Elements Of Data Science - F2024

Week 9: Dimensionality Reduction, Feature Selection and Feature Extraction

11/18/2024

TODOs

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

- HW 3, Due **Mon Dec 2nd, 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]:

```
import numpy
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

from mlxtend.plotting import plot_decision_regions

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

Joing Datasets

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

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

In [3]:

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

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

Joing Datasets

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

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

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

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

	flower_id	name
0	1001	iris
1	1002	rose

	flower_id	price
0	1002	3.99
1	1003	2.25

Joing Datasets On Index

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

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

Out[5]:

	flower_id	name
0	1001	iris
1	1002	rose

Joing Datasets On Index

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

In [5]:
```
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

Joing Datasets On Index

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

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

Out[5]:

	flower_id	name
0	1001	iris
1	1002	rose

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

Out[6]:

	name
flower_id	
1001	iris
1002	rose

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

Out[7]:

	price
flower_id	
1002	3.99
1003	2.25

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

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

In [8]:
```
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 [9]:
```
1 df_flower_name.join(df_flower_price)
2 # df_flower_price.join(df_flower_name)
```

Out[9]:

	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)
```

flower_id	name
1001	iris
1002	rose

flower_id	price
1002	3.99
1003	2.25

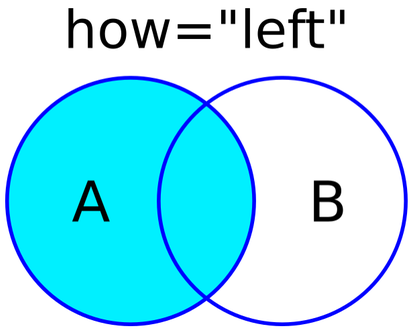
In [9]:
```
1 df_flower_name.join(df_flower_price)
2 # df_flower_price.join(df_flower_name)
```

Out[9]:

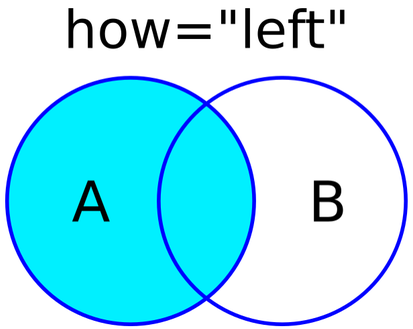
flower_id	name	price
1001	iris	NaN
1002	rose	3.99

- by default, this is a 'Left Join'

Join Types: Left Join



Join Types: Left Join

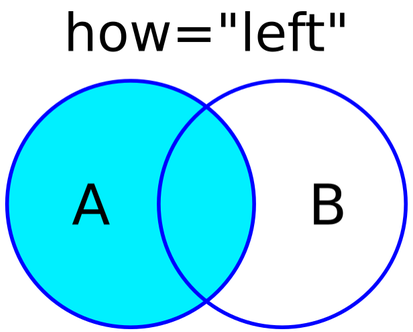


In [10]:
```
1 display(df_flower_name,df_flower_price)
```

	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

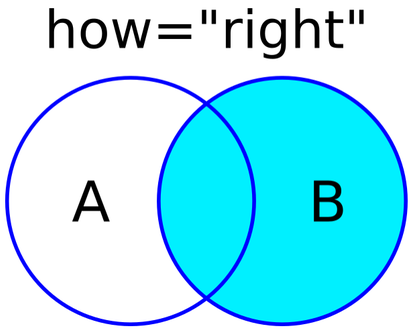
	price
flower_id	
1002	3.99
1003	2.25

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

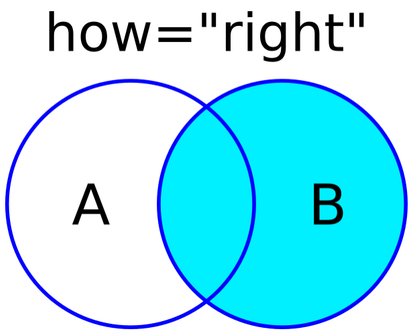
Out[11]:

	name	price
flower_id		
1001	iris	NaN
1002	rose	3.99

Join Types: Right Join



Join Types: Right Join

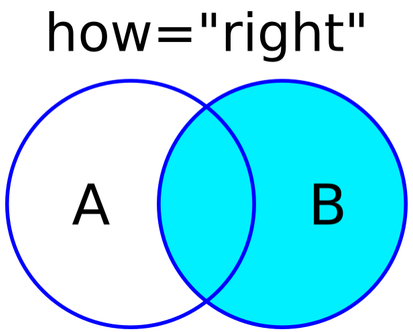


In [12]:
```
1 display(df_flower_name,df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

	price
flower_id	
1002	3.99
1003	2.25

Join Types: Right Join



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

	name
flower_id	
1001	iris
1002	rose

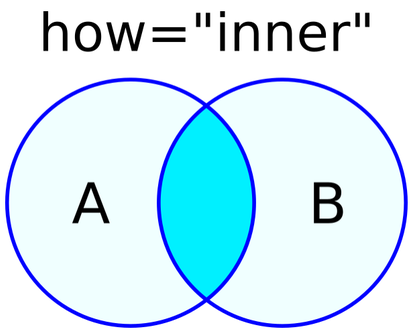
	price
flower_id	
1002	3.99
1003	2.25

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

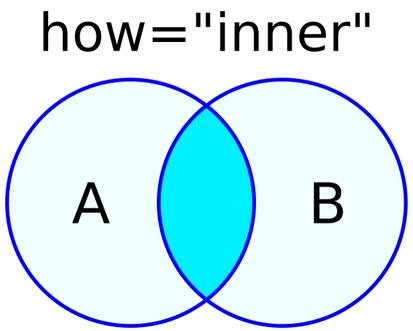
Out[13]:

	name	price
flower_id		
1002	rose	3.99
1003	NaN	2.25

Join Types: Inner Join



Join Types: Inner Join

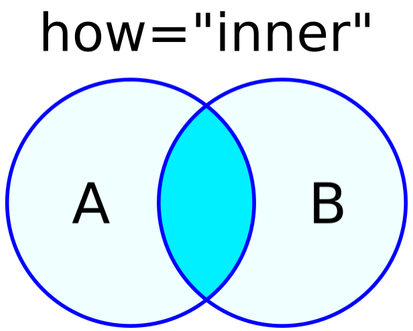


In [14]:
```
1 display(df_flower_name,df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

