# Elements Of Data Science - F2021

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

11/15/2021

# TODOs

- Readings:
    - PML Chapter 6, first 3 sections on Pipelines
    - PML Chapter 8: Applying Machine Learning to Sentiment Analysis

- Quiz 9, Due **Sunday Nov 21st, 11:59pm ET**
- HW3, Due **Tues Nov 23 at 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**
- **Pipelines?**

# 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

# 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'])
```

# 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 in Pandas 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 in Pandas 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 in Pandas 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.copy()
df_flower_price.set_index('flower_id',inplace=True)
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)
```

| flower_id | name |
|---|---|
| 1001 | iris |
| 1002 | rose |

| flower_id | price |
|---|---|
| 1002 | 3.99 |
| 1003 | 2.25 |

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

Out[9]:

| flower_id | name | price |
|---|---|---|
| 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 |

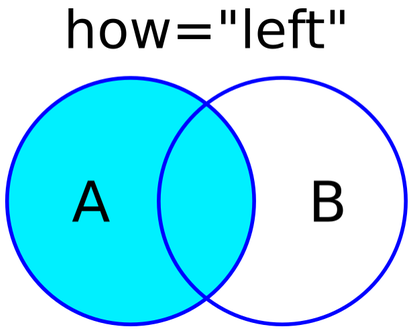
In [9]:
```
df_flower_name.join(df_flower_price)
```

Out[9]:

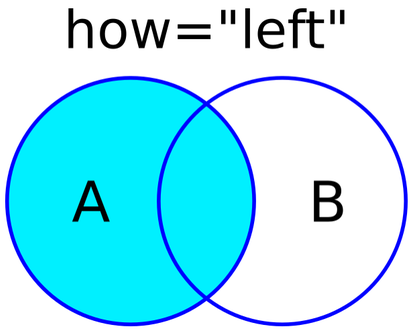
| | name | price |
|---|---|---|
| **flower_id** | | |
| **1001** | iris | NaN |
| **1002** | rose | 3.99 |

- by default, this is a 'Left Join'

# Join Types: Left Join



# Join Types: Left Join

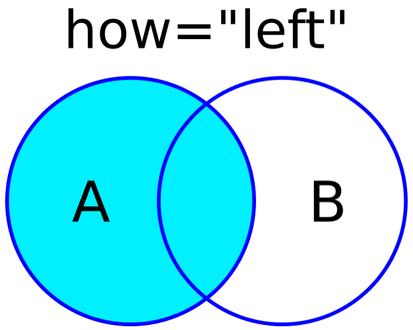



In [10]:
```
display(df_flower_name,df_flower_price)
```

| | name |
|---|---|
| **flower_id** | |
| **1001** | iris |
| **1002** | rose |

| | price |
|---|---|
| **flower_id** | |
| **1002** | 3.99 |
| **1003** | 2.25 |

# Join Types: Left Join




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

| | name |
|---|---|
| **flower_id** | |
| **1001** | iris |
| **1002** | rose |

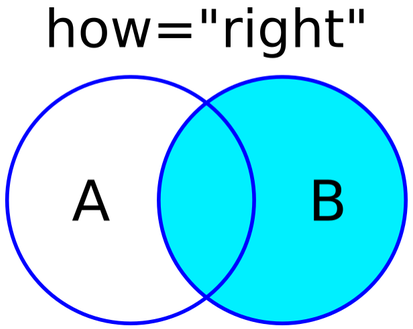
| | price |
|---|---|
| **flower_id** | |
| **1002** | 3.99 |
| **1003** | 2.25 |

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

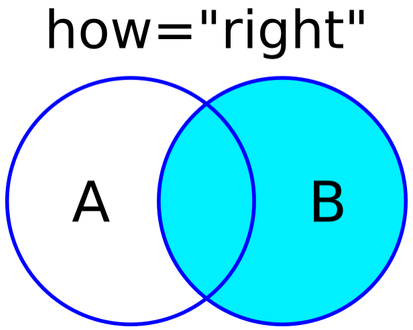
Out[11]:

| | name | price |
|---|---|---|
| **flower_id** | | |
| **1001** | iris | NaN |
| **1002** | rose | 3.99 |

# Join Types: Right Join



# Join Types: Right Join

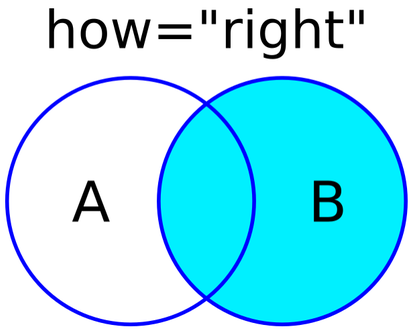



In [12]:
```
display(df_flower_name,df_flower_price)
```

| | name |
|---|---|
| **flower_id** | |
| **1001** | iris |
| **1002** | rose |

| | price |
|---|---|
| **flower_id** | |
| **1002** | 3.99 |
| **1003** | 2.25 |

# Join Types: Right Join




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

| | name |
|---|---|
| **flower_id** | |
| **1001** | iris |
| **1002** | rose |

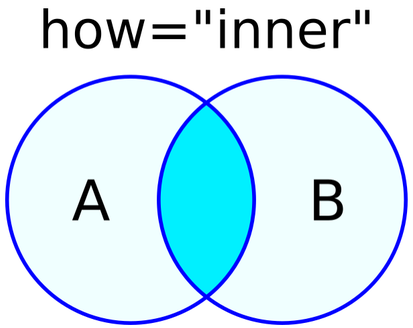
| | price |
|---|---|
| **flower_id** | |
| **1002** | 3.99 |
| **1003** | 2.25 |

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

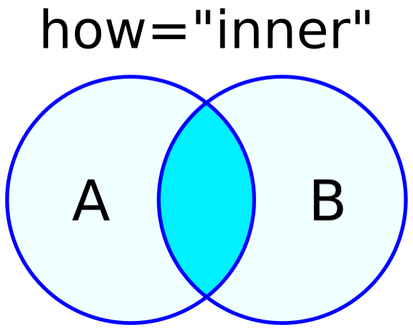
Out[13]:

| | name | price |
|---|---|---|
| **flower_id** | | |
| **1002** | rose | 3.99 |
| **1003** | NaN | 2.25 |

# Join Types: Inner Join



# Join Types: Inner Join

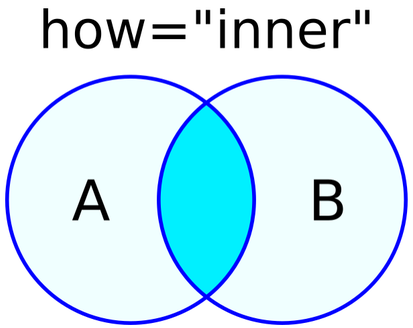



In [14]:
```
display(df_flower_name,df_flower_price)
```

| | 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 |

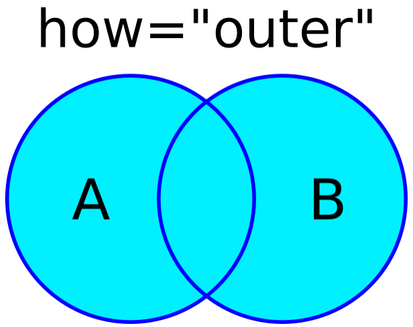
| | price |
|---|---|
| **flower_id** | |
| **1002** | 3.99 |
| **1003** | 2.25 |

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

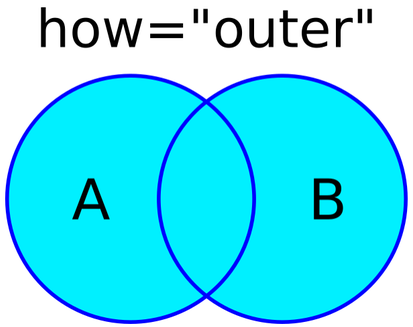
Out[15]:

| | name | price |
|---|---|---|
| **flower_id** | | |
| **1002** | rose | 3.99 |

# Join Types: Outer Join



# Join Types: Outer Join

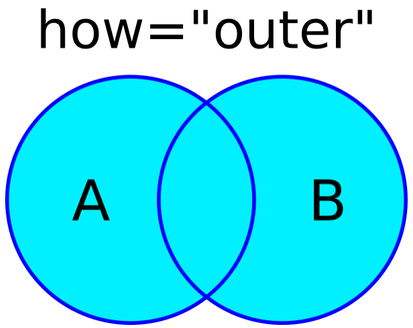



In [16]:
```
display(df_flower_name,df_flower_price)
```

| | 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)
```

| flower_id | name |
|---|---|
| **1001** | iris |
| **1002** | rose |

| flower_id | price |
|---|---|
| **1002** | 3.99 |
| **1003** | 2.25 |

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

Out[17]:

| flower_id | name | price |
|---|---|---|
| **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=`

# Setting the Index When Reading in Data

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

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=`

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'
            ).head(2)
```

