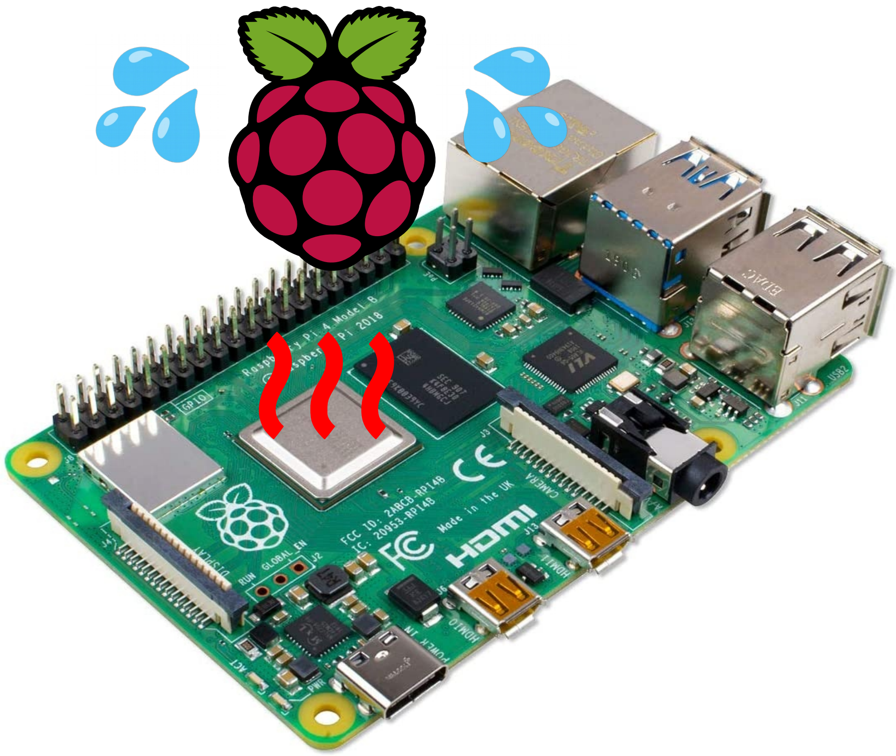
Getting started with ML and Support Vector Classifiers (SVC)

Björn Kasper (kasper.bjoern@bgetem.de)

August 2, 2022



This is a test abstract.

Contents

1 Introduction

This notebook was basically inspired by:

- In Depth: Parameter tuning for SVC
- SVM Hyperparameter Tuning using GridSearchCV:

The goal of this notebook is to show the basic steps in machine learning and the influence of choosing the “right” the kernel of a **support vector classifier (SVC)**. Furthermore, the SVC parameters are described and their effect on the classification result is shown.

Following steps will be shown in next **chapters**:

- STEP 0: Get the data
- STEP 1: Exploring the data
- STEP 2: Prepare the data
- STEP 3: Classify by support vector classifier - SVC
- STEP 4: Evaluate the results - metrics
- STEP 5: Vary parameters

2 Load globally used libraries and set plot parameters

[40]:
```
import time

from IPython.display import HTML

import pandas as pd
import matplotlib.pyplot as plt
from sklearn import svm, metrics
import seaborn as sns
%matplotlib inline
```

3 STEP 0: Get the data

Since this is intended to be an introduction to the world of machine learning (ML), this step does NOT deal with the design of an application suitable for ML and the acquisition of valid measurement data.

In order to get to know the typical work steps and ML tools, the use of **well-known and well-researched data sets** is clearly **recommended**.

In the further course, the famous Iris flower data sets will be used. It can be downloaded on Iris Flower Dataset | Kaggle. Furthermore, the dataset is included in Python in the machine learning package Scikit-learn, so that users can access it without having to find a special source for it.

[1]:
```
# import some data to play with
irisdata_df = pd.read_csv('./datasets/IRIS_flower_dataset_kaggle.csv')
```

4 STEP 1: Exploring the data

4.1 Goals of exploration

The objectives of the exploration of the dataset are as follows:

1. Clarify the **origins history**:
   - Where did the data come from? => Contact persons and licensing permissions?
   - Who obtained the data and with which (measurement) methods? => Did systematic errors occur during the acquisition?
   - What were they originally intended for? => Can they be used for my application?
2. Overview of the internal **structure and organisation** of the data:
   - Which columns are there? => With which methods can they be read in (e.g. import of CSV files)?
   - What do they contain for (physical) measured variables? => Which technical or physical correlations exist?
   - Which data formats or types are there? => Do they have to be converted?
   - In which value ranges do the measurement data vary? => Are normalizations necessary?
3. Identify **anomalies** in the data sets:
   - Do the data have **gaps** or **duplicates**? => Does the data set needs to be cleaned?

  - Are there obvious erroneous entries or measurement outliers? => Does (statistical) filtering have to be carried out?
4. Avoidance of **tendencies due to bias**:
  - Are all possible classes included in the dataset and equally distributed? => Does the data set need to be enriched with additional data for balance?
5. Find a first rough **idea of which correlations** could be in the data set

4.2 Clarify the origins history

> The ***Iris* flower data sets** is a multivariate data set introduced by the British statistician and biologist *Ronald Fisher* in his paper "The use of multiple measurements in taxonomic problems as an example of linear discriminant analysis" (1936). It is sometimes called *Anderson's Iris data set* because Edgar Anderson collected the data to quantify the morphologic variation of Iris flowers of three related species (source: Iris flower data set).

The dataset is published in Public Domain with a CC0-License.

This dataset became a typical test case for many statistical classification techniques in machine learning such as **support vector machines**.

> [..] measurements of the flowers of fifty plants each of the two species *Iris setosa* and *I. versicolor*, found **growing together in the same colony** and measured by Dr E. Anderson [..] (source: R. A. Fisher (1936). "The use of multiple measurements in taxonomic problems". Annals of Eugenics)

> [..] *Iris virginica*, differs from the two other samples in **not being taken from the same natural colony** [..] (source: ibidem)

4.3 Overview of the internal structure and organisation of the data

The data set consists of 50 samples from each of three species of Iris (*Iris setosa*, *Iris virginica* and *Iris versicolor*), so there are 150 total samples. Four features were measured from each sample: the length and the width of the sepals and petals, in centimetres.
Here is a principle illustration of a flower with sepal and petal:

[21]:
```
display(HTML("<figure><img src='./images/Mature_flower_diagram.svg' width='800px'> \
                 <figcaption>Principle illustration of a flower with sepal and␣
↪petal (source: <a href='https://en.wikipedia.org/wiki/File:Mature_flower_diagram.
↪svg'>Mature_flower_diagram.svg</a>)</figcaption> \
              </figure>"))
```

```
<IPython.core.display.HTML object>
```

Here are pictures of the three different Iris species (*Iris setosa*, *Iris virginica* and *Iris versicolor*). Given the dimensions of the flower, it will be possible to predict the class of the flower.

[22]:
```
display(HTML("<table> \
                <tr> \
                <td><figure><img src='./images/Iris_setosa_640px.jpg'␣
↪width='320px'> \
                        <figcaption><i>Iris setosa</i> (source: <a href='https://
↪commons.wikimedia.org/wiki/File:Irissetosa1.jpg'>Irissetosa1.jpg</a>)</
↪figcaption> \
                    </figure></td> \
                <td><figure><img src='./images/Iris_versicolor_640px.jpg'␣
↪width='320px'> \
                        <figcaption><i>Iris versicolor</i> (source: <a href='https:/
↪/en.wikipedia.org/wiki/File:Iris_versicolor_3.jpg'>Iris versicolor 3.jpg</a>)</
↪figcaption> \
                    </figure></td> \
```

```
                <td><figure><img src='./images/Iris_virginica_590px.jpg'␣
↪width='295px'> \
                        <figcaption><i>Iris virginica</i> (source: <a href='https://
↪en.wikipedia.org/wiki/File:Iris_virginica.jpg'>Iris virginica.jpg</a>)</
↪figcaption> \
                    </figure></td> \
                </tr> \
            </table>"))
```

```
<IPython.core.display.HTML object>
```

4.3.1 Inspect structure of dataframe

Print first or last 5 rows of dataframe:

[3]:
```
irisdata_df.head()
```

[3]:
```
   sepal_length  sepal_width  petal_length  petal_width      species
0           5.1          3.5           1.4          0.2  Iris-setosa
1           4.9          3.0           1.4          0.2  Iris-setosa
2           4.7          3.2           1.3          0.2  Iris-setosa
3           4.6          3.1           1.5          0.2  Iris-setosa
4           5.0          3.6           1.4          0.2  Iris-setosa
```

[4]:
```
irisdata_df.tail()
```

[4]:
```
     sepal_length  sepal_width  petal_length  petal_width         species
145           6.7          3.0           5.2          2.3  Iris-virginica
146           6.3          2.5           5.0          1.9  Iris-virginica
147           6.5          3.0           5.2          2.0  Iris-virginica
148           6.2          3.4           5.4          2.3  Iris-virginica
149           5.9          3.0           5.1          1.8  Iris-virginica
```

While printing a dataframe - only an abbreviated view of the dataframe is shown :(
Default setting in the pandas library makes it to display only 5 lines from head and from tail.

