

Elements Of Data Science - F2025

**Week 9: Dimensionality Reduction, Feature Selection and
Feature Extraction**

11/18/2025

TODOs

- Readings:
 - PML Chapter 6.1, Streamlining workflows with Pipelines
 - PML Chapter 8: Applying Machine Learning to Sentiment Analysis
- HW 3, Due **Tue Nov 25th, 11:59pm ET**
- Quiz W9, Due **Tue Nov 25th, 11:59pm ET**

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]: 1 import numpy
        2 import numpy as np
        3 import pandas as pd
        4 import matplotlib.pyplot as plt
        5 import seaborn as sns
        6
        7 from mlxtend.plotting import plot_decision_regions
        8
        9 sns.set_style('darkgrid')
       10 %matplotlib inline
```

Joining Datasets

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

Joining Datasets

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[illegible]

Joining Datasets

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

```
In [3]: 1 df_flower_name_orig = pd.DataFrame([[1001, 'iris'], [1002, 'rose']],
      2                                     columns=['flower_id', 'name'])
      3
      4 df_flower_price_orig = pd.DataFrame([[1002, 3.99], [1003, 2.25]],
      5                                   columns=['flower_id', 'price'])
```

```
In [4]: 1 display(df_flower_name_orig)
      2 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

Joining 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]: 1 df_flower_name_orig
```

```
Out[5]:
```

	flower_id	name
0	1001	iris
1	1002	rose

Joining 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]: 1 df_flower_name_orig
```

Out[5]:

	flower_id	name
0	1001	iris
1	1002	rose

```
In [6]: 1 df_flower_name = df_flower_name_orig.set_index('flower_id') # note: inplace=False, drop=True by default
        2 df_flower_name
```

Out[6]:

	name
flower_id	
1001	iris
1002	rose

Joining 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]: 1 df_flower_name_orig
```

Out[5]:

	flower_id	name
0	1001	iris
1	1002	rose

```
In [6]: 1 df_flower_name = df_flower_name_orig.set_index('flower_id') # note: inplace=False, drop=True by default
2 df_flower_name
```

Out[6]:

	name
flower_id	
1001	iris
1002	rose

```
In [7]: 1 df_flower_price = df_flower_price_orig.set_index('flower_id')
2 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]: 1 display(df_flower_name)
        2 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]: 1 display(df_flower_name)
        2 display(df_flower_price)
```

name	
flower_id	
1001	iris
1002	rose

price	
flower_id	
1002	3.99
1003	2.25

```
In [80]: 1 df_flower_name.join(df_flower_price)
        2 # df_flower_price.join(df_flower_name)
```

Out[80]:

name price		
flower_id		
1001	iris	NaN
1002	rose	3.99

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

```
In [8]: 1 display(df_flower_name)
        2 display(df_flower_price)
```

name	
flower_id	
1001	iris
1002	rose

price	
flower_id	
1002	3.99
1003	2.25

```
In [80]: 1 df_flower_name.join(df_flower_price)
        2 # df_flower_price.join(df_flower_name)
```

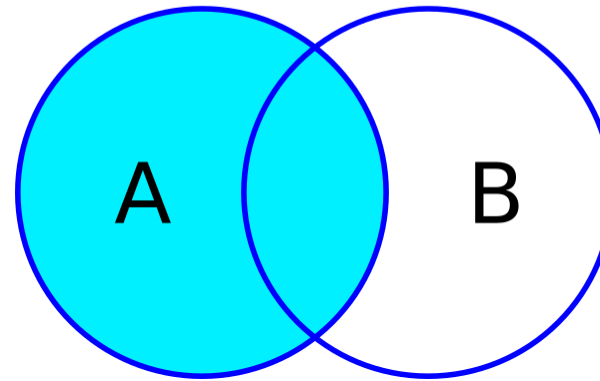
Out[80]:

name price		
flower_id		
1001	iris	NaN
1002	rose	3.99

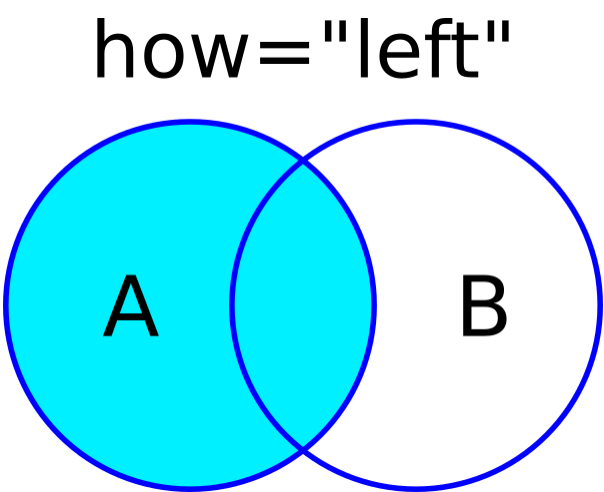
- by default, this is a 'Left Join'

Join Types: Left Join

how="left"



Join Types: Left Join

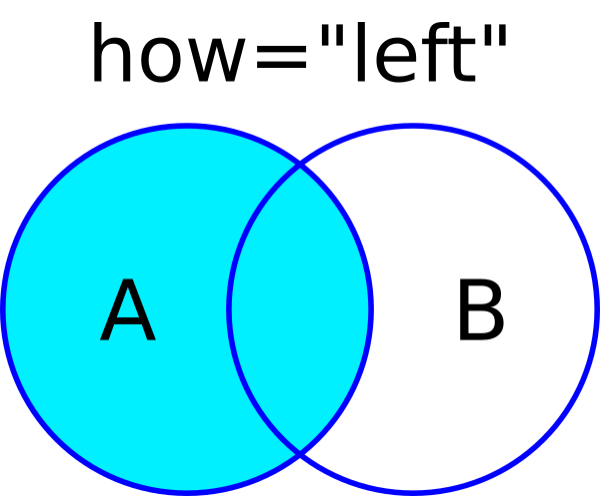


```
In [10]: 1 display(df_flower_name,df_flower_price)
```

name	
flower_id	
1001	iris
1002	rose

price	
flower_id	
1002	3.99
1003	2.25

Join Types: Left Join



```
In [10]: 1 display(df_flower_name,df_flower_price)
```

name	
flower_id	
1001	iris
1002	rose

price	
flower_id	
1002	3.99
1003	2.25

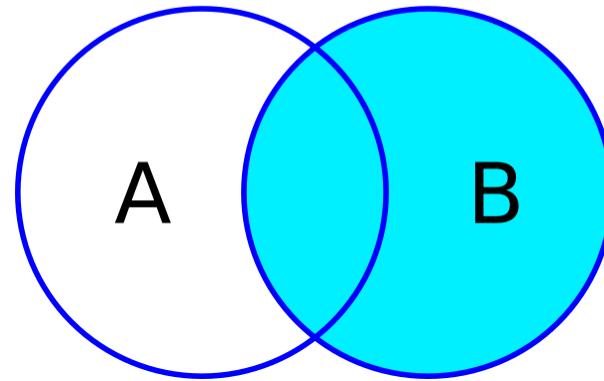
```
In [11]: 1 df_flower_name.join(df_flower_price,how="left") # default for df.join() is left join
```

Out[11]:

name price		
flower_id		
1001	iris	NaN
1002	rose	3.99

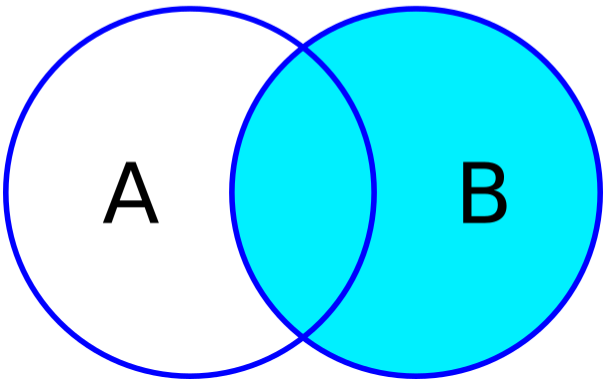
Join Types: Right Join

how="right"



Join Types: Right Join

how="right"

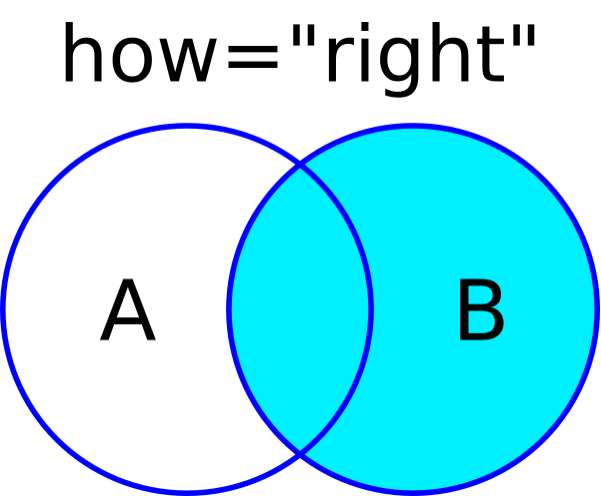


```
In [12]: 1 display(df_flower_name,df_flower_price)
```

name	
flower_id	
1001	iris
1002	rose

price	
flower_id	
1002	3.99
1003	2.25

Join Types: Right Join



```
In [12]: 1 display(df_flower_name,df_flower_price)
```

name	
flower_id	
1001	iris
1002	rose

price	
flower_id	
1002	3.99
1003	2.25

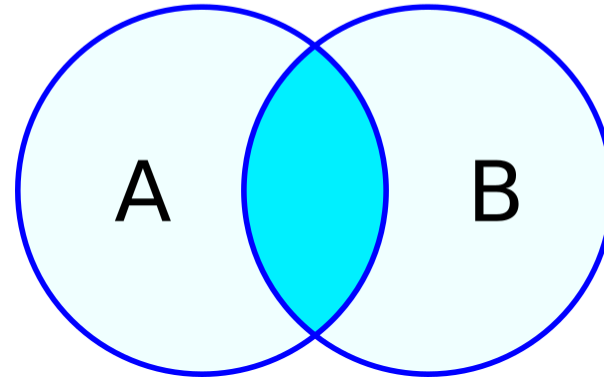
```
In [13]: 1 df_flower_name.join(df_flower_price,how='right')
```

Out[13]:

name price		
flower_id		
1002	rose	3.99
1003	NaN	2.25

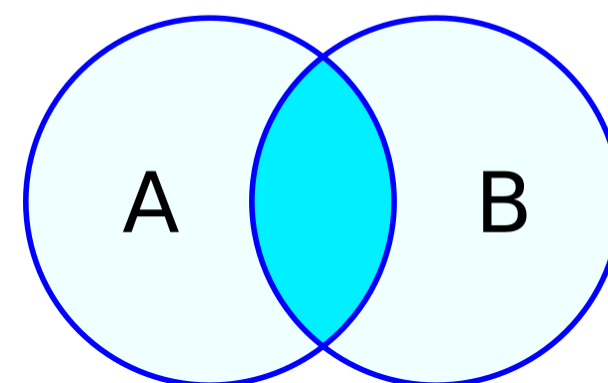
Join Types: Inner Join

how="inner"



Join Types: Inner Join

how="inner"

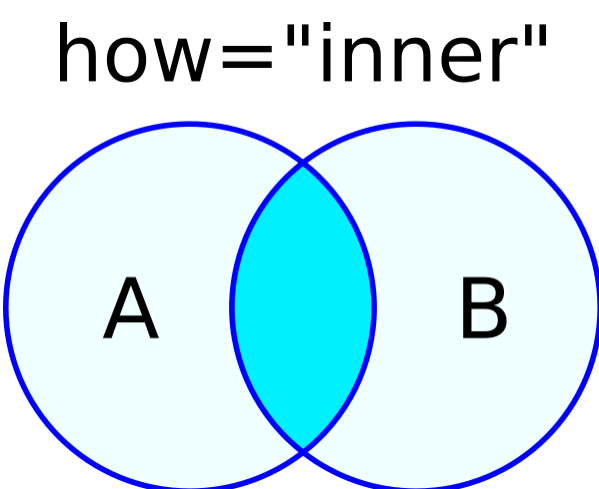


```
In [14]: 1 display(df_flower_name,df_flower_price)
```

name	
flower_id	
1001	iris
1002	rose

price	
flower_id	
1002	3.99
1003	2.25

Join Types: Inner Join



