In [1]:

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

import sklearn.preprocessing as skl_pre
import sklearn.linear_model as skl_lm
import sklearn.discriminant_analysis as skl_da
import sklearn.neighbors as skl_nb

#from IPython.display import set_matplotlib_formats
#set_matplotlib_formats('png')
from IPython.core.pylabtools import figsize
figsize(10, 6) # Width and hight
#plt.style.use('seaborn-white')
```

4.1 Getting started with classification – Breast cancer diagnosis

In this exercise, we will consider the data set <code>data/biopsy.csv</code> with data from breast biopsies, for the purpose of diagnosing breast cancer. For each patient, the data set contains nine different attributes (clump thickness, uniformity of cell size, uniformity of cell shape, marginal adhesion, single epithelial cell size, bare nuclei, bland chromatin, normal nucleoli and mitoses) scored on a scale from 1 to 10, as well as the physician's diagnosis (malign or benign).

Dataset

```
This data frame biopsy contains the following columns:
ID : sample code number (not unique).
V1 : clump thickness.
V2 : uniformity of cell size.
```

V3 : uniformity of cell shape. V4 : marginal adhesion.

V5 : single epithelial cell size.

V6 : bare nuclei (16 values are missing).

V7 : bland chromatin.V8 : normal nucleoli.V9 : mitoses.

class: "benign" or "malignant".

a)

```
Load and familiarize yourself with the data set, using, e.g. info(), describe(), pandas.plotting.scatter_matrix() and print().
```

In [2]:

```
# url = 'data/biopsy.csv'
url = 'https://uu-sml.github.io/course-sml-public/data/biopsy.csv'
biopsy = pd.read_csv(url, na_values='?', dtype={'ID': str}).dropna().reset_index()
```

In [3]:

biopsy.head()

Out[3]:

	index	ID	V1	V2	V3	V4	V5	V6	V7	V8	V9	class
0	0	1000025	5	1	1	1	2	1.0	3	1	1	benign
1	1	1002945	5	4	4	5	7	10.0	3	2	1	benign
2	2	1015425	3	1	1	1	2	2.0	3	1	1	benign
3	3	1016277	6	8	8	1	3	4.0	3	7	1	benign
4	4	1017023	4	1	1	3	2	1.0	3	1	1	benign

In [4]:

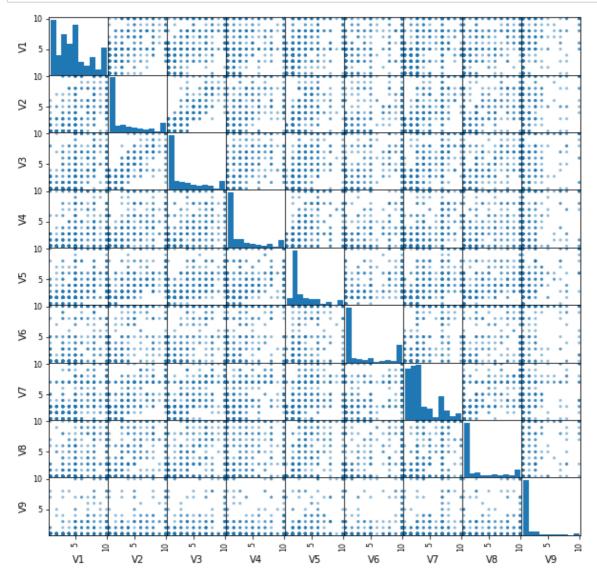
Summary of the variables, note that it does not include the string variables biopsy.describe()

Out[4]:

	index	V 1	V2	V3	V4	V5	V6
count	683.000000	683.000000	683.000000	683.000000	683.000000	683.000000	683.000000
mean	351.355783	4.442167	3.150805	3.215227	2.830161	3.234261	3.544656
std	202.563927	2.820761	3.065145	2.988581	2.864562	2.223085	3.643857
min	0.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000
25%	176.500000	2.000000	1.000000	1.000000	1.000000	2.000000	1.000000
50%	355.000000	4.000000	1.000000	1.000000	1.000000	2.000000	1.000000
75%	526.500000	6.000000	5.000000	5.000000	4.000000	4.000000	6.000000
max	698.000000	10.000000	10.000000	10.000000	10.000000	10.000000	10.000000
4)

In [5]:

```
# scatterplot of the variables V1-V9
pd.plotting.scatter_matrix(biopsy.iloc[:, 2:11], figsize=(10,10))
plt.show()
```



b)

Split the data randomly into a training set and a test set of approximately similar size.

