CAPAIAN PEMBELAJARAN PRAKTIKUM

1. Menjelaskan konsep dari pembelajaran mesin kemudian diterpakan pada berbagai permasalahan – (C2)
2. Mengimplementasikan algoritma dan/atau metode di pembelajaran mesin sehingga mendapatkan pemecahan masalah dan model yang sesuai - (C3)
3. Menghasilkan suatu model terbaik dari permasalahan dan terus melakukan perbaikan jika terdapat perkembangan di bidang rekayasa cerdas – (C6)

MINGGU 7

Klasifikasi Bayes dan Support Vector

DESKRIPSI TEMA

Mahasiswa mempelajari algoritma pembelajaran terbimibng dengan klasifikasi bayes dan klasifikasi berbasis Support Vector serta menerapkannya dengan Bahasa pemrograman Python

CAPAIAN PEMBELAJARAN MINGGUAN (SUB- CAPAIAN PEMBELAJARAN)

Mahasiswa dapat menerapkan algoritma dengan Bayes dan Support Vector sehingga bisa menghasilkan model terbaik dengan bahasa pemrograman Python (SCPMK-07)

PERALATAN YANG DIGUNAKAN

Anaconde Python 3

Laptop atau Personal Computer

LANGKAH-LANGKAH PRAKTIKUM

NAÏVE BAYES CLASSIFIER

Naïve Bayes are a group of extremely fast and simple classification algorithms that are often suitable for very – high dimensional datasets

Bayes Classification

Naive Bayes classifiers are built on Bayesian classification methods. These rely on Bayes's theorem, which is an equation describing the relationship of conditional probabilities of statistical quantities. In Bayesian classification, we're interested in finding the probability of a label given some observed features, which we can write as P(L | features). Bayes's theorem tells us how to express this in terms of quantities we can compute more directly:

$$P(L|Features) = \frac{P(features|L)P(L)}{P(features)}$$

If we are trying to decide between two labels—let's call them L1 and L2—then one way to make this decision is to compute the ratio of the posterior probabilities for each label:

$$\frac{P(L_1|features)}{P(L_1|features)} = \frac{P(features|L_1)P(|L_1)}{P(features|L_2)P(|L_2)}$$

All we need now is some model by which we can compute P(features | Li) for each label. Such a model is called a *generative model* because it specifies the hypothetical random process that generates the data. Specifying this generative model for each label is the main piece of the training of such a Bayesian classifier. The general version of such a training step is a very difficult task, but we can make it simpler through the use of some simplifying assumptions about the form of this model.

This is where the "naive" in "naive Bayes" comes in: if we make very naive assumptions about the generative model for each label, we can find a rough approximation of the generative model for each class, and then proceed with the Bayesian classification. Different types of naive Bayes classifiers rest on different naive assumptions about the data, and we will examine a few of these in the following sections.

1. Begin with standard imports :

```
%matplotlib inline
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns; sns.set()
```

2. Generate Gaussian Naïve Bayes

Perhaps the easiest naive Bayes classifier to understand is Gaussian naive Bayes. In this classifier, the assumption is that *data from each label is drawn from a simple Gaussian distribution*. Imagine that you have the following data :

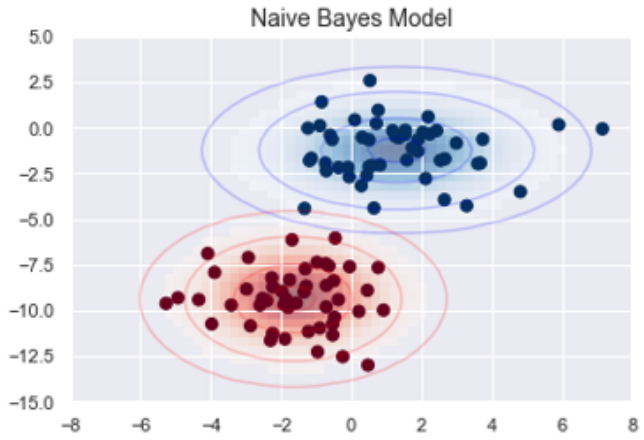
```
from sklearn.datasets import make_blobs
X,y = make_blobs(100,2,centers=2, random_state=2,cluster_std=1.5)
plt.scatter(X[:,0],X[:,1], c=y, s=50, cmap='RdBu')
```

```
<matplotlib.collections.PathCollection at 0x20306039240>
```

One extremely fast way to create a simple model is to assume that the data is described by a Gaussian distribution with no covariance between dimensions. This model can be fit by simply finding the mean and standard deviation of the points within each label, which is all you need to define such a distribution. The result of this naive Gaussian assumption is shown in the following figure which is generate with the following code.

```python
from sklearn.datasets import make_blobs
X, y = make_blobs(100, 2, centers=2, random_state=2, cluster_std=1.5)

fig, ax = plt.subplots()

ax.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='RdBu')
ax.set_title('Naive Bayes Model', size=14)

xlim = (-8, 8)
ylim = (-15, 5)

xg = np.linspace(xlim[0], xlim[1], 60)
yg = np.linspace(ylim[0], ylim[1], 40)
xx, yy = np.meshgrid(xg, yg)
Xgrid = np.vstack([xx.ravel(), yy.ravel()]).T

for label, color in enumerate(['red', 'blue']):
    mask = (y == label)
    mu, std = X[mask].mean(0), X[mask].std(0)
    P = np.exp(-0.5 * (Xgrid - mu) ** 2 / std ** 2).prod(1)
    Pm = np.ma.masked_array(P, P < 0.03)
    ax.pcolorfast(xg, yg, Pm.reshape(xx.shape), alpha=0.5,
                  cmap=color.title() + 's')
    ax.contour(xx, yy, P.reshape(xx.shape),
               levels=[0.01, 0.1, 0.5, 0.9],
               colors=color, alpha=0.2)

ax.set(xlim=xlim, ylim=ylim)
```

```
[(-15, 5), (-8, 8)]
```



The ellipses here represent the Gaussian generative model for each label, with larger probability toward the center of the ellipses. With this generative model in place for each class, we have a simple recipe to compute the likelihood P(features | L1) for any data point, and thus we can quickly compute the posterior ratio and determine which label is the most probable for a given point.