Out[19]:

| purchase_id | lastname | purchase_date | stars | price | favorite_flower |
|---|---|---|---|---|---|
| **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,
         df_flower_price,
         left_on='flower_id',
         right_on='flower_id') # what is the default join for merge?
```

Out[23]:

| | name | price |
|---|---|---|
| **flower_id** | | |
| **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,
         df_flower_price,
         left_on='flower_id',
         right_on='flower_id') # what is the default join for merge?
```

Out[23]:

| | name | price |
|---|---|---|
| **flower_id** | | |
| **1002** | rose | 3.99 |

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

Out[24]:

| | name | price |
|---|---|---|
| **flower_id** | | |
| **1001** | iris | NaN |
| **1002** | rose | 3.99 |
| **1003** | NaN | 2.25 |

# Joining Datasets Review

- Use `.join()` when you can, using dataframe indices
- May need to set the dataframe indices (`.set_index()` or `index_col=`)
- Know the different general join types: Left, Right, Inner, Outer
- Use `pd.merge()` when you need something more complicated

# Questions?

# Dimensionality Reduction

# Recall: Methods for Avoiding Overfitting

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

# Dimensionality Reduction

- Reasons to reduce the number of features:
    - improve *model performance* (reducing complexity reducing chance of overfitting)
    - improve *speed performance* (reducing 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 import datasets
from sklearn.model_selection import train_test_split

wine = datasets.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,random_state=0)
X_train.columns.values
```

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]:
```
from sklearn import datasets
from sklearn.model_selection import train_test_split

wine = datasets.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,random_state=0)
X_train.columns.values
```

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]:
```
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 | prol |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **76** | 13.03 | 0.90 | 1.71 | 16.0 | 86.0 | 1.95 | 2.03 | 0.24 | 1.46 | 4.60 | 1.19 | 2.48 | 392. |
| **78** | 12.33 | 0.99 | 1.95 | 14.8 | 136.0 | 1.90 | 1.85 | 0.35 | 2.76 | 3.40 | 1.06 | 2.31 | 750. |
| **45** | 14.21 | 4.04 | 2.44 | 18.9 | 111.0 | 2.85 | 2.65 | 0.30 | 1.25 | 5.24 | 0.87 | 3.33 | 108( |

# Need to Standardize Features

In [27]:
```
X_train.agg(['mean','std']).T.sort_values('mean',ascending=False)
```

Out[27]:

| | mean | std |
|---|---|---|
| **proline** | 770.381443 | 351.632012 |
| **magnesium** | 99.649485 | 15.215837 |
| **alcalinity_of_ash** | 18.926804 | 3.162986 |
| **alcohol** | 12.876392 | 0.882710 |
| **color_intensity** | 4.112680 | 1.660242 |
| **od280/od315_of_diluted_wines** | 2.933299 | 0.452246 |
| **total_phenols** | 2.479175 | 0.537158 |
| **flavanoids** | 2.426598 | 0.672639 |
| **ash** | 2.338660 | 0.279052 |
| **malic_acid** | 2.033402 | 0.979120 |
| **proanthocyanins** | 1.732474 | 0.520371 |
| **hue** | 1.054082 | 0.179279 |
| **nonflavanoid_phenols** | 0.329794 | 0.105574 |

# Standardize Features

# Standardize Features

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

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

X_test = ss.transform(X_test)
```

# Standardize Features

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

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

X_test = ss.transform(X_test)
```

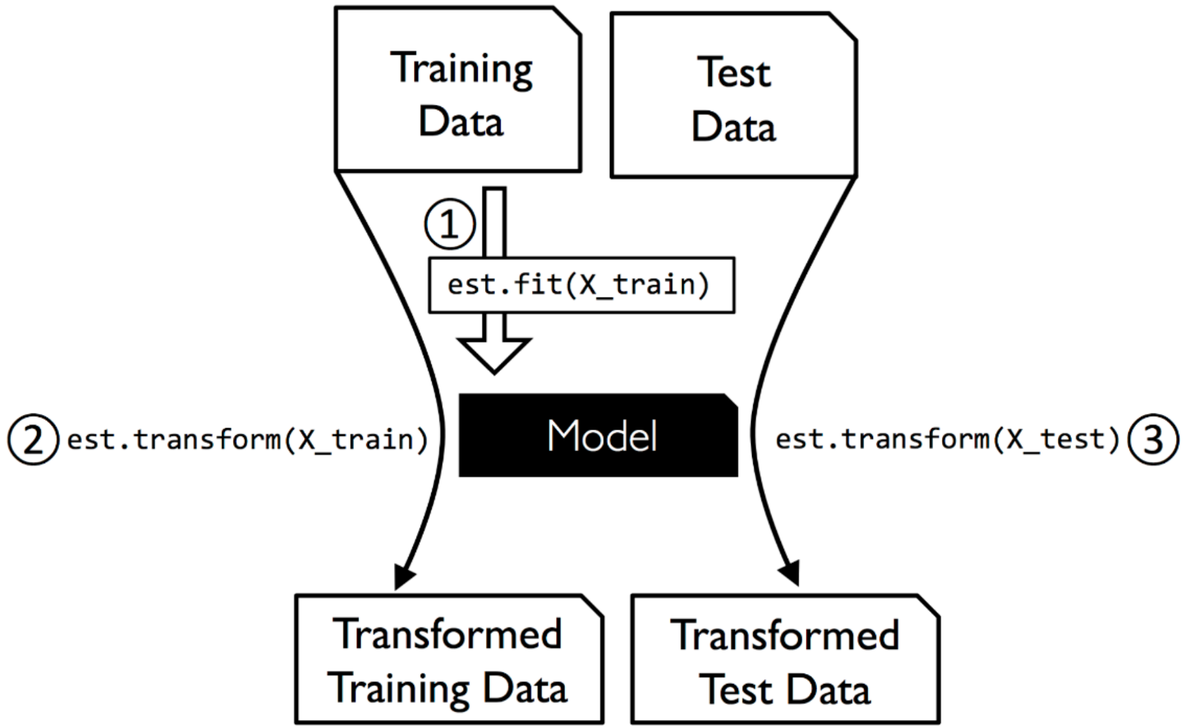
In [29]:
```
X_train.agg(['mean','std']).T.sort_values('mean',ascending=False)
```

Out[29]:

| | mean | std |
|---|---|---|
| **total_phenols** | 2.028160e-15 | 1.005195 |
| **flavanoids** | 6.638447e-16 | 1.005195 |
| **alcalinity_of_ash** | 4.727032e-16 | 1.005195 |
| **magnesium** | 3.694067e-16 | 1.005195 |
| **alcohol** | 1.281907e-16 | 1.005195 |
| **proline** | -3.204767e-17 | 1.005195 |
| **proanthocyanins** | -1.110223e-16 | 1.005195 |
| **nonflavanoid_phenols** | -2.495140e-16 | 1.005195 |
| **color_intensity** | -4.051742e-16 | 1.005195 |
| **malic_acid** | -4.229149e-16 | 1.005195 |
| **od280/od315_of_diluted_wines** | -9.694422e-16 | 1.005195 |
| **hue** | -1.818706e-15 | 1.005195 |
| **ash** | -2.128881e-15 | 1.005195 |

# Recall: Predicting vs Transforming with Train/Test Split

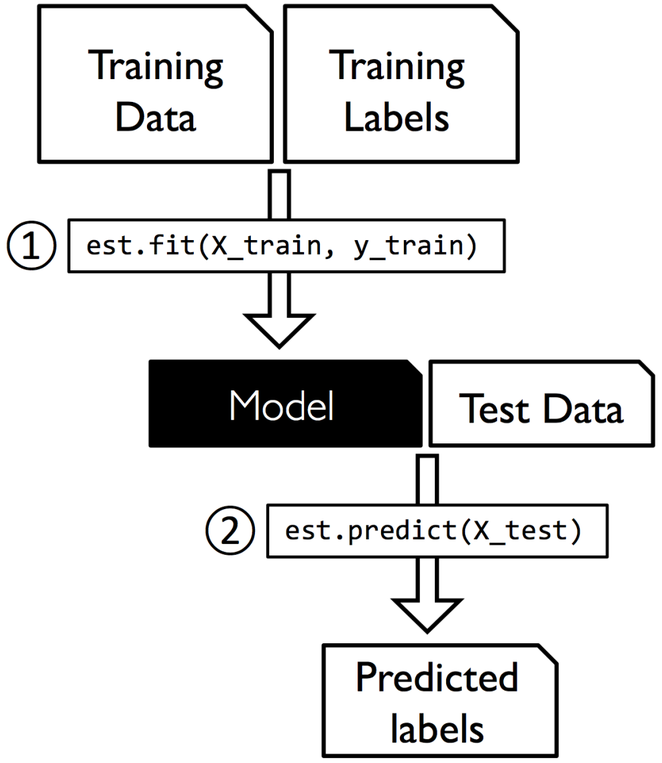
- When transforming data, fit on the training set, transform both train and test




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

# Feature Selection: LASSO (L1)

- LASSO or $\ell_1$ or `l1` regularization drives the coefficient of uninformative features to 0

# Feature Selection: LASSO (L1)

- LASSO or $\ell_1$ or `l1` regularization drives the coefficient of uninformative features to 0