```
In [14]: 1 display(df_flower_name,df_flower_price)
```

name	
flower_id	
1001	iris
1002	rose

price	
flower_id	
1002	3.99
1003	2.25

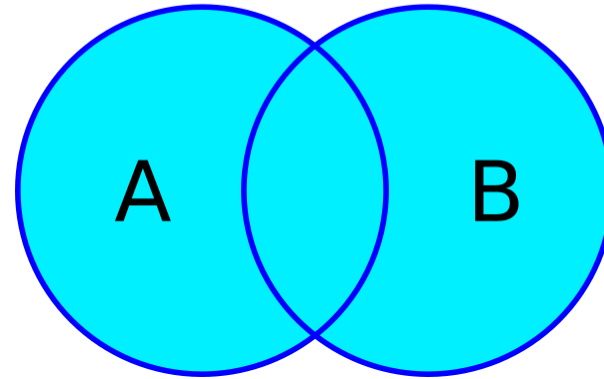
```
In [15]: 1 df_flower_name.join(df_flower_price,how='inner')
```

Out[15]:

name price		
flower_id		
1002	rose	3.99

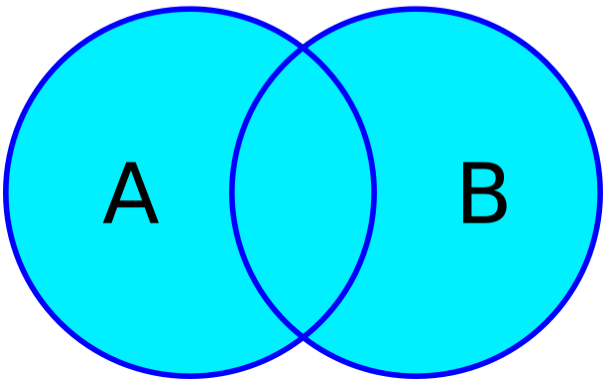
Join Types: Outer Join

how="outer"



Join Types: Outer Join

how="outer"



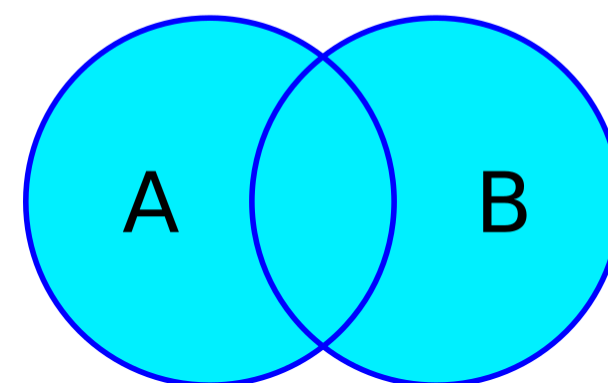
```
In [16]: 1 display(df_flower_name,df_flower_price)
```

name	
flower_id	
1001	iris
1002	rose

price	
flower_id	
1002	3.99
1003	2.25

Join Types: Outer Join

how="outer"



```
In [16]: 1 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]: 1 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]: 1 # this csv has column for purchase_id
          2 pd.read_csv('../data/flowershop_data_with_dups.csv'
          3                   ).head(2)
          4
```

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]: 1 # this csv has column for purchase_id
          2 pd.read_csv('../data/flowershop_data_with_dups.csv')
          3         ).head(2)
          4
```

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]: 1 # can set the index when reading in the csv
          2 pd.read_csv('../data/flowershop_data_with_dups.csv',
          3                 index_col='purchase_id'                # set the index column when reading/loading data
          4                 ).head(2)
          5
```

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]: 1 # imagine that 'name' is a categorical variable  
        2 df_flower_name[['name']]
```

Out[20]:

	name
flower_id	
1001	iris
1002	rose

Joining on the Index using `.join()`

```
In [20]: 1 # imagine that 'name' is a categorical variable
          2 df_flower_name[['name']]
```

Out[20]:

	name
flower_id	
1001	iris
1002	rose

```
In [21]: 1 # converting categorical to one-hot using get_dummies
          2 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]: 1 # imagine that 'name' is a categorical variable
          2 df_flower_name[['name']]
```

Out[20]:

name	
flower_id	
1001	iris
1002	rose

```
In [21]: 1 # converting categorical to one-hot using get_dummies
          2 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]: 1 # can join back using the default index
          2 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]: 1 # using the dataframes before setting index using .set_index()
          2 pd.merge(df_flower_name_orig,df_flower_price_orig,
          3               left_on='flower_id',
          4               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]: 1 # using the dataframes before setting index using .set_index()
          2 pd.merge(df_flower_name_orig,df_flower_price_orig,
          3               left_on='flower_id',
          4               right_on='flower_id') # what is the default join for merge?
```

Out[23]:

	flower_id	name	price
0	1002	rose	3.99

```
In [24]: 1 # if both id columns have the same name, can just use "on="
          2 pd.merge(df_flower_name_orig,
          3               df_flower_price_orig,
          4               on='flower_id',
          5               how='outer')
```

Out[24]:

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

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]: 1 from sklearn.datasets import load_wine
          2 from sklearn.model_selection import train_test_split
          3
          4 wine = load_wine()
          5
          6 X_wine = pd.DataFrame(wine.data, columns=wine.feature_names)
          7 y_wine = wine.target
          8
          9 # reduce to binary classification
         10 X_wine = X_wine.iloc[y_wine < 2]
         11 y_wine = y_wine[y_wine < 2]
         12
         13 X_train, X_test, y_train, y_test = train_test_split(X_wine, y_wine, stratify=y_wine, random_state=0)
         14
         15 wine_feature_names = X_wine.columns.values
         16 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]: 1 from sklearn.datasets import load_wine
2 from sklearn.model_selection import train_test_split
3
4 wine = load_wine()
5
6 X_wine = pd.DataFrame(wine.data, columns=wine.feature_names)
7 y_wine = wine.target
8
9 # reduce to binary classification
10 X_wine = X_wine.iloc[y_wine < 2]
11 y_wine = y_wine[y_wine < 2]
12
13 X_train, X_test, y_train, y_test = train_test_split(X_wine, y_wine, stratify=y_wine, random_state=0)
14
15 wine_feature_names = X_wine.columns.values
16 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]: 1 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	proline
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	495.0
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	465.0
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	1285.0

Need to Standardize Features

Need to Standardize Features

In [27]: `1 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]: 1 from sklearn.preprocessing import StandardScaler
          2
          3 ss = StandardScaler()
          4 X_train_zscore = ss.fit_transform(X_train)
          5 X_train_zscore = pd.DataFrame(X_train_zscore, columns=wine_feature_names)
          6
          7 X_test_zscore = ss.transform(X_test)
```

Standardize Features

```
In [28]: 1 from sklearn.preprocessing import StandardScaler
2
3 ss = StandardScaler()
4 X_train_zscore = ss.fit_transform(X_train)
5 X_train_zscore = pd.DataFrame(X_train_zscore, columns=wine_feature_names)
6
7 X_test_zscore = ss.transform(X_test)
```

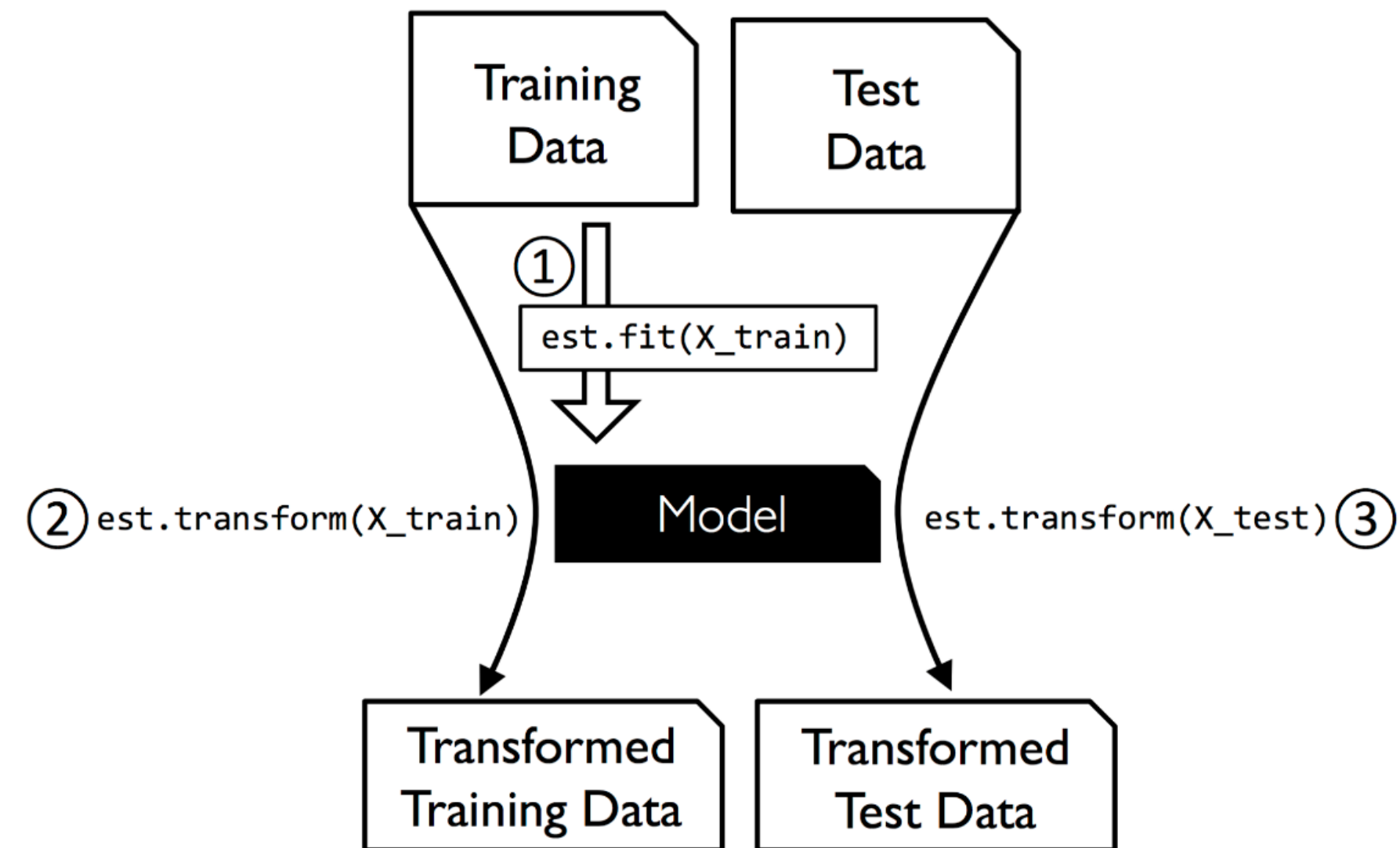
```
In [29]: 1 X_train_zscore.agg(['mean', 'std']).T.round(1)
```

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

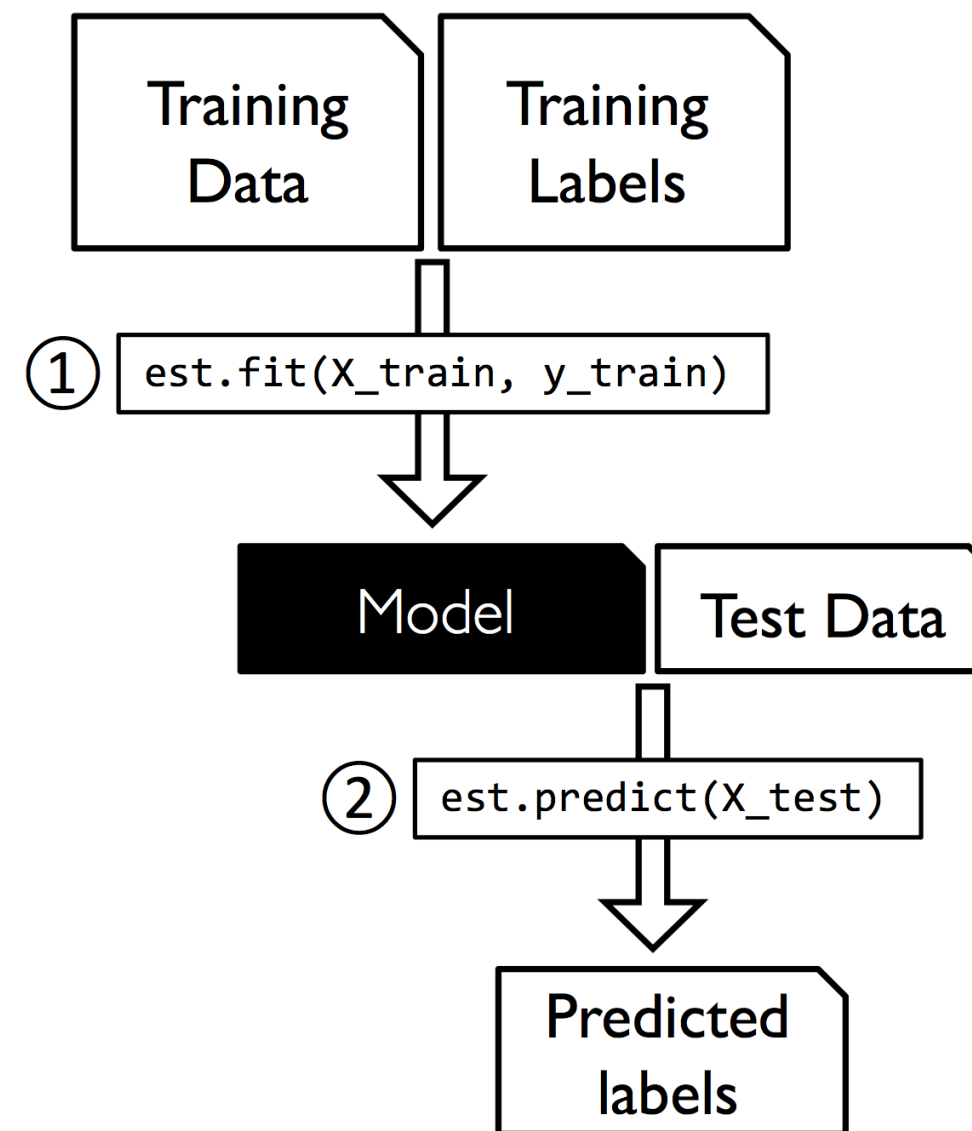
- When transforming data, fit on the training set, transform both train and test



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'

Feature Selection

- Select a subset of features
- Based on how much they contribute to predicting the target 'y'
- 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 11 regularization drives the coefficient of uninformative features to 0

Feature Selection: LASSO (L1)

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

```
In [30]: 1 from sklearn.linear_model import LogisticRegression
2
3 # First, without regularization
4 logr = LogisticRegression(penalty="none", solver="lbfgs", random_state=0)
5 logr.fit(X_train_zscore, y_train)
6 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])
```

```
In [31]: 1 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.