[6]:
```
irisdata_df
```

[6]:
```
     sepal_length  sepal_width  petal_length  petal_width         species
0             5.1          3.5           1.4          0.2     Iris-setosa
1             4.9          3.0           1.4          0.2     Iris-setosa
2             4.7          3.2           1.3          0.2     Iris-setosa
3             4.6          3.1           1.5          0.2     Iris-setosa
4             5.0          3.6           1.4          0.2     Iris-setosa
..            …            …             …            …               …
145           6.7          3.0           5.2          2.3  Iris-virginica
146           6.3          2.5           5.0          1.9  Iris-virginica
147           6.5          3.0           5.2          2.0  Iris-virginica
148           6.2          3.4           5.4          2.3  Iris-virginica
149           5.9          3.0           5.1          1.8  Iris-virginica

[150 rows x 5 columns]
```

To print all rows of a dataframe, the option `display.max_rows` has to set to `None` in pandas:

[7]:
```
pd.set_option('display.max_rows', None)
irisdata_df
```

[7]:

	sepal_length	sepal_width	petal_length	petal_width	species
0	5.1	3.5	1.4	0.2	Iris-setosa
1	4.9	3.0	1.4	0.2	Iris-setosa
2	4.7	3.2	1.3	0.2	Iris-setosa
3	4.6	3.1	1.5	0.2	Iris-setosa
4	5.0	3.6	1.4	0.2	Iris-setosa
5	5.4	3.9	1.7	0.4	Iris-setosa
6	4.6	3.4	1.4	0.3	Iris-setosa
7	5.0	3.4	1.5	0.2	Iris-setosa
8	4.4	2.9	1.4	0.2	Iris-setosa
9	4.9	3.1	1.5	0.1	Iris-setosa
10	5.4	3.7	1.5	0.2	Iris-setosa
11	4.8	3.4	1.6	0.2	Iris-setosa
12	4.8	3.0	1.4	0.1	Iris-setosa
13	4.3	3.0	1.1	0.1	Iris-setosa
14	5.8	4.0	1.2	0.2	Iris-setosa
15	5.7	4.4	1.5	0.4	Iris-setosa
16	5.4	3.9	1.3	0.4	Iris-setosa
17	5.1	3.5	1.4	0.3	Iris-setosa
18	5.7	3.8	1.7	0.3	Iris-setosa
19	5.1	3.8	1.5	0.3	Iris-setosa
20	5.4	3.4	1.7	0.2	Iris-setosa
21	5.1	3.7	1.5	0.4	Iris-setosa
22	4.6	3.6	1.0	0.2	Iris-setosa
23	5.1	3.3	1.7	0.5	Iris-setosa
24	4.8	3.4	1.9	0.2	Iris-setosa
25	5.0	3.0	1.6	0.2	Iris-setosa
26	5.0	3.4	1.6	0.4	Iris-setosa
27	5.2	3.5	1.5	0.2	Iris-setosa
28	5.2	3.4	1.4	0.2	Iris-setosa
29	4.7	3.2	1.6	0.2	Iris-setosa
30	4.8	3.1	1.6	0.2	Iris-setosa
31	5.4	3.4	1.5	0.4	Iris-setosa
32	5.2	4.1	1.5	0.1	Iris-setosa
33	5.5	4.2	1.4	0.2	Iris-setosa
34	4.9	3.1	1.5	0.1	Iris-setosa
35	5.0	3.2	1.2	0.2	Iris-setosa
36	5.5	3.5	1.3	0.2	Iris-setosa
37	4.9	3.1	1.5	0.1	Iris-setosa
38	4.4	3.0	1.3	0.2	Iris-setosa
39	5.1	3.4	1.5	0.2	Iris-setosa
40	5.0	3.5	1.3	0.3	Iris-setosa
41	4.5	2.3	1.3	0.3	Iris-setosa
42	4.4	3.2	1.3	0.2	Iris-setosa
43	5.0	3.5	1.6	0.6	Iris-setosa
44	5.1	3.8	1.9	0.4	Iris-setosa
45	4.8	3.0	1.4	0.3	Iris-setosa
46	5.1	3.8	1.6	0.2	Iris-setosa
47	4.6	3.2	1.4	0.2	Iris-setosa
48	5.3	3.7	1.5	0.2	Iris-setosa
49	5.0	3.3	1.4	0.2	Iris-setosa
50	7.0	3.2	4.7	1.4	Iris-versicolor
51	6.4	3.2	4.5	1.5	Iris-versicolor
52	6.9	3.1	4.9	1.5	Iris-versicolor
53	5.5	2.3	4.0	1.3	Iris-versicolor
54	6.5	2.8	4.6	1.5	Iris-versicolor
55	5.7	2.8	4.5	1.3	Iris-versicolor

56	6.3	3.3	4.7	1.6	Iris-versicolor
57	4.9	2.4	3.3	1.0	Iris-versicolor
58	6.6	2.9	4.6	1.3	Iris-versicolor
59	5.2	2.7	3.9	1.4	Iris-versicolor
60	5.0	2.0	3.5	1.0	Iris-versicolor
61	5.9	3.0	4.2	1.5	Iris-versicolor
62	6.0	2.2	4.0	1.0	Iris-versicolor
63	6.1	2.9	4.7	1.4	Iris-versicolor
64	5.6	2.9	3.6	1.3	Iris-versicolor
65	6.7	3.1	4.4	1.4	Iris-versicolor
66	5.6	3.0	4.5	1.5	Iris-versicolor
67	5.8	2.7	4.1	1.0	Iris-versicolor
68	6.2	2.2	4.5	1.5	Iris-versicolor
69	5.6	2.5	3.9	1.1	Iris-versicolor
70	5.9	3.2	4.8	1.8	Iris-versicolor
71	6.1	2.8	4.0	1.3	Iris-versicolor
72	6.3	2.5	4.9	1.5	Iris-versicolor
73	6.1	2.8	4.7	1.2	Iris-versicolor
74	6.4	2.9	4.3	1.3	Iris-versicolor
75	6.6	3.0	4.4	1.4	Iris-versicolor
76	6.8	2.8	4.8	1.4	Iris-versicolor
77	6.7	3.0	5.0	1.7	Iris-versicolor
78	6.0	2.9	4.5	1.5	Iris-versicolor
79	5.7	2.6	3.5	1.0	Iris-versicolor
80	5.5	2.4	3.8	1.1	Iris-versicolor
81	5.5	2.4	3.7	1.0	Iris-versicolor
82	5.8	2.7	3.9	1.2	Iris-versicolor
83	6.0	2.7	5.1	1.6	Iris-versicolor
84	5.4	3.0	4.5	1.5	Iris-versicolor
85	6.0	3.4	4.5	1.6	Iris-versicolor
86	6.7	3.1	4.7	1.5	Iris-versicolor
87	6.3	2.3	4.4	1.3	Iris-versicolor
88	5.6	3.0	4.1	1.3	Iris-versicolor
89	5.5	2.5	4.0	1.3	Iris-versicolor
90	5.5	2.6	4.4	1.2	Iris-versicolor
91	6.1	3.0	4.6	1.4	Iris-versicolor
92	5.8	2.6	4.0	1.2	Iris-versicolor
93	5.0	2.3	3.3	1.0	Iris-versicolor
94	5.6	2.7	4.2	1.3	Iris-versicolor
95	5.7	3.0	4.2	1.2	Iris-versicolor
96	5.7	2.9	4.2	1.3	Iris-versicolor
97	6.2	2.9	4.3	1.3	Iris-versicolor
98	5.1	2.5	3.0	1.1	Iris-versicolor
99	5.7	2.8	4.1	1.3	Iris-versicolor
100	6.3	3.3	6.0	2.5	Iris-virginica
101	5.8	2.7	5.1	1.9	Iris-virginica
102	7.1	3.0	5.9	2.1	Iris-virginica
103	6.3	2.9	5.6	1.8	Iris-virginica
104	6.5	3.0	5.8	2.2	Iris-virginica
105	7.6	3.0	6.6	2.1	Iris-virginica
106	4.9	2.5	4.5	1.7	Iris-virginica
107	7.3	2.9	6.3	1.8	Iris-virginica
108	6.7	2.5	5.8	1.8	Iris-virginica
109	7.2	3.6	6.1	2.5	Iris-virginica
110	6.5	3.2	5.1	2.0	Iris-virginica
111	6.4	2.7	5.3	1.9	Iris-virginica
112	6.8	3.0	5.5	2.1	Iris-virginica

113	5.7	2.5	5.0	2.0	Iris-virginica
114	5.8	2.8	5.1	2.4	Iris-virginica
115	6.4	3.2	5.3	2.3	Iris-virginica
116	6.5	3.0	5.5	1.8	Iris-virginica
117	7.7	3.8	6.7	2.2	Iris-virginica
118	7.7	2.6	6.9	2.3	Iris-virginica
119	6.0	2.2	5.0	1.5	Iris-virginica
120	6.9	3.2	5.7	2.3	Iris-virginica
121	5.6	2.8	4.9	2.0	Iris-virginica
122	7.7	2.8	6.7	2.0	Iris-virginica
123	6.3	2.7	4.9	1.8	Iris-virginica
124	6.7	3.3	5.7	2.1	Iris-virginica
125	7.2	3.2	6.0	1.8	Iris-virginica
126	6.2	2.8	4.8	1.8	Iris-virginica
127	6.1	3.0	4.9	1.8	Iris-virginica
128	6.4	2.8	5.6	2.1	Iris-virginica
129	7.2	3.0	5.8	1.6	Iris-virginica
130	7.4	2.8	6.1	1.9	Iris-virginica
131	7.9	3.8	6.4	2.0	Iris-virginica
132	6.4	2.8	5.6	2.2	Iris-virginica
133	6.3	2.8	5.1	1.5	Iris-virginica
134	6.1	2.6	5.6	1.4	Iris-virginica
135	7.7	3.0	6.1	2.3	Iris-virginica
136	6.3	3.4	5.6	2.4	Iris-virginica
137	6.4	3.1	5.5	1.8	Iris-virginica
138	6.0	3.0	4.8	1.8	Iris-virginica
139	6.9	3.1	5.4	2.1	Iris-virginica
140	6.7	3.1	5.6	2.4	Iris-virginica
141	6.9	3.1	5.1	2.3	Iris-virginica
142	5.8	2.7	5.1	1.9	Iris-virginica
143	6.8	3.2	5.9	2.3	Iris-virginica
144	6.7	3.3	5.7	2.5	Iris-virginica
145	6.7	3.0	5.2	2.3	Iris-virginica
146	6.3	2.5	5.0	1.9	Iris-virginica
147	6.5	3.0	5.2	2.0	Iris-virginica
148	6.2	3.4	5.4	2.3	Iris-virginica
149	5.9	3.0	5.1	1.8	Iris-virginica

4.3.2 Get data types

[8]:
```
irisdata_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   sepal_length  150 non-null    float64
 1   sepal_width   150 non-null    float64
 2   petal_length  150 non-null    float64
 3   petal_width   150 non-null    float64
 4   species       150 non-null    object
dtypes: float64(4), object(1)
memory usage: 5.3+ KB
```