3. Implement GaussianNB with Scikit-Learn's :

```
1 from sklearn.naive_bayes import GaussianNB
2 model=GaussianNB()
3 model.fit(X,y)
```

```
GaussianNB(priors=None, var_smoothing=1e-09)
```

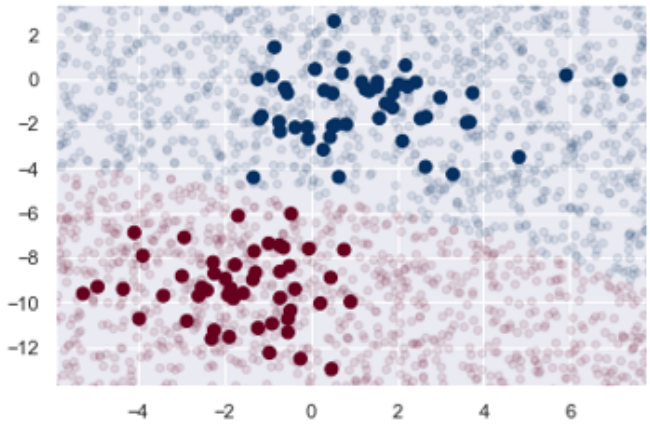
4. Now let's generate some new data and predict the label

```
1 rng=np.random.RandomState(0)
2 Xnew=[-6,-14]+[14,18]*rng.rand(2000,2)
3 ynew = model.predict(Xnew)
```

5. Now, we can plot this new data to get an idea of where the decision boundary is

```
plt.scatter(X[:,0], X[:,1], c=y, s=50,cmap='RdBu')
lim=plt.axis()
plt.scatter(Xnew[:,0],Xnew[:,1],c=ynew,s=20,cmap='RdBu',alpha=0.1)
plt.axis(lim)
```

```
(-5.902170524311957, 7.789182875858786, -13.793829460308247, 3.381339464828492)
```



We see a slightly curved boundary in the classifications—in general, the boundary in Gaussian naive Bayes is quadratic.

6. A nice piece of this Bayesian formalism is that it naturally allows for probabilistic classification, which we can compute using the predict_proba method

```
yprob= model.predict_proba(Xnew)
yprob[-8:].round(2)
```

```
array([[0.89, 0.11],
       [1.  , 0.  ],
       [1.  , 0.  ],
       [1.  , 0.  ],
       [1.  , 0.  ],
       [1.  , 0.  ],
       [0.  , 1.  ],
       [0.15, 0.85]])
```

The columns give the posterior probabilities of the first and second label, respectively. If you are looking for estimates of uncertainty in your classification, Bayesian approaches like this can be a useful approach.

Of course, the final classification will only be as good as the model assumptions that lead to it, which is why Gaussian naive Bayes often does not produce very good results. Still, in many

cases—especially as the number of features becomes large—this assumption is not detrimental enough to prevent Gaussian naive Bayes from being a useful method.

MULTINOMIAL NAÏVE BAYES

The Gaussian assumption just described is by no means the only simple assumption that could be used to specify the generative distribution for each label. Another useful example is multinomial naive Bayes, where the features are assumed to be generated from a simple multinomial distribution. The multinomial distribution describes the probability of observing counts among a number of categories, and thus multinomial naive Bayes is most appropriate for features that represent counts or count rates.

The idea is precisely the same as before, except that instead of modeling the data distribution with the best-fit Gaussian, we model the data distribution with a best-fit multinomial distribution.

Example Classifying Text (using fetch_20newsgroups) : we will use the sparse word count features from the 20 Newsgroups corpus to show how we might classify these short documents into categories.

7. Download the data and take a look the target names

```
from sklearn.datasets import fetch_20newsgroups
data=fetch_20newsgroups()
data.target_names
```

```
['alt.atheism',
 'comp.graphics',
 'comp.os.ms-windows.misc',
 'comp.sys.ibm.pc.hardware',
 'comp.sys.mac.hardware',
 'comp.windows.x',
 'misc.forsale',
 'rec.autos',
 'rec.motorcycles',
 'rec.sport.baseball',
 'rec.sport.hockey',
 'sci.crypt',
 'sci.electronics',
 'sci.med',
 'sci.space',
 'soc.religion.christian',
 'talk.politics.guns',
 'talk.politics.mideast',
 'talk.politics.misc',
 'talk.religion.misc']
```

8. For simplicity here, we will select just a few of these categories and download the training and testing set

```
categories =['talk.religion.misc', 'soc.religion.christian',
             'sci.space','comp.graphics']
train= fetch_20newsgroups(subset='train',categories=categories)
test = fetch_20newsgroups(subset='test',categories=categories)
```

9. The representative entry from the data (5 first data)

```
1 print(train.data[5])
```

```
From: dmcgee@uluhe.soest.hawaii.edu (Don McGee)
Subject: Federal Hearing
Originator: dmcgee@uluhe
Organization: School of Ocean and Earth Science and Technology
Distribution: usa
Lines: 10


Fact or rumor....?  Madalyn Murray O'Hare an atheist who eliminated the
use of the bible reading and prayer in public schools 15 years ago is now
going to appear before the FCC with a petition to stop the reading of the
Gospel on the airways of America.  And she is also campaigning to remove
Christmas programs, songs, etc from the public schools.  If it is true
then mail to Federal Communications Commission 1919 H Street Washington DC
20054 expressing your opposition to her request.  Reference Petition number

2493.
```

10. In order to use this data for machine learning, we need to be able to convert the content of string into a vector of number. Use the TF-IDF vectorizer and create a pipeline that attaches it to a multinomial Naïve Bayes Classifier