In [30]:
```
from sklearn.linear_model import LogisticRegression

# First, without regularization
#   C is the inverse regularization strength: higher means less regularization
logr = LogisticRegression(C=100, penalty="l1", solver="liblinear", random_state=123)
logr.fit(X_train, y_train)
logr.coef_[0,:5]
```

Out[30]:
```
array([-5.74709641, -1.20824931, -2.70057811,  2.47398434, -0.28304842])
```

# Feature Selection: LASSO (L1)

- LASSO or $\ell_1$ or `l1` regularization drives the coefficient of uninformative features to 0

In [30]:
```
from sklearn.linear_model import LogisticRegression

# First, without regularization
#   C is the inverse regularization strength: higher means less regularization
logr = LogisticRegression(C=100, penalty="l1", solver="liblinear", random_state=123)
logr.fit(X_train, y_train)
logr.coef_[0,:5]
```

Out[30]:
```
array([-5.74709641, -1.20824931, -2.70057811,  2.47398434, -0.28304842])
```

In [31]:
```
sorted_tuples = sorted(list(zip(X_train.columns.values,logr.coef_[0])),key=lambda x:x[1],reverse=True)
for feature,coef in sorted_tuples:
    print(f'{feature:30s} : {coef: 0.3f}')
```

```
alcalinity_of_ash              :  2.474
proanthocyanins                :  1.144
hue                            :  1.069
nonflavanoid_phenols           :  0.000
total_phenols                  : -0.146
magnesium                      : -0.283
flavanoids                     : -0.376
color_intensity                : -0.638
od280/od315_of_diluted_wines   : -0.860
malic_acid                     : -1.208
ash                            : -2.701
alcohol                        : -5.747
proline                        : -7.568
```

# Feature Selection: LASSO (L1) Cont.

# Feature Selection: LASSO (L1) Cont.

In [32]:
```
# Now with LASSO
logr = LogisticRegression(C=0.1, penalty="l1", solver="liblinear", random_state=123)
logr.fit(X_train, y_train)

sorted_tuples = sorted(list(zip(X_train.columns.values,logr.coef_[0])),key=lambda x:x[1],reverse=True)
for feature,coef in sorted_tuples:
    print(f'{feature:30s} : {coef: 0.3f}')
```

```
malic_acid                     :  0.000
ash                            :  0.000
alcalinity_of_ash              :  0.000
magnesium                      :  0.000
total_phenols                  :  0.000
nonflavanoid_phenols           :  0.000
proanthocyanins                :  0.000
color_intensity                :  0.000
hue                            :  0.000
od280/od315_of_diluted_wines   :  0.000
flavanoids                     : -0.007
alcohol                        : -0.982
proline                        : -1.102
```

# Feature Selection: LASSO (L1) Cont.

In [32]:
```
# Now with LASSO
logr = LogisticRegression(C=0.1, penalty="l1", solver="liblinear", random_state=123)
logr.fit(X_train, y_train)

sorted_tuples = sorted(list(zip(X_train.columns.values,logr.coef_[0])),key=lambda x:x[1],reverse=True)
for feature,coef in sorted_tuples:
    print(f'{feature:30s} : {coef: 0.3f}')
```

```
malic_acid                     :  0.000
ash                            :  0.000
alcalinity_of_ash              :  0.000
magnesium                      :  0.000
total_phenols                  :  0.000
nonflavanoid_phenols           :  0.000
proanthocyanins                :  0.000
color_intensity                :  0.000
hue                            :  0.000
od280/od315_of_diluted_wines   :  0.000
flavanoids                     : -0.007
alcohol                        : -0.982
proline                        : -1.102
```

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

Out[33]:
```
Index(['alcohol', 'flavanoids', '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

# 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

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

rf = RandomForestClassifier(random_state=123).fit(X_train,y_train)
rf.feature_importances_ # (normalized) total reduction of function measuring impurity
```

Out[34]:
```
array([0.27332426, 0.01783127, 0.01145411, 0.05480187, 0.05158374,
       0.05521824, 0.10260545, 0.01117794, 0.01033494, 0.13339066,
       0.00759636, 0.0216486 , 0.24903258])
```