Oracle

Feature Selection: LASSO (L1) Cont.

Oracle

```
In [82]: 1
          2 # Now with LASSO
          3 # C is the inverse regularization strength: higher means less regularization
          4 logr_l1 = LogisticRegression(C= .1, penalty="l1", solver="liblinear", random_state=0)
          5 logr_l1.fit(X_train_zscore, y_train)
          6
          7 pd.Series(logr_l1.coef_[0], index=wine_feature_names).sort_values(ascending=False).round(5)
```

```
Out[82]: 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.

Oracle

```
In [82]: 1
          2 # Now with LASSO
          3 # C is the inverse regularization strength: higher means less regularization
          4 logr_l1 = LogisticRegression(C= .1, penalty="l1", solver="liblinear", random_state=0)
          5 logr_l1.fit(X_train_zscore, y_train)
          6
          7 pd.Series(logr_l1.coef_[0], index=wine_feature_names).sort_values(ascending=False).round(5)
```

```
Out[82]: 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
```

```
In [33]: 1 # which columns were kept?
          2 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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- We can rank the feature based on how much impurity they remove

```
In [34]: 1 from sklearn.ensemble import RandomForestClassifier
          2
          3 rf = RandomForestClassifier(random_state=0).fit(X_train_zscore,y_train)
          4 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])

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]: 1 from sklearn.ensemble import RandomForestClassifier
          2
          3 rf = RandomForestClassifier(random_state=0).fit(X_train_zscore,y_train)
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```

```
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])
```

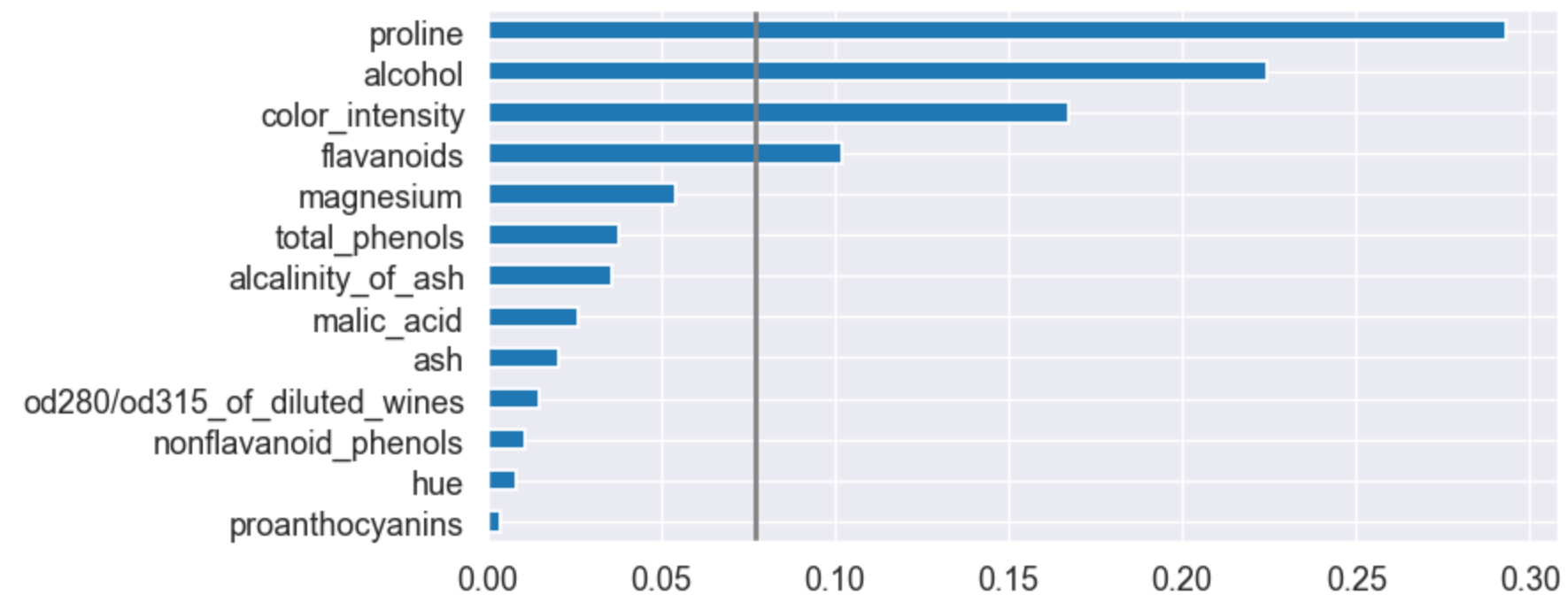
```
In [35]: 1 rf_feature_importances = pd.Series(rf.feature_importances_,index=wine_feature_names)
          2 rf_feature_importances.sort_values(ascending=False).round(3)
```

```
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

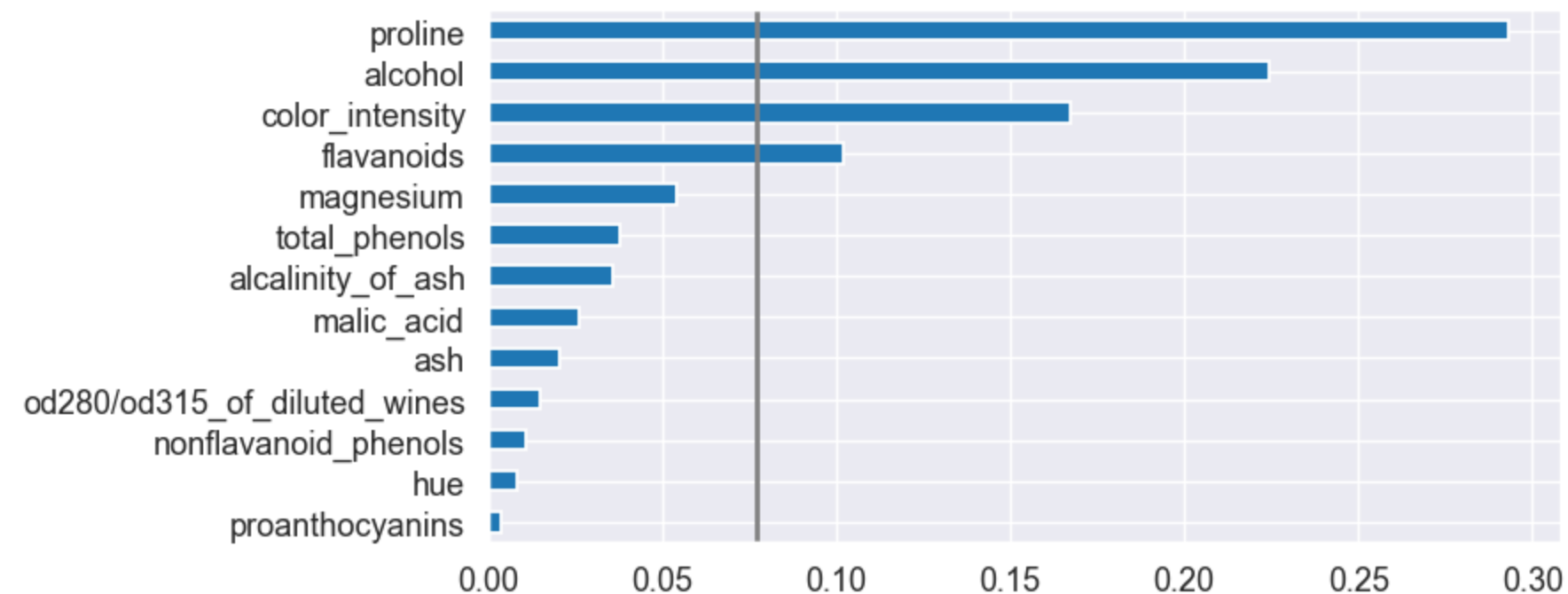
Feature Selection: Tree Based Model Feature Importance

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



Feature Selection: Tree Based Model Feature Importance

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



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

Feature Selection: SelectFromModel

Feature Selection: SelectFromModel

```
In [37]: 1 from sklearn.feature_selection import SelectFromModel
2
3 sfm_lr = SelectFromModel(logr_l1,
4                           threshold=None, # if model uses l1 regularization: abs val > 1e-5, otherwise mean
5                           prefit=True,   # don't need to refit, but may give warnings about missing feature names
6                           )
7
8 sfm_lr.get_support() # boolean mask of features selected
```

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

Feature Selection: SelectFromModel

```
In [37]: 1 from sklearn.feature_selection import SelectFromModel
2
3 sfm_lr = SelectFromModel(logr_l1,
4                           threshold=None, # if model uses l1 regularization: abs val > 1e-5, otherwise mean
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6                           )
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8 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])
```

```
In [38]: 1 wine_feature_names[sfm_lr.get_support()]
```

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

Feature Selection: SelectFromModel

```
In [37]: 1 from sklearn.feature_selection import SelectFromModel
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3 sfm_lr = SelectFromModel(logr_l1,
4                           threshold=None, # if model uses l1 regularization: abs val > 1e-5, otherwise mean
5                           prefit=True,    # don't need to refit, but may give warnings about missing feature names
6                           )
7
8 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])
```

```
In [38]: 1 wine_feature_names[sfm_lr.get_support()]
```

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

```
In [39]: 1 X_train_subset = sfm_lr.transform(X_train_zscore)
2 X_train_subset.shape
```

```
/Users/andi/miniconda3/envs/sigma2/lib/python3.8/site-packages/sklearn/base.py:443: UserWarning: X has feature names, but SelectFromModel was fitted without feature names
  warnings.warn(
```

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

Feature Selection: SelectFromModel

```
In [37]: 1 from sklearn.feature_selection import SelectFromModel
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3 sfm_lr = SelectFromModel(logr_ll,
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```

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

```
In [38]: 1 wine_feature_names[sfm_lr.get_support()]
```

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

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In [39]: 1 X_train_subset = sfm_lr.transform(X_train_zscore)
2 X_train_subset.shape
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/Users/andi/miniconda3/envs/sigma2/lib/python3.8/site-packages/sklearn/base.py:443: UserWarning: X has feature names, but SelectFromModel was fitted without feature names
  warnings.warn(
```

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

```
In [40]: 1 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]: 1 sfm_rf = SelectFromModel(RandomForestClassifier(),  
2                                     threshold='mean',    # return all features with value greater than the mean (default)  
3                                     prefit=False         # will refit (default)  
4                                     ).fit(X_train_zscore,y_train)  
5  
6 wine_feature_names[sfm_rf.get_support()]
```

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

Feature Selection: SelectFromModel Cont.

```
In [41]: 1 sfm_rf = SelectFromModel(RandomForestClassifier(),  
2                                     threshold='mean',    # return all features with value greater than the mean (default)  
3                                     prefit=False        # will refit (default)  
4                                     ).fit(X_train_zscore,y_train)  
5  
6 wine_feature_names[sfm_rf.get_support()]
```

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

```
In [42]: 1 sfm_rf.estimator_.feature_importances_.mean().round(3)
```

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

Feature Selection: SelectFromModel Cont.

```
In [41]: 1 sfm_rf = SelectFromModel(RandomForestClassifier(),
2                                   threshold='mean',    # return all features with value greater than the mean (default)
3                                   prefit=False        # will refit (default)
4                                   ).fit(X_train_zscore,y_train)
5
6 wine_feature_names[sfm_rf.get_support()]
```

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

```
In [42]: 1 sfm_rf.estimator_.feature_importances_.mean().round(3)
```

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

```
In [43]: 1 sfm_rf_feature_importances = pd.Series(sfm_rf.estimator_.feature_importances_,index=wine_feature_names)
2 sfm_rf_feature_importances.sort_values(ascending=False).round(3)
```

```
Out[43]: proline                0.308
          color_intensity        0.177
          alcohol                0.150
          flavanoids             0.117
          magnesium              0.080
          alcalinity_of_ash       0.031
          total_phenols           0.028
          malic_acid              0.027
          od280/od315_of_diluted_wines 0.023
          hue                    0.021
          ash                    0.018
          nonflavanoid_phenols    0.015
          proanthocyanins         0.006
          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

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

```
In [83]: 1 from sklearn.feature_selection import SelectKBest, f_classif
          2
          3 # select 3 best features
          4 kbest = SelectKBest(score_func=f_classif, # default,
          5                               k=2        # how many features to keep
          6                               ).fit(X_train, y_train)
          7 wine_feature_names[kbest.get_support()]
```

```
Out[83]: array(['alcohol', '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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- Likely prohibitively expensive/time-consuming
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- Requires a model that assigns weights or importance to features

```
In [45]: 1 from sklearn.feature_selection import RFE
          2
          3 rfe = RFE(LogisticRegression(penalty='none',max_iter=1000), # turn off regularization
          4               n_features_to_select=3,                       # number of feature to retain
          5               step=1,                                         # number of features to eliminate each round
          6               ).fit(X_train_zscore,y_train)
          7
          8 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`
- **Exhaustive 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
- Additional features explain more variance

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$$R_{adj}^2 = 1 - (1 - R^2) \frac{n - 1}{n - m - 1}$$

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

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$$R^2_{adj} = 1 - (1 - R^2) \frac{n - 1}{n - m - 1}$$

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

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

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

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

```
In [47]: 1 from sklearn.linear_model import LinearRegression
2
3 X_r = X_train_zscore.loc[:, wine_feature_names != 'alcohol'] # get all features except alcohol
4 y_r = X_train_zscore.loc[:, 'alcohol'] # predict alcohol from other features
5
6 lr = LinearRegression()
7 print('R2 with 3 features :', lr.fit(X_r.iloc[:, :3], y_r).score(X_r.iloc[:, :3], y_r).round(2))
8 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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Is this due to a better model or just adding features?