	price
flower_id	
1002	3.99
1003	2.25

Join Types: Inner Join



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

	name
flower_id	
1001	iris
1002	rose

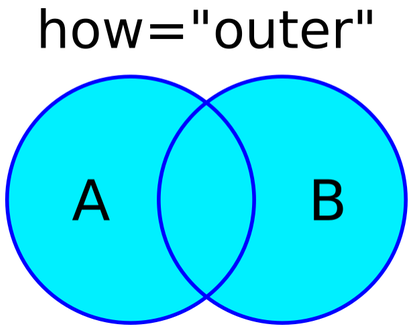
	price
flower_id	
1002	3.99
1003	2.25

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

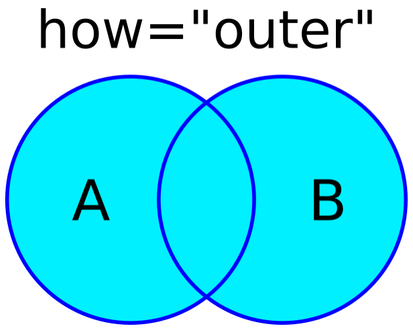
Out[15]:

	name	price
flower_id		
1002	rose	3.99

Join Types: Outer Join



Join Types: Outer Join

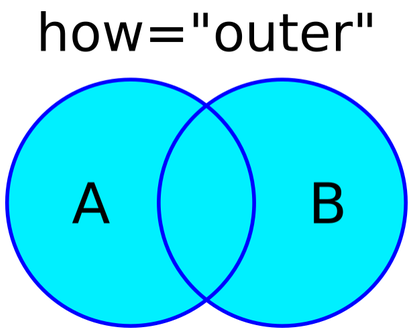


In [16]:
```
1 display(df_flower_name,df_flower_price)
```

	name
flower_id	
1001	iris
1002	rose

	price
flower_id	
1002	3.99
1003	2.25

Join Types: Outer Join



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

```

Out[18]:

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

Setting the Index When Reading in Data

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

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

```

Out[18]:

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

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

```

Out[19]:

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]:

flower_id	name
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_id	flower_name_iris	flower_name_rose
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]:

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

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

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

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

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

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

Out[23]:

	flower_id	name	price
0	1002	rose	3.99

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

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

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

Out[23]:

	flower_id	name	price
0	1002	rose	3.99

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

Out[24]:

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

Questions about joining datasets?

Dimensionality Reduction

Recall: Methods for Avoiding Overfitting

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

Dimensionality Reduction

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

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

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

Load Binary Wine Classification

Load Binary Wine Classification

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

wine = load_wine()

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

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

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

wine_feature_names = X_wine.columns.values
wine_feature_names
```

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

Load Binary Wine Classification

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

wine = load_wine()

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

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

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

wine_feature_names = X_wine.columns.values
wine_feature_names
```

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

In [26]:
```
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]:

```
from sklearn.preprocessing import StandardScaler

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

X_test_zscore = ss.transform(X_test)
```

Standardize Features

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

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

X_test_zscore = ss.transform(X_test)
```

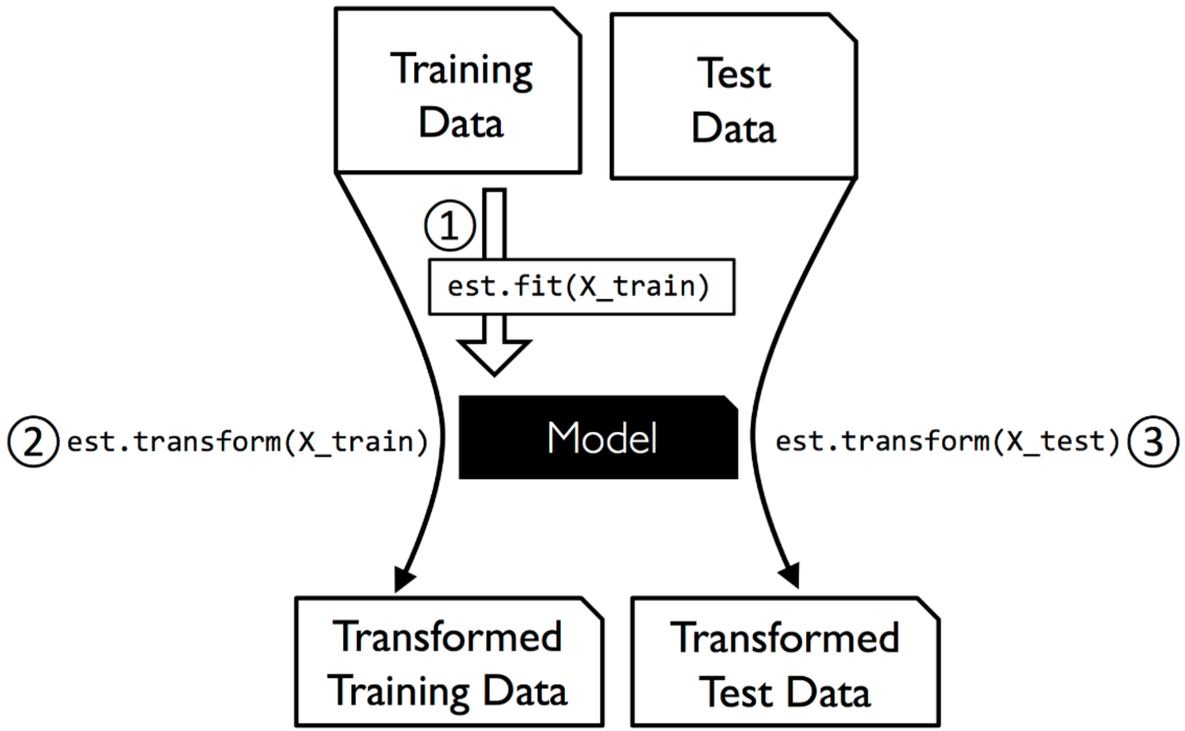
In [29]:
```
X_train_zscore.agg(['mean','std']).T.round(1)
```

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

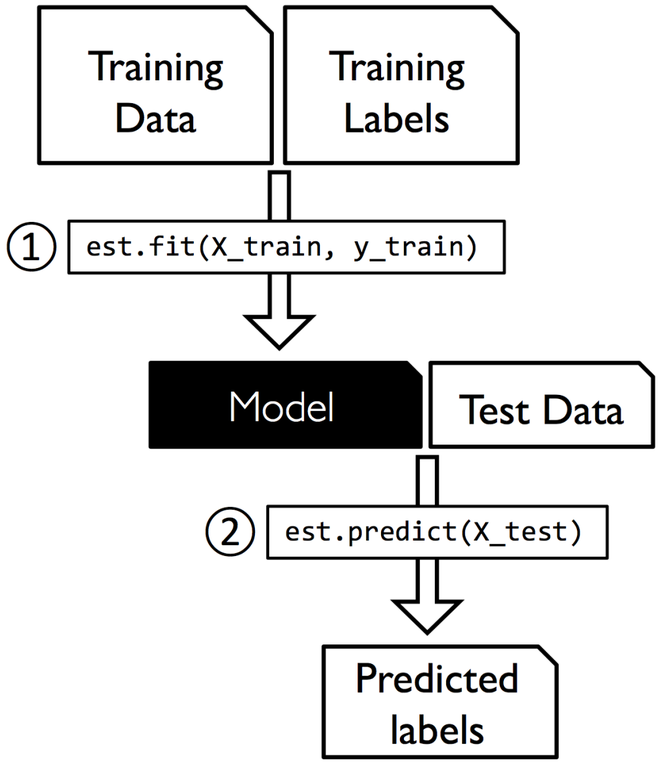
- When transforming data, fit on the training set, transform both train and test



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 `l1` regularization drives the coefficient of uninformative features to 0

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

# First, without regularization
logr = LogisticRegression(penalty="none", solver="lbfgs", random_state=0)
logr.fit(X_train_zscore, y_train)
logr.coef_[0].round(2)
```