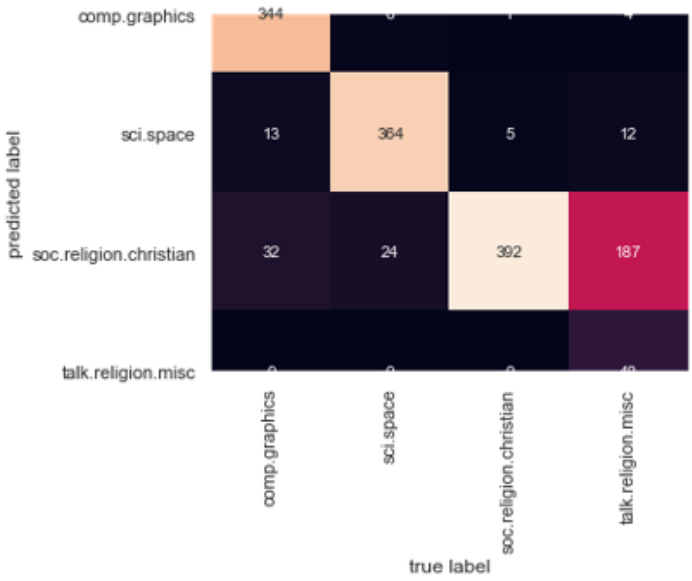
```
1 from sklearn.feature_extraction.text import TfidfVectorizer
2 from sklearn.naive_bayes import MultinomialNB
3 from sklearn.pipeline import make_pipeline
4
5 model = make_pipeline(TfidfVectorizer(),MultinomialNB())
```

11. With this pipeline, we can apply the model to the training data and predict labels for the test data

```
1 model.fit(train.data, train.target)
2 labels =model.predict(test.data)
```

12. Now that we have predicted the labels for the test data, we can evaluate them to learn about the performance of the estimator. For the example, here is the confusion matrix between the true and predicted labels for the test data.

```
from sklearn.metrics import confusion_matrix
mat = confusion_matrix(test.target, labels)
sns.heatmap(mat.T, square=True, annot=True, fmt='d', cbar=False,
            xticklabels=train.target_names, yticklabels=train.target_names)
plt.xlabel('true label')
plt.ylabel('predicted label');
```



13. Predict for a single string

```
predict_category('sending a payload to the ISS')
```

```
'sci.space'
```

```
predict_category('discussing islam vs atheism')
```

```
'soc.religion.christian'
```

```
predict_category('deterining the screen resolution')
```

```
'comp.graphics'
```

SUPPORT VECTOR MACHINE (SVM)

SVM are an extension that allows for more complex models that are not defined simply by hyperplanes in the input space. While there are support vector machines for classification and regression, we will restrict ourselves to the classification cases as implemented in SVC. Similar concepts apply to support vector regression as implemented in SVR.

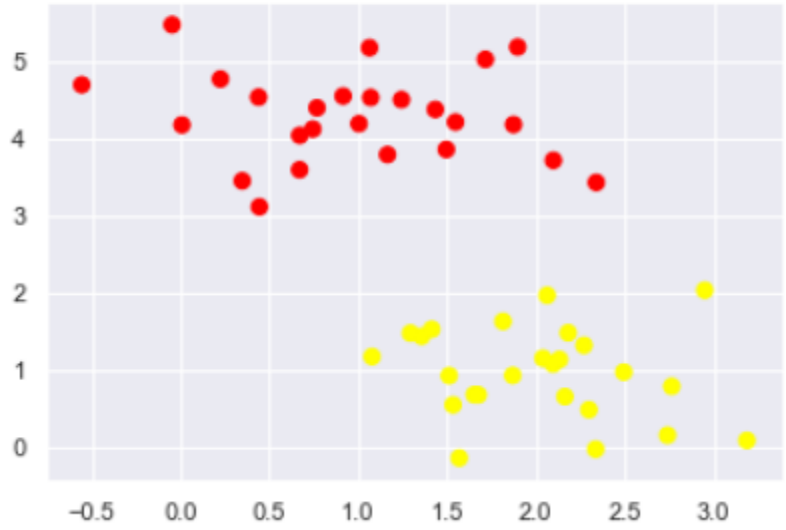
14. We begin with the standard import :

```
%matplotlib inline
import numpy as np
import matplotlib.pyplot as plt
from scipy import stats

# use seaborn plotting defaults
import seaborn as sns; sns.set()
```

As part of our discussion of Bayessian Classification, we learned a simple model describing the distribution of each underlying class and used these generative models to probabilistically determine the labels for new points. That was example of generative classification; here we will consider instead discriminative classification; rather than modeling each class, we simply fine a line or curve (in 2 dimension) or manifold (in multiple dimension) that divides the classes from each other.

15. As an example of this, consider the simple case of a classification task, in which the two classes are well separated :

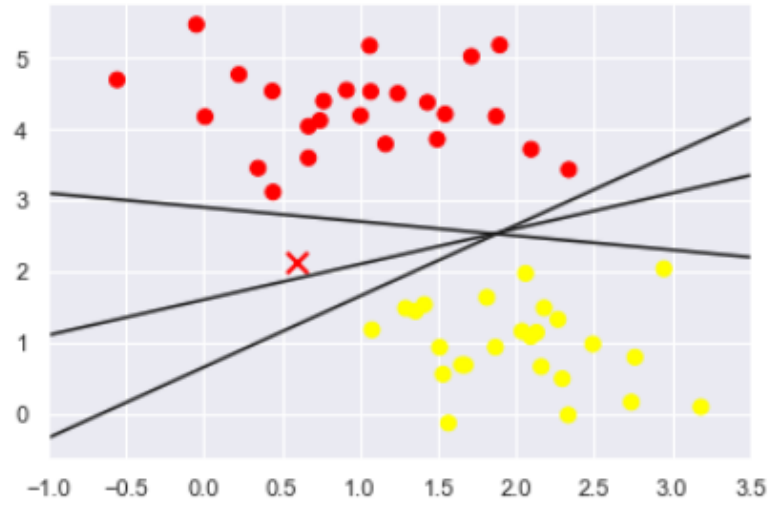
```
from sklearn.datasets.samples_generator import make_blobs
X, y = make_blobs(n_samples=50, centers=2,
                  random_state=0, cluster_std=0.60)
plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn');
```



A linear discriminative classifier would attempt to draw a straight line separating the two sets of data and thereby create a model for classification. For two dimensional data, like that shown here, this is a task we could do by hand. But immediately we see a problem : there is more than possible dividing line that can perfectly discriminate between the two classes!