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```

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

Is this due to a better model or just adding features?

```
In [48]: 1 print('Adj R2 with 3 features :', adj_r2(lr.fit(X_r.iloc[:, :3], y_r), X_r.iloc[:, :3], y_r).round(2))
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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In [47]: 1 from sklearn.linear_model import LinearRegression
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```

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

Is this due to a better model or just adding features?

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In [48]: 1 print('Adj R2 with 3 features :', adj_r2(lr.fit(X_r.iloc[:, :3], y_r), X_r.iloc[:, :3], y_r).round(2))
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
```

- 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.

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

```
In [49]: 1 from statsmodels.api import OLS
          2
          3 model = OLS(y_r,X_r).fit()
          4 print(model.rsquared_adj.round(3))
          5 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:	Tue, 18 Nov 2025	Prob (F-statistic):	1.06e-15
Time:	17:54:26	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

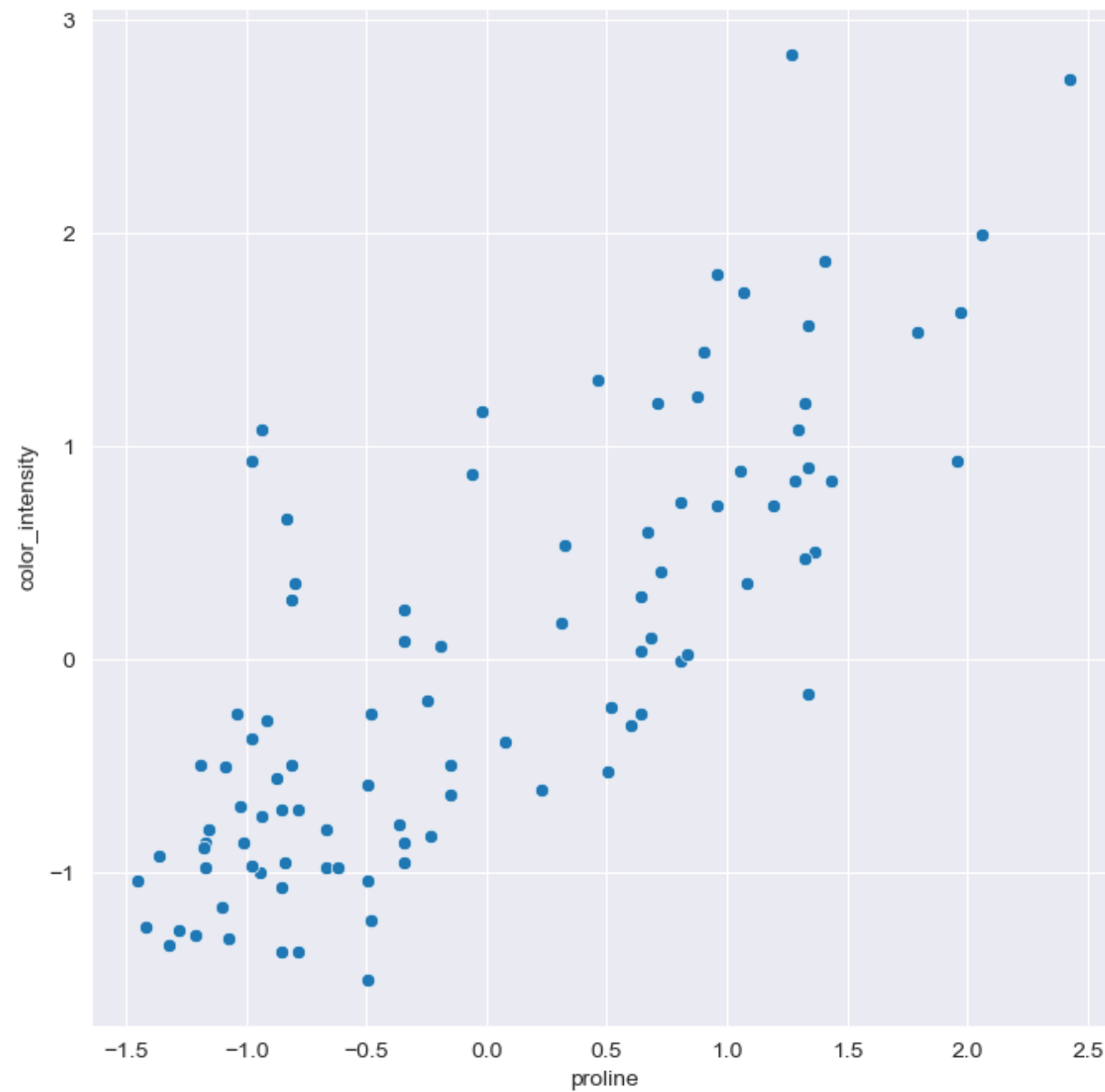
Principal Component Analysis (PCA)

- 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

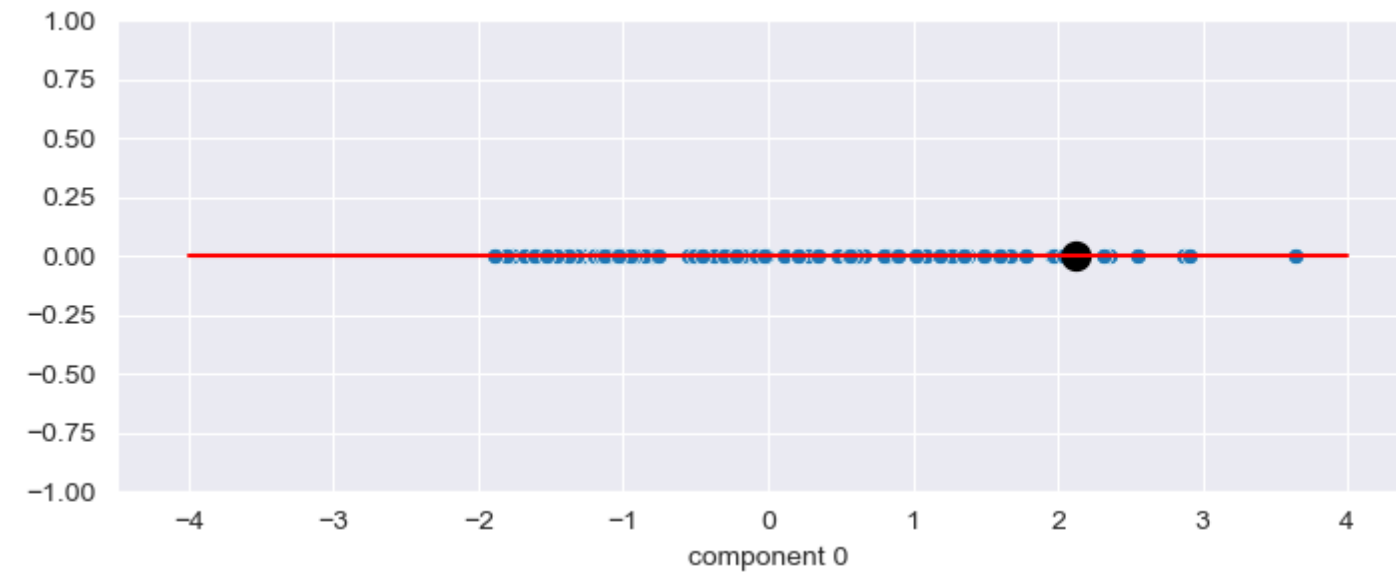
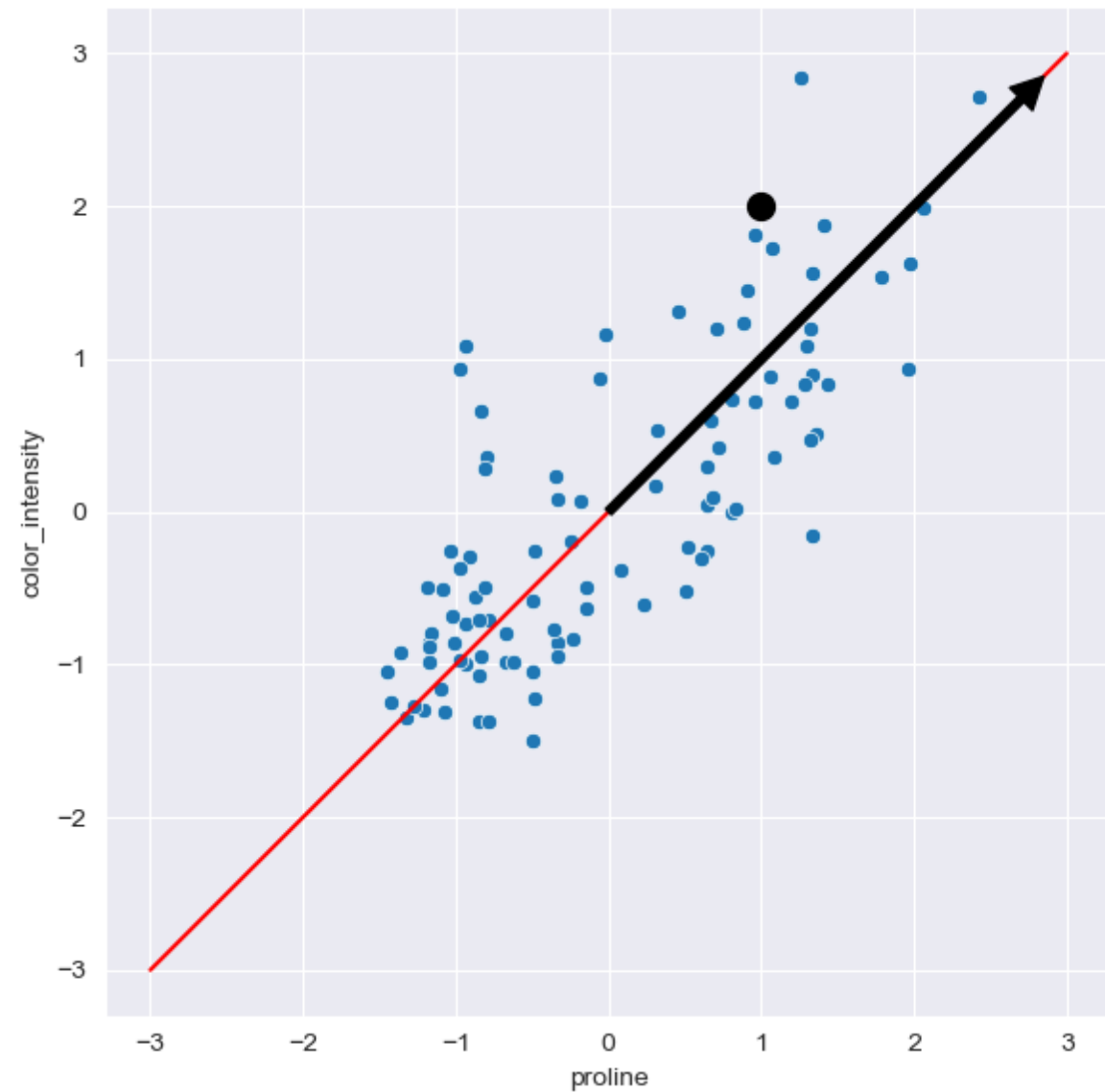
```
In [51]: 1 fig,ax = plt.subplots(1,1,figsize=(8,8))  
2 sns.scatterplot(x='proline',y='color_intensity',data=X_train_zscore,ax=ax);
```



PCA Example Cont.

PCA Example Cont.

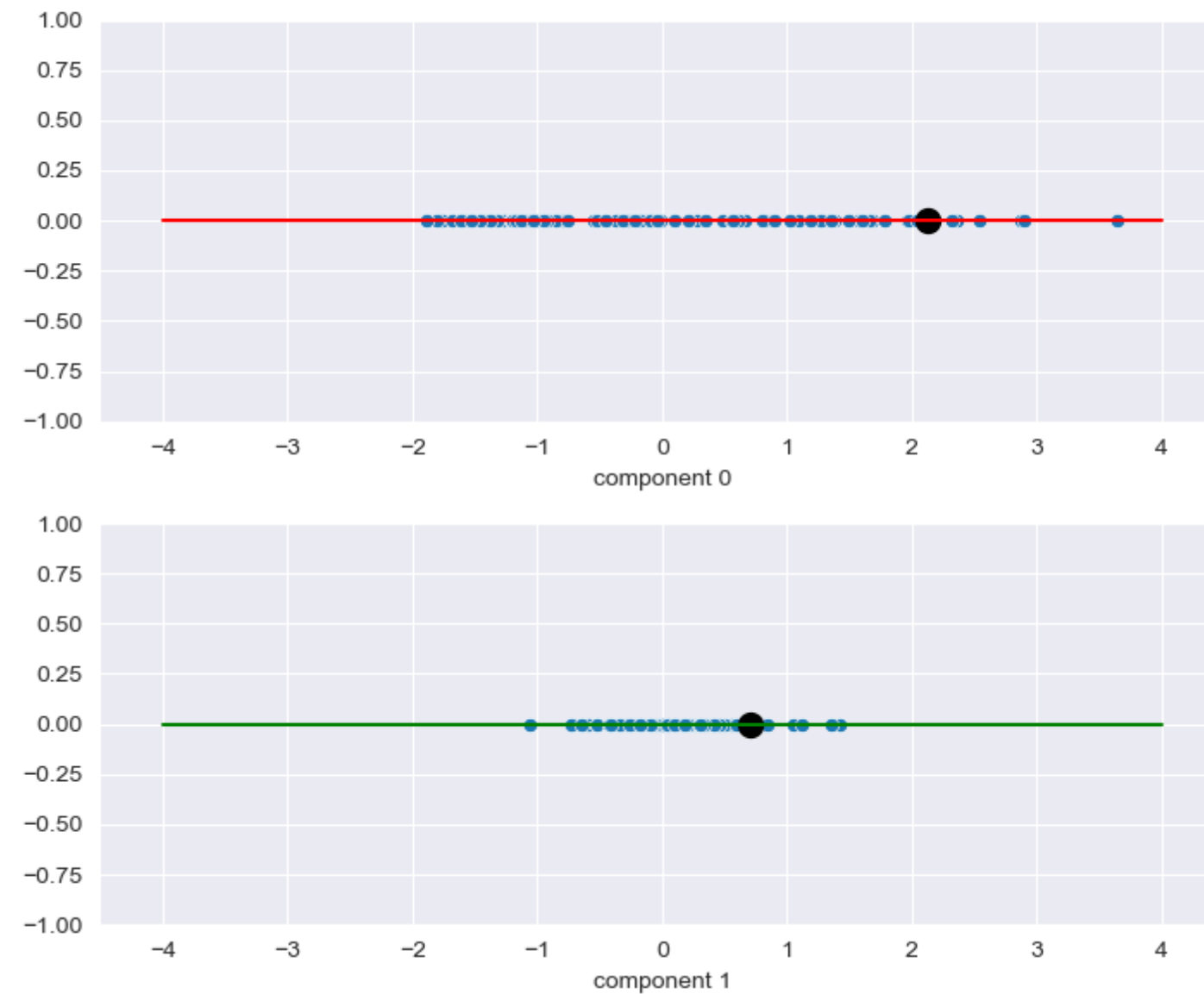
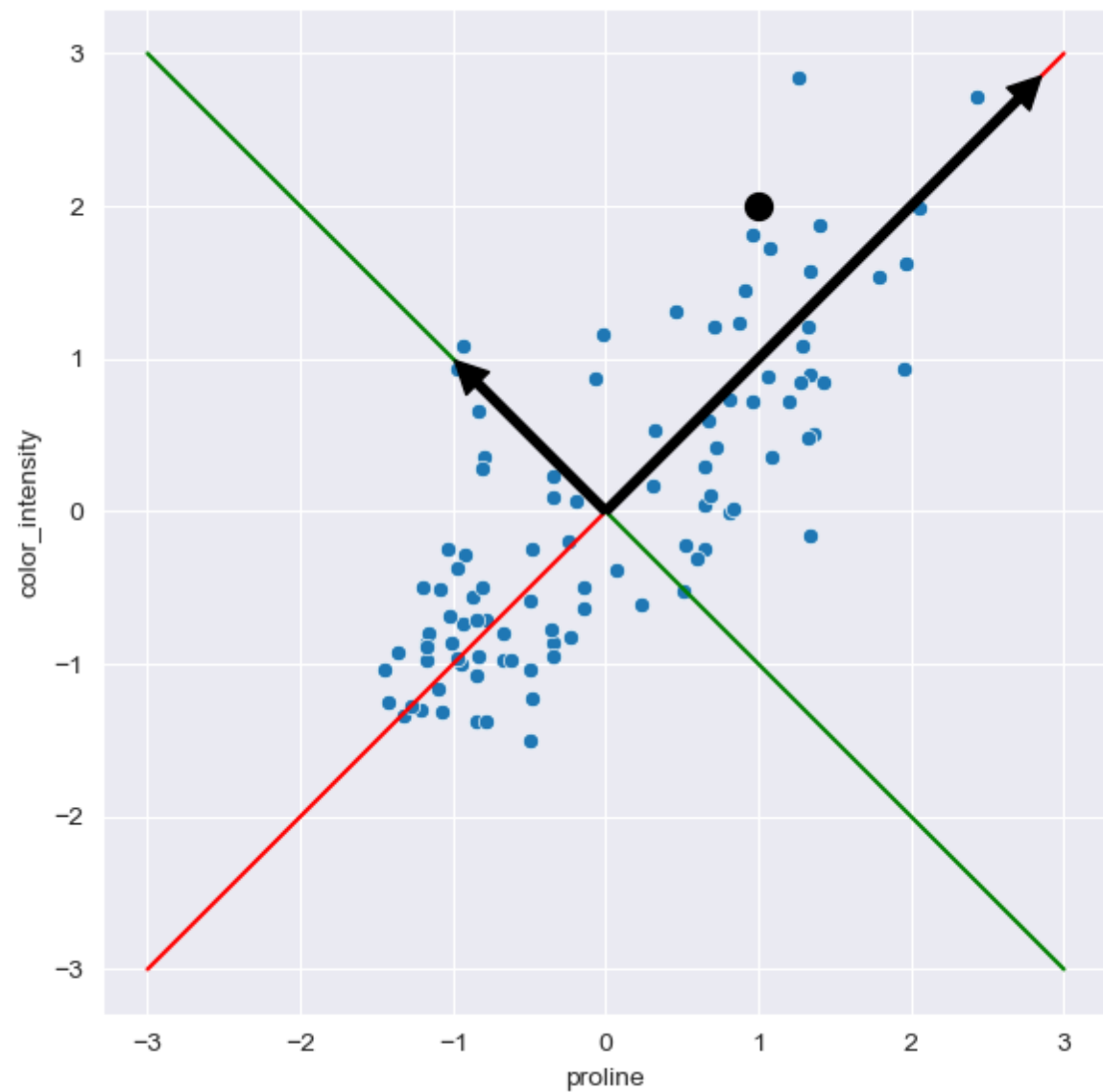
```
In [53]: 1 plot_pca(X_train_zscore[['proline', 'color_intensity']],pca,num_components=1)
        2 plt.tight_layout()
```



PCA Example Cont.

PCA Example Cont.