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

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

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Out[30]:
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         0.91,  -1.55,   0.2 ,  -3.87, -14.43])
```

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

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

Feature Selection: LASSO (L1) Cont.

Oracle

Feature Selection: LASSO (L1) Cont.

Oracle

In [32]:
```
# Now with LASSO
#   C is the inverse regularization strength: higher means less regularization
logr_l1 = LogisticRegression(C= .1, penalty="l1", solver="liblinear", random_state=0)
logr_l1.fit(X_train_zscore, y_train)

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

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

Feature Selection: LASSO (L1) Cont.

Oracle

In [32]:
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# Now with LASSO
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logr_l1.fit(X_train_zscore, y_train)

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```

Out[32]:
```
malic_acid                      0.00000
ash                             0.00000
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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]:
```
# which columns were kept?
wine_feature_names[logr_l1.coef_[0] != 0]
```

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

Feature Selection: Tree Based Model Feature Importance

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

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

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

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

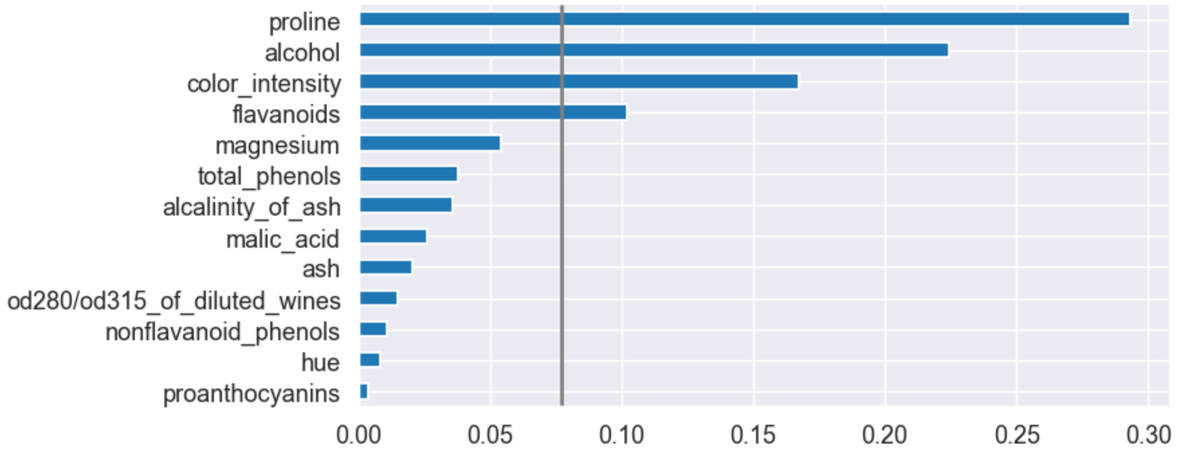
Out[35]:
```
proline                         0.293
alcohol                         0.225
color_intensity                 0.167
flavanoids                      0.102
magnesium                       0.054
total_phenols                   0.038
alcalinity_of_ash               0.036
malic_acid           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

Feature Selection: Tree Based Model Feature Importance

Feature Selection: Tree Based Model Feature Importance

In [36]:

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



Feature Selection: Tree Based Model Feature Importance

In [36]:
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fig,ax = plt.subplots(1,1,figsize=(6,3),dpi=130)
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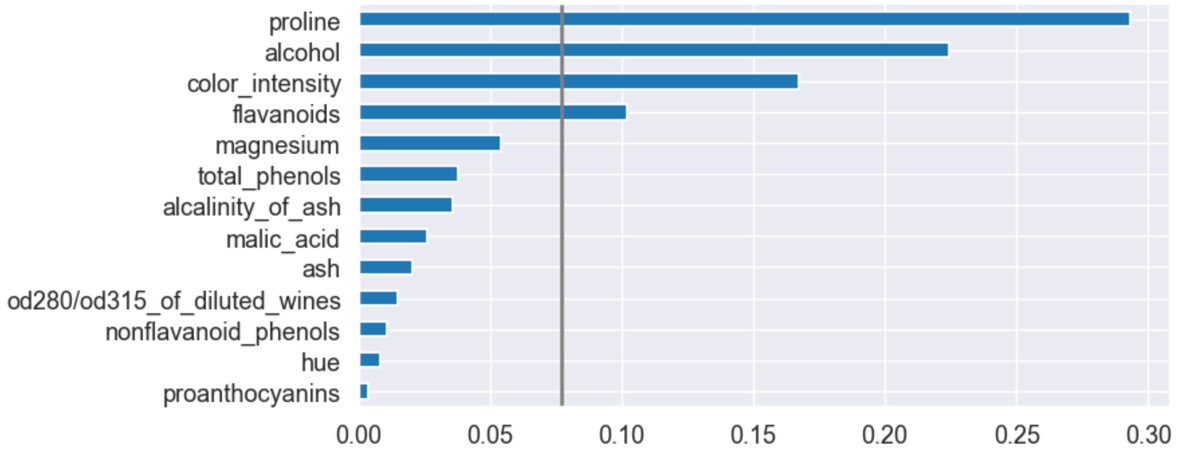

- Which of these features should we keep?
  - Elbow method
  - Threshold at mean

Feature Selection: SelectFromModel

Feature Selection: SelectFromModel

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

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

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

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

Feature Selection: SelectFromModel

In [37]:
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sfm_lr.get_support() # boolean mask of features selected
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Out[37]:
```
array([ True, False, False, False, False, False, False, False, False,
       False, False, False,  True])
```

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

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

Feature Selection: SelectFromModel

In [37]:
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from sklearn.feature_selection import SelectFromModel

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

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

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

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

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

Feature Selection: SelectFromModel

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array([ True, False, False, False, False, False, False, False, False,
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In [38]:
```
wine_feature_names[sfm_lr.get_support()]
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tFromModel was fitted without feature names
  warnings.warn(
```

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

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

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

Feature Selection: SelectFromModel Cont.

Feature Selection: SelectFromModel Cont.