16. We can draw them as follows :

```
xfit = np.linspace(-1, 3.5)
plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
plt.plot([0.6], [2.1], 'x', color='red', markeredgewidth=2, markersize=10)

for m, b in [(1, 0.65), (0.5, 1.6), (-0.2, 2.9)]:
    plt.plot(xfit, m * xfit + b, '-k')

plt.xlim(-1, 3.5);
```

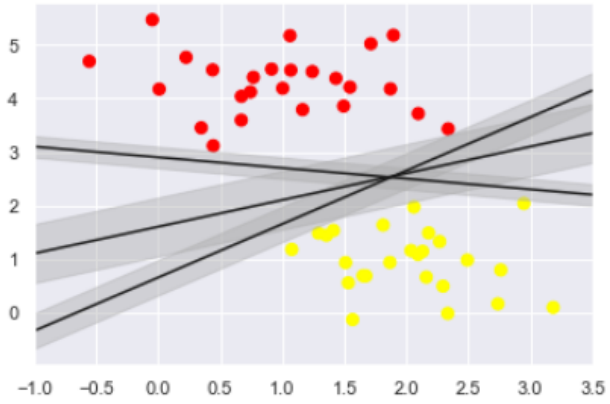


These are three very different separators which, nevertheless, perfectly discriminate between these samples. Depending on which we choose a new data point (e.g the one marked by the “x”) will be assigned a different label. Evidently our simple intuition of “drawing a line between classes” is not enough and we need to think a bit deeper.

Support Vector Machines : maximizing the *Margin*

17. SVM offer one way to improve on this. The intuition is this : rather than simply drawing a zero – width line between the class, we can draw around each line a margin of some width, up to the nearest point. Here is an example this might look:

```
xfit = np.linspace(-1, 3.5)
plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')

for m, b, d in [(1, 0.65, 0.33), (0.5, 1.6, 0.55), (-0.2, 2.9, 0.2)]:
    yfit = m * xfit + b
    plt.plot(xfit, yfit, '-k')
    plt.fill_between(xfit, yfit - d, yfit + d, edgecolor='none',
                     color='#AAAAAA', alpha=0.4)

plt.xlim(-1, 3.5);
```



In SVM, the line that maximizes this margin is the one we will choose as the optimal model. SVM are an example of such a *maximum margin* estimator.

Fitting a Support Vector Machine

18. Let's see the result of an actual fit to this data: we will use Scikit-Learn's support vector classifier to train an SVM model on this data. For the time being, we will use a linear kernel and set the C parameter to a very large number.

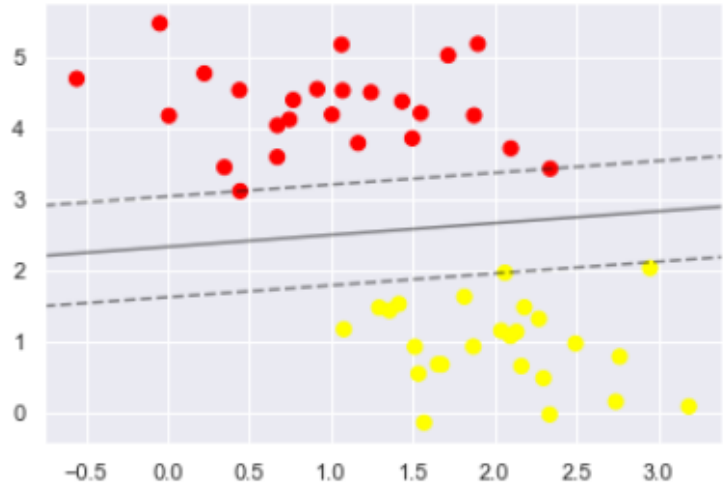
```
1  from sklearn.svm import SVC # "Support vector classifier"
2  model = SVC(kernel='linear', C=1E10)
3  model.fit(X, y)
```

```
Out[5]: SVC(C=10000000000.0, cache_size=200, class_weight=None, coef0=0.0,
            decision_function_shape='ovr', degree=3, gamma='auto_deprecated',
            kernel='linear', max_iter=-1, probability=False, random_state=None,
            shrinking=True, tol=0.001, verbose=False)
```

19. To better visualize what's happening here, let's create a quick convenience function that will plot SVM decision boundaries for us:

```python
def plot_svc_decision_function(model, ax=None, plot_support=True):
    """Plot the decision function for a 2D SVC"""
    if ax is None:
        ax = plt.gca()
    xlim = ax.get_xlim()
    ylim = ax.get_ylim()

    # create grid to evaluate model
    x = np.linspace(xlim[0], xlim[1], 30)
    y = np.linspace(ylim[0], ylim[1], 30)
    Y, X = np.meshgrid(y, x)
    xy = np.vstack([X.ravel(), Y.ravel()]).T
    P = model.decision_function(xy).reshape(X.shape)

    # plot decision boundary and margins
    ax.contour(X, Y, P, colors='k',
               levels=[-1, 0, 1], alpha=0.5,
               linestyles=['--', '-', '--'])

    # plot support vectors
    if plot_support:
        ax.scatter(model.support_vectors_[:, 0],
                   model.support_vectors_[:, 1],
                   s=300, linewidth=1, facecolors='none');
    ax.set_xlim(xlim)
    ax.set_ylim(ylim)
```

```python
plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
plot_svc_decision_function(model);
```



This is the dividing line that maximizes the margin between the two sets of points. Notice that a few of the training points just touch the margin: they are indicated by the black circles in this figure.