```
In [6]:
```

```
# sampling indices for training
np.random.seed(1)
trainI = np.random.choice(biopsy.shape[0], size=300, replace=False)
trainIndex = biopsy.index.isin(trainI)
train = biopsy.iloc[trainIndex] # training set
test = biopsy.iloc[~trainIndex] # test set
```

c) Logistic regression

Perform logistic regression with class as output variable and V3, V4 and V5 as input variables. Do a prediction on the test set, and compute (i) the fraction of correct predictions and (ii) the confusion matrix (using, for examnple, pandas.crosstab()). The commands skl_lm.LogisticRegression() and model.predict() are useful. Is the performance any good, and what does the confusion matrix tell you?

```
In [7]:
```

```
model = skl lm.LogisticRegression(solver='lbfgs')
X_train = train[['V3', 'V4', 'V5']]
Y_train = train['class']
X_test = test[['V3', 'V4', 'V5']]
Y_test = test['class']
model.fit(X train, Y train)
print('Model summary:')
print(model)
Model summary:
LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=Tru
e,
                   intercept scaling=1, l1 ratio=None, max iter=100,
                   multi_class='auto', n_jobs=None, penalty='12',
                   random state=None, solver='lbfgs', tol=0.0001, verbose=
0,
                   warm start=False)
In [8]:
predict_prob = model.predict_proba(X_test)
print('The class order in the model:')
print(model.classes )
print('Examples of predicted probablities for the above classes:')
predict_prob[0:5] # inspect the first 5 predictions
The class order in the model:
['benign' 'malignant']
Examples of predicted probablities for the above classes:
Out[8]:
array([[0.01147602, 0.98852398],
       [0.99038093, 0.00961907],
       [0.99038093, 0.00961907],
       [0.97523155, 0.02476845],
       [0.99038093, 0.00961907]])
```

```
In [9]:
```

```
prediction = np.empty(len(X_test), dtype=object)
prediction = np.where(predict_prob[:, 0]>=0.5, 'benign', 'malignant')
prediction[0:5] # Inspect the first 5 predictions after labeling.
```

Out[9]:

array(['malignant', 'benign', 'benign', 'benign'], dtype='<U9')</pre>

In [10]:

```
# Confusion matrix
print("Confusion matrix:\n")
print(pd.crosstab(prediction, Y_test), '\n')

# Accuracy
print(f"Accuracy: {np.mean(prediction == Y_test):.3f}")
```

Confusion matrix:

class benign malignant
row_0
benign 239 14
malignant 11 119

Accuracy: 0.935

d) LDA

Repeat (\underline{c}) using LDA. A useful command is sklearn.discriminant_analysis.LinearDiscriminantAnalysis(). sklearn.discriminant_analysis is imported as skl_da

In [11]:

```
model = skl_da.LinearDiscriminantAnalysis()
model.fit(X_train, Y_train)
```

Out[11]:

```
In [12]:
```

```
predict prob = model.predict proba(X test)
print('The class order in the model:')
print(model.classes )
print('Examples of predicted probablities for the above classes:')
with np.printoptions(suppress=True, precision=3): # Supress scientific notaion, e.g. 1.
0e-2.
    print(predict_prob[0:5]) # inspect the first 5 predictions
The class order in the model:
['benign' 'malignant']
Examples of predicted probablities for the above classes:
[[0.078 0.922]
 [0.999 0.001]
 [0.999 0.001]
 [0.998 0.002]
 [0.999 0.001]]
In [13]:
prediction = np.empty(len(X_test), dtype=object)
prediction = np.where(predict_prob[:, 0]>=0.5, 'benign', 'malignant')
print("First five predictions:")
print(prediction[0:5], '\n') # Inspect the first 5 predictions after labeling.
# Confusion matrix
print("Consufion matrix:")
print(pd.crosstab(prediction, Y test),'\n')
# Accuracy
print(f"Accuracy: {np.mean(prediction == Y_test):.3f}")
First five predictions:
['malignant' 'benign' 'benign' 'benign']
Consufion matrix:
class
           benign malignant
row 0
benign
              243
                          25
                         108
malignant
                7
Accuracy: 0.916
```

e) QDA

Repeat (c) using QDA. A useful command is sklearn.discriminant_analysis.QuadraticDiscriminantAnalysis().