[9]:
```
irisdata_df.describe()
```

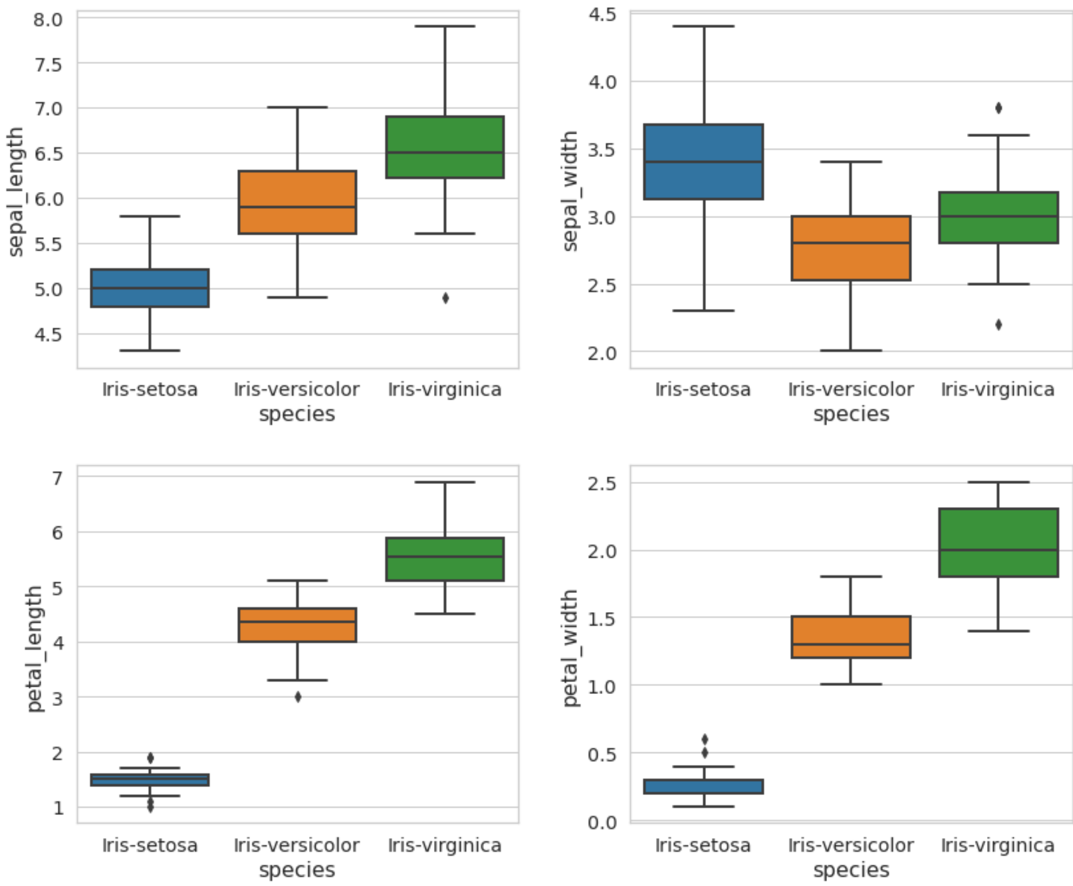
[9]:

	sepal_length	sepal_width	petal_length	petal_width
count	150.000000	150.000000	150.000000	150.000000
mean	5.843333	3.054000	3.758667	1.198667
std	0.828066	0.433594	1.764420	0.763161
min	4.300000	2.000000	1.000000	0.100000
25%	5.100000	2.800000	1.600000	0.300000
50%	5.800000	3.000000	4.350000	1.300000
75%	6.400000	3.300000	5.100000	1.800000
max	7.900000	4.400000	6.900000	2.500000

4.3.3 Get data ranges with Boxplots

Boxplots can be used to explore the data ranges in the data set. These also provide information about **outliers**.

[157]:
```
sns.set_context("notebook", font_scale=1.3, rc={"lines.linewidth": 2.0})
sns.set_style("whitegrid")
#sns.set_style("white")

fig, axs = plt.subplots(2, 2, figsize=(12, 10))

fn = ['sepal_length', 'sepal_width', 'petal_length', 'petal_width']
cn = ['Iris-setosa', 'Iris-versicolor', 'Iris-virginica']
box1 = sns.boxplot(x = 'species', y = 'sepal_length',
                   data = irisdata_df, order = cn, ax = axs[0,0])
box2 = sns.boxplot(x = 'species', y = 'sepal_width',
                   data = irisdata_df, order = cn, ax = axs[0,1])
box3 = sns.boxplot(x = 'species', y = 'petal_length',
                   data = irisdata_df, order = cn, ax = axs[1,0])
box4 = sns.boxplot(x = 'species', y = 'petal_width',
                   data = irisdata_df,  order = cn, ax = axs[1,1])

# add some spacing between subplots
fig.tight_layout(pad=2.0)

plt.show()
```



4.4 Identify anomalies in the data sets

4.4.1 Find gaps in dataset

This section was inspired by Working with Missing Data in Pandas.

Checking for missing values using `isnull()` In order to check for missing values in Pandas DataFrame, we use the function `isnull()`. This function returns a dataframe of Boolean values which are True for **NaN values**.

[37]:
```
pd.set_option('display.max_rows', 40)
pd.set_option('display.min_rows', 30)
```

[38]:
```
irisdata_df.isnull()
```

[38]:

	sepal_length	sepal_width	petal_length	petal_width	species
0	False	False	False	False	False
1	False	False	False	False	False
2	False	False	False	False	False
3	False	False	False	False	False
4	False	False	False	False	False
5	False	False	False	False	False
6	False	False	False	False	False
7	False	False	False	False	False
8	False	False	False	False	False
9	False	False	False	False	False

```
10          False        False        False        False     False
11          False        False        False        False     False
12          False        False        False        False     False
13          False        False        False        False     False
14          False        False        False        False     False
..            …            …            …          …         …
135         False        False        False        False     False
136         False        False        False        False     False
137         False        False        False        False     False
138         False        False        False        False     False
139         False        False        False        False     False
140         False        False        False        False     False
141         False        False        False        False     False
142         False        False        False        False     False
143         False        False        False        False     False
144         False        False        False        False     False
145         False        False        False        False     False
146         False        False        False        False     False
147         False        False        False        False     False
148         False        False        False        False     False
149         False        False        False        False     False

[150 rows x 5 columns]
```

Show only the gaps:

[5]:
```
irisdata_df_gaps = irisdata_df[irisdata_df.isnull().any(axis=1)]
irisdata_df_gaps
```

[5]:
```
Empty DataFrame
Columns: [sepal_length, sepal_width, petal_length, petal_width, species]
Index: []
```

Fine - this dataset seems to be complete :)

So let's look for something else for exercise: employes.csv

[159]:
```
# import data to dataframe from csv file
employees_df = pd.read_csv("./datasets/employees_edit.csv")

employees_df
```

[159]:
```
     First Name  Gender  Start Date Last Login Time  Salary   Bonus %  \
0       Douglas    Male    8/6/1993        12:42 PM   97308   6945.00
1        Thomas    Male   3/31/1996         6:53 AM   61933      4.17
2         Maria  Female   4/23/1993        11:17 AM  130590  11858.00
3         Jerry    Male    3/4/2005         1:00 PM  138705      9.34
4         Larry    Male   1/24/1998         4:47 PM  101004   1389.00
…           …      …         …           …        …        …
999       Henry     NaN  11/23/2014         6:09 AM  132483  16655.00
1000    Phillip    Male   1/31/1984         6:30 AM   42392  19675.00
1001    Russell    Male   5/20/2013        12:39 PM   96914   1421.00
1002      Larry    Male   4/20/2013         4:45 PM   60500  11985.00
1003     Albert    Male   5/15/2012         6:24 PM  129949  10169.00

     Senior Management           Team
0                 True      Marketing
1                 True            NaN
```

```
2              False              Finance
3               True              Finance
4               True      Client Services
…                  …                    …
999            False         Distribution
1000           False              Finance
1001           False              Product
1002           False  Business Development
1003            True                Sales

[1004 rows x 8 columns]
```

Show only the gaps from this gappy dataset again:

[160]:
```
employees_df_gaps = employees_df[employees_df.isnull().any(axis=1)]
employees_df_gaps
```

[160]:
```
    First Name  Gender  Start Date Last Login Time  Salary   Bonus %  \
1       Thomas    Male   3/31/1996        6:53 AM   61933      4.17
7          NaN  Female   7/20/2015       10:43 AM   45906  11598.00
10      Louise  Female   8/12/1980        9:01 AM   63241  15132.00
20        Lois     NaN   4/22/1995        7:18 PM   64714   4934.00
22      Joshua     NaN    3/8/2012        1:58 AM   90816  18816.00
..         …       …         …              …       …        …
965    Antonio     NaN   6/18/1989        9:37 PM  103050      3.05
976     Victor     NaN   7/28/2006        2:49 PM   76381  11159.00
989    Stephen     NaN   7/10/1983        8:10 PM   85668   1909.00
993     Justin     NaN   2/10/1991        4:58 PM   38344   3794.00
999      Henry     NaN  11/23/2014        6:09 AM  132483  16655.00

    Senior Management              Team
1                True               NaN
7                 NaN           Finance
10               True               NaN
20               True             Legal
22               True   Client Services
..                 …                 …
965             False             Legal
976              True             Sales
989             False             Legal
993             False             Legal
999             False      Distribution

[237 rows x 8 columns]
```

Fill the missing values with `fillna()` Now we are going to fill all the null (NaN) values in Gender column with *"No Gender"*.

Attention: We are doing that directly in this dataframe with `inplace = True` - we don't make a deep copy!

[161]:
```
# filling a null values using fillna()
employees_df["Gender"].fillna("No Gender", inplace = True)
employees_df
```

[161]:
```
     First Name     Gender  Start Date Last Login Time  Salary   Bonus %  \
0       Douglas       Male    8/6/1993       12:42 PM   97308   6945.00
```

```
1        Thomas       Male   3/31/1996         6:53 AM   61933       4.17
2         Maria     Female   4/23/1993        11:17 AM  130590   11858.00
3         Jerry       Male    3/4/2005         1:00 PM  138705       9.34
4         Larry       Male   1/24/1998         4:47 PM  101004    1389.00
…           …         …         …          …       …       …
999       Henry  No Gender  11/23/2014         6:09 AM  132483   16655.00
1000    Phillip       Male   1/31/1984         6:30 AM   42392   19675.00
1001    Russell       Male   5/20/2013        12:39 PM   96914    1421.00
1002      Larry       Male   4/20/2013         4:45 PM   60500   11985.00
1003     Albert       Male   5/15/2012         6:24 PM  129949   10169.00

     Senior Management                  Team
0                 True             Marketing
1                 True                   NaN
2                False               Finance
3                 True               Finance
4                 True       Client Services
…                  …                   …
999              False          Distribution
1000             False               Finance
1001             False               Product
1002             False  Business Development
1003              True                 Sales

[1004 rows x 8 columns]
```

Dropping missing values using `dropna()` In order to drop null values from a dataframe, we use `dropna()` function. This function drops rows or columns of datasets with NaN values in different ways.