These points are the pivotal elements of this fit, and are known as the *support vectors*, and give the algorithm its name

20. In Scikit-Learn, the identity of these points are stored in the support_vectors_ attribute of the classifier:

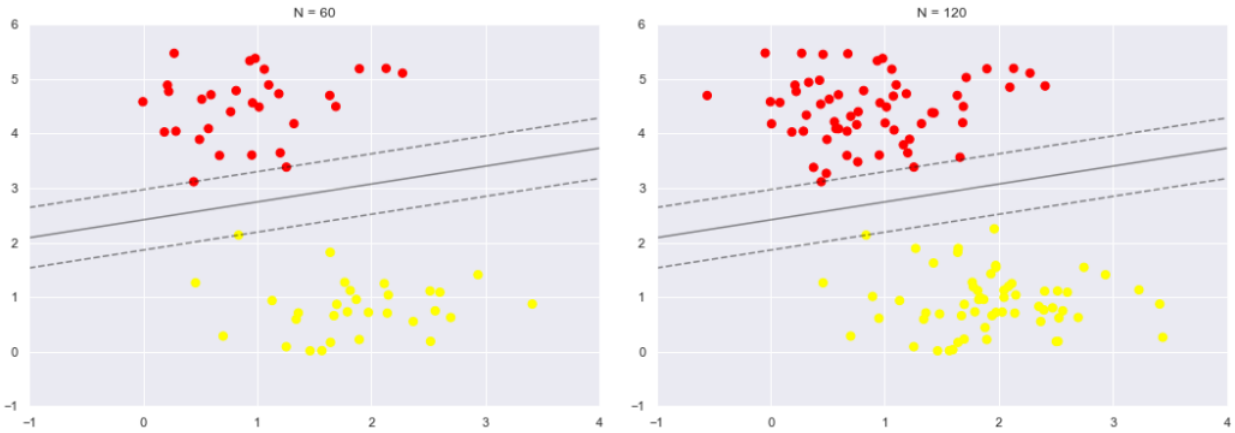
```
model.support_vectors_
```

```
array([[0.44359863, 3.11530945],
       [2.33812285, 3.43116792],
       [2.06156753, 1.96918596]])
```

A key to this classifier's success is that for the fit, only the position of the support vectors matter; any points further from the margin which are on the correct side do not modify the fit! Technically, this is because these points do not contribute to the loss function used to fit the model, so their position and number do not matter so long as they do not cross the margin.

21. We can see this, for example, if we plot the model learned from the first 60 points and first 120 points of this dataset:

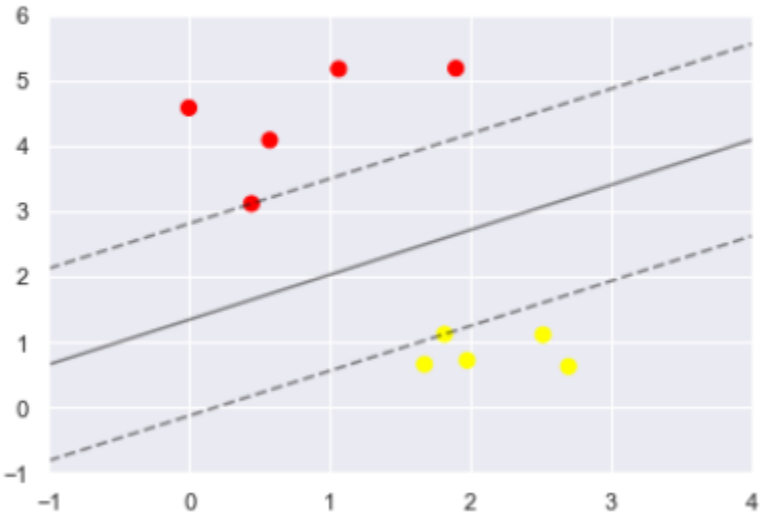
```
def plot_svm(N=10, ax=None):
    X, y = make_blobs(n_samples=200, centers=2,
                      random_state=0, cluster_std=0.60)
    X = X[:N]
    y = y[:N]
    model = SVC(kernel='linear', C=1E10)
    model.fit(X, y)

    ax = ax or plt.gca()
    ax.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
    ax.set_xlim(-1, 4)
    ax.set_ylim(-1, 6)
    plot_svc_decision_function(model, ax)

fig, ax = plt.subplots(1, 2, figsize=(16, 6))
fig.subplots_adjust(left=0.0625, right=0.95, wspace=0.1)
for axi, N in zip(ax, [60, 120]):
    plot_svm(N, axi)
    axi.set_title('N = {0}'.format(N))
```



In the left panel, we see the model and the support vectors for 60 training points. In the right panel, we have doubled the number of training points, but the model has not changed: the three support vectors from the left panel are still the support vectors from the right panel. This insensitivity to the exact behavior of distant points is one of the strengths of the SVM model.