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

wine_feature_names[sfm_rf.get_support()]
```

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

Feature Selection: SelectFromModel Cont.

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

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

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

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

Feature Selection: SelectFromModel Cont.

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

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

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

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

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

Out[43]:
```
proline                         0.279
alcohol                         0.254
color_intensity                 0.168
magnesium                       0.079
flavanoids                      0.059
alcalinity_of_ash               0.036
total_phenols                   0.035
malic_acid                      0.022
od280/od315_of_diluted_wines    0.020
ash                             0.016
hue                             0.013
proanthocyanins                 0.010
nonflavanoid_phenols            0.009
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

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

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

Feature Selection: Recursive Feature Elimination

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

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

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

wine_feature_names[rfe.get_support()]
```

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

Feature Selection: Other Methods

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

Questions on Feature Selection?

When changing number of features: Use Adjusted R^2

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

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- 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]:

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

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

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

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

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

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```

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

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

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

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

In [47]:
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R2 with 3 features   : 0.37
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```

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

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

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

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.round(3))
model.summary()
```

```
0.621
```

Out[49]:

OLS Regression Results

Dep. Variable:	alcohol	**R-squared (uncentered):**	0.668
Model:	OLS	**Adj. R-squared (uncentered):**	0.621
Method:	Least Squares	**F-statistic:**	14.23
Date:	Wed, 11 Dec 2024	**Prob (F-statistic):**	1.06e-15
Time:	23:26:03	**Log-Likelihood:**	-84.207
No. Observations:	97	**AIC:**	192.4
Df Residuals:	85	**BIC:**	223.3
Df Model:	12		
Covariance Type:	nonrobust		

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

Questions re Adjusted R^2?

Feature Extraction

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

Principal Component Analysis (PCA)

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

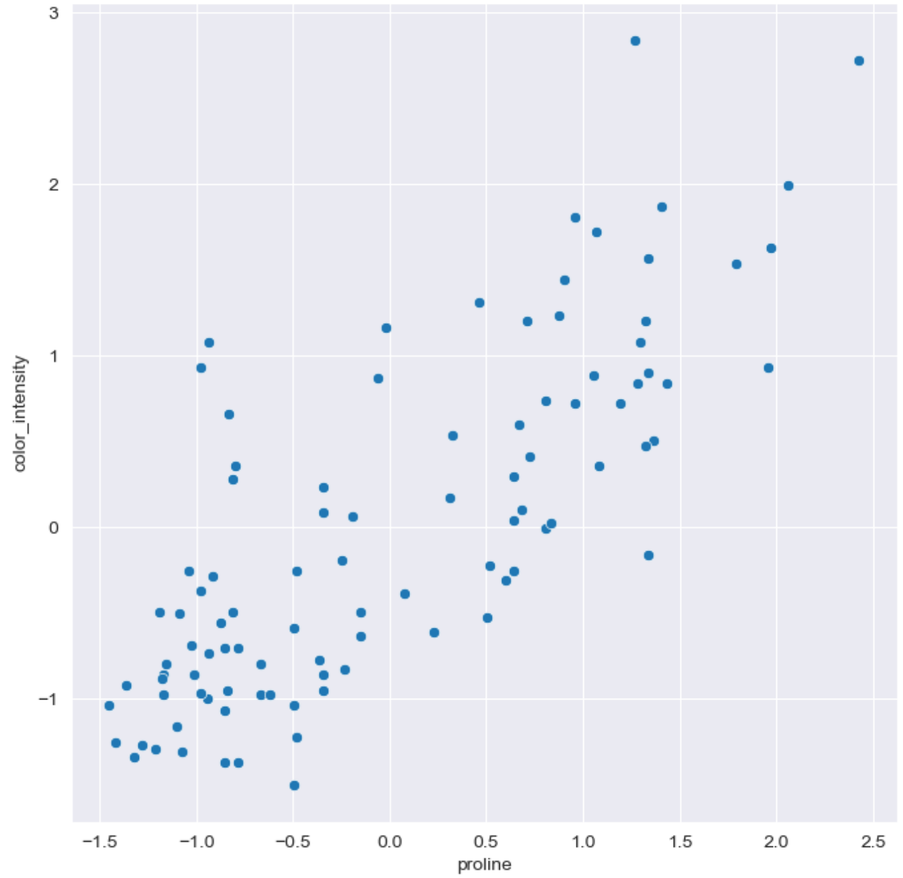
Principal Component Analysis (PCA)

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

PCA Example

PCA Example

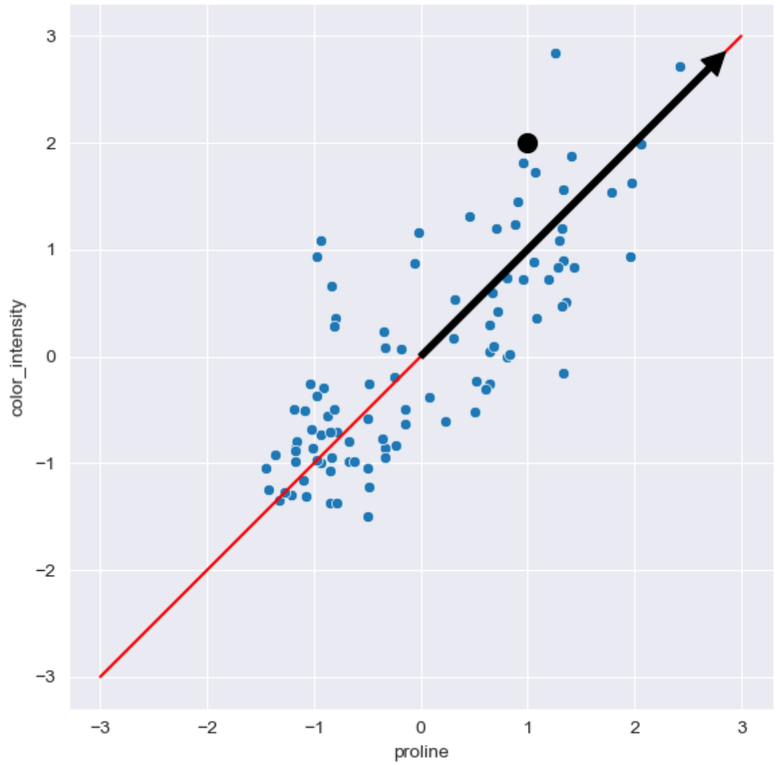
In [51]:
```
fig,ax = plt.subplots(1,1,figsize=(8,8))
sns.scatterplot(x='proline',y='color_intensity',data=X_train_zscore,ax=ax);
```

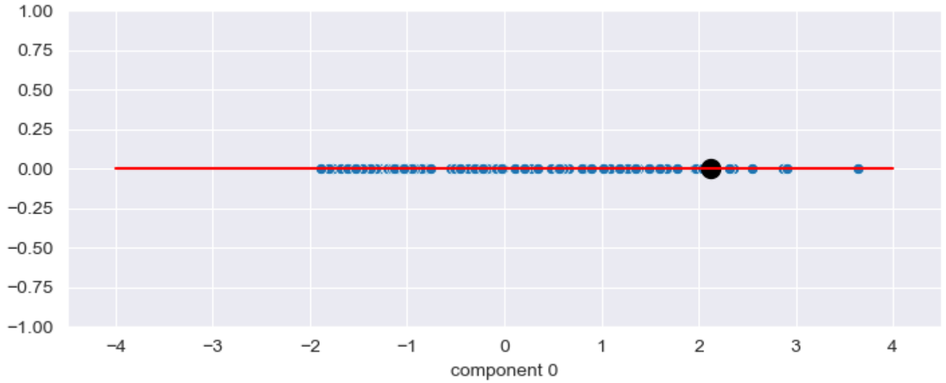


PCA Example Cont.

