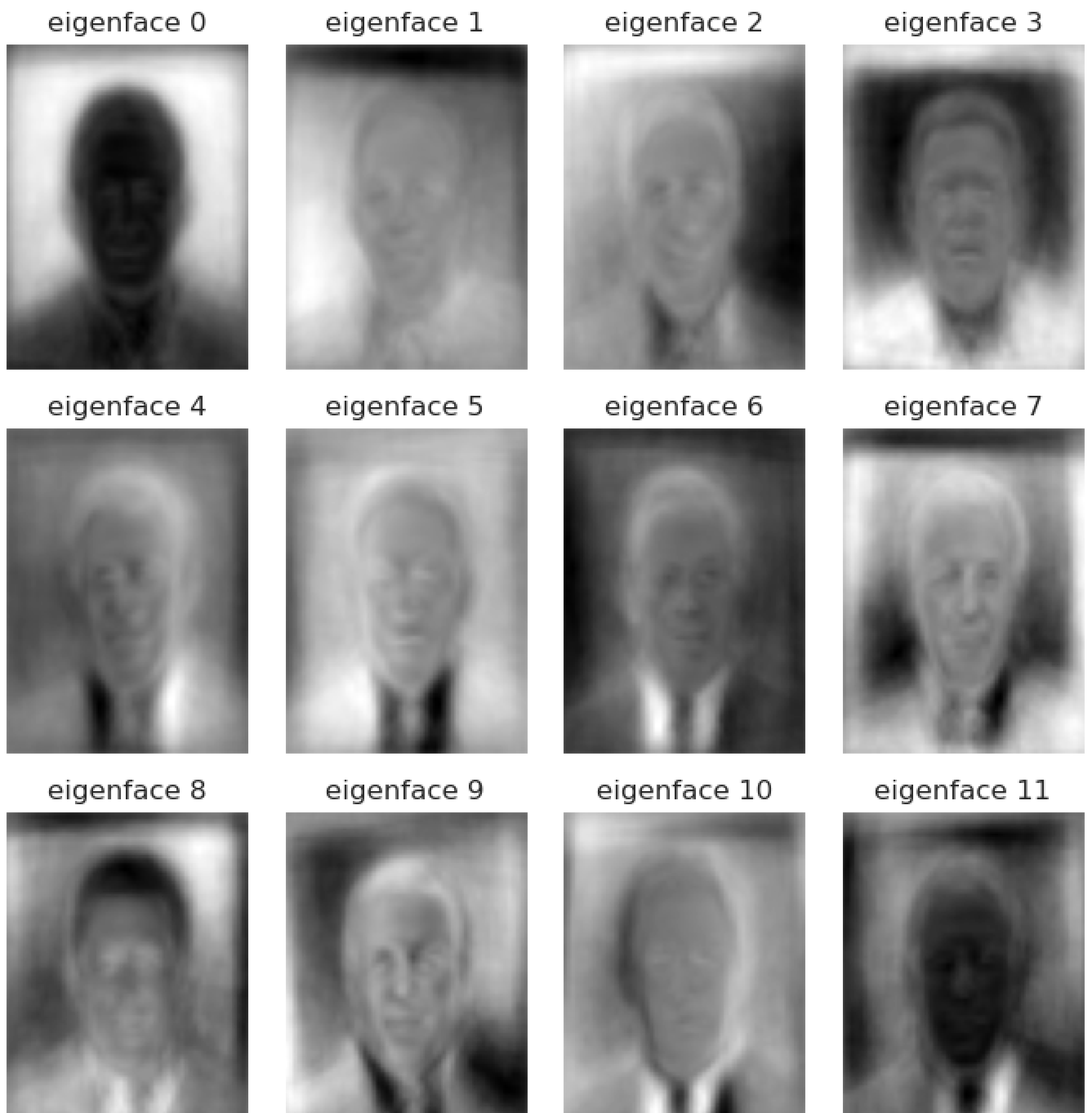
Eigenfaces

- What if we plot the top 12 components (eigenfaces) using .reshape(h,w)?