22. If we are running this notebook live, you can use IPython's interactive widgets to view this feature of the SVM model interactively:

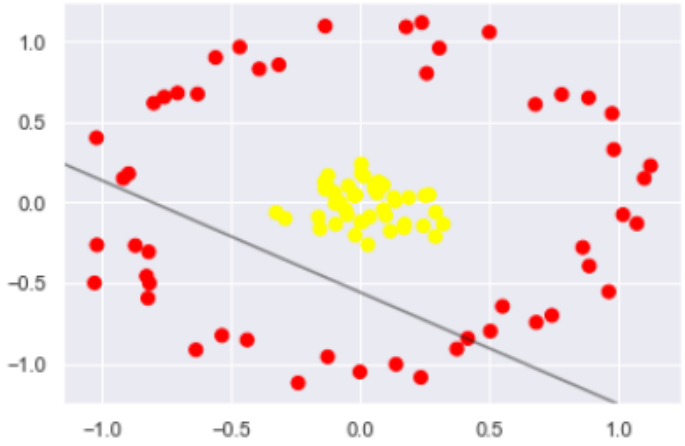
```
from ipywidgets import interact, fixed
interact(plot_svm, N=[10, 200], ax=fixed(None));
```



Beyond linear boundaries : Kernel SVM

23. In SVM models, we can use a version of the same idea. To motivate the need for kernels, let's look at some data that is not linearly separable:

```
from sklearn.datasets.samples_generator import make_circles
X, y = make_circles(100, factor=.1, noise=.1)

clf = SVC(kernel='linear').fit(X, y)

plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
plot_svc_decision_function(clf, plot_support=False);
```

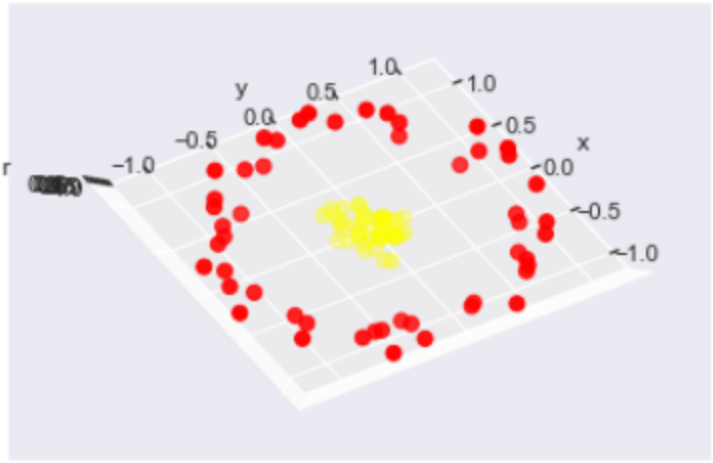


24. For example, one simple projection we could use would be to compute a *radial basis function* centered on the middle clump:

```
r = np.exp(-(X ** 2).sum(1))
```

25. We can visualize this extra data dimension using a three-dimensional plot—if you are running this notebook live, you will be able to use the sliders to rotate the plot:

```python
from mpl_toolkits import mplot3d

def plot_3D(elev=30, azim=30, X=X, y=y):
    ax = plt.subplot(projection='3d')
    ax.scatter3D(X[:, 0], X[:, 1], r, c=y, s=50, cmap='autumn')
    ax.view_init(elev=elev, azim=azim)
    ax.set_xlabel('x')
    ax.set_ylabel('y')
    ax.set_zlabel('r')

interact(plot_3D, elev=[-90, 90], azip=(-180, 180),
         X=fixed(X), y=fixed(y));
```



We can see that with this additional dimension, the data becomes trivially linearly separable, by drawing a separating plane at, say, *r*=0.7.

Here we had to choose and carefully tune our projection: if we had not centered our radial basis function in the right location, we would not have seen such clean, linearly separable results. In general, the need to make such a choice is a problem: we would like to somehow automatically find the best basis functions to use.

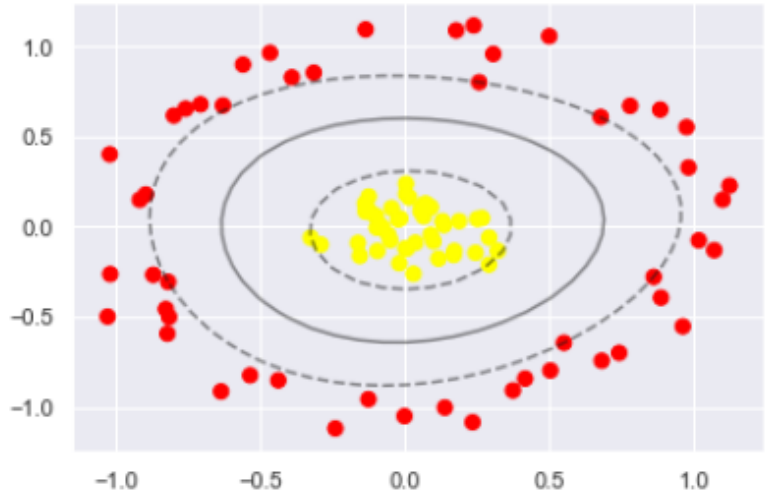
One strategy to this end is to compute a basis function centered at *every* point in the dataset, and let the SVM algorithm sift through the results. This type of basis function transformation is known as a *kernel transformation*, as it is based on a similarity relationship (or kernel) between each pair of points.

A potential problem with this strategy – projecting N points into N dimension – is that it might become very computationally intensive as N grows large. However, because of a neat little procedure known as the kernel trick, a fit on kernel-transformed data can be implicitly – that is, without ever building the full N-dimension representation of the kernel projection. This kernel trick is built into the SVM and is one of the reasons the method is powerful.

26. In Scikit-Learn, we can apply kernelized SVM simply by changing our linear kernel to an RBF (radial basis function) kernel, using the kernel model hyperparameter:

```
clf = SVC(kernel='rbf', C=1E6)
clf.fit(X, y)
```

```
plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
plot_svc_decision_function(clf)
plt.scatter(clf.support_vectors_[:, 0], clf.support_vectors_[:, 1],
            s=300, lw=1, facecolors='none');
```