```
In [54]: 1 plot_pca(X_train_zscore[['proline', 'color_intensity']],pca,num_components=2)
        2 plt.tight_layout()
```



PCA in sklearn

PCA in sklearn

```
In [55]: 1 from sklearn.decomposition import PCA
          2
          3 pca = PCA().fit(X_train_zscore)
          4
          5 print(f'num input features: {X_train_zscore.shape[1]}')
          6 print(f'num pca components: {pca.n_components_}')
```

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

```
In [56]: 1 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]: 1 from sklearn.decomposition import PCA
          2
          3 pca = PCA().fit(X_train_zscore)
          4
          5 print(f'num input features: {X_train_zscore.shape[1]}')
          6 print(f'num pca components: {pca.n_components_}')
```

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

```
In [56]: 1 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]: 1 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

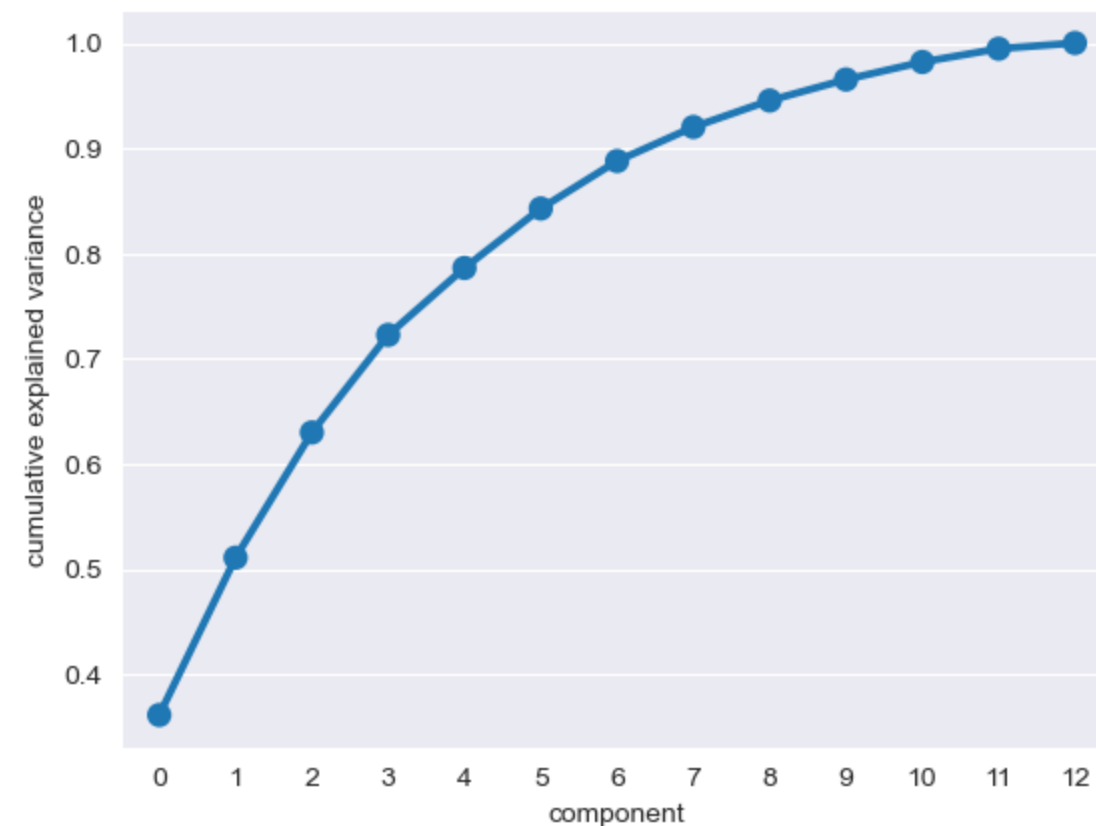
- How much of the variance in the dataset is explained by each component?

PCA: Explained Variance

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

```
In [58]: 1 pca = PCA().fit(X_train_zscore)
2
3 print(f'explained_variance           : {pca.explained_variance_.round(2)}')
4 print(f'explained_variance_ratio_    : {pca.explained_variance_ratio_.round(2)}')
5 print(f'cumulative explained variance : {pca.explained_variance_ratio_.cumsum().round(2)}')
6 df_var = pd.DataFrame({'component':range(pca.n_components_),
7                        'cumulative explained variance':pca.explained_variance_ratio_.cumsum()})
8 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]: 1 pca_2d = PCA(n_components=2)
2 X_pca = pca_2d.fit_transform(X_train_zscore)
3 X_pca = pd.DataFrame(X_pca, columns=[ 'component0', 'component1' ])
4
5 fig, ax=plt.subplots(1,2,figsize=(14,6))
6 sns.scatterplot(x='proline',y='color_intensity',data=X_train_zscore,ax=ax[0]);
7 sns.scatterplot(x='component0',y='component1',data=X_pca,ax=ax[1]);
8 ax[0].axis('equal');ax[1].axis('equal');
```