Default is to drop rows with at least 1 null value (NaN). Giving the parameter `how = 'all'` the function drops rows with all data missing or contain null values (NaN).

[162]:
```python
# making a new dataframe with dropped NaN values
employees_df_dropped = employees_df.dropna(axis = 0, how ='any')
employees_df_dropped
```

[162]:
```
     First Name     Gender  Start Date Last Login Time  Salary    Bonus %  \
0       Douglas       Male    8/6/1993        12:42 PM   97308    6945.00
2         Maria     Female   4/23/1993        11:17 AM  130590   11858.00
3         Jerry       Male    3/4/2005         1:00 PM  138705       9.34
4         Larry       Male   1/24/1998         4:47 PM  101004    1389.00
5        Dennis       Male   4/18/1987         1:35 AM  115163   10125.00
…           …         …         …          …       …       …
999       Henry  No Gender  11/23/2014         6:09 AM  132483   16655.00
1000    Phillip       Male   1/31/1984         6:30 AM   42392   19675.00
1001    Russell       Male   5/20/2013        12:39 PM   96914    1421.00
1002      Larry       Male   4/20/2013         4:45 PM   60500   11985.00
1003     Albert       Male   5/15/2012         6:24 PM  129949   10169.00

     Senior Management                  Team
0                 True             Marketing
2                False               Finance
3                 True               Finance
4                 True       Client Services
5                False                 Legal
…                  …                   …
999              False          Distribution
```

```
1000            False               Finance
1001            False               Product
1002            False  Business Development
1003             True                 Sales

[903 rows x 8 columns]
```

Finally we compare the sizes of dataframes so that we learn how many rows had at least 1 Null value.

[163]:
```
print("Old data frame length:", len(employees_df))
print("New data frame length:", len(employees_df_dropped))
print("Number of rows with at least 1 NaN value: ",
      (len(employees_df)-len(employees_df_dropped)))
```

```
Old data frame length: 1004
New data frame length: 903
Number of rows with at least 1 NaN value:  101
```

4.4.2 Find and remove duplicates in dataset

This section was inspired by: - How to Find Duplicates in Pandas DataFrame (With Examples) - How to Drop Duplicate Rows in a Pandas DataFrame

Checking for duplicate values using `duplicated()` In order to check for duplicate values in Pandas DataFrame, we use a function `duplicated()`. This function can be used in two ways: - find duplicate rows across **all columns** with `duplicateRows = df[df.duplicated()]` - find duplicate rows across **specific columns** `duplicateRows = df[df.duplicated(subset=['col1', 'col2'])]`

Find duplicate rows across **all columns**:

[44]:
```
# import (again) data to dataframe from csv file
employees_df = pd.read_csv("./datasets/employees_edit.csv")
```

[45]:
```
# find duplicate rows across all columns
duplicateRows = employees_df[employees_df.duplicated()]
duplicateRows
```

[45]:
```
    First Name  Gender  Start Date Last Login Time  Salary  Bonus %  \
112      Karen  Female  11/30/1999         7:46 AM  102488  17653.0
127      Linda  Female   5/25/2000         5:45 PM  119009  12506.0
296    Brandon     NaN   11/3/1997         8:17 PM  121333  15295.0
580   Nicholas    Male    3/1/2013         9:26 PM  101036   2826.0

    Senior Management                  Team
112              True               Product
127              True  Business Development
296             False  Business Development
580              True       Human Resources
```

[46]:
```
# argument keep='last' displays the first duplicate rows instead of the last
duplicateRows = employees_df[employees_df.duplicated(keep='last')]
duplicateRows
```

[46]:
```
    First Name  Gender  Start Date Last Login Time  Salary  Bonus %  \
55       Karen  Female  11/30/1999         7:46 AM  102488  17653.0
92       Linda  Female   5/25/2000         5:45 PM  119009  12506.0
153    Brandon     NaN   11/3/1997         8:17 PM  121333  15295.0
```

```
442   Nicholas    Male    3/1/2013         9:26 PM  101036   2826.0

    Senior Management                  Team
55                True              Product
92                True  Business Development
153              False  Business Development
442               True       Human Resources
```

Find duplicate rows across **specific columns**:

[164]:
```
# identify duplicate rows across 'First Name' and 'Last Login Time' columns
duplicateRows = employees_df[employees_df.duplicated(
                    subset=['First Name', 'Last Login Time'])]
duplicateRows
```

[164]:
```
    First Name    Gender  Start Date Last Login Time  Salary  Bonus %  \
112      Karen    Female  11/30/1999         7:46 AM  102488  17653.0
127      Linda    Female   5/25/2000         5:45 PM  119009  12506.0
296    Brandon No Gender   11/3/1997         8:17 PM  121333  15295.0
577        NaN    Female   1/13/2009         1:01 PM  118736   7421.0
580   Nicholas      Male    3/1/2013         9:26 PM  101036   2826.0
632        NaN No Gender    9/2/1988        12:49 PM  147309   1702.0
881        NaN      Male    9/5/1980         7:36 AM  114896  13823.0
929        NaN    Female   8/23/2000         4:19 PM   95866  19388.0
934      Nancy    Female   9/10/2001        11:57 PM   85213   2386.0
973      Linda    Female    2/4/2010         8:49 PM   44486  17308.0

    Senior Management                  Team
112               True              Product
127               True  Business Development
296              False  Business Development
577                NaN       Client Services
580               True       Human Resources
632                NaN          Distribution
881                NaN       Client Services
929                NaN                 Sales
934               True             Marketing
973               True           Engineering
```

[165]:
```
# argument keep='last' displays the first duplicate rows instead of the last
duplicateRows = employees_df[employees_df.duplicated(
                    subset=['First Name', 'Last Login Time'], keep='last')]
duplicateRows
```

[165]:
```
    First Name    Gender  Start Date Last Login Time  Salary   Bonus %  \
23         NaN      Male   6/14/2012         4:19 PM  125792   5042.00
37       Linda    Female  10/19/1981         8:49 PM   57427   9557.00
55       Karen    Female  11/30/1999         7:46 AM  102488  17653.00
66       Nancy    Female  12/15/2012        11:57 PM  125250   2672.00
92       Linda    Female   5/25/2000         5:45 PM  119009  12506.00
153    Brandon No Gender   11/3/1997         8:17 PM  121333  15295.00
222        NaN    Female   6/17/1991        12:49 PM   71945      5.56
269        NaN      Male    2/4/2005         1:01 PM   40451  16044.00
442   Nicholas      Male    3/1/2013         9:26 PM  101036   2826.00
778        NaN    Female   6/18/2000         7:36 AM  106428  10867.00

    Senior Management                  Team
```

```
23              NaN                   NaN
37             True       Client Services
55             True               Product
66             True  Business Development
92             True  Business Development
153           False  Business Development
222             NaN             Marketing
269             NaN          Distribution
442            True       Human Resources
778             NaN                   NaN
```

Dropping duplicate values using `drop_duplicates()` In order to drop duplicate values from a dataframe, we use `drop_duplicates()` function.

This function can be used in two ways: - remove duplicate rows across **all columns** with `df.drop_duplicates()` - find duplicate rows across **specific columns** `df.drop_duplicates(subset=['col1', 'col2'])`

Attention: We are doing that directly in this dataframe with `inplace = True` - we don't make a deep copy!

Remove duplicate rows across **all columns**:

[49]:
```
# remove duplicate rows across all columns
employees_df.drop_duplicates(inplace=True)
employees_df
```

[49]:
```
     First Name  Gender  Start Date Last Login Time  Salary   Bonus %  \
0       Douglas    Male    8/6/1993        12:42 PM   97308   6945.00
1        Thomas    Male   3/31/1996         6:53 AM   61933      4.17
2         Maria  Female   4/23/1993        11:17 AM  130590  11858.00
3         Jerry    Male    3/4/2005         1:00 PM  138705      9.34
4         Larry    Male   1/24/1998         4:47 PM  101004   1389.00
5        Dennis    Male   4/18/1987         1:35 AM  115163  10125.00
6          Ruby  Female   8/17/1987         4:20 PM   65476  10012.00
7           NaN  Female   7/20/2015        10:43 AM   45906  11598.00
8        Angela  Female  11/22/2005         6:29 AM   95570  18523.00
9       Frances  Female    8/8/2002         6:51 AM  139852   7524.00
10       Louise  Female   8/12/1980         9:01 AM   63241  15132.00
11        Julie  Female  10/26/1997         3:19 PM  102508  12637.00
12      Brandon    Male   12/1/1980         1:08 AM  112807  17492.00
13         Gary    Male   1/27/2008        11:40 PM  109831   5831.00
14     Kimberly  Female   1/14/1999         7:13 AM   41426  14543.00
…           …       …         …               …       …         …
989     Stephen     NaN   7/10/1983         8:10 PM   85668   1909.00
990       Donna  Female  11/26/1982         7:04 AM   82871  17999.00
991      Gloria  Female   12/8/2014         5:08 AM  136709  10331.00
992       Alice  Female   10/5/2004         9:34 AM   47638  11209.00
993      Justin     NaN   2/10/1991         4:58 PM   38344   3794.00
994       Robin  Female   7/24/1987         1:35 PM  100765  10982.00
995        Rose  Female   8/25/2002         5:12 AM  134505  11051.00
996     Anthony    Male  10/16/2011         8:35 AM  112769  11625.00
997        Tina  Female   5/15/1997         3:53 PM   56450     19.04
998      George    Male   6/21/2013         5:47 PM   98874   4479.00
999       Henry     NaN  11/23/2014         6:09 AM  132483  16655.00
1000    Phillip    Male   1/31/1984         6:30 AM   42392  19675.00
1001    Russell    Male   5/20/2013        12:39 PM   96914   1421.00
1002      Larry    Male   4/20/2013         4:45 PM   60500  11985.00
```

```
1003      Albert     Male   5/15/2012          6:24 PM  129949  10169.00

     Senior Management                  Team
0                 True             Marketing
1                 True                   NaN
2                False               Finance
3                 True               Finance
4                 True       Client Services
5                False                 Legal
6                 True               Product
7                  NaN               Finance
8                 True           Engineering
9                 True  Business Development
10                True                   NaN
11                True                 Legal
12                True       Human Resources
13               False                 Sales
14                True               Finance
…                    …                     …
989              False                 Legal
990              False             Marketing
991               True               Finance
992              False       Human Resources
993              False                 Legal
994               True       Client Services
995               True             Marketing
996               True               Finance
997               True           Engineering
998               True             Marketing
999              False          Distribution
1000             False               Finance
1001             False               Product
1002             False  Business Development
1003              True                 Sales

[1000 rows x 8 columns]
```