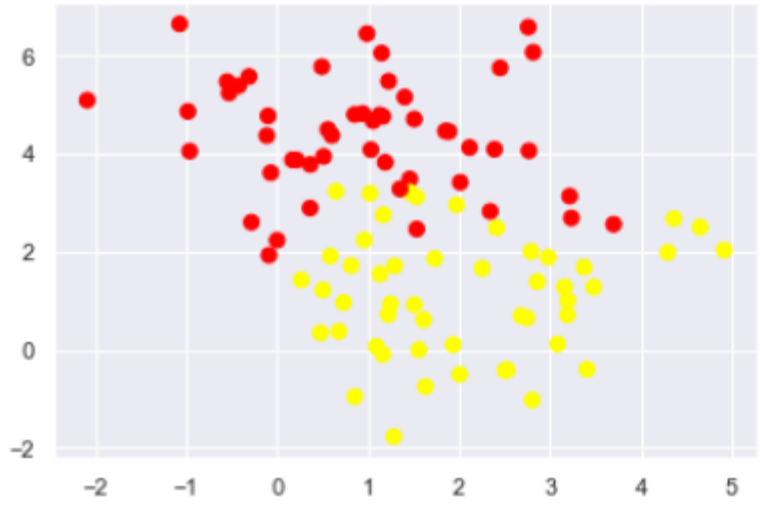


Using this kernelized support vector machine, we learn a suitable nonlinear decision boundary. This kernel transformation strategy is used often in machine learning to turn fast linear methods into fast nonlinear methods, especially for models in which the kernel trick can be used.

Tuning the SVM : Softening Margins

27. Our discussion thus far has centered around very clean datasets, in which a perfect decision boundary exists. But what if your data has some amount of overlap? For example, you may have data like this:

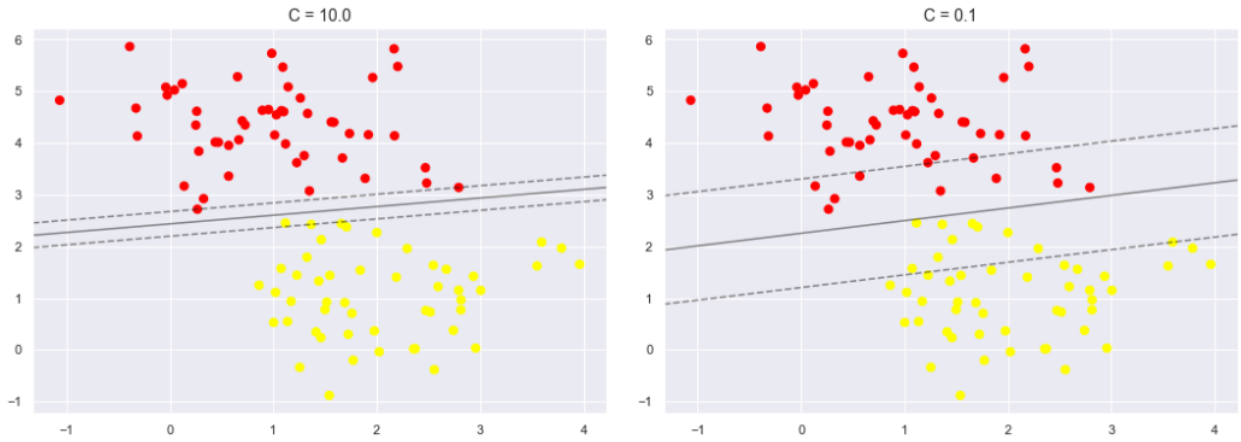
```
X, y = make_blobs(n_samples=100, centers=2,
                  random_state=0, cluster_std=1.2)
plt.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn');
```



To handle this case, the SVM implementation has a bit of a fudge-factor which "softens" the margin: that is, it allows some of the points to creep into the margin if that allows a better fit. The hardness of the margin is controlled by a tuning parameter, most often known as C. For very large C, the margin is hard, and points cannot lie in it. For smaller C, the margin is softer, and can grow to encompass some points

28. The plot shown below gives a visual picture of how a changing C parameter affects the final fit, via the softening of the margin :

```
X, y = make_blobs(n_samples=100, centers=2,
                  random_state=0, cluster_std=0.8)

fig, ax = plt.subplots(1, 2, figsize=(16, 6))
fig.subplots_adjust(left=0.0625, right=0.95, wspace=0.1)

for axi, C in zip(ax, [10.0, 0.1]):
    model = SVC(kernel='linear', C=C).fit(X, y)
    axi.scatter(X[:, 0], X[:, 1], c=y, s=50, cmap='autumn')
    plot_svc_decision_function(model, axi)
    axi.scatter(model.support_vectors_[:, 0],
                model.support_vectors_[:, 1],
                s=300, lw=1, facecolors='none');
    axi.set_title('C = {0:.1f}'.format(C), size=14)
```



Example : Face Recognition

29. As an example of support vector machines in action, let's take a look at the facial recognition problem. We will use the Labeled Faces in the Wild dataset, which consists of several thousand collated photos of various public figures. A fetcher for the dataset is built into Scikit-Learn:

```
from sklearn.datasets import fetch_lfw_people
faces = fetch_lfw_people(min_faces_per_person=60)
print(faces.target_names)
print(faces.images.shape)
```

```
['Ariel Sharon' 'Colin Powell' 'Donald Rumsfeld' 'George W Bush'
 'Gerhard Schroeder' 'Hugo Chavez' 'Junichiro Koizumi' 'Tony Blair']
(1348, 62, 47)
```

30. Let's plot a few of these faces to see what we're working with:

```
fig, ax = plt.subplots(3, 5)
for i, axi in enumerate(ax.flat):
    axi.imshow(faces.images[i], cmap='bone')
    axi.set(xticks=[], yticks=[],
            xlabel=faces.target_names[faces.target[i]])
```

31. Each image contains [62×47] or nearly 3,000 pixels. We could proceed by simply using each pixel value as a feature, but often it is more effective to use some sort of preprocessor to extract more meaningful features; here we will use a principal component analysis (PCA) to extract 150 fundamental components to feed into our support vector machine classifier. We can do this most straightforwardly by packaging the preprocessor and the classifier into a single pipeline:

```
from sklearn.svm import SVC
from sklearn.decomposition import PCA as RandomizedPCA
from sklearn.pipeline import make_pipeline

pca = RandomizedPCA(n_components=150, whiten=True, random_state=42)
svc = SVC(kernel='rbf', class_weight='balanced')
model = make_pipeline(pca, svc)
```