# 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

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

rf = RandomForestClassifier(random_state=123).fit(X_train,y_train)
rf.feature_importances_ # (normalized) total reduction of function measuring impurity
```

Out[34]:
```
array([0.27332426, 0.01783127, 0.01145411, 0.05480187, 0.05158374,
       0.05521824, 0.10260545, 0.01117794, 0.01033494, 0.13339066,
       0.00759636, 0.0216486 , 0.24903258])
```

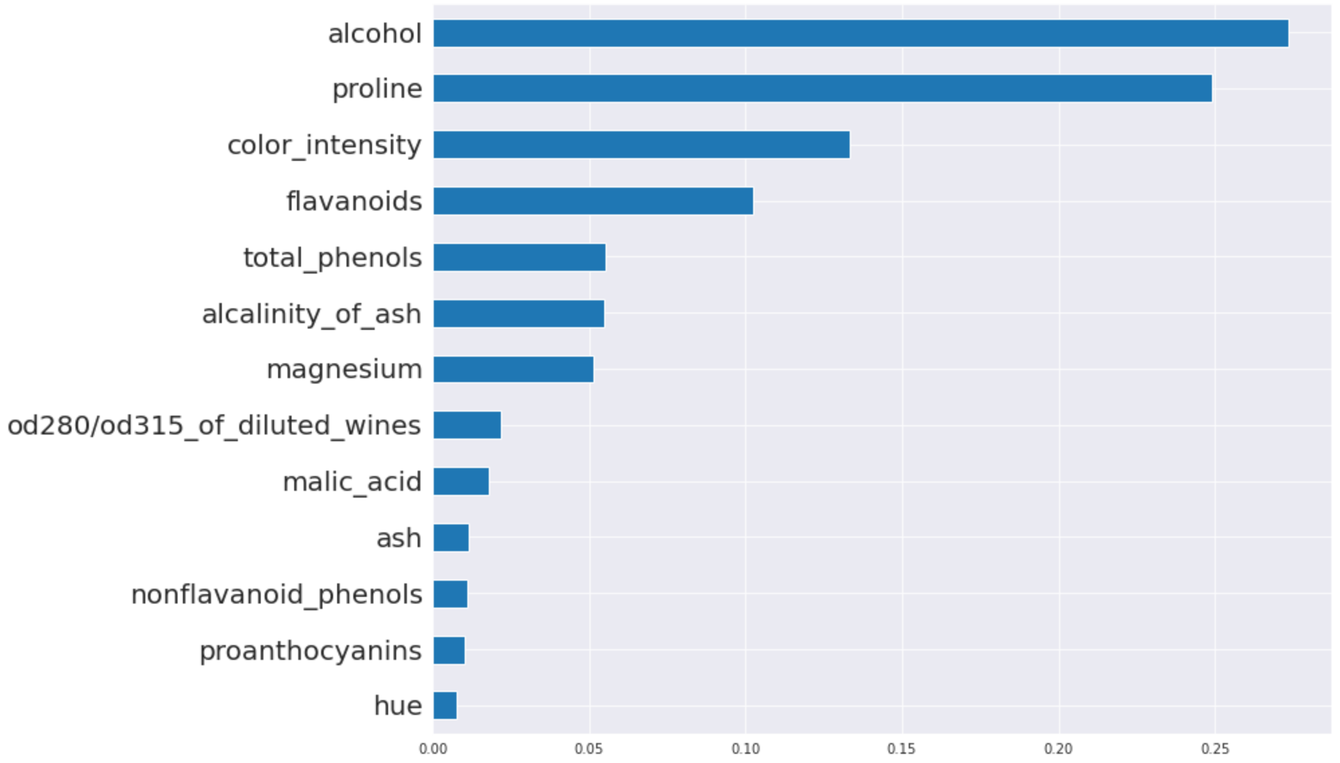
In [35]:
```
feature_importances = pd.Series(rf.feature_importances_,index=X_train.columns)
feature_importances.sort_values(ascending=False).round(3)
```

Out[35]:
```
alcohol                         0.273
proline                         0.249
color_intensity                 0.133
flavanoids                      0.103
total_phenols                   0.055
alcalinity_of_ash               0.055
magnesium                       0.052
od280/od315_of_diluted_wines    0.022
malic_acid                      0.018
ash                             0.011
nonflavanoid_phenols            0.011
proanthocyanins                 0.010
hue                             0.008
dtype: float64
```

# Feature Selection: Tree Based Model Feature Importance

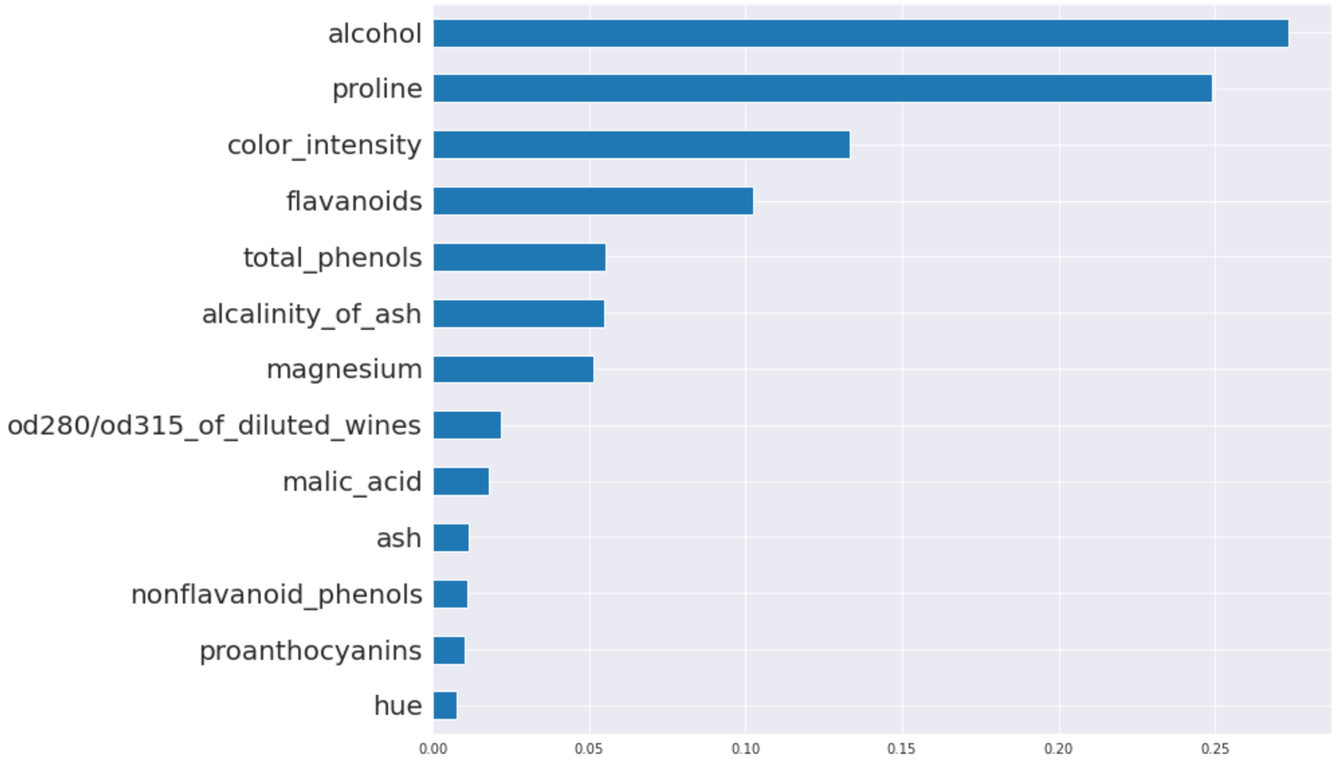
# Feature Selection: Tree Based Model Feature Importance

In [36]:
```
fig,ax = plt.subplots(1,1,figsize=(12,10))
feature_importances.sort_values().plot.barh(ax=ax);
ax.set_yticklabels(ax.get_yticklabels(),fontsize=20);
```



# Feature Selection: Tree Based Model Feature Importance

In [36]:
```
fig,ax = plt.subplots(1,1,figsize=(12,10))
feature_importances.sort_values().plot.barh(ax=ax);
ax.set_yticklabels(ax.get_yticklabels(),fontsize=20);
```




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

# Feature Selection: SelectFromModel

# Feature Selection: SelectFromModel

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

sfm = SelectFromModel(logr,
                      threshold=None, # if model uses l1 regularization, anything greater than 1e-5, otherwise mean
                      prefit=True     # do not need to re-fit
                     )

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

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

# Feature Selection: SelectFromModel

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

sfm = SelectFromModel(logr,
                      threshold=None, # if model uses l1 regularization, anything greater than 1e-5, otherwise mean
                      prefit=True     # do not need to re-fit
                     )

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

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

In [38]:
```
X_train.columns[sfm.get_support()]
```

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

# Feature Selection: SelectFromModel

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

sfm = SelectFromModel(logr,
                      threshold=None, # if model uses l1 regularization, anything greater than 1e-5, otherwise mean
                      prefit=True     # do not need to re-fit
                     )

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

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

In [38]:
```
X_train.columns[sfm.get_support()]
```

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

In [39]:
```
X_train_subset = sfm.transform(X_train)
X_train_subset.shape
```

Out[39]:
```
(97, 3)
```

# Feature Selection: SelectFromModel

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

sfm = SelectFromModel(logr,
                      threshold=None, # if model uses l1 regularization, anything greater than 1e-5, otherwise mean
                      prefit=True     # do not need to re-fit
                     )

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

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

In [38]:
```
X_train.columns[sfm.get_support()]
```

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

In [39]:
```
X_train_subset = sfm.transform(X_train)
X_train_subset.shape
```

Out[39]:
```
(97, 3)
```

In [40]:
```
X_train_subset[:3] # note that this is no-longer a dataframe
```

Out[40]:
```
array([[ 0.17492287, -0.59267761, -1.08166225],
       [-0.62220886, -0.86167036, -0.05826353],
       [ 1.51865922,  0.33385297,  0.88509284]])
```

# 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
                         prefit=False        # will refit
                        ).fit(X_train,y_train)

X_train.columns[sfm_rf.get_support()]

sfm_rf = SelectFromModel(RandomForestClassifier(),threshold='mean')
X_train_subset = sfm_rf.fit_transform(X_train,y_train)
X_test_subset = sfm_rf.transform(X_test)
```

# Feature Selection: SelectFromModel Cont.

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

X_train.columns[sfm_rf.get_support()]

sfm_rf = SelectFromModel(RandomForestClassifier(),threshold='mean')
X_train_subset = sfm_rf.fit_transform(X_train,y_train)
X_test_subset = sfm_rf.transform(X_test)
```

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

Out[42]:
```
0.07692307692307693
```

# Feature Selection: SelectFromModel Cont.

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

X_train.columns[sfm_rf.get_support()]

sfm_rf = SelectFromModel(RandomForestClassifier(),threshold='mean')
X_train_subset = sfm_rf.fit_transform(X_train,y_train)
X_test_subset = sfm_rf.transform(X_test)
```

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

Out[42]:
```
0.07692307692307693
```

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

Out[43]:
```
proline                         0.284
alcohol                         0.229
color_intensity                 0.157
flavanoids                      0.101
total_phenols                   0.058
magnesium                       0.057
alcalinity_of_ash               0.048
od280/od315_of_diluted_wines    0.015
nonflavanoid_phenols            0.014
ash                             0.010
hue                             0.010
proanthocyanins                 0.009
malic_acid                      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

# 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 [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)
list(X_wine.columns[kbest.get_support()])
```

Out[44]:
```
['alcohol', 'color_intensity', 'proline']
```

# 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

# 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

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

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

X_train.columns[rfe.get_support()]
```

Out[45]:
```
Index(['alcohol', 'alcalinity_of_ash', '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?

# Changing number of features: Use Adjusted $R^2$

# Changing number of features: Use Adjusted $R^2$

- Adding features guarantees an increase in $R^2$
- $R^2$ describes the proportion of explained variance
- Additional features explain more variance

# Changing number of features: Use Adjusted $R^2$

- Adding features guarantees an increase in $R^2$
- $R^2$ describes the proportion of explained variance
- Additional features explain more variance

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

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

# Changing number of features: Use Adjusted $R^2$

- Adding features guarantees an increase in $R^2$
- $R^2$ describes the proportion of explained variance
- Additional features explain more variance

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

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

In [46]:
```
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.

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

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

X_r = X_train.iloc[:,1:]
y_r = X_train.iloc[:,0]  # predict alcohol from other features

lr = LinearRegression()
print(lr.fit(X_r.iloc[:,:3],y_r).score(X_r.iloc[:,:3],y_r))
print(lr.fit(X_r.iloc[:,:],y_r).score(X_r.iloc[:,:],y_r))
```

```
0.3940307310415285
0.7455685143343734
```

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

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

X_r = X_train.iloc[:,1:]
y_r = X_train.iloc[:,0]  # predict alcohol from other features

lr = LinearRegression()
print(lr.fit(X_r.iloc[:,:3],y_r).score(X_r.iloc[:,:3],y_r))
print(lr.fit(X_r.iloc[:,:],y_r).score(X_r.iloc[:,:],y_r))
```

```
0.3940307310415285
0.7455685143343734
```

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

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

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

X_r = X_train.iloc[:,1:]
y_r = X_train.iloc[:,0]  # predict alcohol from other features

lr = LinearRegression()
print(lr.fit(X_r.iloc[:,:3],y_r).score(X_r.iloc[:,:3],y_r))
print(lr.fit(X_r.iloc[:,:],y_r).score(X_r.iloc[:,:],y_r))
```

```
0.3940307310415285
0.7455685143343734
```

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

In [48]:
```
print(adj_r2(lr.fit(X_r.iloc[:,:3],y_r),X_r.iloc[:,:3],y_r))
print(adj_r2(lr.fit(X_r.iloc[:,:],y_r),X_r.iloc[:,:],y_r))
```

```
0.3744833352686746
0.7092211592392839
```