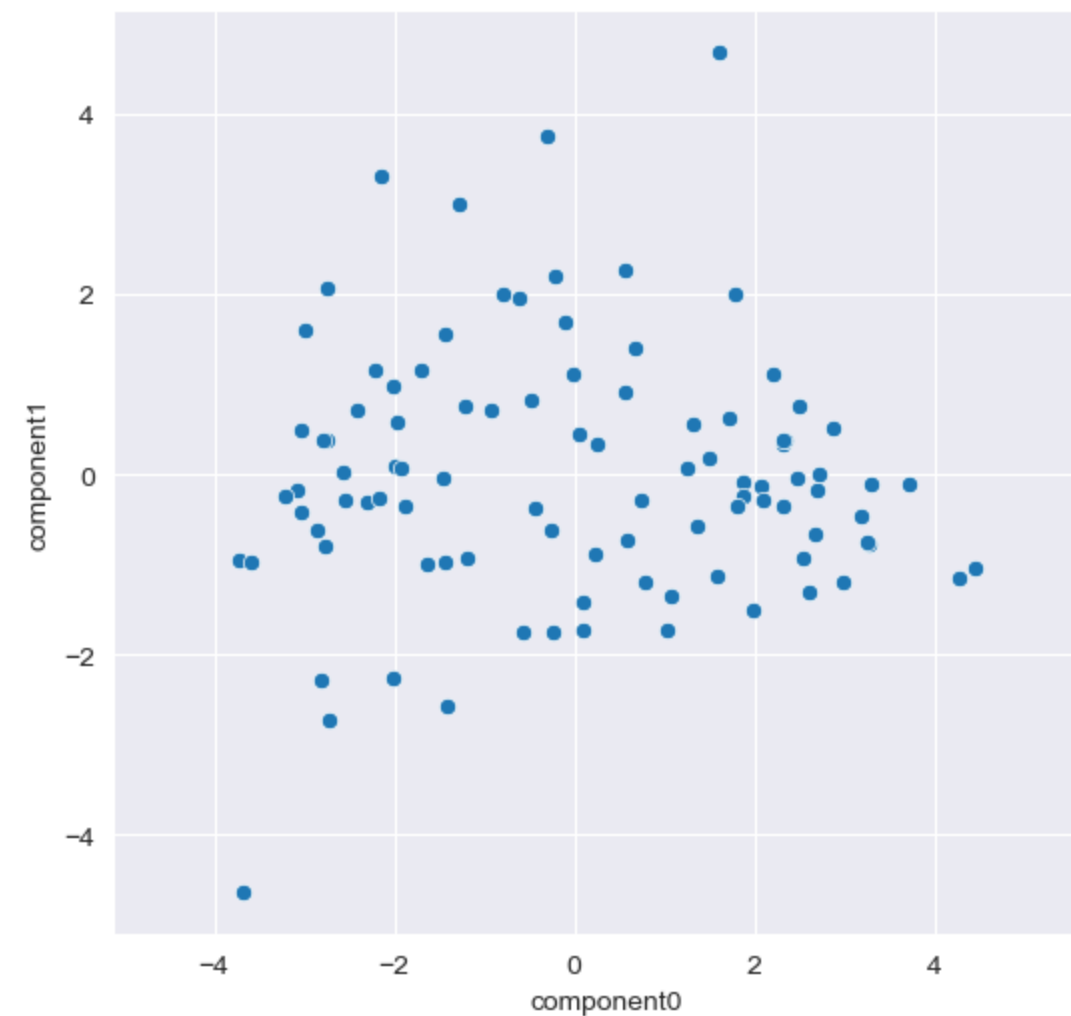
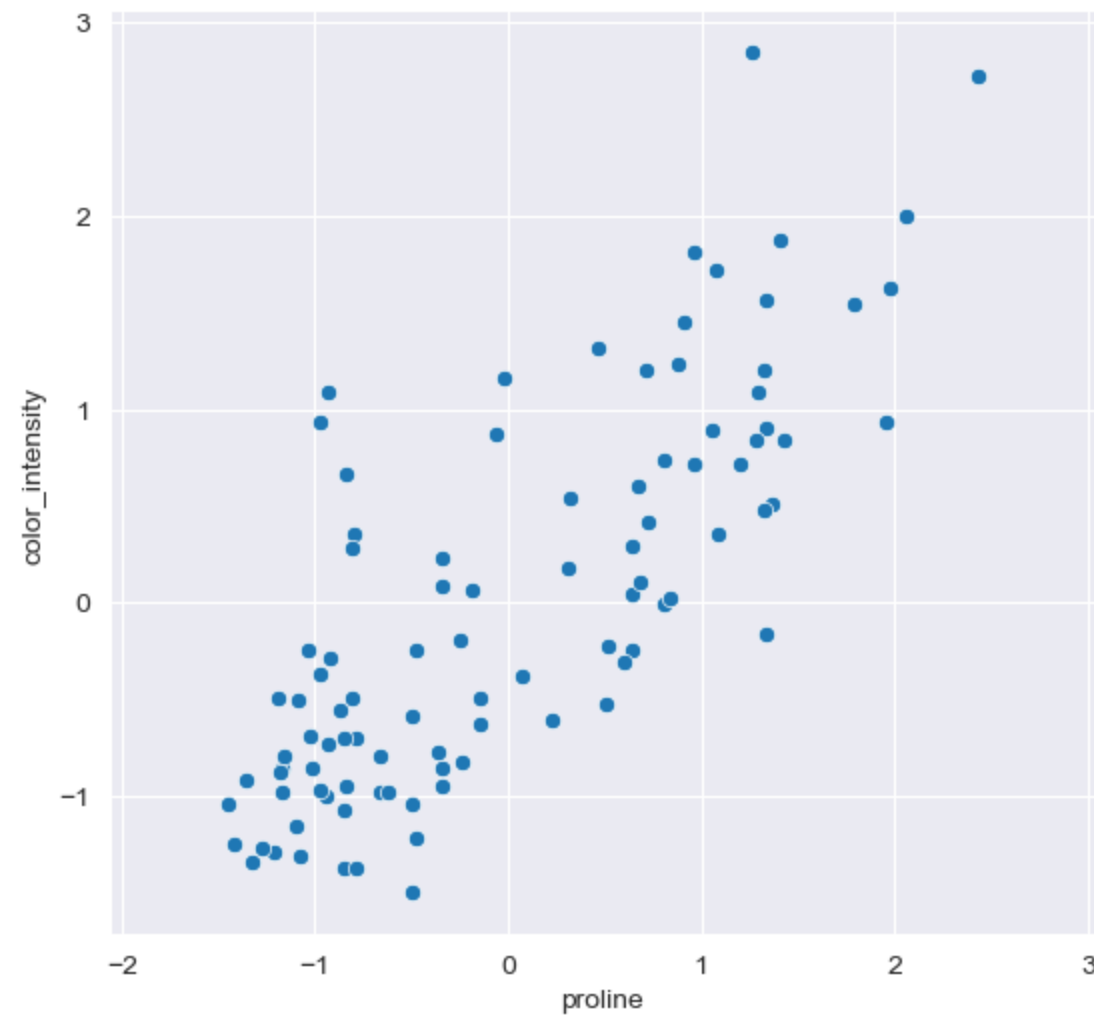


Image Recognition Example

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)
- 1024×1024 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 the Wild (LFW)

Labeled Faces in the Wild

Example Dataset: Labeled Faces in th Wild (LFW)

Labeled Faces in the Wild

```
In [60]: 1 from sklearn.datasets import fetch_lfw_people
          2
          3 lfw_people = fetch_lfw_people(min_faces_per_person=70, resize=0.6)
```

```
In [61]: 1 [lfw_people.target_names[i] for i in range(6)]
```

```
Out[61]: ['Ariel Sharon',
          'Colin Powell',
          'Donald Rumsfeld',
          'George W Bush',
          'Gerhard Schroeder',
          'Hugo Chavez']
```

Example Dataset: Labeled Faces in th Wild (LFW)

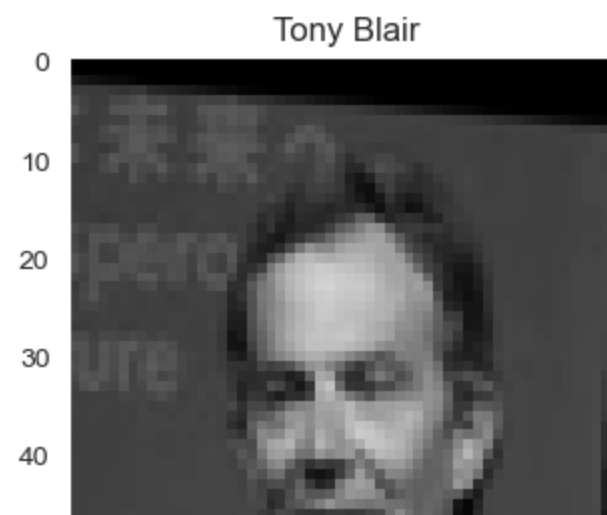
Labeled Faces in the Wild

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In [60]: 1 from sklearn.datasets import fetch_lfw_people
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          3 lfw_people = fetch_lfw_people(min_faces_per_person=70, resize=0.6)
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In [61]: 1 [lfw_people.target_names[i] for i in range(6)]
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```
Out[61]: ['Ariel Sharon',
          'Colin Powell',
          'Donald Rumsfeld',
          'George W Bush',
          'Gerhard Schroeder',
          'Hugo Chavez']
```

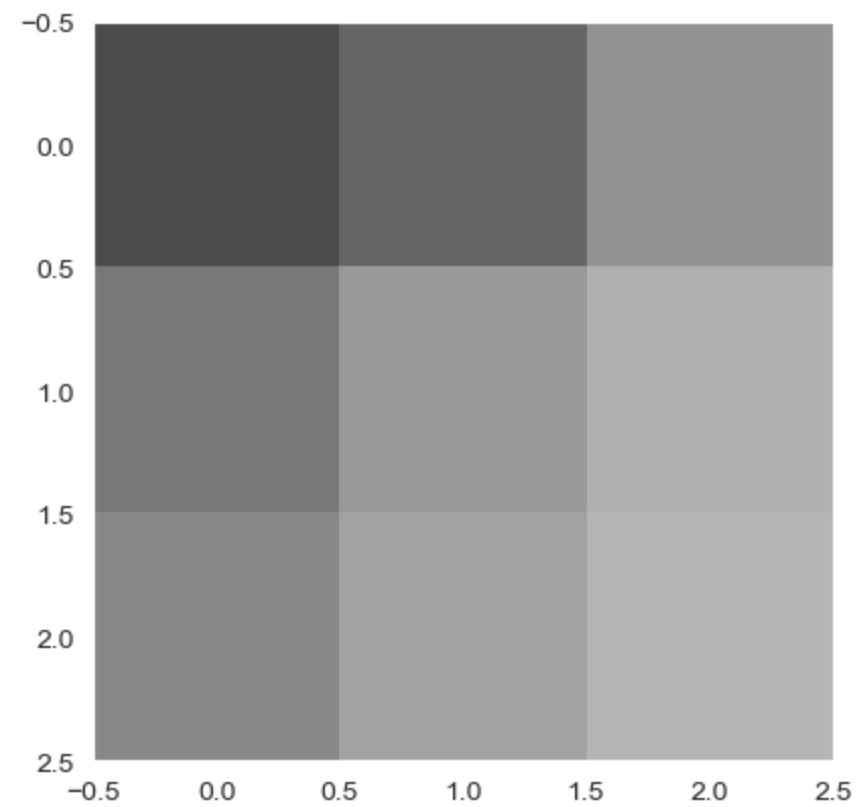
```
In [62]: 1 sns.set_style('dark')
          2 plt.imshow(lfw_people.images[1], cmap=plt.cm.gray, vmin=0, vmax=1)
          3 plt.title(lfw_people.target_names[lfw_people.target[1]], size=12);
```



Example Pixel Values

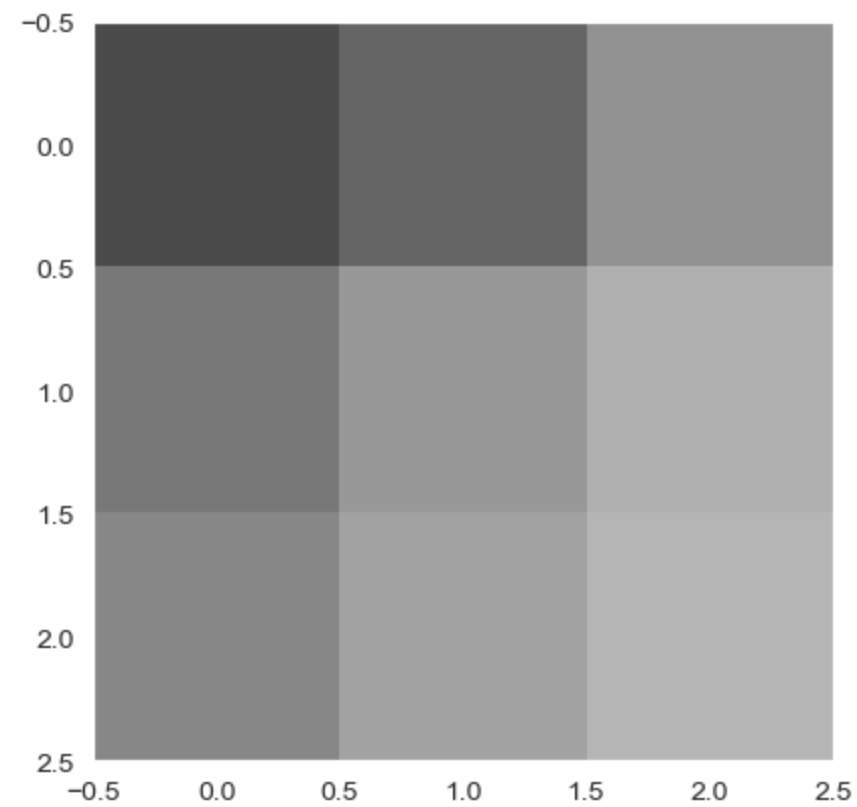
Example Pixel Values

```
In [63]: 1 # sample of 3x3 set of pixels
          2 plt.imshow(lfw_people.images[1][20:23,20:23], cmap=plt.cm.gray, vmin=0, vmax=1);
```



Example Pixel Values

```
In [63]: 1 # sample of 3x3 set of pixels
          2 plt.imshow(lfw_people.images[1][20:23,20:23],cmap=plt.cm.gray,vmin=0, vmax=1);
```



```
In [64]: 1 lfw_people.images[1][20:23,20:23].round(2)
```

```
Out[64]: array([[0.29, 0.4 , 0.57],
                [0.47, 0.6 , 0.69],
                [0.53, 0.64, 0.71]], dtype=float32)
```

Representing each Image: Flatten

- Grid as a fixed length feature vector?

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- Grid as a fixed length feature vector?

```
In [65]: 1 lfw_people.images[1].shape
```

```
Out[65]: (75, 56)
```

Representing each Image: Flatten

- Grid as a fixed length feature vector?

```
In [65]: 1 lfw_people.images[1].shape
```

```
Out[65]: (75, 56)
```

```
In [66]: 1 x = lfw_people.images[1].reshape(1,-1)
          2 x
```

```
Out[66]: array([[0.00261438, 0.00261438, 0.          , ..., 0.01830065, 0.          ,
                  0.          ]], dtype=float32)
```


Representing each Image: Flatten

- Grid as a fixed length feature vector?