```
In [14]:
model = skl da.QuadraticDiscriminantAnalysis()
model.fit(X_train, Y_train)
Out[14]:
QuadraticDiscriminantAnalysis(priors=None, reg_param=0.0,
                              store_covariance=False, tol=0.0001)
In [15]:
predict_prob = model.predict_proba(X_test)
print('The class order in the model:')
print(model.classes , '\n')
print('Examples of predicted probablities for the above classes:')
with np.printoptions(suppress=True, precision=3):
    print(predict_prob[0:5])
                             # inspect the first 5 predictions
The class order in the model:
['benign' 'malignant']
Examples of predicted probablities for the above classes:
 [0.999 0.001]
 [0.999 0.001]
 [0.998 0.002]
 [0.999 0.001]]
In [16]:
prediction = np.empty(len(X_test), dtype=object)
prediction = np.where(predict_prob[:, 0]>=0.5, 'benign', 'malignant')
print('Frist five predictions:')
print(prediction[0:5], '\n') # Inspect the first 5 predictions after labeling.
# Confusion matrix
print('Confusion matrix:\n')
print(pd.crosstab(prediction, Y_test), '\n')
# Accuracy
print('Accuracy:')
print(f"{np.mean(prediction == Y_test):.3f}")
Frist five predictions:
['malignant' 'benign' 'benign' 'benign']
Confusion matrix:
class
           benign
                  malignant
row 0
              237
benign
                          12
malignant
               13
                         121
```

Accuracy: 0.935

f) KNN

Repeat $\underline{(c)}$ using k-NN (with k=1). A useful commands is sklearn.neighbors.KNeighborsClassifier() .

In [17]:

```
model = skl_nb.KNeighborsClassifier(n_neighbors=1)
model.fit(X_train, Y_train)
```

Out[17]:

In [18]:

```
prediction = model.predict(X_test)
print('Confusion matrix:\n')
print(pd.crosstab(prediction, Y_test), '\n')
print(f"Accuracy: {np.mean(prediction == Y_test):.3f}")
```

Confusion matrix:

class benign malignant
row_0
benign 238 19
malignant 12 114

Accuracy: 0.919

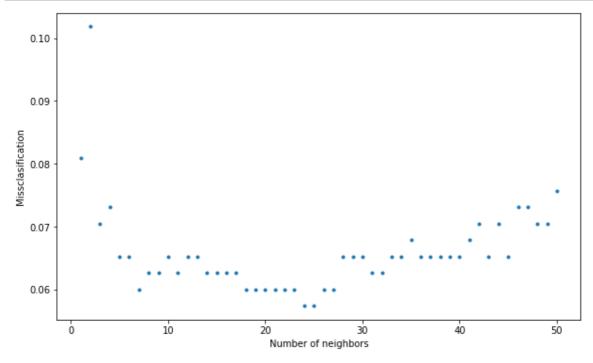
g) Try different values for KNN

Use a for -loop to explore the performance of k-NN for different values of k, and plot the fraction of correct predictions as a function of k.

In [19]:

```
misclassification = []
for k in range(50): # Try n_neighbors = 1, 2, ...., 50
    model = skl_nb.KNeighborsClassifier(n_neighbors=k+1)
    model.fit(X_train, Y_train)
    prediction = model.predict(X_test)
    misclassification.append(np.mean(prediction != Y_test))

K = np.linspace(1, 50, 50)
plt.plot(K, misclassification,'.')
plt.ylabel('Missclassification')
plt.xlabel('Number of neighbors')
plt.show()
```

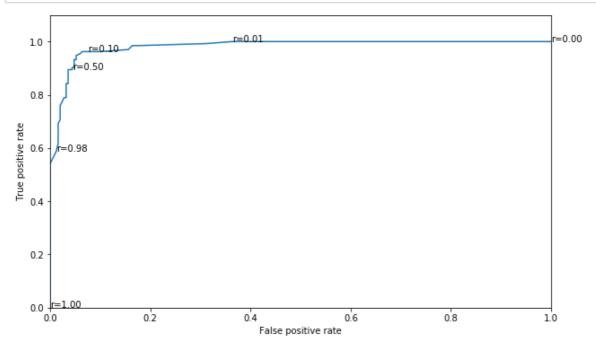


h) ROC for logistic regression

Use a for -loop to explore how the true and false positive rates in logistic regression are affected by different threshold values, and plot the result as a ROC curve . (see Figure 4.7 and Table 4.1 in the book).

In [20]:

```
true postive rate = []
false_positive_rate = []
positive_class = 'malignant'
negative class = 'benign'
P = np.sum(Y_test == positive_class) # Number of positive examples in test data
N = np.sum(Y_test == negative_class) # Number of negative samples in test data
threshold = np.linspace(0.00, 1, 101)
model = skl_lm.LogisticRegression(solver='lbfgs')
model.fit(X_train, Y_train)
predict_prob = model.predict_proba(X_test)
positive_class_index = np.argwhere(model.classes_ == positive_class).squeeze()
for r in threshold:
    prediction = np.where(predict_prob[:, positive_class_index] > r,
                          positive_class,
                          negative_class)
    FP = np.sum((prediction==positive_class)&(Y_test==negative_class)) # False Positive
    TP = np.sum((prediction==positive_class)&(Y_test==positive_class)) # True positive
    false_positive_rate.append(FP/N)
    true_postive_rate.append(TP/P)
plt.plot(false_positive_rate, true_postive_rate);
for idx in [0, 1, 10, 50, 98, 100]:
    plt.text(false_positive_rate[idx], true_postive_rate[idx], f"r={threshold[idx]:.2f}
")
plt.xlim([0,1])
plt.ylim([0,1.1]);
plt.xlabel('False positive rate')
plt.ylabel('True positive rate');
```





Try to find another set of inputs (perhaps by also considering transformations of the attributes) which gives a better result than you have achieved so far. You may also play with the threshold values. ("Better" is on purpose left vague. For this problem, the implications of a false negative (= benign) misclassification is probably more severe than a false positive (= malignant) misclassification.)

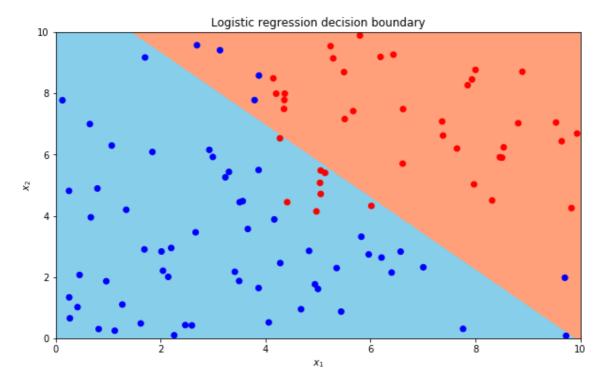
In []:

4.2 Decision boundaries

The following code generates some data with x_1 and x_2 both in [0, 10] and y either 0 or 1, and plots the decision boundary for a logistic regression model.

In [21]:

```
# generate data
np.random.seed(2)
N = 100
x1 = np.random.uniform(0, 10, N)
x2 = np.random.uniform(0, 10, N)
y = np.ones(N)
y[x1<4] = 0
y[x2<4] = 0
X = pd.DataFrame({'x1': x1, 'x2': x2})
# learn a logistic regression model
model = skl_lm.LogisticRegression(solver='lbfgs')
model.fit(X, y)
# classify the points in the whole domain
res = 0.01 # resolution of the squares
xs1 = np.arange(0, 10 + res, res)
xs2 = np.arange(0, 10 + res, res)
xs1, xs2 = np.meshgrid(xs1, xs2) # Creating the grid for all the data points
X_all = pd.DataFrame({'x1': xs1.flatten(), 'x2': xs2.flatten()})
prediction = model.predict(X_all)
from matplotlib.colors import LinearSegmentedColormap
mycmap = LinearSegmentedColormap.from_list('mycmap', ['skyblue', 'lightsalmon'])
plt.imshow(prediction.reshape(xs1.shape[0],-1),
           cmap=mycmap,
           origin='lower',
           extent=[0,10,0,10],
           aspect='auto')
# Plot of the data points and their label
plt.scatter(x1, x2, c=y, cmap='bwr') # blue - white -red colormap
plt.title('Logistic regression decision boundary')
plt.xlim([0,10])
plt.ylim([0,10])
plt.xlabel('$x 1$')
plt.ylabel('$x_2$')
plt.show()
```



(a)

Run the code and verify that it reproduces the figure, and make sure you understand the figure. What is the misclassification rate here?

In [22]:

```
# In this problem, the misclassification rate for the logistic regression is 13%
# (the number of points that are in the wrong region in the figure)
y_hat = model.predict(X)
print("Misclassification rate:", 100*np.sum(y_hat != y)/y.shape[0], "%")
```

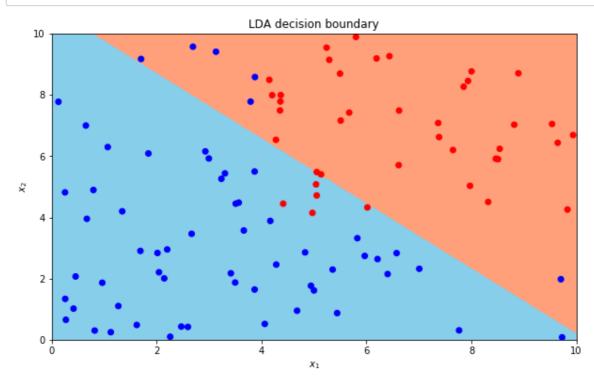
Misclassification rate: 13.0 %

(b)

Modify the code to plot the decision boundary for a LDA classifier. What differences do you see? What is the misclassification rate?

In [23]:

```
# Learn a LDA model
model = skl_da.LinearDiscriminantAnalysis()
model.fit(X, y)
# classify many points, and plot a colored square around each point
prediction = model.predict(X_all)
# Plot of the prediction for all the points in the space
plt.imshow(prediction.reshape(xs1.shape[0],-1),
           cmap=mycmap,
           origin='lower',
           extent=[0,10,0,10],
           aspect='auto')
# Plot of the data points and their label
plt.scatter(x1, x2, c=y, cmap='bwr')
plt.title('LDA decision boundary')
plt.xlim([0,10])
plt.ylim([0,10])
plt.xlabel('$x_1$')
plt.ylabel('$x_2$')
plt.show()
# Misclassification rate 11%.
# Note that the decision boundaries for both logistic regression and
# LDA are linear, but not identical.
y_hat = model.predict(X)
print("Misclassification rate:", 100*np.sum(y_hat != y)/y.shape[0], "%")
```



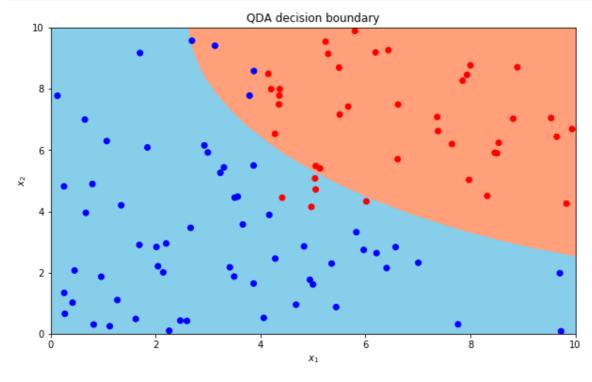
Misclassification rate: 11.0 %



Modify the code to plot the decision boundary for a QDA classifier. What differences do you see? What is the misclassification rate?

In [24]:

```
# Learn a QDA model
model = skl_da.QuadraticDiscriminantAnalysis()
model.fit(X, y)
# classify many points, and plot a colored square around each point
prediction = model.predict(X_all)
# Plot of the prediction for all the points in the space
plt.imshow(prediction.reshape(xs1.shape[0],-1),
           cmap=mycmap,
           origin='lower',
           extent=[0,10,0,10],
           aspect='auto')
# Plot of the data points and their label
plt.scatter(x1, x2, c=y, cmap='bwr')
plt.title('QDA decision boundary')
plt.xlim([0,10])
plt.ylim([0,10])
plt.xlabel('$x_1$')
plt.ylabel('$x_2$')
plt.show()
y_hat = model.predict(X)
print("Misclassification rate:", 100*np.sum(y_hat != y)/y.shape[0], "%")
# Misclassification rate 9%. The decision boundary of QDA is not linear.
```



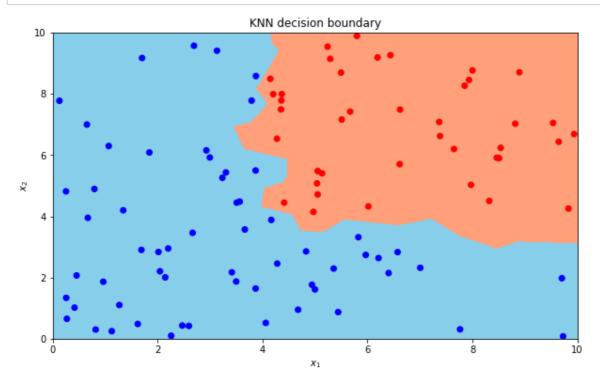
Misclassification rate: 9.0 %

(d)

Modify the code to plot the decision boundary for a k-NN classifier. What differences do you see? What is the misclassification rate?

In [25]:

```
# Learn a KNN model with k=1
model = skl_nb.KNeighborsClassifier(n_neighbors=1)
model.fit(X, y)
# classify many points, and plot a colored square around each point
prediction = model.predict(X_all)
# Plot of the prediction for all the points in the space
plt.imshow(prediction.reshape(xs1.shape[0],-1),
           cmap=mycmap,
           origin='lower',
           extent=[0,10,0,10],
           aspect='auto')
# Plot of the data points and their label
plt.scatter(x1, x2, c=y, cmap='bwr')
plt.title('KNN decision boundary')
plt.xlim([0,10])
plt.ylim([0,10])
plt.xlabel('$x_1$')
plt.ylabel('$x_2$')
plt.show()
y_hat = model.predict(X)
print("Misclassification rate:", 100*np.sum(y_hat != y)/y.shape[0], "%")
# The misclassification rate is 0\% (which always is the case when k = 1).
# The misclassification rate for a test data set could still be much worse.
```



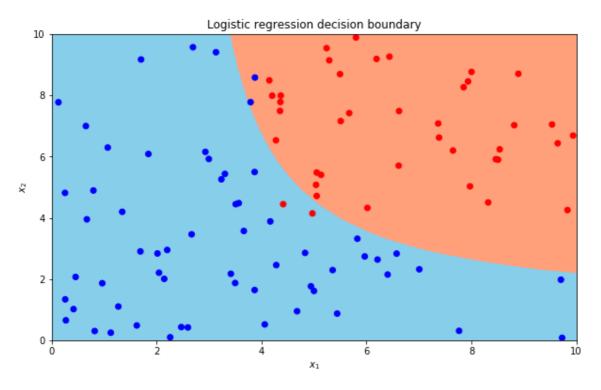
Misclassification rate: 0.0 %



What happens with the decision boundary for logistic regression if you include the term x_1x_2 as an input? What is the misclassification rate?

In [26]:

```
# learn a logistic regression model including the term X1*X2 as an input
X['x1x2'] = X['x1']*X['x2']
model = skl lm.LogisticRegression(solver='lbfgs')
model.fit(X, y)
# classify many points, and plot a colored square around each point
X_{all}['x1x2'] = X_{all}['x1'] * X_{all}['x2']
prediction = model.predict(X_all)
# Plot of the prediction for all the points in the space
plt.imshow(prediction.reshape(xs1.shape[0],-1),
           cmap=mycmap,
           origin='lower',
           extent=[0,10,0,10],
           aspect='auto')
# Plot of the data points and their label
plt.scatter(x1, x2, c=y, cmap='bwr')
plt.title('Logistic regression decision boundary')
plt.xlim([0,10])
plt.ylim([0,10])
plt.xlabel('$x_1$')
plt.ylabel('$x_2$')
plt.show()
y_hat = model.predict(X)
print("Misclassification rate:", 100*np.sum(y_hat != y)/y.shape[0], "%")
# Misclassification rate 4%. Using nonlinear transformations of the inputs
# is one way to create a nonlinear decision boundary in a linear model.
# However, the decision boundary in a 3D-plot plot with axes
# `x1`, `x2` and `x1x2` would still be linear.
```



Misclassification rate: 4.0 %

4.3 Why not linear regression?

In this exercise, we explore why linear regression might not be well suited for classification problems.

(a)

Construct and plot a data set as follows: Let x_i be samples $x_i=i$ in a sequence from i=1 to i=40. Let $y_i=0$ for all i=1:40, except for i=34,38,39,40 where $y_i=1$. Hence, y belongs to either of two classes, 0 and 1.

```
In [27]:
```

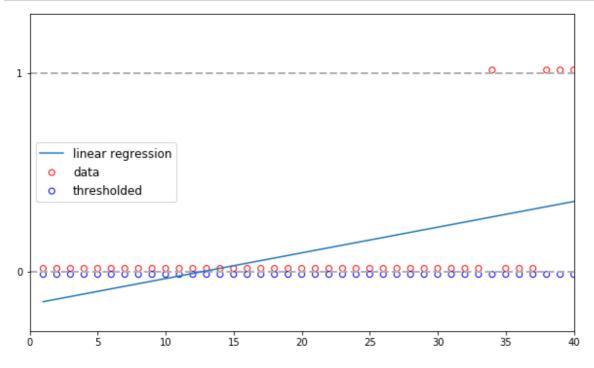
```
x = np.arange(40)+1
y = np.repeat(0, 40)
y[[33, 37, 38, 39]] = 1
```

(b)

Now, the problem is to fit a model which is able to predict the output y from the input x. Start with a linear regression model (command skl_lm.LinearRegression()), and simply threshold its predictions at 0.5 (the average of 0 and 1, the two classes). Plot the prediction. How good is the prediction?

In [28]:

```
model = skl_lm.LinearRegression()
                               # reshape because the model requires input to be a 2D-
model.fit(x.reshape(-1,1), y)
array
prediction = model.predict(x.reshape(-1,1))
prediction_class = np.zeros(40)
prediction_class[prediction>=0.5] = 1
plt.plot(x, prediction, label='linear regression')
plt.scatter(x, y+.015, marker='o', facecolors='none', edgecolors='r', label='data')
plt.scatter(x,
            prediction_class-.015,
            marker='o',
            facecolors='none',
            edgecolors='b',
            label='thresholded')
plt.yticks([0,1])
plt.grid(axis='y', linewidth=2, linestyle='dashed')
plt.xlim(0, 40)
plt.ylim([-0.3,1.3])
plt.legend(loc='center left', fontsize='large')
plt.show()
```

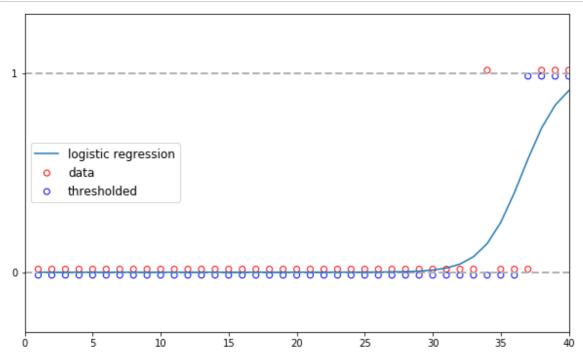


(c)

Try instead logistic regression using $skl_lm.LogisticRegression()$ command (set the parameter C to 1000) and plot the prediction. How good is the prediction, and what advantages does logistic regression have over linear regression for this classification problem?

In [29]:

```
# c)
model = skl_lm.LogisticRegression(C=1000, solver='lbfgs')
model.fit(x.reshape(-1,1), y)
prediction = model.predict_proba(x.reshape(-1,1))
prediction_class = np.repeat(0, 40)
prediction_class[prediction[:, 1]>=0.5] = 1
plt.plot(x, prediction[:, 1], label='logistic regression')
plt.scatter(x, y+.015, marker='o', facecolors='none', edgecolors='r', label='data')
plt.scatter(x,
            prediction_class-.015,
            marker='o',
            facecolors='none',
            edgecolors='b',
            label='thresholded')
plt.yticks([0,1])
plt.grid(axis='y', linewidth=2, linestyle='dashed')
plt.xlim(0, 40)
plt.ylim([-0.3,1.3])
plt.legend(loc='center left', fontsize='large')
plt.show()
```



4.4 k-NN

In this exercise, we are going to explore an important user aspect of k-NN.

(a)

Make 200 draws x_1 from a $\mathcal{N}(0,1^2)$ distribution, and 200 draws x_2 from $\mathcal{N}(0,10^4)$. Also construct y such that y=1 if $x_1\cdot x_2$ is positive, and 0 otherwise. Split the data set randomly into a test and a training data set (equally sized).

In [30]:

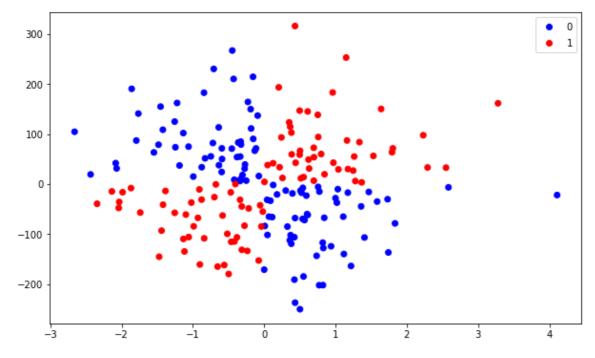
```
np.random.seed(2)
N = 200
x1 = np.random.normal(0, 1**2, 200)
x2 = np.random.normal(0, 10**2, 200)

y_a = np.zeros(N)
y_a[x1*x2 > 0] = 1

X_a = pd.DataFrame({'x1': x1, 'x2': x2})

X_a_train = X_a.iloc[:100, :]
X_a_test = X_a.iloc[-100:, :]
y_a_train = y_a[:100]
y_a_test = y_a[-100:]

scatter = plt.scatter(X_a['x1'], X_a['x2'], c=y_a, cmap='bwr');
plt.legend(*scatter.legend_elements());
```



(b)

Use k-NN (choose k yourself) to predict the test output y using x_1 and x_2 as inputs. How well do you perform?

In [31]:

```
model = skl_nb.KNeighborsClassifier(n_neighbors=2)
model.fit(X_a_train, y_a_train)
prediction_a = model.predict(X_a_test)
print(f"Accuracy: {np.mean(prediction_a == y_a_test)}")
```

Accuracy: 0.52

(c)

Now replace x_2 with 200 draws from $\mathcal{N}(0,1^2)$, and perform k-NN classification anew. How well do you perform this time? Explain the difference!

In [32]:

```
# c)
np.random.seed(2)
N = 200
x1 = np.random.normal(size=N)
x2 = np.random.normal(size=N)

y_b = 1*(x1*x2>0)

X_b = pd.DataFrame({'x1': x1, 'x2': x2})

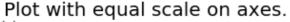
X_b_train = X_b.iloc[:100, :]
X_b_test = X_b.iloc[-100:, :]
y_b_train = y_b[:100]
y_b_test = y_b[-100:]

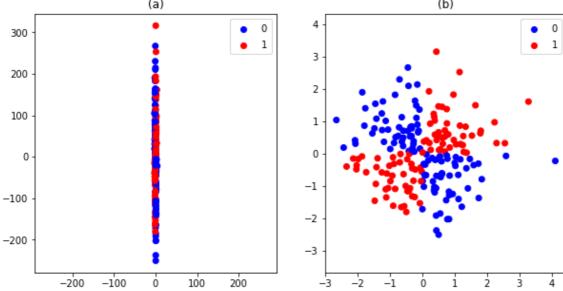
model = skl_nb.KNeighborsClassifier(n_neighbors=3)
model.fit(X_b_train, y_b_train)
prediction_b = model.predict(X_b_test)
print(f"Accuracy: {np.mean(prediction_b == y_b_test)}")
```

Accuracy: 0.92

In [33]:

```
# k-NN is based on the Euclidian distance between data points. In our
# problem in (b), the values of x2 is on average 100 times larger than
# the values of x1, and hence does the prediction essentially only
# depend on x2 (e.g., the distance between (0.1,10) and (0.1,-10)
# is larger than the distance between (0.1,10) and (-0.1,-9),
# e.g., X_1 does effectively not matter when determining the k nearest
# neighbors). However, since y depends both on x1 and x2, the
# performance is deteriorated. Now, when removing the magnitude
# difference between x1 and x2, both inputs will impact the k-NN
# prediction equally.
fig, ax = plt.subplots(1,2, figsize=(10,5))
scatter_a = ax[0].scatter(X_a['x1'], X_a['x2'], c=y_a, cmap='bwr');
scatter_b = ax[1].scatter(X_b['x1'], X_b['x2'], c=y_b, cmap='bwr');
ax[0].legend(*scatter_a.legend_elements());
ax[1].legend(*scatter_b.legend_elements());
ax[0].axis('equal')
ax[1].axis('equal');
fig.suptitle('Plot with equal scale on axes.', fontsize=20)
ax[0].set_title('(a)')
ax[1].set_title('(b)');
```





(d)

Explore how the sklearn.preprocessing.scale() function can help for such problems encountered in (b)!

In [34]:

```
# scale() can be used to standarize a dataset.
# You can do this before splitting up the
# dataset in traineng and test data.
# However, you have to do the same scaling
# of future, yet unseen, data. We use
# StandardScaler() for return a scaler
# that remembers the transofmration
# so we can reuse it for new data.

scaler = skl_pre.StandardScaler().fit(X_a_train)

model = skl_nb.KNeighborsClassifier(n_neighbors=2)
model.fit(scaler.transform(X_a_train), y_a_train)
prediction = model.predict(scaler.transform(X_a_test))

print(f"Accuracy: {np.mean(prediction == y_a_test)}")
```

Accuracy: 0.92

4.5 Multiclass classification

In the course, we have focused on the classification problem for 2 classes. The methods can, however, be generalized to more than two classes. In Python, the commands

skl_da.LinearDiscriminantAnalysis(), skl_da.QuadraticDiscriminantAnalysis() and skl_nb.KNeighborsClassifier() can all be used directly for multi-class problems as well, which we will do in this exercise.

(a)

Load and familiarize yourself with the data set iris, and split it randomly into a training and a test data set.

Description

This famous (Fisher's or Anderson's) iris data set gives the measurements in centimeters of the variables sepal length and width and petal length and width, respectively, for 50 flowers from each of 3 species of iris. The species are Iris setosa, versicolor, and virginica.

Format

iris is a data frame with 150 cases (rows) and 5 variables (columns) named Sepal.Length , Sepal.Width , Petal.Length , Petal.Width , and Species .

```
In [35]:
```

```
# url = 'data/iris.csv'
url = 'https://uu-sml.github.io/course-sml-public/data/iris.csv'
iris = pd.read_csv(url)
```

In [36]:

```
# sampling indices for training
np.random.seed(1)
iris.info()
trainI = np.random.choice(iris.shape[0], size=100, replace=False)
trainIndex = iris.index.isin(trainI)
iris_train = iris.iloc[trainIndex] # training set
iris_test = iris.iloc[~trainIndex] # test set

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
# Column Non-Null Count Dtype
```

```
Column
                 Non-Null Count Dtype
                 _____
   Sepal.Length 150 non-null
                                float64
0
   Sepal.Width 150 non-null
                                float64
1
    Petal.Length 150 non-null
                                float64
2
                                float64
3
    Petal.Width 150 non-null
    Species
                 150 non-null
                                object
dtypes: float64(4), object(1)
memory usage: 6.0+ KB
```

(b)

Use all inputs (Sepal.Length, Sepal.Width, Petal.Length, Petal.Width) to predict the output Species (setosa, versicolor and virginica) using LDA, QDA, and k-NN, respectively.

In [37]:

```
input_variables = ['Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width']
X_train = iris_train[input_variables]
Y_train = iris_train['Species']
X_test = iris_test[input_variables]
Y_test = iris_test['Species']
# LDA
model = skl da.LinearDiscriminantAnalysis()
model.fit(X_train, Y_train)
prediction = model.predict(X_test)
print(f"Accuracy LDA: {np.mean(prediction == Y_test)}")
# ODA
model = skl da.QuadraticDiscriminantAnalysis()
model.fit(X_train, Y_train)
prediction = model.predict(X test)
print(f"Accuracy QDA: {np.mean(prediction == Y_test)}")
# KNN
model = skl nb.KNeighborsClassifier(n neighbors=2)
model.fit(X_train, Y_train)
prediction = model.predict(X_test)
print(f"Accuracy KNN: {np.mean(prediction == Y_test)}")
```

Accuracy LDA: 0.96 Accuracy QDA: 0.94 Accuracy KNN: 0.9