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

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

X_r = X_train.iloc[:,1:]
y_r = X_train.iloc[:,0]  # predict alcohol from other features

lr = LinearRegression()
print(lr.fit(X_r.iloc[:,:3],y_r).score(X_r.iloc[:,:3],y_r))
print(lr.fit(X_r.iloc[:,:],y_r).score(X_r.iloc[:,:],y_r))
```

```
0.3940307310415285
0.7455685143343734
```

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

In [48]:
```
print(adj_r2(lr.fit(X_r.iloc[:,:3],y_r),X_r.iloc[:,:3],y_r))
print(adj_r2(lr.fit(X_r.iloc[:,:],y_r),X_r.iloc[:,:],y_r))
```

```
0.3744833352686746
0.7092211592392839
```

- 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]:
```
from statsmodels.api import OLS

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

```
0.709648775181579
```

Out[49]:

OLS Regression Results

| | | | |
|---|---|---|---|
| **Dep. Variable:** | alcohol | **R-squared (uncentered):** | 0.746 |
| **Model:** | OLS | **Adj. R-squared (uncentered):** | 0.710 |
| **Method:** | Least Squares | **F-statistic:** | 20.76 |
| **Date:** | Mon, 15 Nov 2021 | **Prob (F-statistic):** | 2.12e-20 |
| **Time:** | 14:22:21 | **Log-Likelihood:** | -71.254 |
| **No. Observations:** | 97 | **AIC:** | 166.5 |
| **Df Residuals:** | 85 | **BIC:** | 197.4 |
| **Df Model:** | 12 | | |
| **Covariance Type:** | nonrobust | | |

| | coef | std err | t | P>\|t\| | [0.025 | 0.975] |
|---|---|---|---|---|---|---|
| **malic_acid** | 0.1412 | 0.064 | 2.201 | 0.030 | 0.014 | 0.269 |
| **ash** | -0.0380 | 0.080 | -0.473 | 0.637 | -0.197 | 0.122 |
| **alcalinity_of_ash** | -0.0283 | 0.082 | -0.347 | 0.730 | -0.191 | 0.134 |
| **magnesium** | 0.1268 | 0.072 | 1.763 | 0.081 | -0.016 | 0.270 |
| **total_phenols** | -0.1925 | 0.116 | -1.665 | 0.100 | -0.422 | 0.037 |
| **flavanoids** | 0.2984 | 0.149 | 1.996 | 0.049 | 0.001 | 0.596 |
| **nonflavanoid_phenols** | -0.0106 | 0.087 | -0.122 | 0.903 | -0.183 | 0.162 |
| **proanthocyanins** | -0.1724 | 0.076 | -2.257 | 0.027 | -0.324 | -0.021 |
| **color_intensity** | 0.3969 | 0.116 | 3.423 | 0.001 | 0.166 | 0.627 |
| **hue** | -0.0260 | 0.064 | -0.410 | 0.683 | -0.152 | 0.100 |

# 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

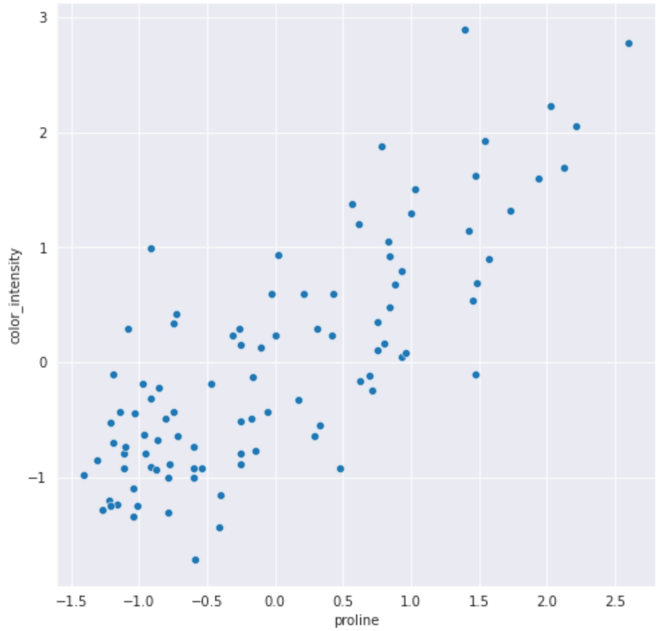
# Principal Component Analysis (PCA)

- How it works:
    0. first center the data (subtract the means)
    1. first component:
        - direction (combination of features)
        - explains maximum variance
    2. 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

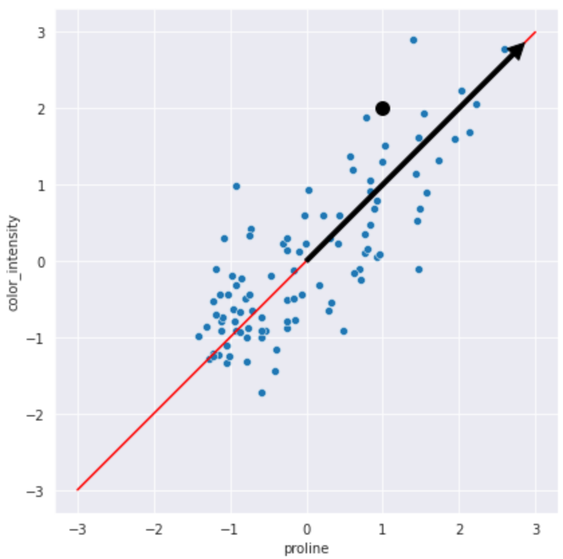
In [51]:
```
fig,ax = plt.subplots(1,1,figsize=(8,8))
sns.scatterplot(x='proline',y='color_intensity',data=X_train,ax=ax);
```