Eigenfaces

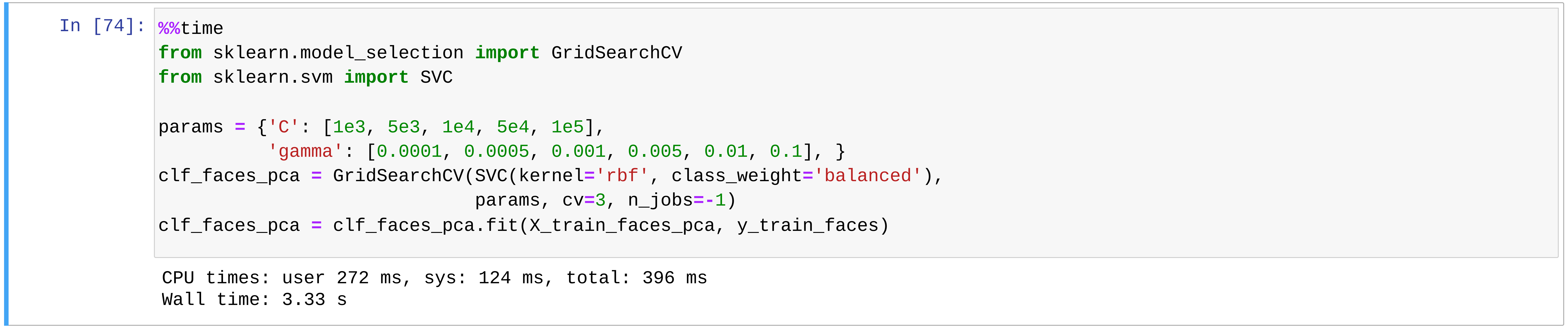
- What if we plot the top 12 components (eigenfaces) using .reshape(h,w)?

```
In [73]: eigenface_titles = ["eigenface %d" % i for i in range(eigenfaces.shape[0])]
         plot_gallery(eigenfaces, eigenface_titles, h, w)
```



Train and Tune SVC

Train and Tune SVC



In [74]:

```
%%time
from sklearn.model_selection import GridSearchCV
from sklearn.svm import SVC

params = {'C': [1e3, 5e3, 1e4, 5e4, 1e5],
          'gamma': [0.0001, 0.0005, 0.001, 0.005, 0.01, 0.1], }
clf_faces_pca = GridSearchCV(SVC(kernel='rbf', class_weight='balanced'),
                             params, cv=3, n_jobs=-1)
clf_faces_pca = clf_faces_pca.fit(X_train_faces_pca, y_train_faces)
```

```
CPU times: user 272 ms, sys: 124 ms, total: 396 ms
Wall time: 3.33 s
```

Train and Tune SVC

In [74]:
```
%%time
from sklearn.model_selection import GridSearchCV
from sklearn.svm import SVC

params = {'C': [1e3, 5e3, 1e4, 5e4, 1e5],
          'gamma': [0.0001, 0.0005, 0.001, 0.005, 0.01, 0.1], }
clf_faces_pca = GridSearchCV(SVC(kernel='rbf', class_weight='balanced'),
                             params, cv=3, n_jobs=-1)
clf_faces_pca = clf_faces_pca.fit(X_train_faces_pca, y_train_faces)
```

```
CPU times: user 272 ms, sys: 124 ms, total: 396 ms
Wall time: 3.33 s
```

In [75]:
```
print(f"best_params : {clf_faces_pca.best_params_}")
print(f"best_score  : {clf_faces_pca.best_score_:0.2f}")
```

```
best_params : {'C': 1000.0, 'gamma': 0.001}
best_score  : 0.72
```