Remove duplicate rows across **specific columns**:

[166]:
```
# remove duplicate rows across 'First Name' and 'Last Login Time' columns
employees_df.drop_duplicates(
    subset=['First Name', 'Last Login Time'], keep='last', inplace=True)
employees_df
```

[166]:
```
     First Name     Gender  Start Date Last Login Time  Salary   Bonus %  \
0       Douglas       Male    8/6/1993        12:42 PM   97308   6945.00
1        Thomas       Male   3/31/1996         6:53 AM   61933      4.17
2         Maria     Female   4/23/1993        11:17 AM  130590  11858.00
3         Jerry       Male    3/4/2005         1:00 PM  138705      9.34
4         Larry       Male   1/24/1998         4:47 PM  101004   1389.00
…           …          …           …               …       …         …
999       Henry  No Gender  11/23/2014         6:09 AM  132483  16655.00
1000    Phillip       Male   1/31/1984         6:30 AM   42392  19675.00
1001    Russell       Male   5/20/2013        12:39 PM   96914   1421.00
1002      Larry       Male   4/20/2013         4:45 PM   60500  11985.00
1003     Albert       Male   5/15/2012         6:24 PM  129949  10169.00

     Senior Management                  Team
```

```
0               True           Marketing
1               True                 NaN
2              False             Finance
3               True             Finance
4               True     Client Services
…                  …                   …
999            False        Distribution
1000           False             Finance
1001           False             Product
1002           False Business Development
1003            True               Sales

[994 rows x 8 columns]
```

4.5 Avoidance of tendencies due to bias

The description of the Iris dataset says, that it consists of **50 samples** from **each of three species** of Iris (Iris setosa, Iris virginica and Iris versicolor), so there are **150 total samples**.

But how to prove it?

4.5.1 Count occurrences of unique values

To prove whether all possible classes included in the dataset and equally distributed, you can use the function `df.value_counts`.

Following parameters can be used for fine tuning: - `dropna=False` causes that NaN values are included - `normalize=True`: relative frequencies of the unique values are returned - `ascending=False`: sort resulting classes descending

[167]:
```
# import (again) data to dataframe from csv file
employees_df = pd.read_csv("./datasets/employees_edit.csv")
```

[168]:
```
# count unique values without missing values in a column,
# ordered descending and normalized
irisdata_df['species'].value_counts(ascending=False, dropna=False, normalize=True)
```

[168]:
```
Iris-setosa        0.333333
Iris-versicolor    0.333333
Iris-virginica     0.333333
Name: species, dtype: float64
```

[169]:
```
# count unique values and missing values in a column,
# ordered descending and not absolute values
employees_df['Team'].value_counts(ascending=False, dropna=False, normalize=False)
```

[169]:
```
Client Services         106
Business Development    103
Finance                 102
Marketing                98
Product                  96
Sales                    94
Engineering              92
Human Resources          92
Distribution             90
Legal                    88
NaN                      43
```

```
Name: Team, dtype: int64
```

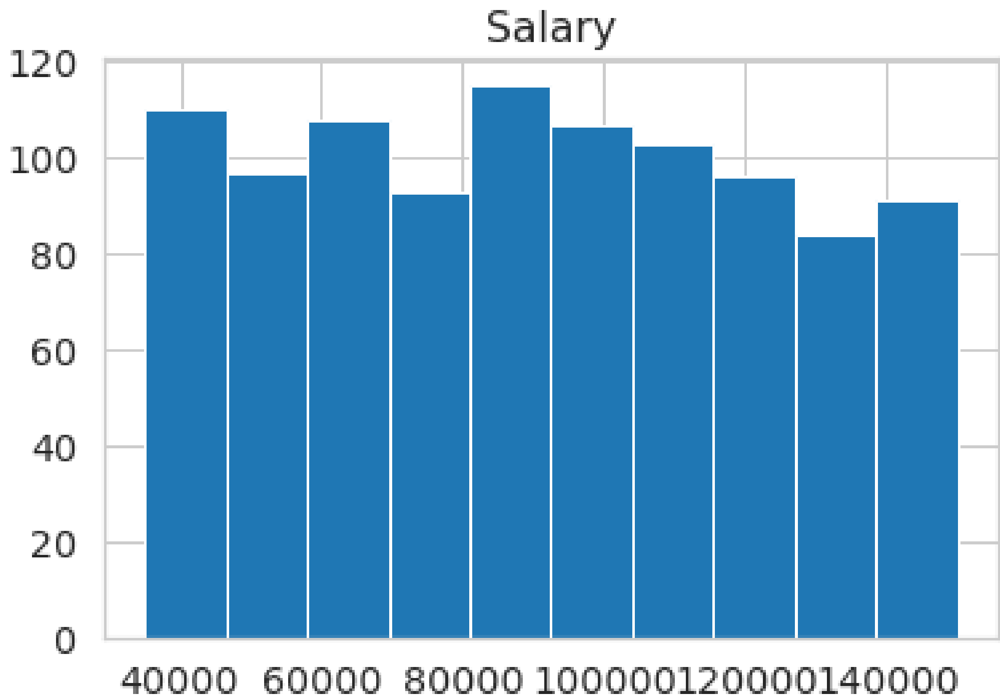
4.5.2 Display Histogram

This section was inspired by: Pandas Histogram – DataFrame.hist().

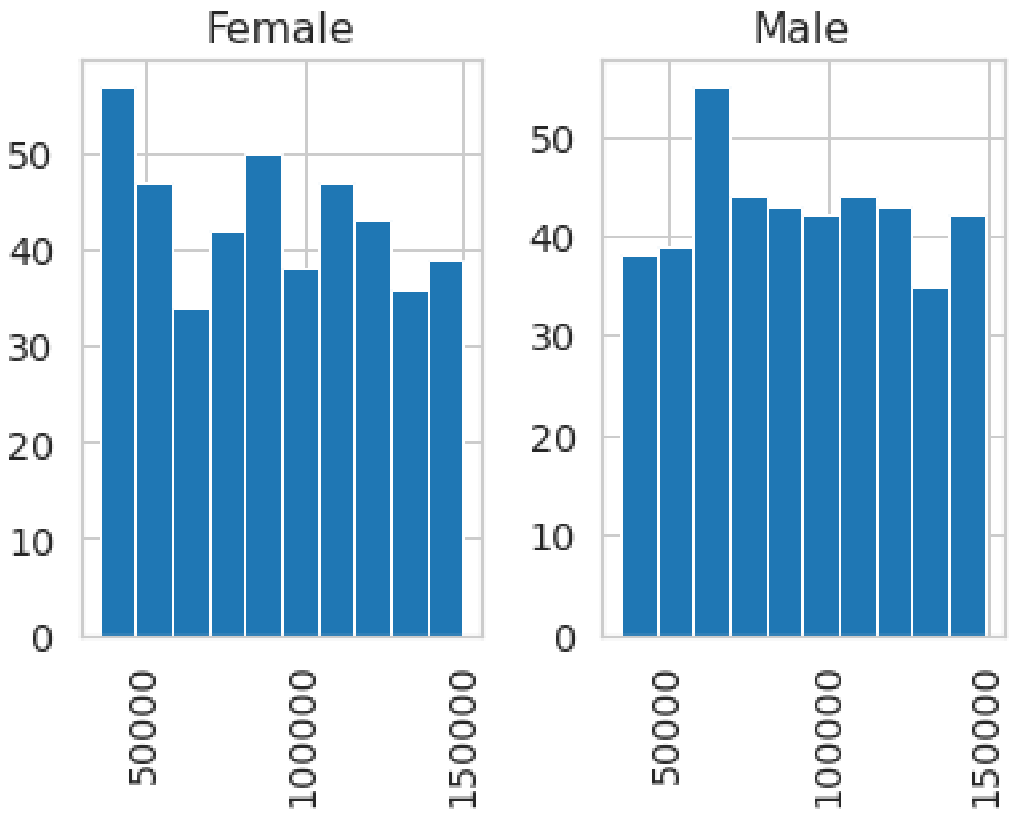
Histograms represent **frequency distributions** graphically. This requires the separation of the data into classes (so-called **bins**).

These classes are represented in the histogram as rectangles of equal or variable width. The height of each rectangle then represents the (relative or absolute) **frequency density**.

[176]:
```
employees_df.hist(column=['Salary'])
plt.show()
```



[175]:
```
employees_df.hist(column='Salary', by='Gender')
plt.show()
```



4.6 First idea of correlations in data set

To get a rough idea of the **dependencies** and **correlations** in the data set, it can be helpful to visualize the whole dataset in a **correlation heatmap**. They show in a glance which variables are correlated, to what degree and in which direction.

Later, 2 particularly well correlated variables are selected from the data set and plotted in a **scatterplot**.

4.6.1 Visualise data with correlation heatmap

This section was inspired by How to Create a Seaborn Correlation Heatmap in Python?.

> **Correlation matrices** are an **essential tool of exploratory data analysis**. Correlation heatmaps contain the same information in a visually appealing way. What more: they show in a glance which variables are correlated, to what degree, in which direction, and alerts us to potential multicollinearity problems (source: ibidem).