32. For the sake of testing our classifier output, we will split the data into a training and testing set:

```
from sklearn.model_selection import train_test_split
Xtrain, Xtest, ytrain, ytest = train_test_split(faces.data, faces.target,
                                                random_state=42)
```

33. Finally, we can use a grid search cross-validation to explore combinations of parameters. Here we will adjust C (which controls the margin hardness) and gamma (which controls the size of the radial basis function kernel), and determine the best model:

```
from sklearn.model_selection import GridSearchCV
param_grid = {'svc__C': [1, 5, 10, 50],
              'svc__gamma': [0.0001, 0.0005, 0.001, 0.005]}
grid = GridSearchCV(model, param_grid)

%time grid.fit(Xtrain, ytrain)
print(grid.best_params_)
```

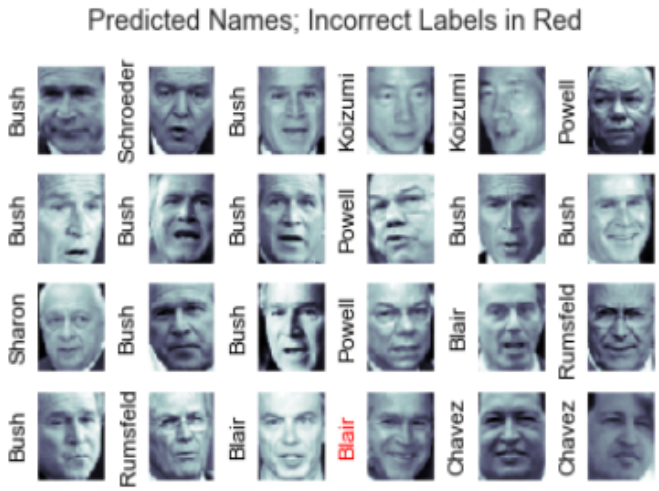
The optimal values fall toward the middle of our grid; if they fell at the edges, we would want to expand the grid to make sure we have found the true optimum.

34. Now with this cross-validated model, we can predict the labels for the test data, which the model has not yet seen:

```
model = grid.best_estimator_
yfit = model.predict(Xtest)
```

35. Let's take a look at a few of the test images along with their predicted values:

```
fig, ax = plt.subplots(4, 6)
for i, axi in enumerate(ax.flat):
    axi.imshow(Xtest[i].reshape(62, 47), cmap='bone')
    axi.set(xticks=[], yticks=[])
    axi.set_ylabel(faces.target_names[yfit[i]].split()[-1],
                   color='black' if yfit[i] == ytest[i] else 'red')
fig.suptitle('Predicted Names; Incorrect Labels in Red', size=14);
```



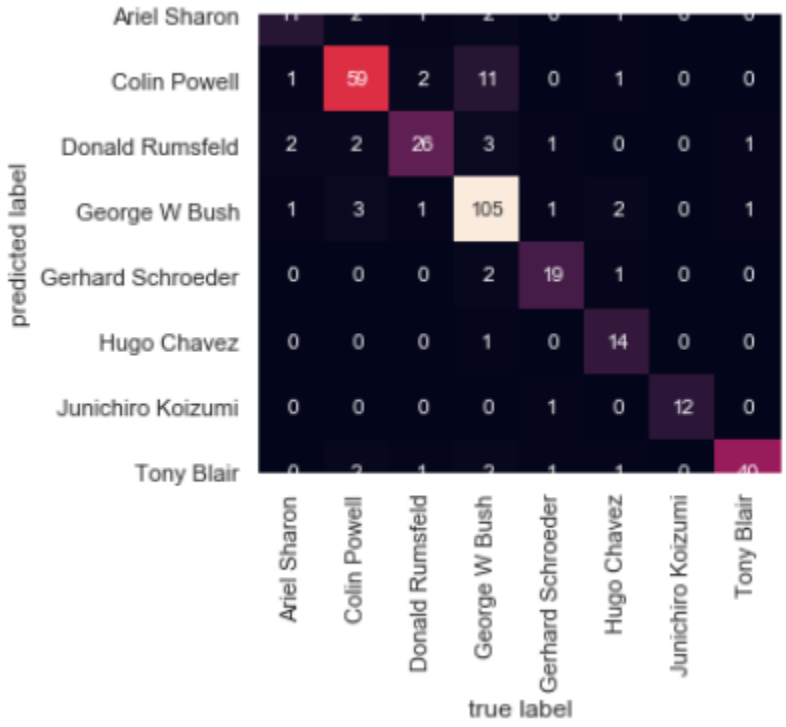
36. Out of this small sample, our optimal estimator mislabeled only a single face (Bush's face in the bottom row was mislabeled as Blair). We can get a better sense of our estimator's performance using the classification report, which lists recovery statistics label by label:

```
from sklearn.metrics import classification_report
print(classification_report(ytest, yfit,
                            target_names=faces.target_names))
```

	precision	recall	f1-score	support
Ariel Sharon	0.65	0.73	0.69	15
Colin Powell	0.80	0.87	0.83	68
Donald Rumsfeld	0.74	0.84	0.79	31
George W Bush	0.92	0.83	0.88	126
Gerhard Schroeder	0.86	0.83	0.84	23
Hugo Chavez	0.93	0.70	0.80	20
Junichiro Koizumi	0.92	1.00	0.96	12
Tony Blair	0.85	0.95	0.90	42
accuracy			0.85	337
macro avg	0.83	0.84	0.84	337
weighted avg	0.86	0.85	0.85	337

37. We might also display the confusion matrix between these classes:

```python
from sklearn.metrics import confusion_matrix
mat = confusion_matrix(ytest, yfit)
sns.heatmap(mat.T, square=True, annot=True, fmt='d', cbar=False,
            xticklabels=faces.target_names,
            yticklabels=faces.target_names)
plt.xlabel('true label')
plt.ylabel('predicted label');
```



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