Evaluate on the test set

Evaluate on the test set

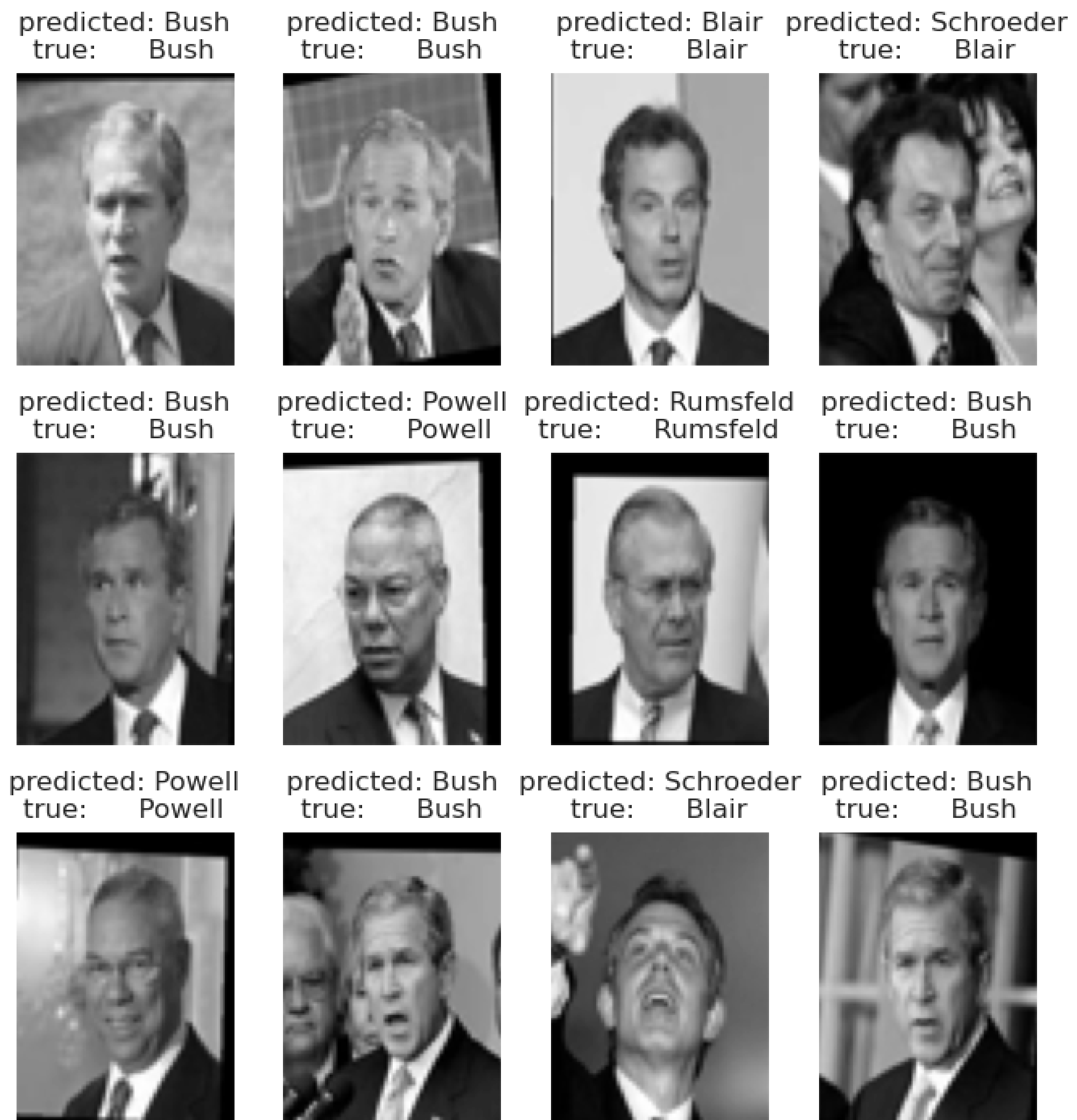
In [76]:
```
from sklearn.metrics import classification_report

y_pred_pca = clf_faces_pca.predict(X_test_faces_pca)
print(classification_report(y_test_faces, y_pred_pca, target_names=target_names))
```

```
                   precision    recall  f1-score   support

     Ariel Sharon       0.65      0.58      0.61        19
     Colin Powell       0.74      0.73      0.74        59
  Donald Rumsfeld       0.76      0.63      0.69        30
    George W Bush       0.80      0.91      0.85       133
Gerhard Schroeder       0.77      0.63      0.69        27
      Hugo Chavez       0.64      0.50      0.56        18
       Tony Blair       0.77      0.75      0.76        36

         accuracy                           0.77       322
        macro avg       0.73      0.68      0.70       322
     weighted avg       0.76      0.77      0.76       322
```

Prediction Examples

Prediction Examples

```
In [77]: prediction_titles = [title(y_pred_pca, y_test_faces, target_names, i)
                              for i in range(y_pred_pca.shape[0])]

         plot_gallery(X_test_faces[10:], prediction_titles[10:], h, w)
         plt.tight_layout()
```