Simple correlation matrix Because **string values can never be correlated**, the class names (species) have to be converted first:

[170]:
```
# encoding the class column
irisdata_df_enc = irisdata_df.replace({"species":  {"Iris-setosa":0,
                                                    "Iris-versicolor":1,
                                                    "Iris-virginica":2}})

irisdata_df_enc
```

[170]:
```
     sepal_length  sepal_width  petal_length  petal_width  species
0             5.1          3.5           1.4          0.2        0
```

1	4.9	3.0	1.4	0.2	0
2	4.7	3.2	1.3	0.2	0
3	4.6	3.1	1.5	0.2	0
4	5.0	3.6	1.4	0.2	0
..	…	…	…	…	…
145	6.7	3.0	5.2	2.3	2
146	6.3	2.5	5.0	1.9	2
147	6.5	3.0	5.2	2.0	2
148	6.2	3.4	5.4	2.3	2
149	5.9	3.0	5.1	1.8	2

[150 rows x 5 columns]

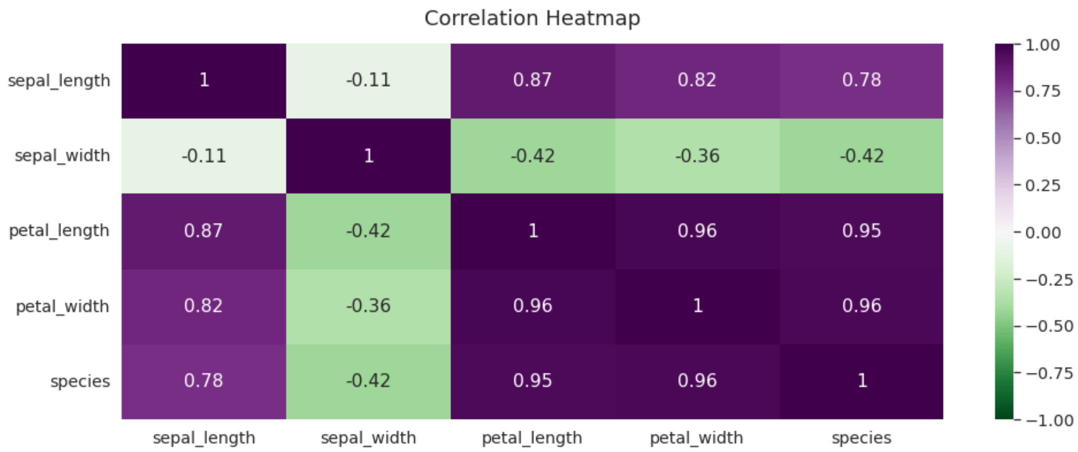
[92]:
```
irisdata_df_enc.corr()
```

[92]:

	sepal_length	sepal_width	petal_length	petal_width	species
sepal_length	1.000000	-0.109369	0.871754	0.817954	0.782561
sepal_width	-0.109369	1.000000	-0.420516	-0.356544	-0.419446
petal_length	0.871754	-0.420516	1.000000	0.962757	0.949043
petal_width	0.817954	-0.356544	0.962757	1.000000	0.956464
species	0.782561	-0.419446	0.949043	0.956464	1.000000

Correlation heatmap Choose the color sets from color map.

[174]:
```
# increase the size of the heatmap
plt.figure(figsize=(16, 6))

# store heatmap object in a variable to easily access it
# when you want to include more features (such as title)
# set the range of values to be displayed on the colormap from -1 to 1,
# and set 'annotation=True' to display the correlation values on the heatmap
heatmap = sns.heatmap(irisdata_df_enc.corr(), vmin=-1, vmax=1,
                      annot=True, cmap='PRGn_r')

# give a title to the heatmap
# 'pad=12' defines the distance of the title from the top of the heatmap
heatmap.set_title('Correlation Heatmap', fontdict={'fontsize':18}, pad=16)
plt.show()
```



Triangle correlation heatmap When looking at the correlation heatmaps above, you would not lose any information by **cutting** away half of it **along the diagonal** line marked by 1-s.

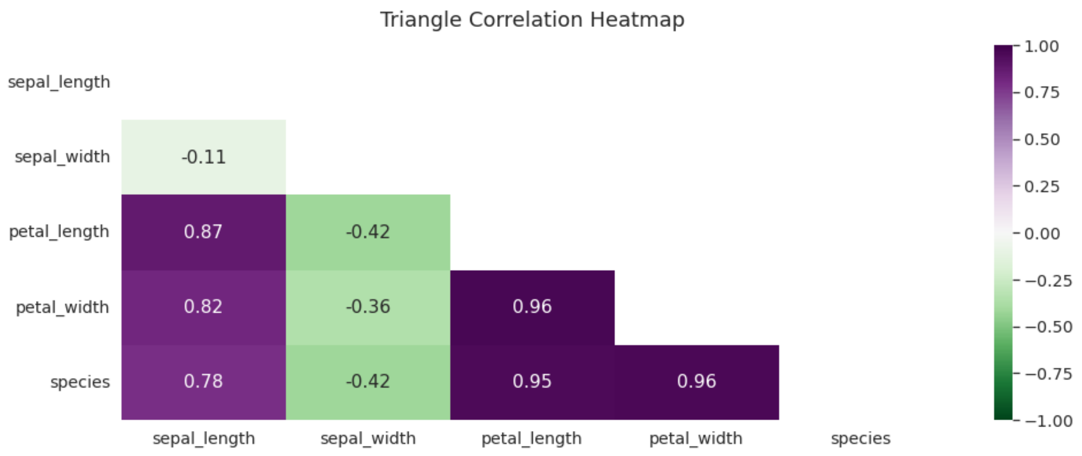
The **numpy** function `np.triu()` can be used to isolate the upper triangle of a matrix while turning all the values in the lower triangle into 0.

[94]:
```
import numpy as np

np.triu(np.ones_like(irisdata_df_enc.corr()))
```

[94]:
```
array([[1., 1., 1., 1., 1.],
       [0., 1., 1., 1., 1.],
       [0., 0., 1., 1., 1.],
       [0., 0., 0., 1., 1.],
       [0., 0., 0., 0., 1.]])
```

Use this mask to cut the heatmap along the diagonal:

[173]:
```
plt.figure(figsize=(16, 6))

# define the mask to set the values in the upper triangle to 'True'
mask = np.triu(np.ones_like(irisdata_df_enc.corr(), dtype=bool))

heatmap = sns.heatmap(irisdata_df_enc.corr(), mask=mask,
                      vmin=-1, vmax=1, annot=True, cmap='PRGn_r')

heatmap.set_title('Triangle Correlation Heatmap', fontdict={'fontsize':18}, pad=16)
plt.show()
```



As a result from the **heatmaps** we can see, that the shape of the **petals** are the **most correlationed columns** (0.96) with the **type of flowers** (species classes).

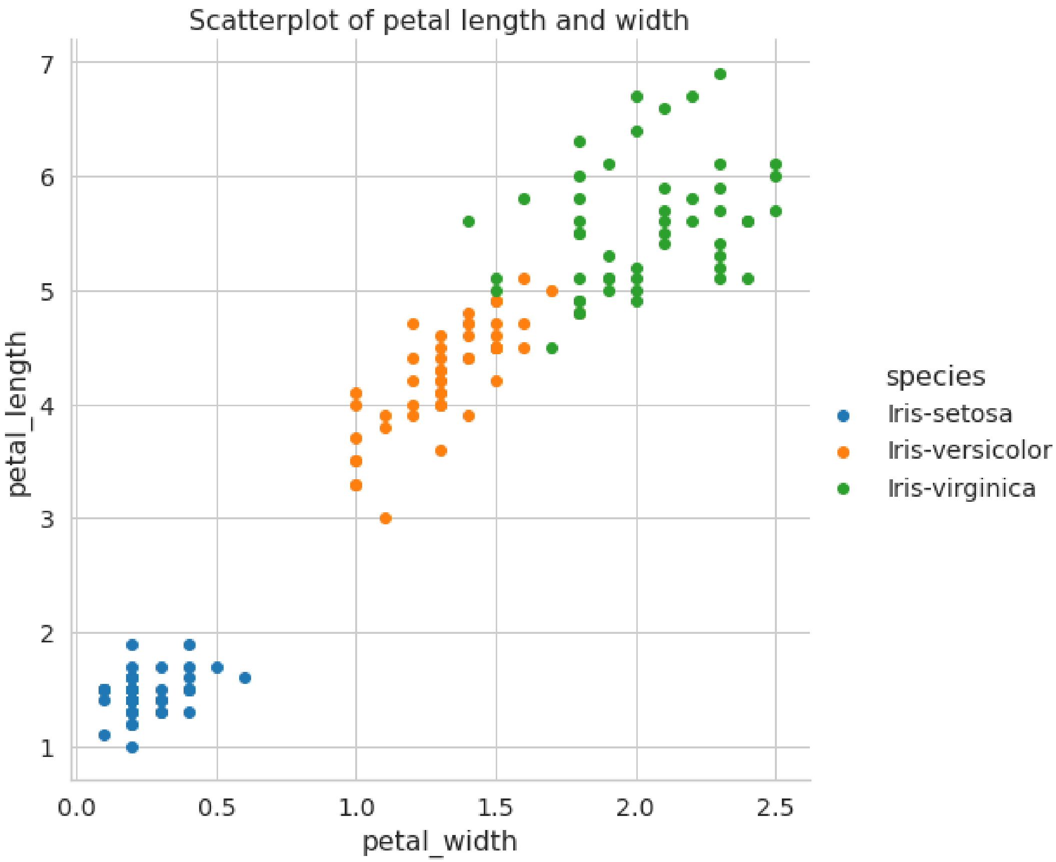
Somewhat lower correlates **sepal length** with **petal length** (0.87).

4.6.2 Visualise data with scatter plot

In the following, Seaborn is applied which is a library for making statistical graphics in Python. It is built on top of matplotlib and closely integrated with pandas data structures.

To investigate whether there are dependencies (e.g. correlations) in `irisdata_df` between individual variables in the data set, it is advisable to plot them in a **scatter plot**.