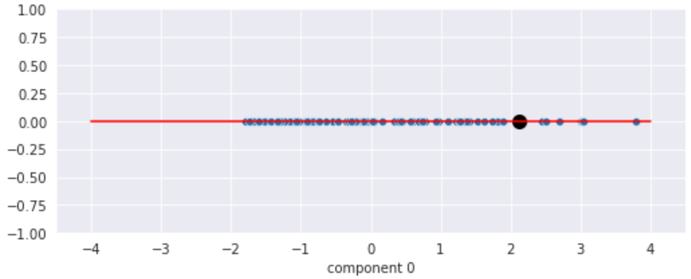


# PCA Example Cont.

# PCA Example Cont.

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

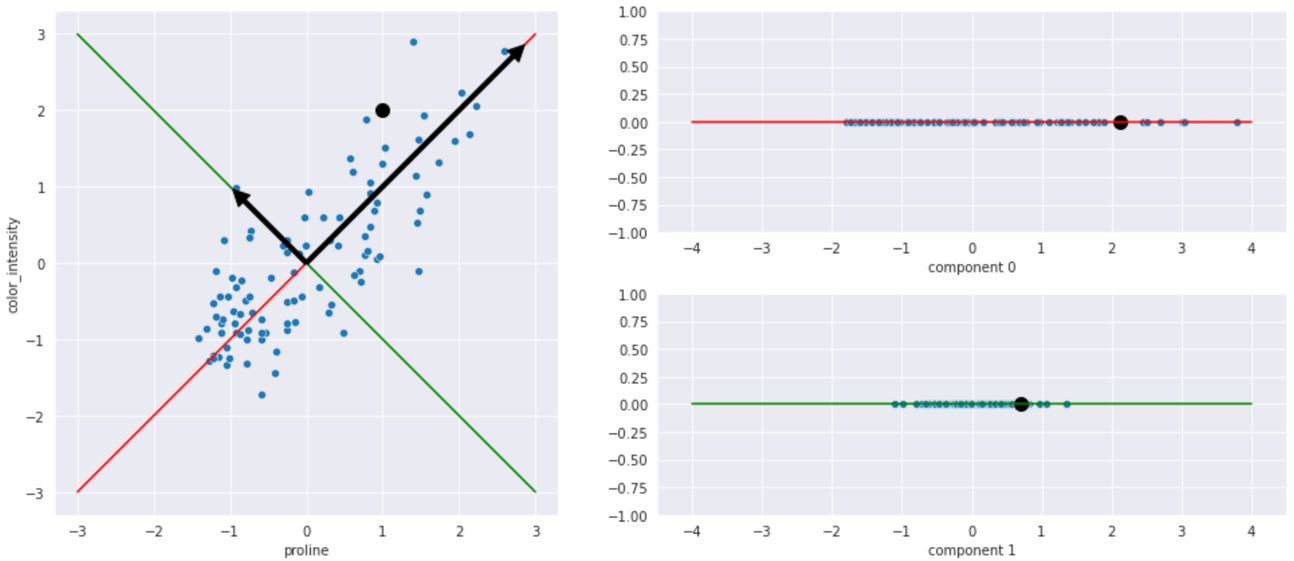


# PCA Example Cont.

# PCA Example Cont.

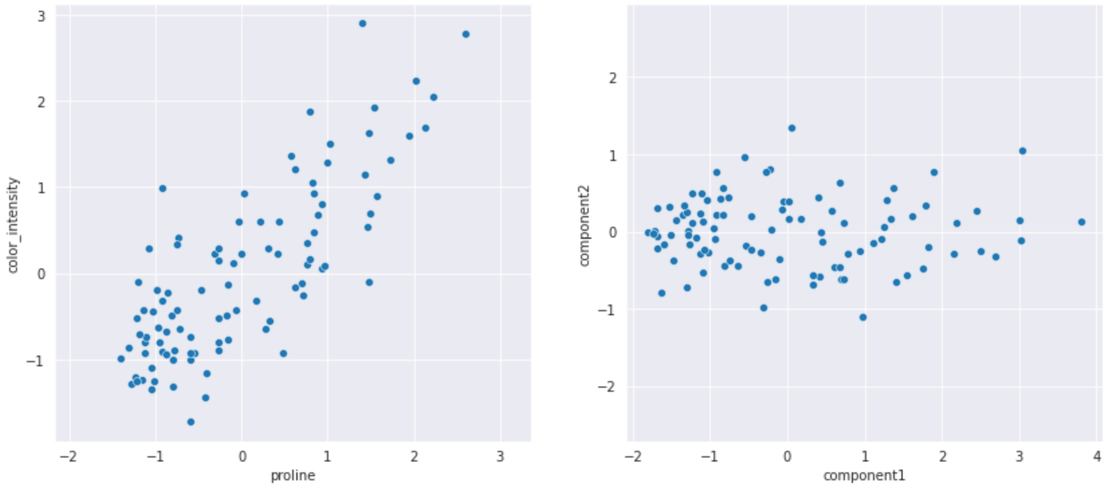
In [54]:
```
plot_pca(X_train[['proline','color_intensity']],pca,num_components=2)
plt.tight_layout()
```



# PCA in sklearn

# PCA in sklearn

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

# extract the first 2 principle compenents
pca = PCA(n_components=2)
X_pca = pca.fit_transform(X_train[['proline','color_intensity']])

X_pca = pd.DataFrame(X_pca,columns=['component1','component2'])


fig,ax=plt.subplots(1,2,figsize=(14,6))
sns.scatterplot(x='proline',y='color_intensity',data=X_train,ax=ax[0]);
sns.scatterplot(x='component1',y='component2',data=X_pca,ax=ax[1]);
ax[0].axis('equal');ax[1].axis('equal');
```



# PCA: Explained Variance

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

# PCA: Explained Variance

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

In [56]:
```
pca.explained_variance_ratio_
```

Out[56]:
```
array([0.89808764, 0.10191236])
```

# PCA: Principle Components

- What does the first component (vector) look like?

# PCA: Principle Components

- What does the first component (vector) look like?

In [57]:
```
pca.components_[0]
```

Out[57]:
```
array([0.70710678, 0.70710678])
```

# PCA: Principle Components

- What does the first component (vector) look like?

In [57]:
```
pca.components_[0]
```

Out[57]:
```
array([0.70710678, 0.70710678])
```

- And the second?

# PCA: Principle Components

- What does the first component (vector) look like?

In [57]:
```
pca.components_[0]
```

Out[57]:
```
array([0.70710678, 0.70710678])
```

- And the second?

In [58]:
```
pca.components_[1]
```

Out[58]:
```
array([-0.70710678,  0.70710678])
```

# PCA: Principle Components

- What does the first component (vector) look like?

```
In [57]: pca.components_[0]
```

```
Out[57]: array([0.70710678, 0.70710678])
```

- And the second?

```
In [58]: pca.components_[1]
```

```
Out[58]: array([-0.70710678,  0.70710678])
```

- All components returned

# PCA: Principle Components

- What does the first component (vector) look like?

In [57]:
```
pca.components_[0]
```

Out[57]:
```
array([0.70710678, 0.70710678])
```

- And the second?

In [58]:
```
pca.components_[1]
```

Out[58]:
```
array([-0.70710678,  0.70710678])
```

- All components returned

In [59]:
```
pca.components_
```

Out[59]:
```
array([[ 0.70710678,  0.70710678],
       [-0.70710678,  0.70710678]])
```

# PCA: Principle Components

- What does the first component (vector) look like?

In [57]:
```
pca.components_[0]
```

Out[57]:
```
array([0.70710678, 0.70710678])
```

- And the second?

In [58]:
```
pca.components_[1]
```

Out[58]:
```
array([-0.70710678,  0.70710678])
```

- All components returned

In [59]:
```
pca.components_
```

Out[59]:
```
array([[ 0.70710678,  0.70710678],
       [-0.70710678,  0.70710678]])
```

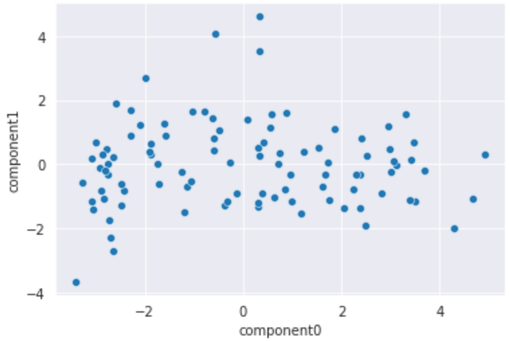
In [60]:
```
# Can also return the singular values themselves
pca.singular_values_
```

Out[60]:
```
array([13.1995834 ,  4.44645904])
```

# Dimensionality Reduction with PCA

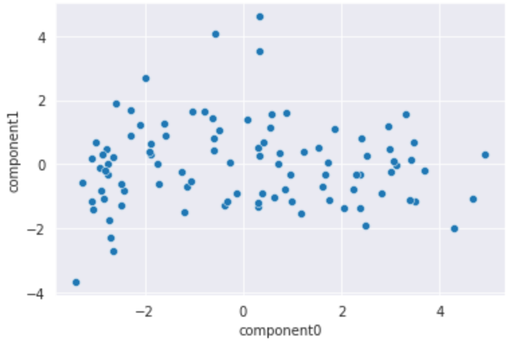
# Dimensionality Reduction with PCA

In [61]:
```
pca_2d = PCA(n_components=2)
X_2d = pca_2d.fit_transform(X_train)
X_2d = pd.DataFrame(X_2d, columns=["component"+str(i) for i in range(2)])
sns.scatterplot(x='component0',y='component1',data=X_2d);
```



# Dimensionality Reduction with PCA

In [61]:
```
pca_2d = PCA(n_components=2)
X_2d = pca_2d.fit_transform(X_train)
X_2d = pd.DataFrame(X_2d, columns=["component"+str(i) for i in range(2)])
sns.scatterplot(x='component0',y='component1',data=X_2d);
```




In [62]:
```
print(' + \n'.join([f'{w: 0.2f}*{f}' for f,w in sorted(zip(X_train.columns,pca_2d.components_[0]),key=lambda x:x[1])]))
```

```
-0.28*nonflavanoid_phenols +
-0.26*alcalinity_of_ash +
-0.03*hue +
 0.01*malic_acid +
 0.11*ash +
 0.21*proanthocyanins +
 0.23*magnesium +
 0.25*od280/od315_of_diluted_wines +
 0.36*proline +
 0.36*color_intensity +
 0.36*total_phenols +
 0.37*alcohol +
 0.39*flavanoids
```

# 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

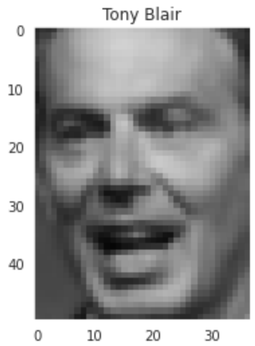
In [64]:
```
from sklearn.datasets import fetch_lfw_people

lfw_people = fetch_lfw_people(min_faces_per_person=70, resize=0.4)
```

# Example Dataset: Labeled Faces in th Wild (LFW)

## Labeled Faces in the Wild

In [64]:
```
from sklearn.datasets import fetch_lfw_people

lfw_people = fetch_lfw_people(min_faces_per_person=70, resize=0.4)
```

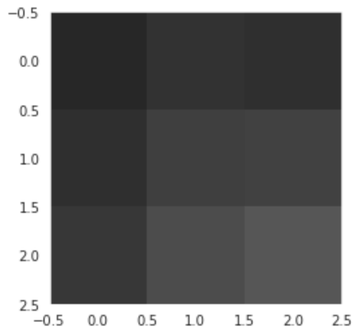
In [65]:
```
sns.set_style('dark')
plt.imshow(lfw_people.images[1], cmap=plt.cm.gray, vmin=0, vmax=255)
plt.title(lfw_people.target_names[lfw_people.target[1]], size=12);
```



# Example Pixel Values

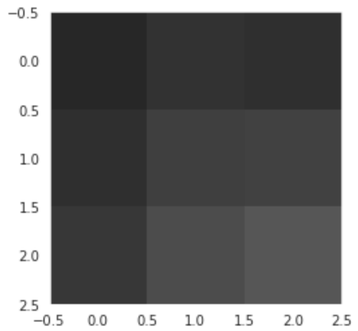
# Example Pixel Values

In [66]:
```
# first 3x3 set of pixels
plt.imshow(lfw_people.images[1][:3,:3],cmap=plt.cm.gray,vmin=0, vmax=255);
```



# Example Pixel Values

In [66]:
```
# first 3x3 set of pixels
plt.imshow(lfw_people.images[1][:3,:3],cmap=plt.cm.gray,vmin=0, vmax=255);
```




In [67]:
```
lfw_people.images[1][:3,:3]
```

Out[67]:
```
array([[39.666668, 50.333332, 47.      ],
       [47.666668, 63.      , 65.333336],
       [55.333332, 76.666664, 86.333336]], 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 [68]:
```
lfw_people.images[1].shape
```

Out[68]:
```
(50, 37)
```

# Representing each Image: Flatten

- Grid as a fixed length feature vector?