Performance without PCA: Train

Performance without PCA: Train

```
%%time

# Warning: this cell takes up to 3 minutes to execute on an Intel i7 1.8Ghz w/ 8 cores

params = {'C': [1e3, 5e3, 1e4, 5e4, 1e5],
          'gamma': [0.0001, 0.0005, 0.001, 0.005, 0.01, 0.1],}
clf_faces_nopca = GridSearchCV(SVC(kernel='rbf', class_weight='balanced'),
                                   params, cv=3, n_jobs=-1)
clf_faces_nopca = clf_faces_nopca.fit(X_train_faces, y_train_faces)

#CPU times: user 2.08 s, sys: 53.3 ms, total: 2.13 s
#Wall time: 2min 42s

print(f"best_params : {clf_faces_nopca.best_params_}")
print(f"best_score  : {clf_faces_nopca.best_score_:0.2f}")

#best_params : {'C': 1000.0, 'gamma': 0.0001}
#best_score  : 0.78
```

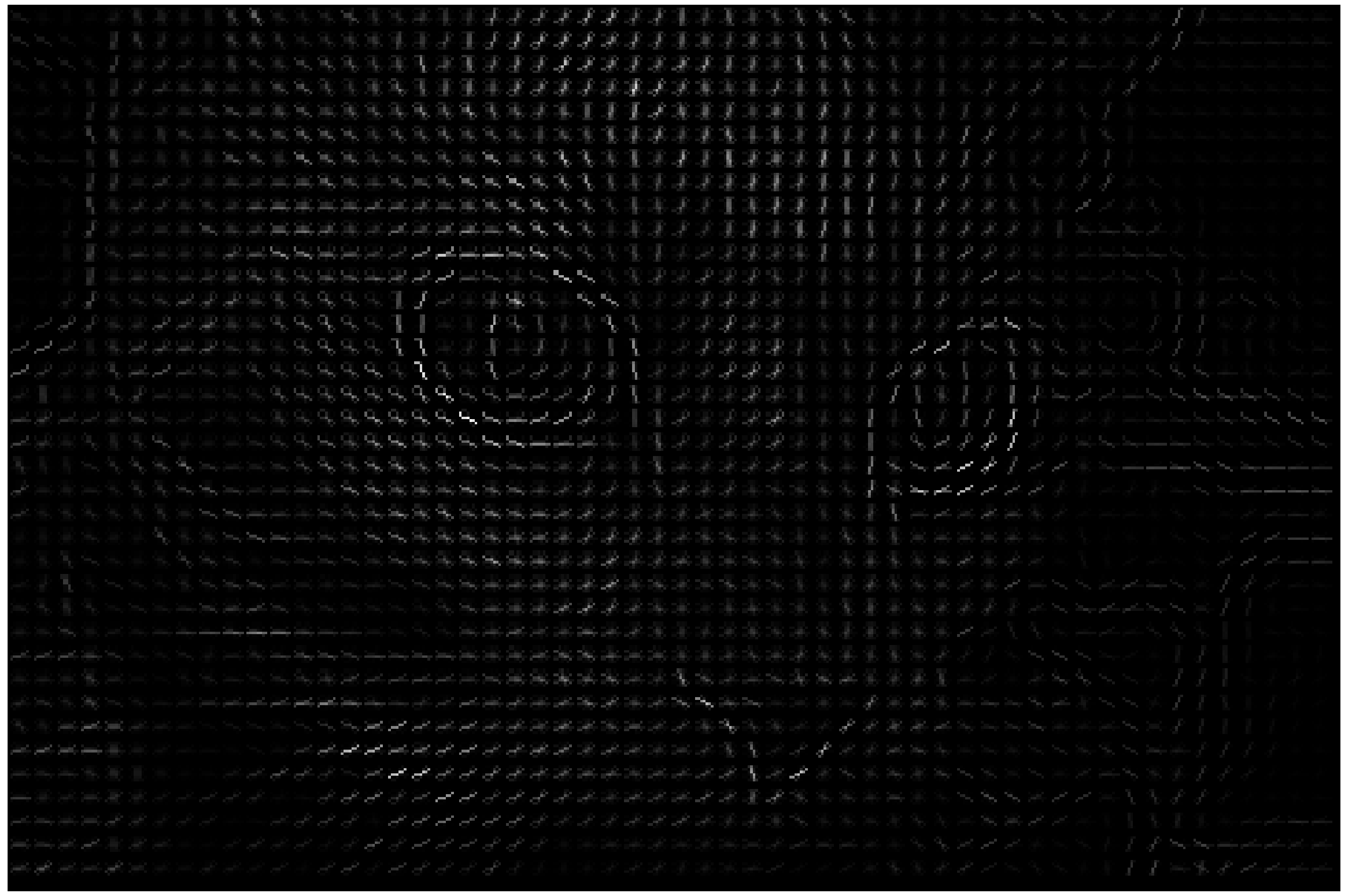
Performance without PCA: Evaluate

Performance without PCA: Evaluate

```
y_pred_nopca = clf_faces_nopca.predict(X_test_faces)
print(classification_report(y_test_faces, y_pred_nopca, target_names=target_names))