```
In [65]: 1 lfw_people.images[1].shape
```

```
Out[65]: (75, 56)
```

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```

```
Out[66]: array([[0.00261438, 0.00261438, 0.          , ..., 0.01830065, 0.          ,
                  0.          ]], dtype=float32)
```

```
In [67]: 1 x.shape
```

```
Out[67]: (1, 4200)
```

Representing each Image: Flatten

- Grid as a fixed length feature vector?

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In [65]: 1 lfw_people.images[1].shape
```

```
Out[65]: (75, 56)
```

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In [66]: 1 x = lfw_people.images[1].reshape(1,-1)
2 x
```

```
Out[66]: array([[0.00261438, 0.00261438, 0.          , ..., 0.01830065, 0.          ,
                  0.          ]], dtype=float32)
```

```
In [67]: 1 x.shape
```

```
Out[67]: (1, 4200)
```

What information do we lose when we do this?

Create a Dataset

Create a Dataset

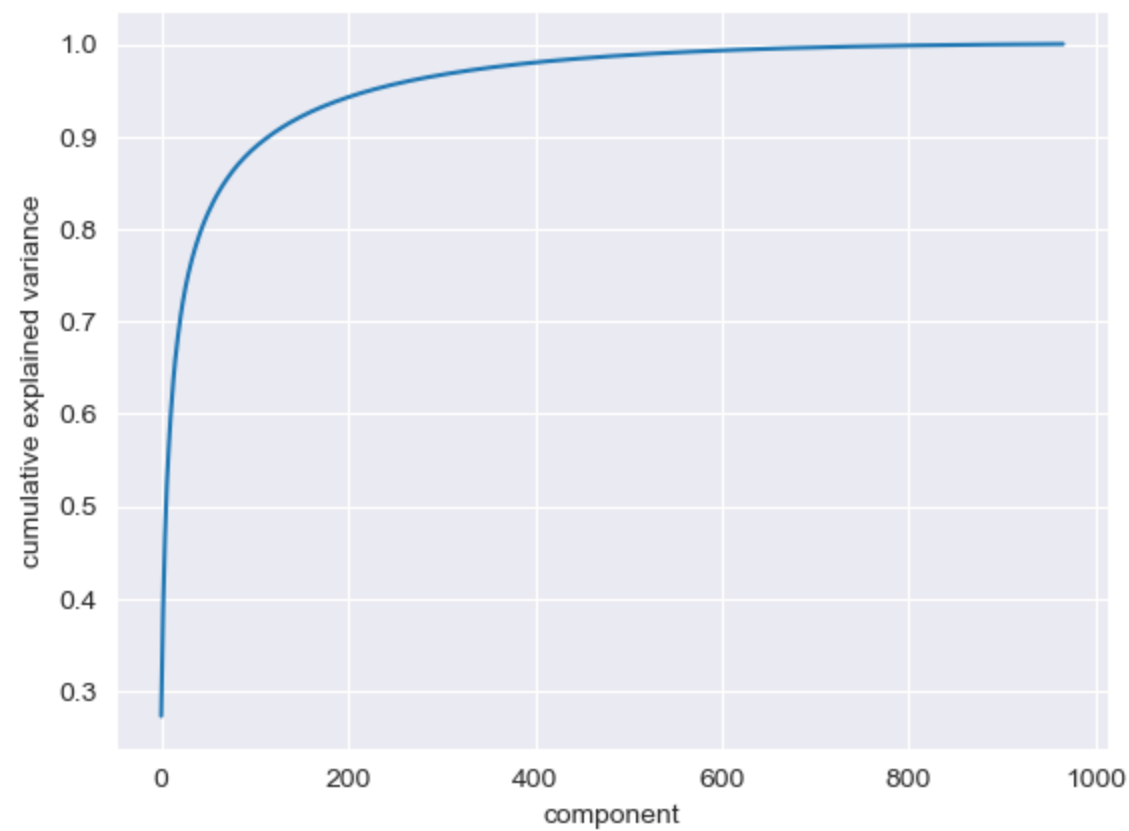
```
In [68]: 1 # get the shape of images for plotting the
          2 n_samples, h, w = lfw_people.images.shape
          3
          4 # use actual pixel values, ignoring relative position
          5 X_faces = lfw_people.data
          6 n_features = X_faces.shape[1]
          7
          8 # the label to predict is the id of the person
          9 y_faces = lfw_people.target
         10 target_names = lfw_people.target_names
         11 n_classes = target_names.shape[0]
         12
         13 # create train/test split
         14 X_train_faces, X_test_faces, y_train_faces, y_test_faces = train_test_split(X_faces, y_faces,
         15                                                                                   test_size=0.25,
         16                                                                                   stratify=y_faces,
         17                                                                                   random_state=0)
         18 print(f"image_size: {h}x{w}")
         19 print("n_features: %d" % n_features)
         20 print("n_classes : %d" % n_classes)
         21 print(f"n_train   : {len(X_train_faces)}")
         22 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 [69]: 1 pca_faces = PCA().fit(X_train_faces)
2
3 df_var_faces = pd.DataFrame({'component':range(pca_faces.n_components_),
4                               'cumulative explained variance':pca_faces.explained_variance_ratio_.cumsum()})
5 # using lineplot here instead of pointplot because of the large number of components
6 with sns.axes_style('darkgrid'):
7     sns.lineplot(x='component',y='cumulative explained variance',data=df_var_faces);
```



Compute PCA and Transform

Compute PCA and Transform

```
In [70]: 1 # set the number of dimensions we want to retain
2 n_components = 200
3
4 # instantiate and fit on X_train
5 pca_faces = PCA(n_components=n_components,
6                 svd_solver='randomized',
7                 whiten=True).fit(X_train_faces)
8
9 # extract and reshape components into eigenfaces for plotting
10 eigenfaces = pca_faces.components_.reshape((n_components, h, w))
11
12 # transform the training and test set for classification
13 X_train_faces_pca = pca_faces.transform(X_train_faces)
14 X_test_faces_pca = pca_faces.transform(X_test_faces)
```


Compute PCA and Transform

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In [70]: 1 # set the number of dimensions we want to retain
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12 # transform the training and test set for classification
13 X_train_faces_pca = pca_faces.transform(X_train_faces)
14 X_test_faces_pca = pca_faces.transform(X_test_faces)
```

```
In [71]: 1 pca_faces.components_[0].round(2)
```

```
Out[71]: array([0.01, 0.01, 0.01, ..., 0.  , 0.  , 0.  ], dtype=float32)
```

Compute PCA and Transform

```
In [70]: 1 # set the number of dimensions we want to retain
          2 n_components = 200
          3
          4 # instantiate and fit on X_train
          5 pca_faces = PCA(n_components=n_components,
          6                  svd_solver='randomized',
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          8
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         10 eigenfaces = pca_faces.components_.reshape((n_components, h, w))
         11
         12 # transform the training and test set for classification
         13 X_train_faces_pca = pca_faces.transform(X_train_faces)
         14 X_test_faces_pca = pca_faces.transform(X_test_faces)
```

```
In [71]: 1 pca_faces.components_[0].round(2)
```

```
Out[71]: array([0.01, 0.01, 0.01, ..., 0. , 0. , 0. ], dtype=float32)
```

```
In [72]: 1 pca_faces.singular_values_.round(2)
```

```
Out[72]: 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,
                15.07,  14.87,  14.88,  14.68,  14.6 ,  14.48,  14.33,  14.28,
```

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]: 1 def plot_gallery(images, titles, h, w, n_row=3, n_col=4):
2         """Helper function to plot a gallery of portraits"""
3         plt.figure(figsize=(1.8 * n_col, 2.4 * n_row))
4         plt.subplots_adjust(bottom=0, left=.01, right=.99, top=.90, hspace=.35)
5         for i in range(n_row * n_col):
6             plt.subplot(n_row, n_col, i + 1)
7             plt.imshow(images[i].reshape((h, w)), cmap=plt.cm.gray)
8             plt.title(titles[i], size=12)
9             plt.xticks(())
10            plt.yticks(())
11            plt.tight_layout()
12
13 # plot the result of the prediction on a portion of the test set
14 def title(y_pred, y_test, target_names, i):
15     pred_name = target_names[y_pred[i]].rsplit(' ', 1)[-1]
16     true_name = target_names[y_test[i]].rsplit(' ', 1)[-1]
17     return 'predicted: %s\ntrue:      %s' % (pred_name, true_name)
```

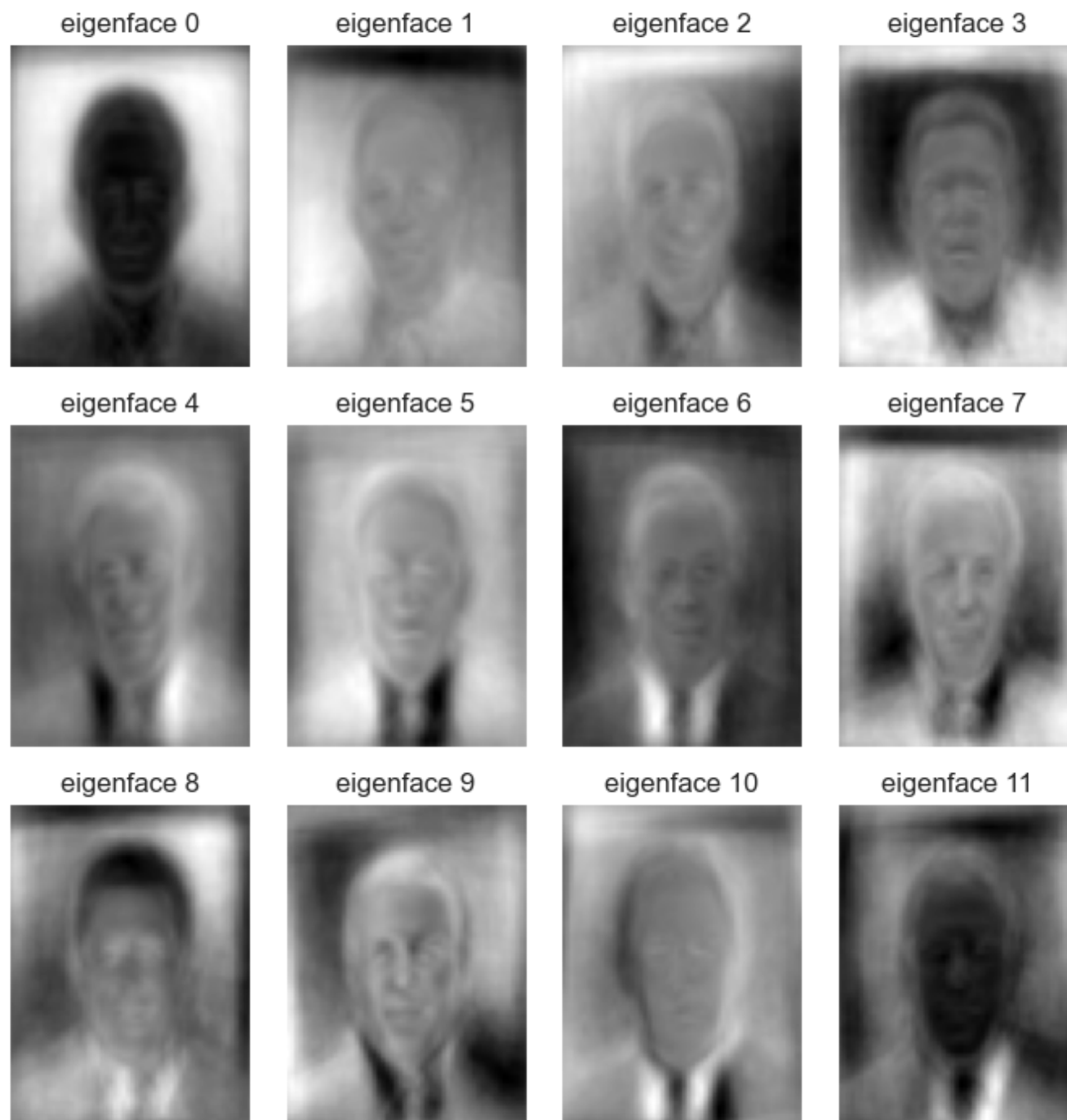
Eigenfaces

- 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 [74]: 1 eigenface_titles = ["eigenface %d" % i for i in range(eigenfaces.shape[0])]
          2 plot_gallery(eigenfaces, eigenface_titles, h, w)
```



Train and Tune SVC

Train and Tune SVC

```
In [75]: 1 %%time
          2 from sklearn.model_selection import GridSearchCV
          3 from sklearn.svm import SVC
          4
          5 params = {'C': [1e3, 5e3, 1e4, 5e4, 1e5],
          6             'gamma': [0.0001, 0.0005, 0.001, 0.005, 0.01, 0.1], }
          7 clf_faces_pca = GridSearchCV(SVC(kernel='rbf', class_weight='balanced'),
          8                               params, cv=3, n_jobs=-1)
          9 clf_faces_pca = clf_faces_pca.fit(X_train_faces_pca, y_train_faces)
```

```
CPU times: user 482 ms, sys: 253 ms, total: 735 ms
Wall time: 6.03 s
```


Train and Tune SVC

```
In [75]: 1 %%time
2 from sklearn.model_selection import GridSearchCV
3 from sklearn.svm import SVC
4
5 params = {'C': [1e3, 5e3, 1e4, 5e4, 1e5],
6           'gamma': [0.0001, 0.0005, 0.001, 0.005, 0.01, 0.1], }
7 clf_faces_pca = GridSearchCV(SVC(kernel='rbf', class_weight='balanced'),
8                               params, cv=3, n_jobs=-1)
9 clf_faces_pca = clf_faces_pca.fit(X_train_faces_pca, y_train_faces)
```