In [68]:
```
lfw_people.images[1].shape
```

Out[68]:
```
(50, 37)
```

In [69]:
```
x = lfw_people.images[1].reshape(1,-1)
x
```

Out[69]:
```
array([[ 39.666668,  50.333332,  47.      , ..., 117.666664, 115.      ,
         133.66667 ]], dtype=float32)
```

# Representing each Image: Flatten

- Grid as a fixed length feature vector?

In [68]:
```
lfw_people.images[1].shape
```

Out[68]:
```
(50, 37)
```

In [69]:
```
x = lfw_people.images[1].reshape(1,-1)
x
```

Out[69]:
```
array([[ 39.666668,  50.333332,  47.      , ..., 117.666664, 115.      ,
        133.66667 ]], dtype=float32)
```

In [70]:
```
x.shape
```

Out[70]:
```
(1, 1850)
```

# Representing each Image: Flatten

- Grid as a fixed length feature vector?

In [68]:
```
lfw_people.images[1].shape
```

Out[68]:
```
(50, 37)
```

In [69]:
```
x = lfw_people.images[1].reshape(1,-1)
x
```

Out[69]:
```
array([[ 39.666668,  50.333332,  47.      , ..., 117.666664, 115.      ,
        133.66667 ]], dtype=float32)
```

In [70]:
```
x.shape
```

Out[70]:
```
(1, 1850)
```

What information do we lose when we do this?

# Create a Dataset

# Create a Dataset

In [71]:
```
# 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=123)

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: 50x37
n_features: 1850
n_classes : 7
n_train   : 966
n_test    : 322
```

# Compute PCA and Transform

# Compute PCA and Transform

In [72]:
```
# set the number of dimensions we want to retain
n_components = 150

# 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_pca_faces = pca_faces.transform(X_train_faces)
X_test_pca_faces = pca_faces.transform(X_test_faces)
```

# Compute PCA and Transform

In [72]:
```
# set the number of dimensions we want to retain
n_components = 150

# 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_pca_faces = pca_faces.transform(X_train_faces)
X_test_pca_faces = pca_faces.transform(X_test_faces)
```

In [73]:
```
pca_faces.components_[0]
```

Out[73]:
```
array([-0.01278668, -0.01292658, -0.01463957, ..., -0.00385124,
       -0.00411337, -0.0045574 ], dtype=float32)
```

# Compute PCA and Transform

In [72]:
```
# set the number of dimensions we want to retain
n_components = 150

# 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_pca_faces = pca_faces.transform(X_train_faces)
X_test_pca_faces = pca_faces.transform(X_test_faces)
```

In [73]:
```
pca_faces.components_[0]
```

Out[73]:
```
array([-0.01278668, -0.01292658, -0.01463957, ..., -0.00385124,
       -0.00411337, -0.0045574 ], dtype=float32)
```

In [74]:
```
pca_faces.singular_values_
```

Out[74]:
```
array([21388.467  , 19735.988  , 13733.558  , 12266.252  , 11349.948  ,
        8755.401  ,  7928.223  ,  7296.223  ,  7035.028  ,  6864.7207 ,
        6348.1304 ,  6118.6055 ,  5526.047  ,  5221.793  ,  4977.621  ,
        4962.2236 ,  4785.6265 ,  4679.6924 ,  4524.9766 ,  4275.846  ,
        4209.652  ,  4032.5813 ,  3924.0525 ,  3801.2917 ,  3723.4976 ,
        3675.6616 ,  3581.645  ,  3497.1353 ,  3378.749  ,  3268.003  ,
        3137.3608 ,  3030.9197 ,  3017.3242 ,  2981.4546 ,  2897.5417 ,
        2858.5464 ,  2792.041  ,  2762.1348 ,  2726.447  ,  2702.855  ,
        2661.0544 ,  2591.7307 ,  2543.3933 ,  2526.289  ,  2459.802  ,
        2429.5876 ,  2417.179  ,  2379.5273 ,  2339.4941 ,  2332.3047 ,
        2293.3118 ,  2283.203  ,  2221.0967 ,  2194.8472 ,  2160.4968 ,
```

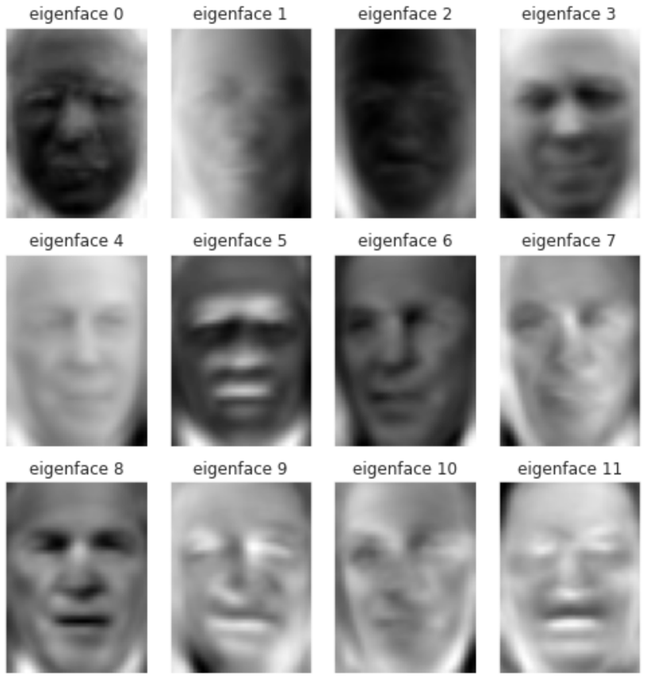
# Eigenfaces

- 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 [76]:
```
eigenface_titles = ["eigenface %d" % i for i in range(eigenfaces.shape[0])]
plot_gallery(eigenfaces, eigenface_titles, h, w)
plt.tight_layout()
```



# Train and Tune SVC

# Train and Tune SVC

In [77]:
```
%%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 = GridSearchCV(SVC(kernel='rbf', class_weight='balanced'),
                         params, cv=3, n_jobs=-1)
clf_faces = clf_faces.fit(X_train_pca_faces, y_train_faces)
```

```
CPU times: user 258 ms, sys: 133 ms, total: 391 ms
Wall time: 2.71 s
```

# Train and Tune SVC

In [77]:
```
%%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 = GridSearchCV(SVC(kernel='rbf', class_weight='balanced'),
                         params, cv=3, n_jobs=-1)
clf_faces = clf_faces.fit(X_train_pca_faces, y_train_faces)
```

```
CPU times: user 258 ms, sys: 133 ms, total: 391 ms
Wall time: 2.71 s
```

In [78]:
```
print(f"best_params : {clf_faces.best_params_}")
print(f"best_score  : {clf_faces.best_score_:0.2f}")
```

```
best_params : {'C': 1000.0, 'gamma': 0.005}
best_score  : 0.79
```

# Evaluate on the test set

# Evaluate on the test set

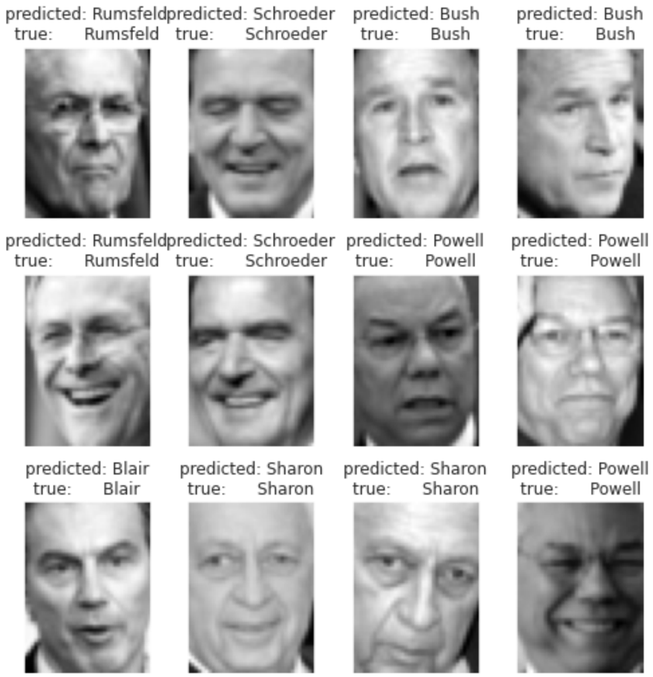
In [79]:
```
y_pred = clf_faces.predict(X_test_pca_faces)
from sklearn.metrics import classification_report
print(classification_report(y_test_faces, y_pred, target_names=target_names))
```

```
                   precision    recall  f1-score   support

     Ariel Sharon       0.93      0.74      0.82        19
     Colin Powell       0.82      0.86      0.84        59
  Donald Rumsfeld       0.89      0.83      0.86        30
    George W Bush       0.84      0.97      0.90       133
Gerhard Schroeder       1.00      0.52      0.68        27
      Hugo Chavez       1.00      0.61      0.76        18
       Tony Blair       0.84      0.89      0.86        36

         accuracy                           0.86       322
        macro avg       0.90      0.77      0.82       322
     weighted avg       0.87      0.86      0.85       322
```