[181]:
```
# There are five preset seaborn themes: darkgrid, whitegrid, dark, white, and ticks.
sns.set_style("whitegrid")
# set scale of fonts
sns.set_context("notebook", font_scale=1.3, rc={"lines.linewidth": 2.5})

# 'sepal_length', 'petal_length' are iris feature data
# 'height' used to define height of graph
# 'hue' stores the class/label of iris dataset
sns.FacetGrid(irisdata_df, hue ="species",
              height = 7).map(plt.scatter,
                              'petal_width',
                              'petal_length').add_legend()


plt.title('Scatterplot of petal length and width')
plt.show()
```



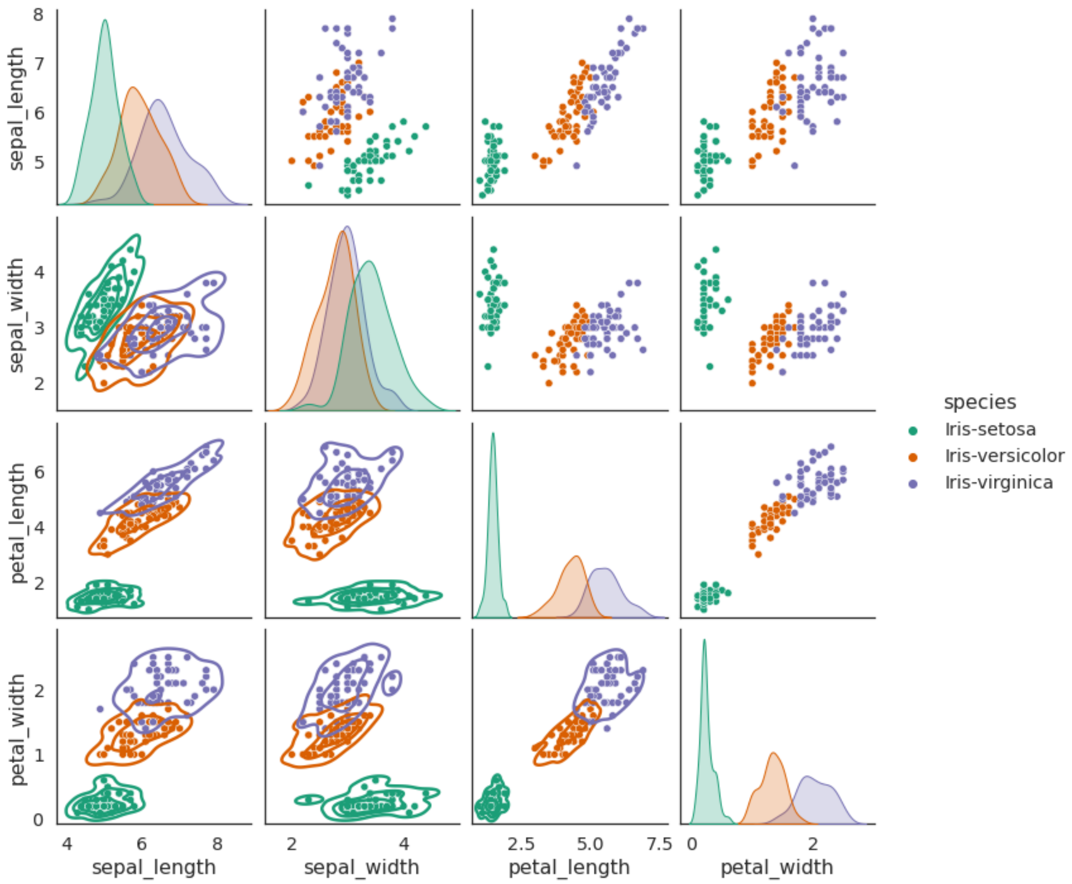
4.6.3 Visualise data with pairs plot

For systematic investigation of dependencies, all variables (each against each) are plotted in separate scatter plots.

With this so called **pairs plot** it is possible to see both **relationships** between two variables and **distribution** of single variables.

This function will create a grid of Axes such that **each numeric variable** in `irisdata_df` will by shared in the y-axis across a single row and in the x-axis across a single column.

[184]:
```
sns.set_style("white")
g = sns.pairplot(irisdata_df, diag_kind="kde", hue='species',
                 palette='Dark2', height=2.5)

g.map_lower(sns.kdeplot, levels=4, color=".2")

plt.show()
```



5 STEP 2: Prepare the data

Through the intensive exploration of the data in Step 1 (STEP 1: Exploring the data), we know that special **preparation** of the data is **not necessary**. The values are **complete** and **without gaps** and there are **no duplicates**. The values are in similar ranges, which **does not require normalization** of the data.

Furthermore, we know that the **classes** are very **evenly distributed** and thus bias tendencies should be avoided.

6 STEP 3: Classify by support vector classifier - SVC

6.1 Operating principal

Support Vectors Classifier tries to **find the best hyperplane to separate** the different classes by maximizing the distance between sample points and the hyperplane (source: In Depth: Parameter tuning for SVC).

Following graphic shows the operating principal of SVC: the hyperplane *H1* does not separate the classes. *H2* does, but only with a small margin. *H3* separates them with the maximal margin (source: Support-vector machine).

```
[7]: display(HTML("<figure><img src='./images/SVM_separating_hyperplanes.svg'␣
     ↪width='400px'> \
                    <figcaption>SVC seperate the data in classes by finding the best␣
     ↪hyperplane (source: <a href='https://en.wikipedia.org/wiki/File:
     ↪Svm_separating_hyperplanes_(SVG).svg'>Svm separating hyperplanes (SVG).svg</a>)</
     ↪figcaption> \
                 </figure>"))
```

```
<IPython.core.display.HTML object>
```

6.2 Split the dataset

In the next very important step, the dataset is split into **2 subsets**: a **training dataset** and a **test dataset**. As the names suggest, the training dataset is used to train the ML algorithm. The test data set is then used to check the quality of the trained ML algorithm (here the **recognition rate**). For this purpose, the **class labels** are **removed** from the training data set - after all, these are to be predicted.

Typically, the **test dataset** should contain about **20%** of the entire dataset.

```
[43]: from sklearn.model_selection import train_test_split

X = irisdata_df.drop('species', axis=1)
y = irisdata_df['species']

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.20)
```

For training, do not use only the variables that correlate best with each other, but all of them.

Otherwise, the result of the prediction would be significantly worse. Maybe this is already an indication of **overfitting** of the ML model.

```
[42]: # DO NOT USE THIS!!
X_train, X_test, y_train, y_test = train_test_split(X[['sepal_length',
                                                       'sepal_width']],
                                                    y, test_size = 0.20)
```

6.3 Create the SVM model

In this step we create the SVC model and fit it to our training data.

```
[44]: from sklearn.svm import SVC
classifier = SVC(kernel = 'linear', random_state = 0)

# fit the model for the data
classifier.fit(X_train, y_train)
```

```
[44]: SVC(kernel='linear', random_state=0)
```

6.4 Make predictions

[45]:
```
y_pred = classifier.predict(X_test)
#X_test
```

7 STEP 4: Evaluate the results - metrics

And finally for checking the accuracy of the model, the **confusion matrix** is used for the **cross validation**.

By using the function `sklearn.metrics.confusion_matrix()` a confusion matrix of the true digit values versus the predicted digit values is plotted.

7.1 Textual confusion matrix

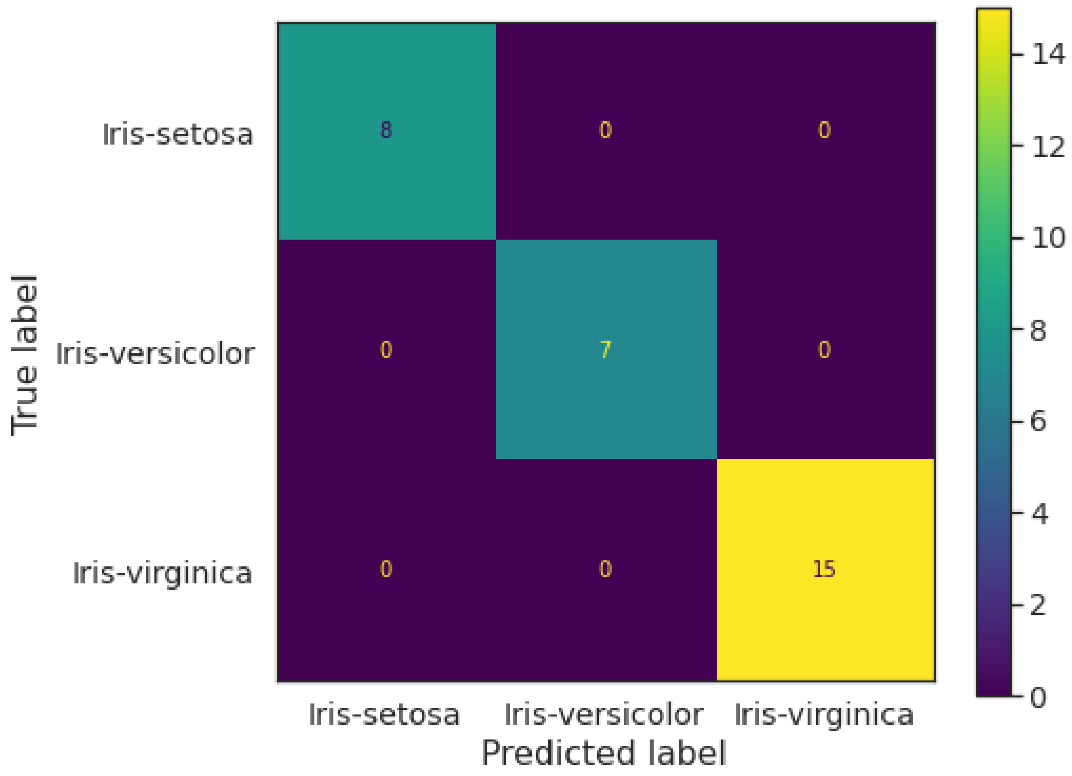
[46]:
```
cm = metrics.confusion_matrix(y_test, y_pred)
print(cm)
```

```
[[ 8  0  0]
 [ 0  7  0]
 [ 0  0 15]]
```

7.2 Colored confusion matrix

The function `sklearn.metrics.ConfusionMatrixDisplay()` plots a colored confusion matrix.

[58]:
```
sns.set_style("white")

# print colored confusion matrix
cm_colored = metrics.ConfusionMatrixDisplay.from_predictions(y_test, y_pred)

#cm_colored.figure_.suptitle("Confusion Matrix")
cm_colored.figure_.set_figwidth(7)
cm_colored.figure_.set_figheight(6)

cm_colored.confusion_matrix
plt.show()
```



[185]:
```
from sklearn.model_selection import cross_val_score

accuracies = cross_val_score(estimator = classifier, X = X_train,
                             y = y_train, cv = 10)

print("Accuracy: {:.2f} %".format(accuracies.mean()*100))
print("Standard Deviation: {:.2f} %".format(accuracies.std()*100))
```

```
Accuracy: 96.67 %
Standard Deviation: 5.53 %
```

8 STEP 5: Vary parameters

This section was inspired by In Depth: Parameter tuning for SVC

In this section, the 4 SVC parameters `kernel`, `gamma`, `C` and `degree` will be introduced one by one. Furthermore, their influence on the classification result by varying these single parameters will be shown.

Disclaimer: In order to show the effects of varying the individual parameters in 2D graphs, only the best correlating variables `petal_length` and `petal_width` are used to train the SVC.