CPU times: user 482 ms, sys: 253 ms, total: 735 ms
Wall time: 6.03 s

```
In [76]: 1 print(f"best_params : {clf_faces_pca.best_params_}")
2 print(f"best_score  : {clf_faces_pca.best_score_:0.2f}")
```

best_params : {'C': 1000.0, 'gamma': 0.001}
best_score : 0.73

Evaluate on the test set

Evaluate on the test set

```
In [77]: 1 from sklearn.metrics import classification_report
2
3 y_pred_pca = clf_faces_pca.predict(X_test_faces_pca)
4 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	0.76	0.75	59
Donald Rumsfeld	0.69	0.60	0.64	30
George W Bush	0.80	0.88	0.84	133
Gerhard Schroeder	0.60	0.44	0.51	27
Hugo Chavez	0.64	0.50	0.56	18
Tony Blair	0.74	0.78	0.76	36
accuracy			0.75	322
macro avg	0.69	0.65	0.67	322
weighted avg	0.74	0.75	0.74	322

Prediction Examples

Prediction Examples

```
In [78]: 1 prediction_titles = [title(y_pred_pca, y_test_faces, target_names, i)
2           for i in range(y_pred_pca.shape[0])]
3
4 plot_gallery(X_test_faces[10:], prediction_titles[10:], h, w)
5 plt.tight_layout()
```



Performance without PCA: Train

Performance without PCA: Train

```
1 %%time
2
3 # Warning: this cell takes up to 3 minutes to execute on an Intel i7 1.8Ghz w/ 8 cores
4
5 params = {'C': [1e3, 5e3, 1e4, 5e4, 1e5],
6           'gamma': [0.0001, 0.0005, 0.001, 0.005, 0.01, 0.1],}
7 clf_faces_nopca = GridSearchCV(SVC(kernel='rbf', class_weight='balanced'),
8                                params, cv=3, n_jobs=-1)
9 clf_faces_nopca = clf_faces_nopca.fit(X_train_faces, y_train_faces)
10
11 #CPU times: user 2.08 s, sys: 53.3 ms, total: 2.13 s
12 #Wall time: 2min 42s
13
14 print(f"best_params : {clf_faces_nopca.best_params_}")
15 print(f"best_score  : {clf_faces_nopca.best_score_:0.2f}")
16
17 #best_params : {'C': 1000.0, 'gamma': 0.0001}
18 #best_score  : 0.78
```

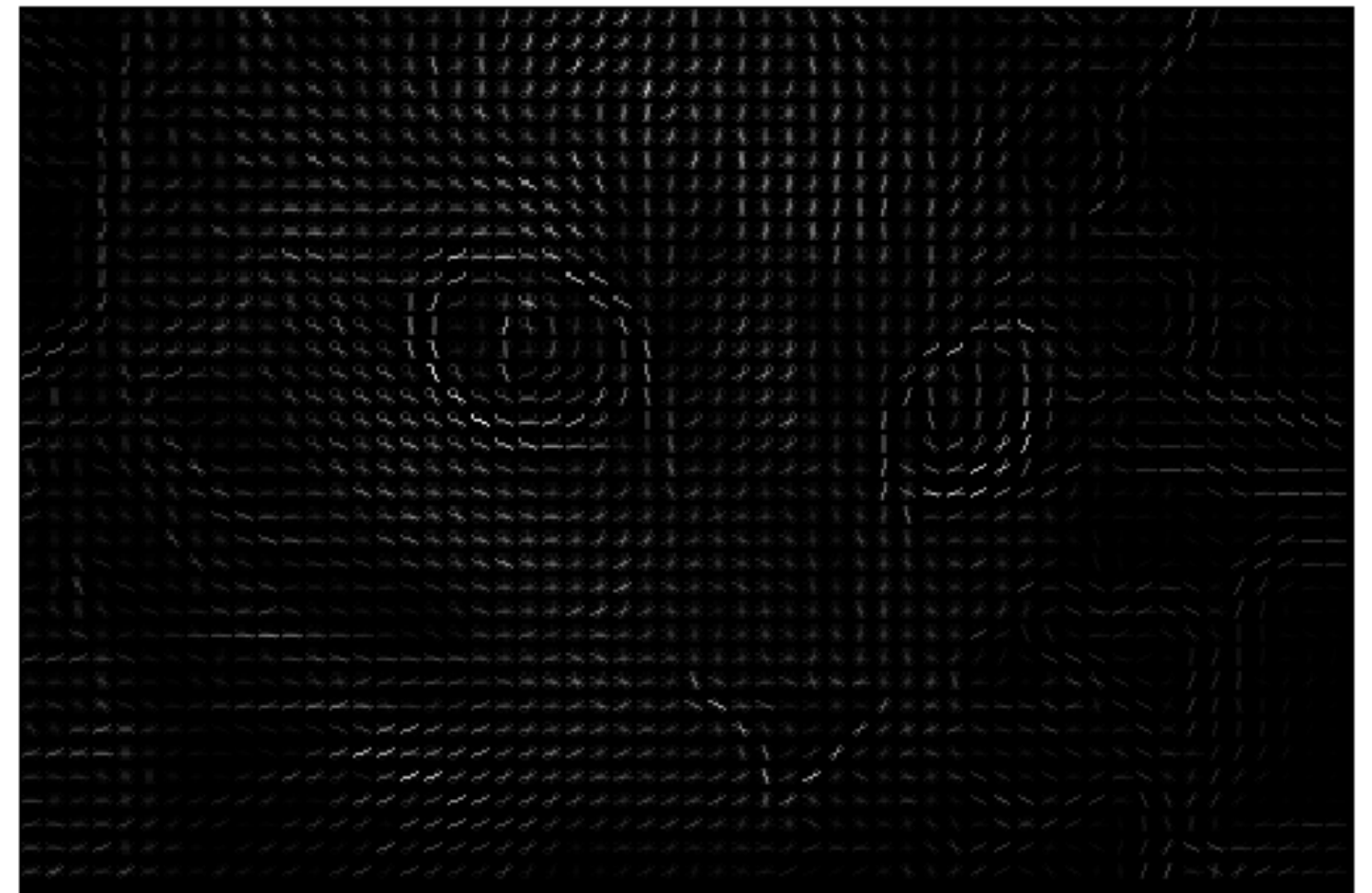
Performance without PCA: Evaluate

Performance without PCA: Evaluate

```
1 y_pred_nopca = clf_faces_nopca.predict(X_test_faces)
2 print(classification_report(y_test_faces, y_pred_nopca, target_names=target_names))
3
4 #                precision    recall  f1-score   support
5
6 #      Ariel Sharon           0.65      0.79      0.71         19
7 #      Colin Powell          0.82      0.69      0.75         59
8 #      Donald Rumsfeld        0.60      0.60      0.60         30
9 #      George W Bush          0.82      0.90      0.86        133
10 #      Gerhard Schroeder      0.56      0.56      0.56         27
11 #      Hugo Chavez            0.71      0.28      0.40         18
12 #      Tony Blair            0.71      0.75      0.73         36
13
14 #              accuracy              0.75        322
15 #              macro avg          0.70      0.65      0.66        322
16 #              weighted avg          0.75      0.75      0.74        322
```

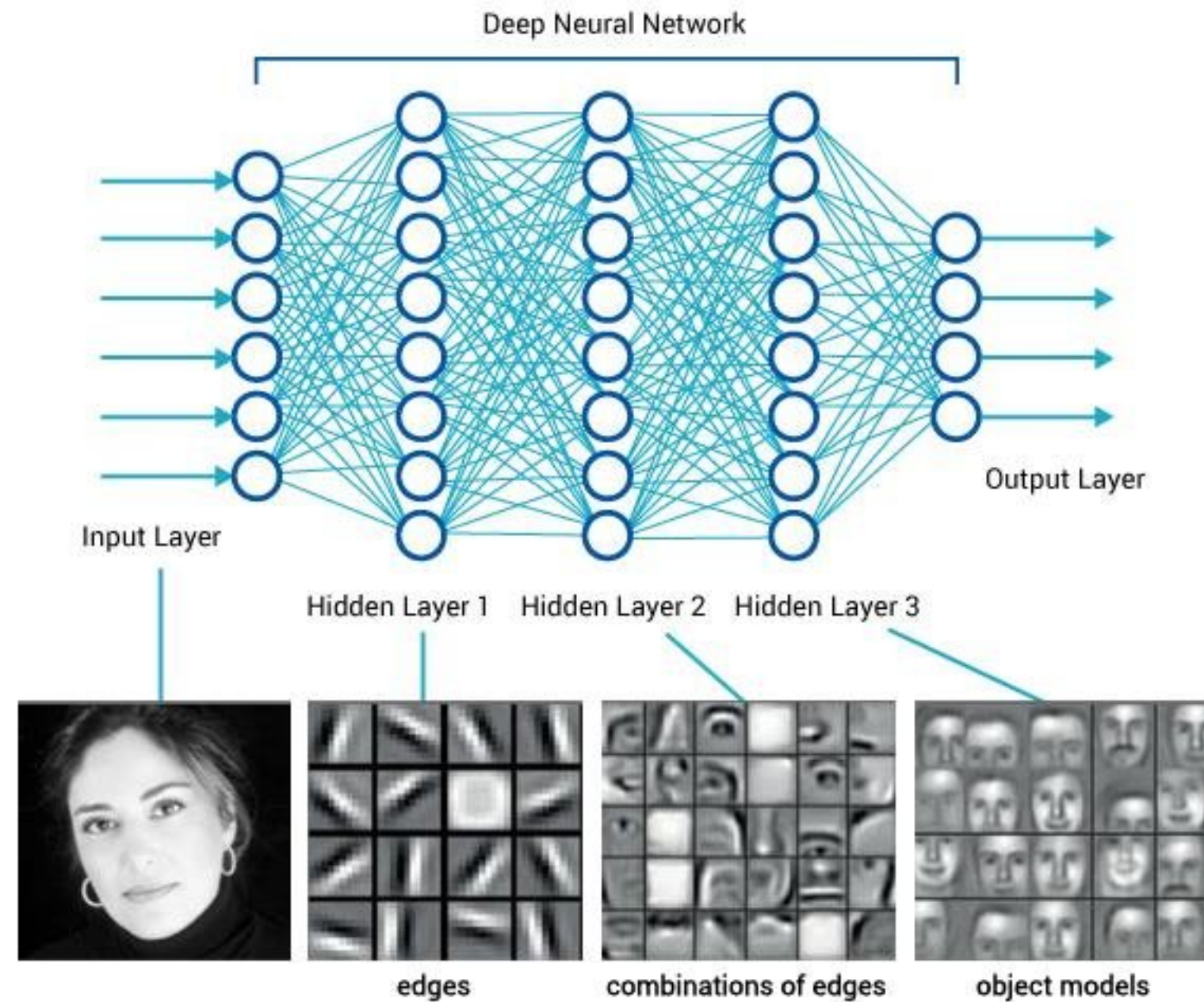
Other Image Recognition Methods

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



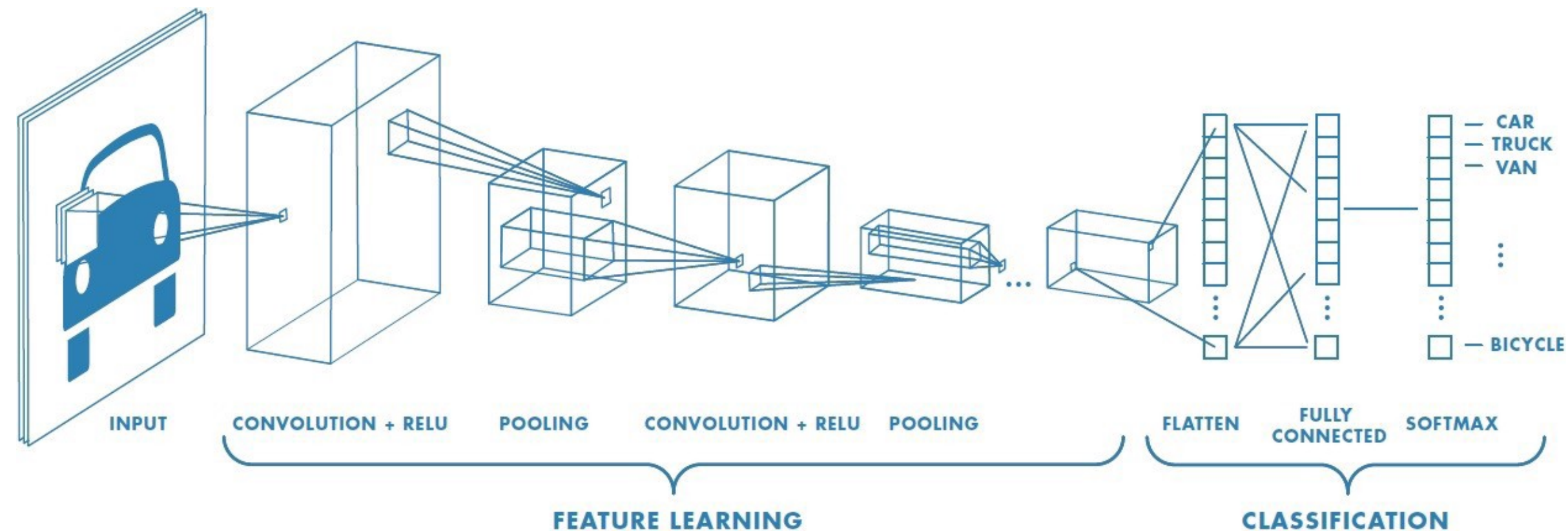
Other Image Recognition Methods: Deep Neural Networks

- With Deep Neural Nets



Other Image Recognition Methods: Deep Neural Networks

- With Convolutional Neural Networks [Good Example](#)



Questions re Feature Extraction and PCA?

Next time: NLP and Pipelines