#                    precision    recall  f1-score   support

#      Ariel Sharon       0.65      0.79      0.71        19
#      Colin Powell       0.82      0.69      0.75        59
#   Donald Rumsfeld       0.60      0.60      0.60        30
#     George W Bush       0.82      0.90      0.86       133
# Gerhard Schroeder       0.56      0.56      0.56        27
#       Hugo Chavez       0.71      0.28      0.40        18
#        Tony Blair       0.71      0.75      0.73        36

#          accuracy                           0.75       322
#         macro avg       0.70      0.65      0.66       322
#      weighted avg       0.75      0.75      0.74       322
```

Other Image Recognition Methods

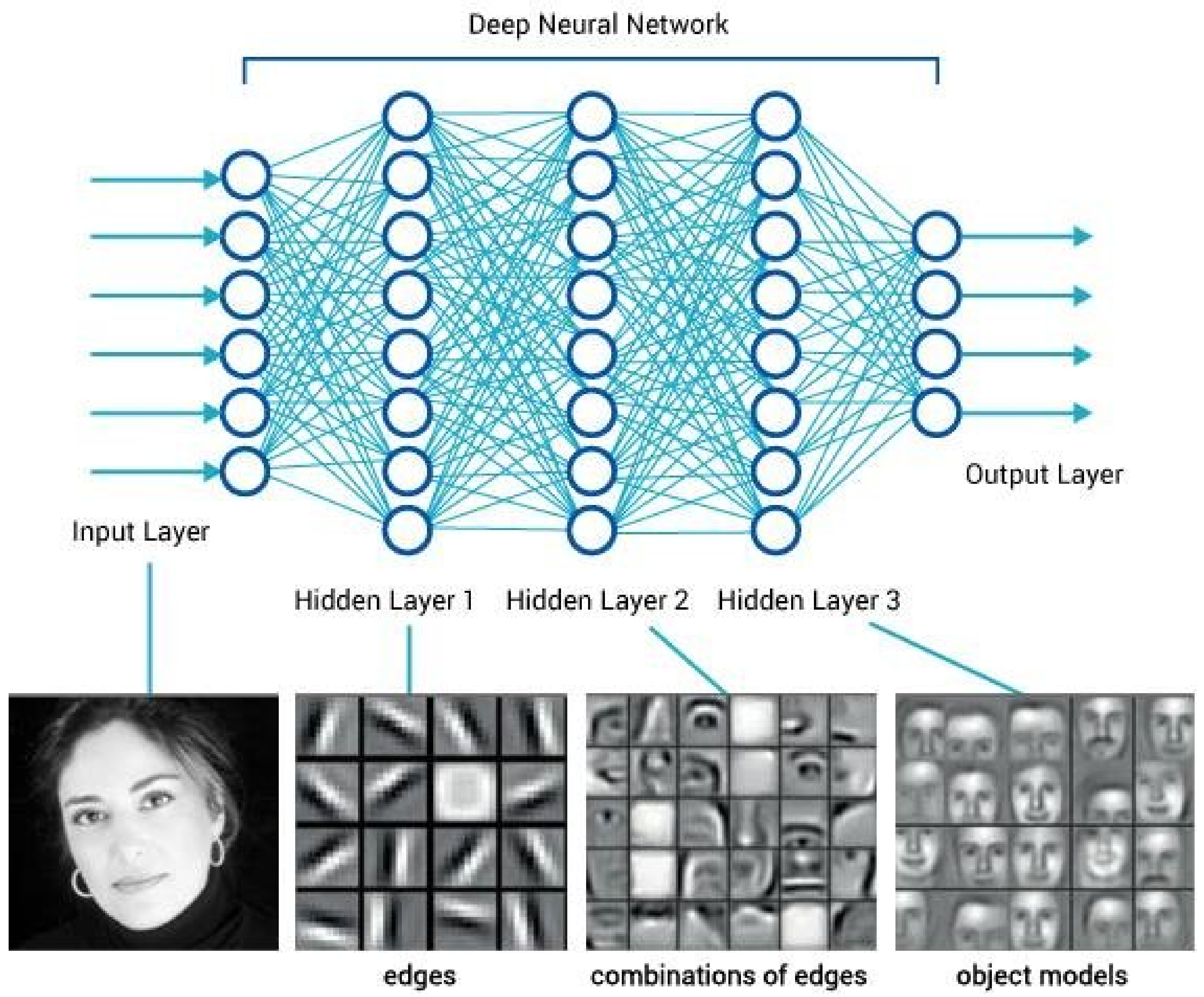
- With Feature Engineering and general models
    - ex: Histogram of Oriented Gradients or HOG (See PDSH Chap 5)
    - many more (See scikit-image)