# Prediction Examples

# Prediction Examples

In [80]:
```
prediction_titles = [title(y_pred, y_test_faces, target_names, i)
                     for i in range(y_pred.shape[0])]

plot_gallery(X_test_faces, prediction_titles, h, w)
plt.tight_layout()
```



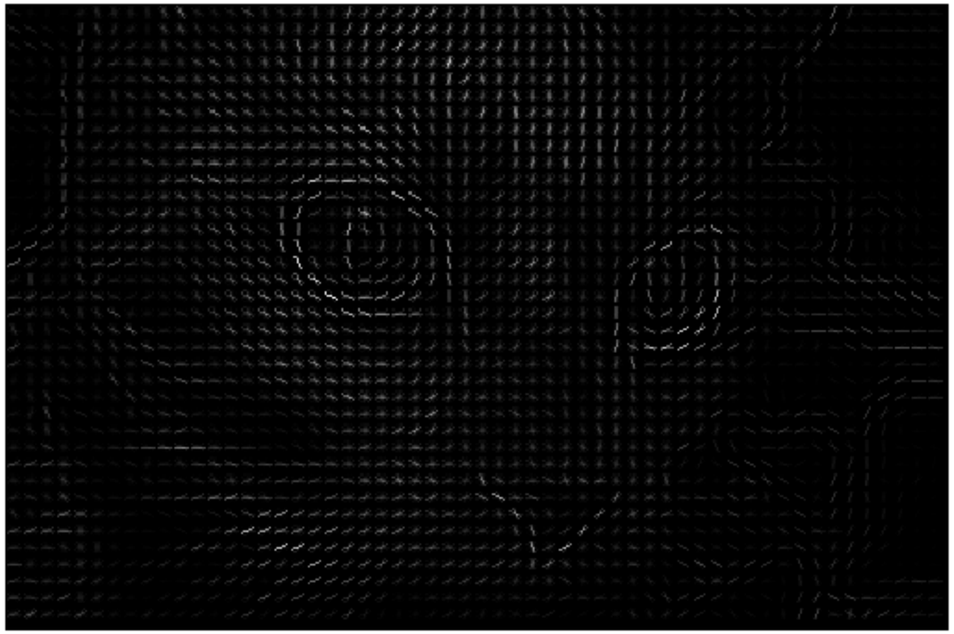
# Performance without PCA

# Performance without PCA

```
%%time

# Warning: this cell takes up to 2 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 = GridSearchCV(SVC(kernel='rbf', class_weight='balanced'),
                         params, cv=3, n_jobs=-1)
clf_faces = clf_faces.fit(X_train_faces, y_train_faces)

# CPU times: user 9.57 s, sys: 72.1 ms, total: 9.64 s
# Wall time: 1min 18s

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

# best_params : {'C': 1000.0, 'gamma': 0.0001}
# best_score  : 0.41
```

# Other Image Recognition Methods

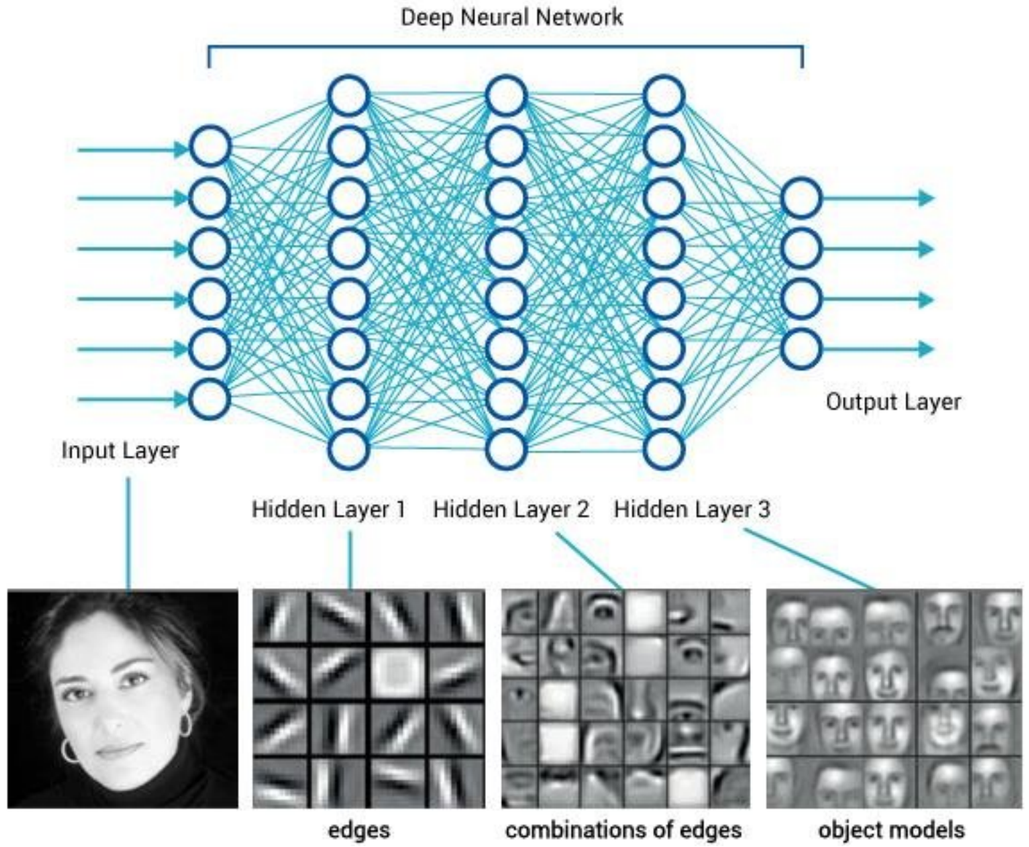
- With Feature Engineering and general models
  - ex: Histogram of Oriented Gradients or HOG (See PDSH Chap 5)
  - many more (See scikit-image)



From PDSH

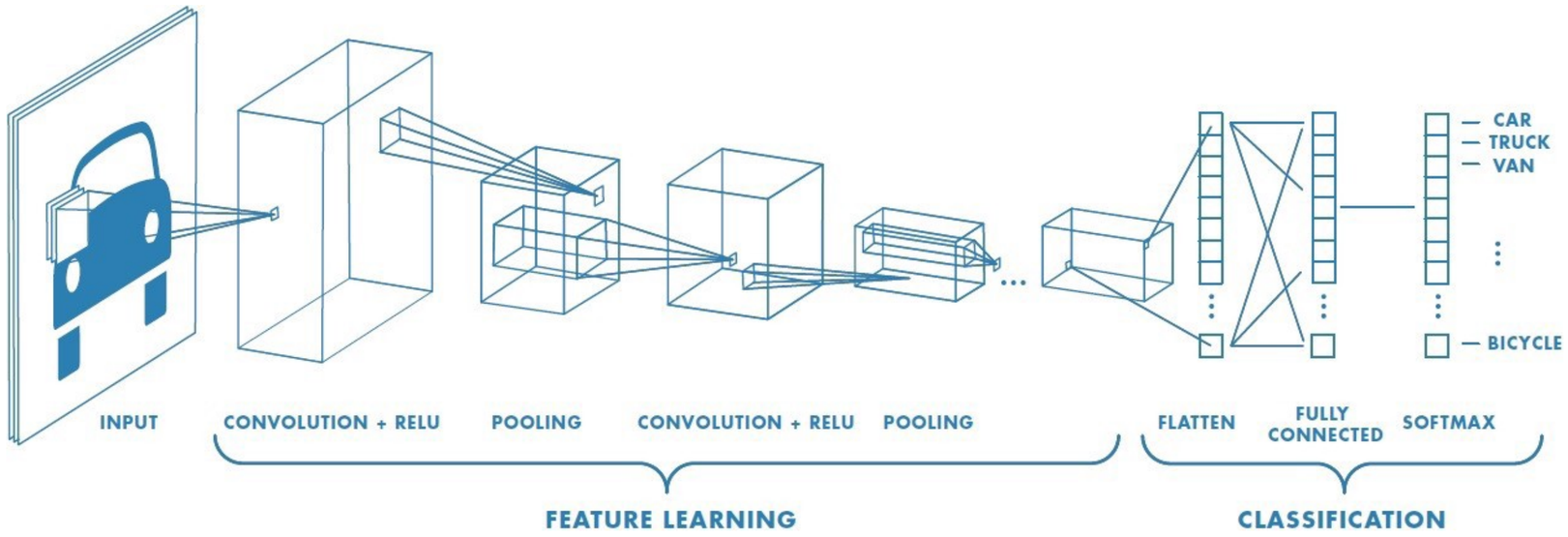
# Other Image Recognition Methods: Deep Neural Networks

- 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