PCA Example Cont.

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

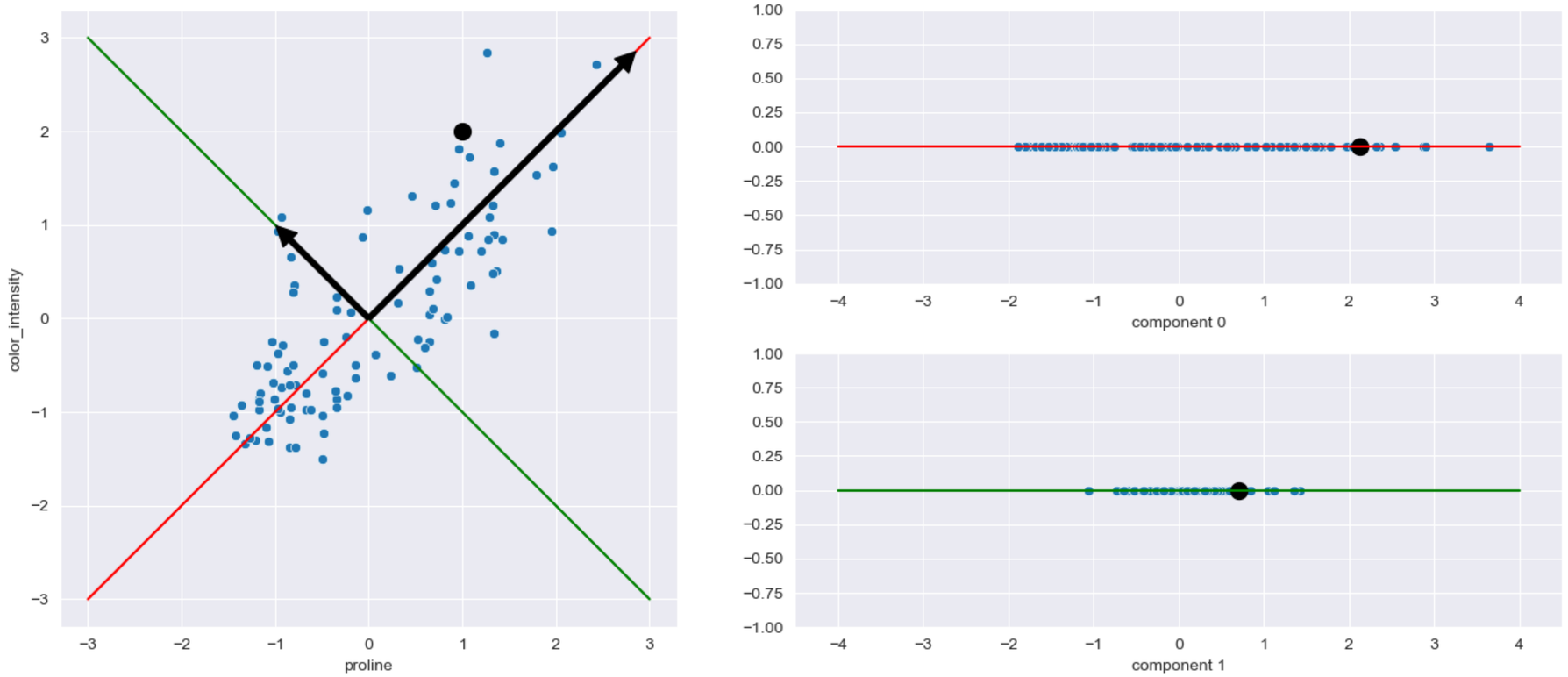




PCA Example Cont.

PCA Example Cont.

In [54]:
```
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]:
```
from sklearn.decomposition import PCA

pca = PCA().fit(X_train_zscore)

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

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

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

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

PCA in sklearn

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

pca = PCA().fit(X_train_zscore)

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

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

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

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

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

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

PCA: Explained Variance

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

PCA: Explained Variance

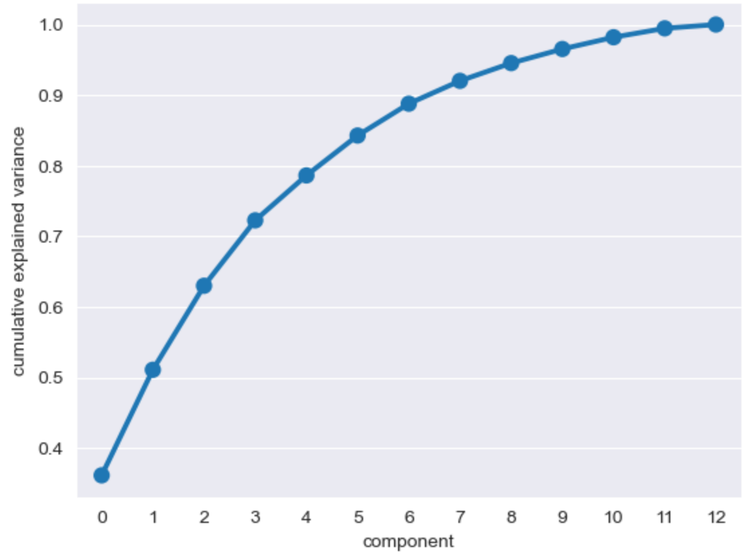
- How much of the variance in the dataset is explained by each component?