From PDSH

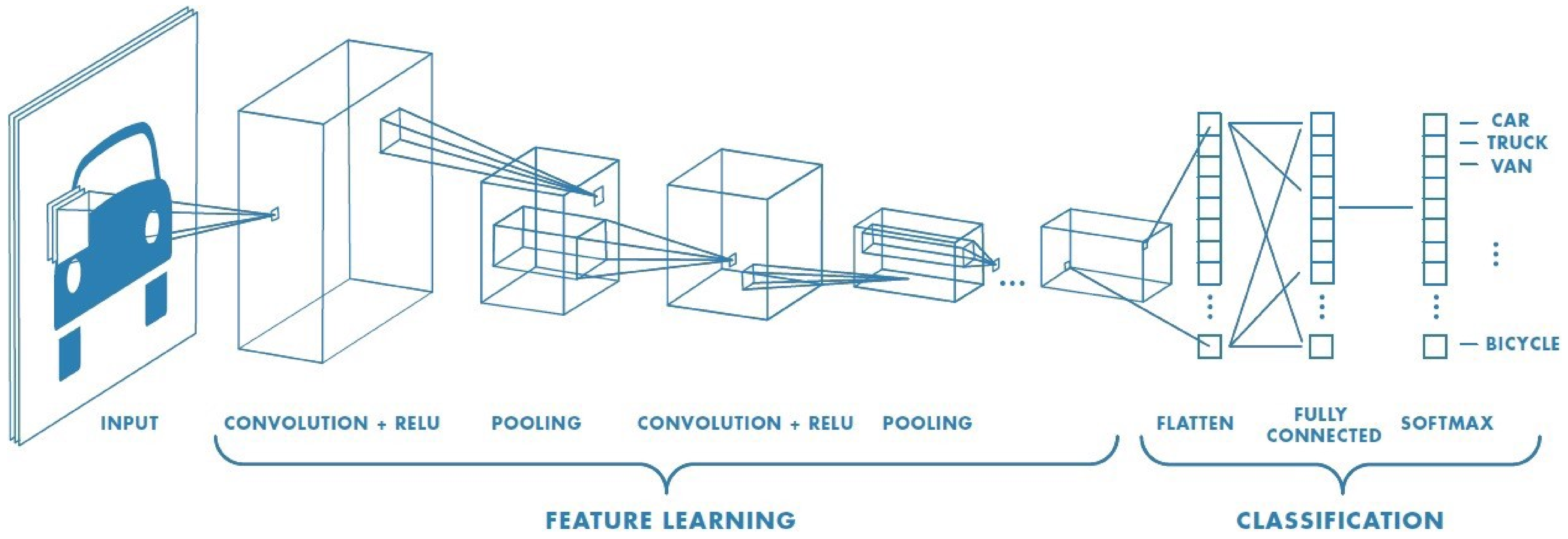
Other Image Recognition Methods: Deep Neural Networks

- With Deep Neural Nets



Other Image Recognition Methods: Deep Neural Networks

- With Convolutional Neural Networks Good Example



From https://towardsdatascience.com/a-comprehensive-guide-to-convolutional-neural-networks-the-eli5-way-3bd2b1164a53

Questions re Feature Extraction and PCA?

Next time: NLP and Pipelines