In [58]:

```
pca = PCA().fit(X_train_zscore)

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

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



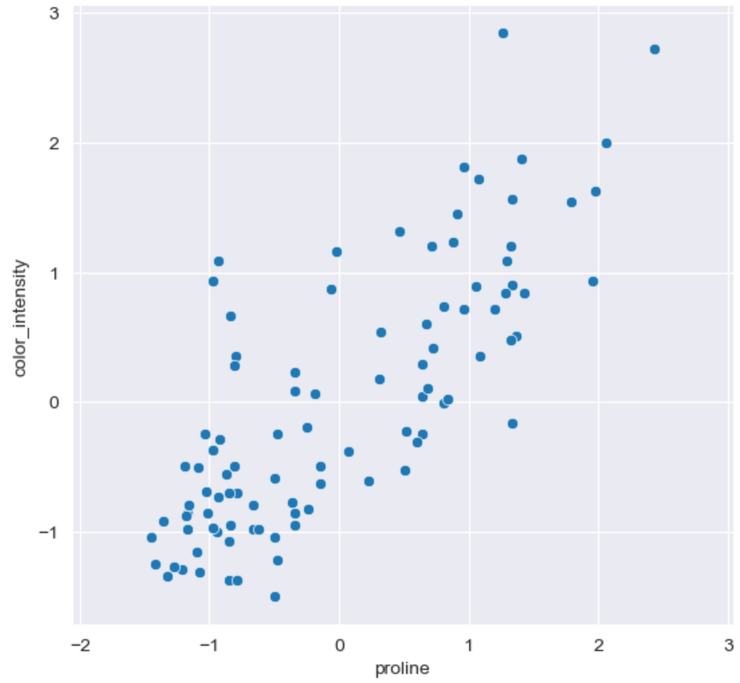
Dimensionality Reduction with PCA

Dimensionality Reduction with PCA

In [59]:

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

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



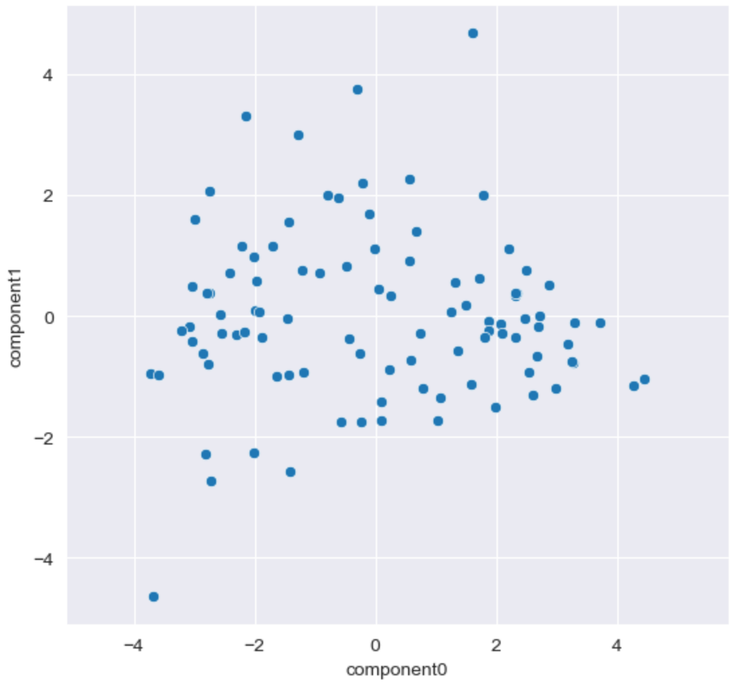


Image Recognition Example

PCA and Image Recognition

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

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

Example Dataset: Labeled Faces in th Wild (LFW)

Labeled Faces in the Wild

Example Dataset: Labeled Faces in th Wild (LFW)

Labeled Faces in the Wild

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

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

In [61]:
```
[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

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

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

In [61]:
```
[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']
```

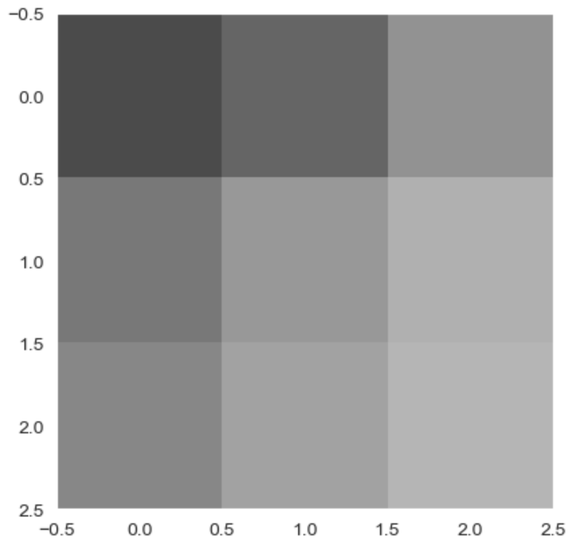
In [62]:
```
sns.set_style('dark')
plt.imshow(lfw_people.images[1], cmap=plt.cm.gray, vmin=0, vmax=1)
plt.title(lfw_people.target_names[lfw_people.target[1]], size=12);
```

Example Pixel Values

Example Pixel Values

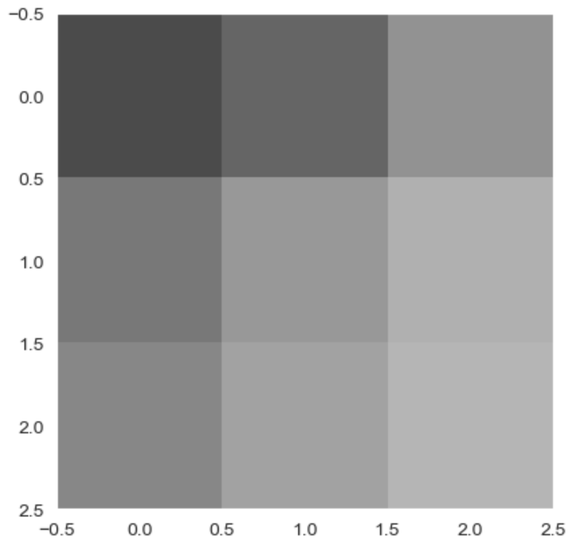
In [63]:

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



Example Pixel Values

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



In [64]:
```
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?

Representing each Image: Flatten

- 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)
```

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)
```

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)
```

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]:

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

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

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

# create train/test split
X_train_faces, X_test_faces, y_train_faces, y_test_faces = train_test_split(X_faces, y_faces,
                                                                            test_size=0.25,
                                                                            stratify=y_faces,
                                                                            random_state=0)
print(f"image_size: {h}x{w}")
print("n_features: %d" % n_features)
print("n_classes : %d" % n_classes)
print(f"n_train   : {len(X_train_faces)}")
print(f"n_test    : {len(X_test_faces)}")
```

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

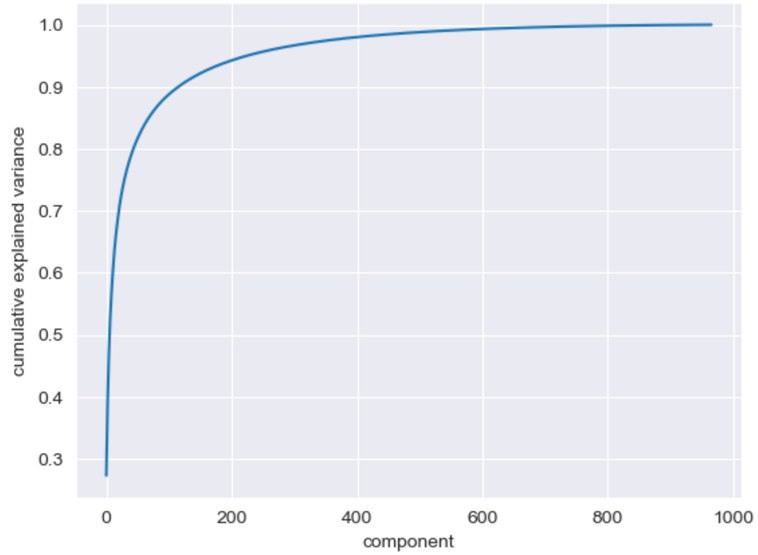
Variance explained by PCA

Variance explained by PCA

In [69]:

```
pca_faces = PCA().fit(X_train_faces)

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



Compute PCA and Transform

Compute PCA and Transform

In [70]:

```
# set the number of dimensions we want to retain
n_components = 200

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

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

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

Compute PCA and Transform

In [70]:
```
# set the number of dimensions we want to retain
n_components = 200

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

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

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

In [71]:
```
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]:
```
# set the number of dimensions we want to retain
n_components = 200

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

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

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

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

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

In [72]:
```
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,
```

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]:

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

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

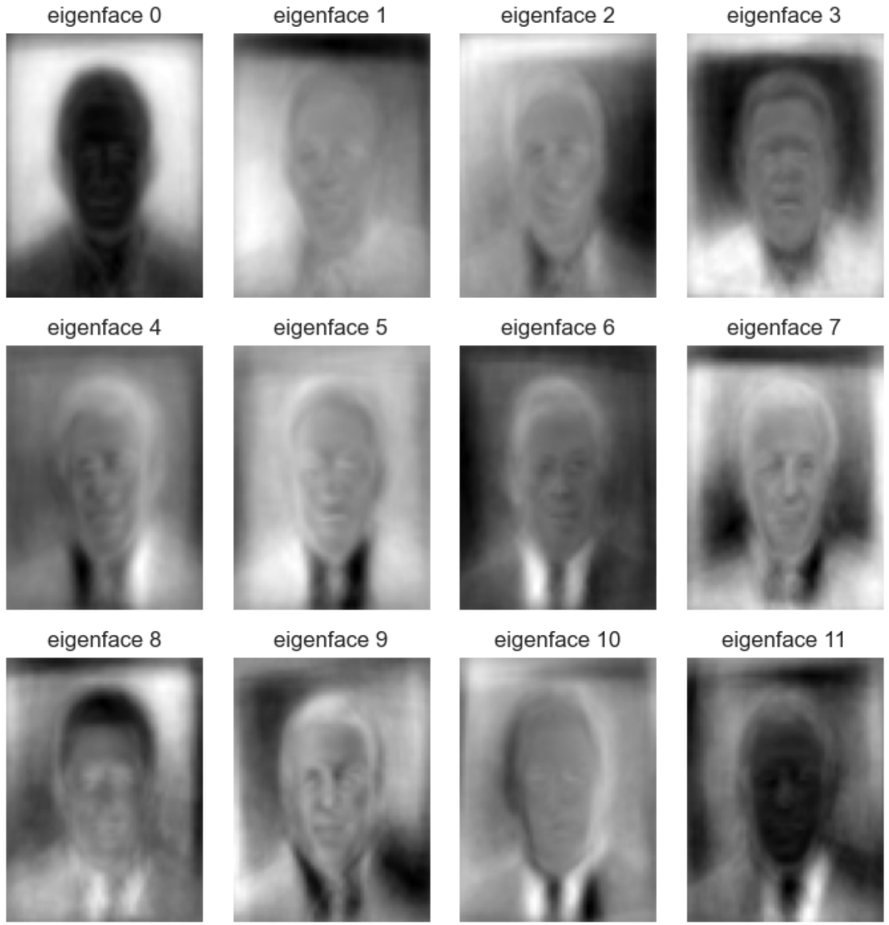
Eigenfaces

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

Eigenfaces

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

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



Train and Tune SVC

Train and Tune SVC

In [75]:

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

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

```
CPU times: user 340 ms, sys: 157 ms, total: 497 ms
Wall time: 4.22 s
```

Train and Tune SVC

In [75]:
```
%%time
from sklearn.model_selection import GridSearchCV
from sklearn.svm import SVC

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

```
CPU times: user 340 ms, sys: 157 ms, total: 497 ms
Wall time: 4.22 s
```

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

```
best_params : {'C': 1000.0, 'gamma': 0.001}
best_score  : 0.74
```

Evaluate on the test set

Evaluate on the test set

In [77]:

```
from sklearn.metrics import classification_report

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

```
                   precision    recall  f1-score   support

     Ariel Sharon       0.52      0.58      0.55        19
     Colin Powell       0.73      0.76      0.74        59
  Donald Rumsfeld       0.74      0.67      0.70        30
    George W Bush       0.80      0.89      0.85       133
Gerhard Schroeder       0.65      0.41      0.50        27
      Hugo Chavez       0.89      0.44      0.59        18
       Tony Blair       0.74      0.78      0.76        36

         accuracy                           0.75       322
        macro avg       0.72      0.65      0.67       322
     weighted avg       0.75      0.75      0.74       322
```

Prediction Examples

Prediction Examples

In [78]:

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

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

Performance without PCA: Train

Performance without PCA: Train

```
%%time

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

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

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

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

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

Performance without PCA: Evaluate

Performance without PCA: Evaluate

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

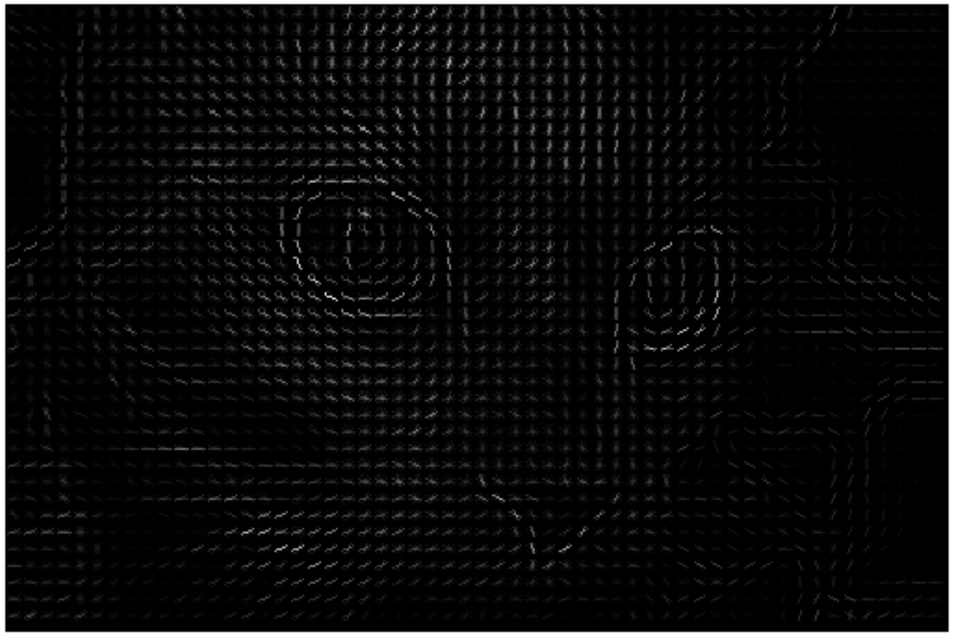
#                    precision    recall  f1-score   support

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

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

Other Image Recognition Methods

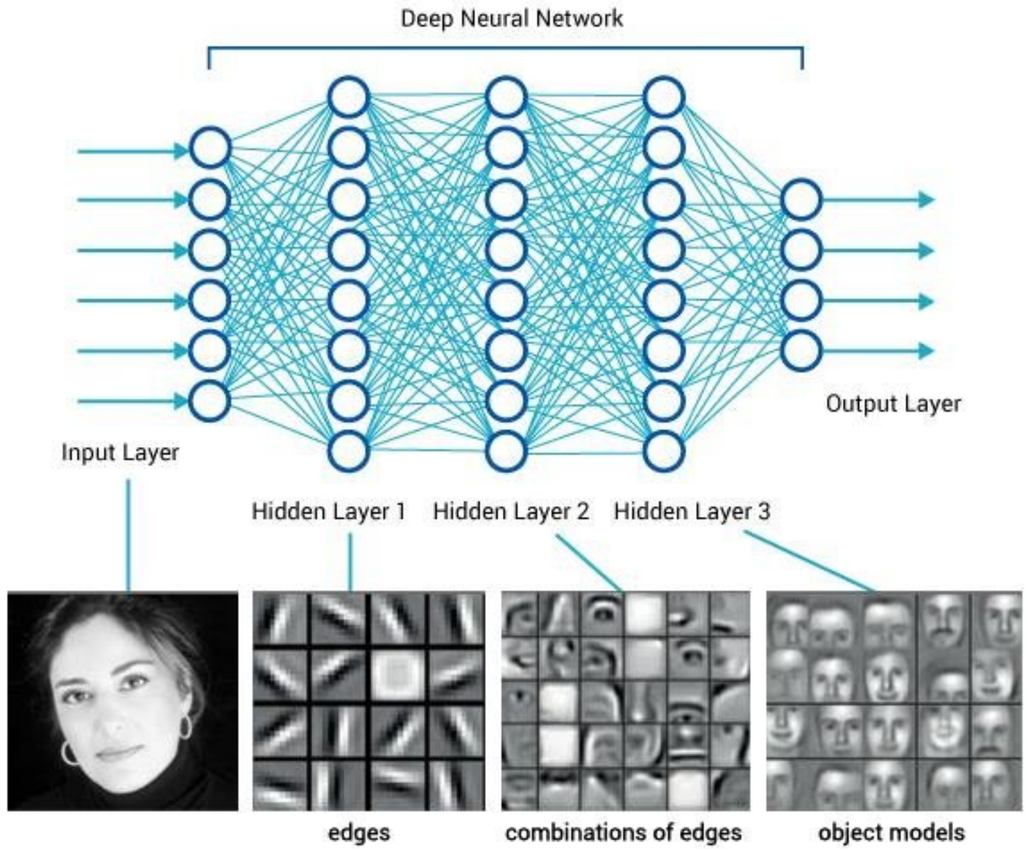
- With Feature Engineering and general models
  - ex: Histogram of Oriented Gradients or HOG (See PDSH Chap 5)
  - many more (See scikit-image)



From PDSH

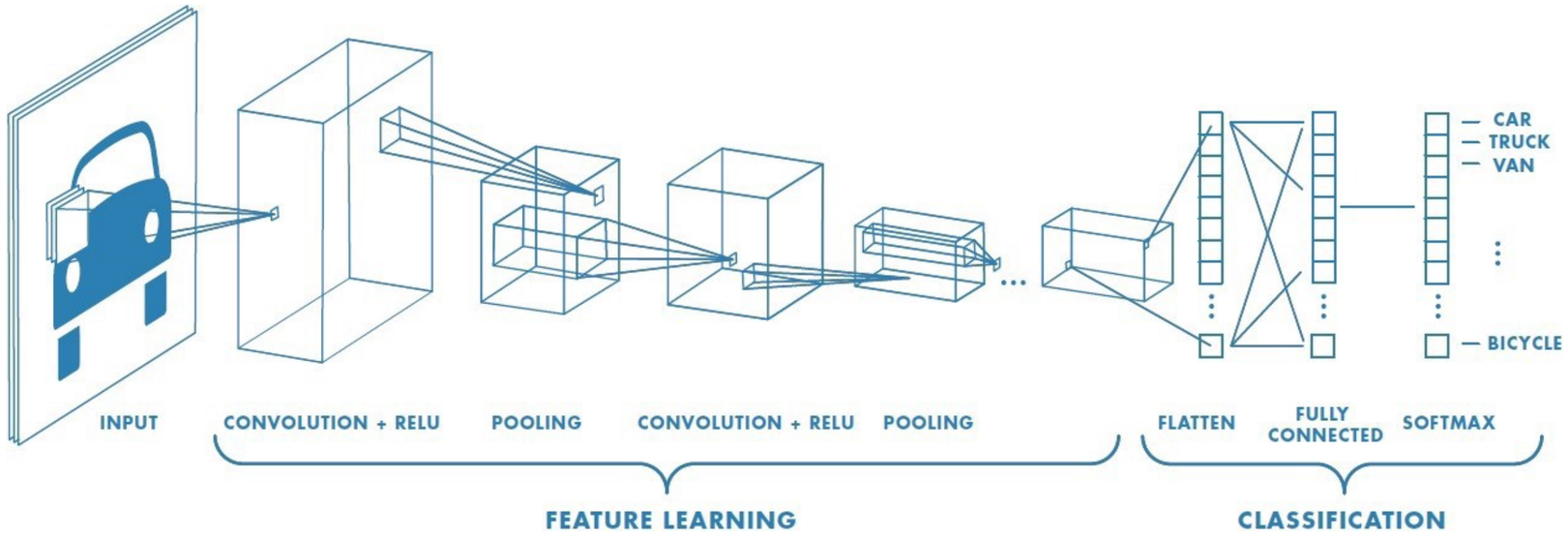
Other Image Recognition Methods: Deep Neural Networks

- With Deep Neural Nets



Other Image Recognition Methods: Deep Neural Networks

- With Convolutional Neural Networks Good Example



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

Questions re Feature Extraction and PCA?

Next time: NLP and Pipelines