8.1 Prepare dataset

[186]:
```
# import iris dataset again
irisdata_df = pd.read_csv('./datasets/IRIS_flower_dataset_kaggle.csv')

# encode the class column from class strings to integer equivalents
irisdata_df_enc = irisdata_df.replace({"species":  {"Iris-setosa":0,
                                                     "Iris-versicolor":1,
```

```
                                                 "Iris-virginica":2}})
irisdata_df_enc
```

[186]:
```
     sepal_length  sepal_width  petal_length  petal_width  species
0             5.1          3.5           1.4          0.2        0
1             4.9          3.0           1.4          0.2        0
2             4.7          3.2           1.3          0.2        0
3             4.6          3.1           1.5          0.2        0
4             5.0          3.6           1.4          0.2        0
..            …            …             …            …          …
145           6.7          3.0           5.2          2.3        2
146           6.3          2.5           5.0          1.9        2
147           6.5          3.0           5.2          2.0        2
148           6.2          3.4           5.4          2.3        2
149           5.9          3.0           5.1          1.8        2

[150 rows x 5 columns]
```

[116]:
```
# copy only 2 feature columns
# and convert pandas dataframe to numpy array
X = irisdata_df_enc[['petal_length', 'petal_width']].to_numpy(copy=True)
#X = irisdata_df_enc[['sepal_length', 'sepal_width']].to_numpy(copy=True)
#X
```

[118]:
```
# convert pandas dataframe to numpy array
# and get a flat 1D copy of 2D numpy array
y = irisdata_df_enc[['species']].to_numpy(copy=True).flatten()
#y
```

8.2 Plotting function

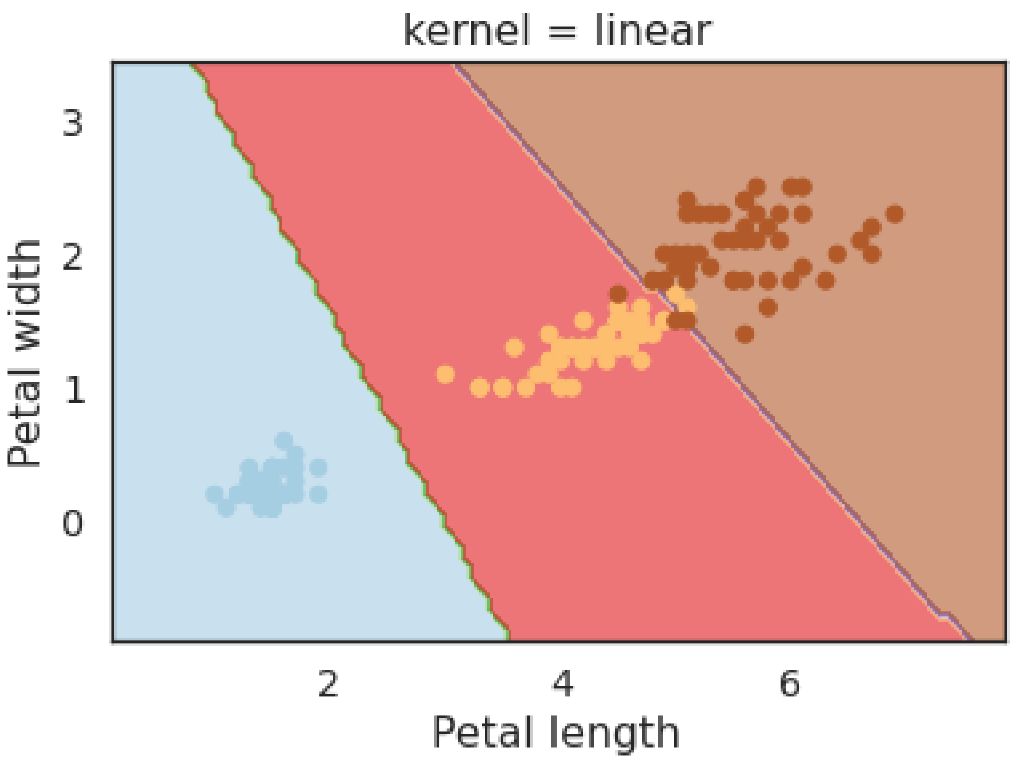
This function helps to visualize the modifications by varying the individual SVC parameters.

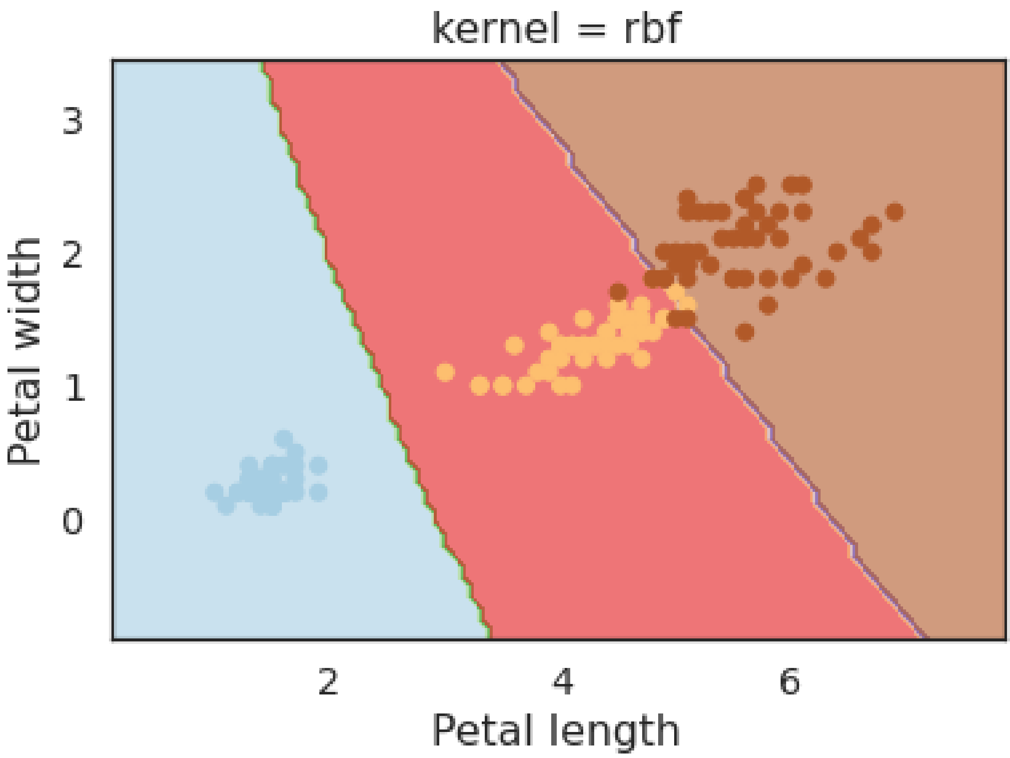
[101]:
```
def plotSVC(title, xlabel, ylabel):
    # create a mesh to plot in
    x_min, x_max = X[:, 0].min() - 1, X[:, 0].max() + 1
    y_min, y_max = X[:, 1].min() - 1, X[:, 1].max() + 1

    # prevent division by zero
    if x_min == 0.0:
        x_min = 0.1

    h = (x_max / x_min)/1000
    xx, yy = np.meshgrid(np.arange(x_min, x_max, h), np.arange(y_min, y_max, h))

    plt.subplot(1, 1, 1)
    Z = svc.predict(np.c_[xx.ravel(), yy.ravel()])
    Z = Z.reshape(xx.shape)

    plt.contourf(xx, yy, Z, cmap=plt.cm.Paired, alpha=0.6)
    plt.scatter(X[:, 0], X[:, 1], c=y, cmap=plt.cm.Paired)
    plt.xlabel(xlabel)
    plt.ylabel(ylabel)
    plt.xlim(xx.min(), xx.max())
    plt.title(title)
    plt.show()
```

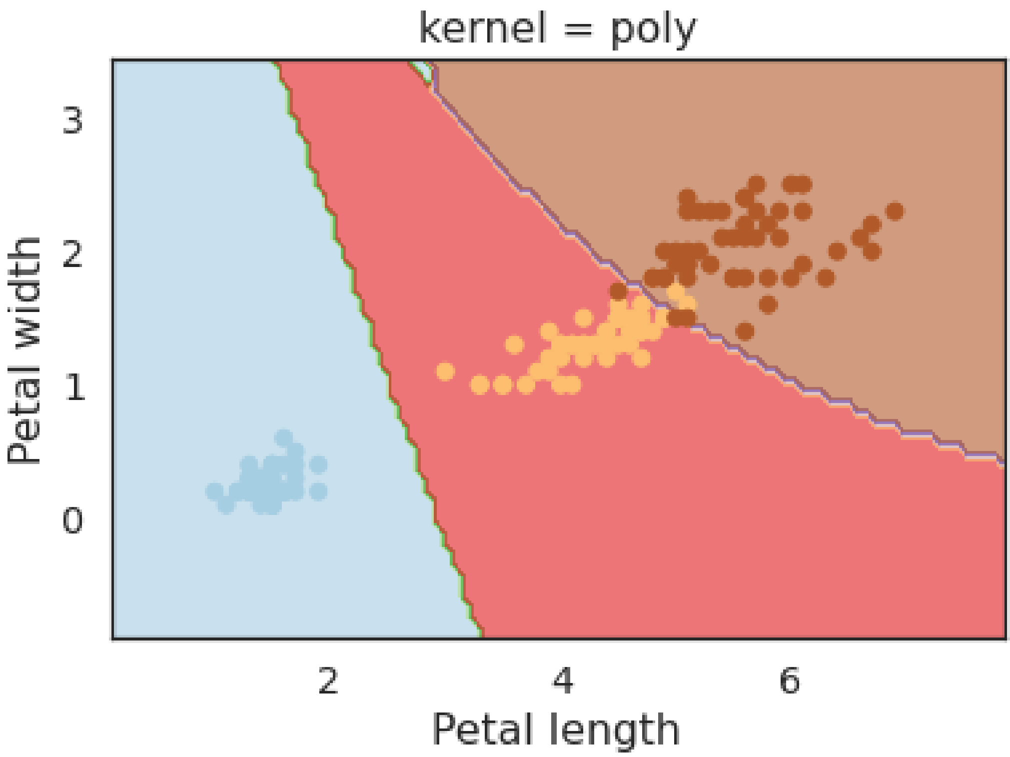
8.3 Vary `kernel` parameter

The `kernel` parameter selects the type of hyperplane that is used to separate the data. Using `linear` (linear classifier) kernel will use a linear hyperplane (a line in the case of 2D data). The `rbf` (radial basis function kernel) and `poly` (polynomial kernel) kernel use non linear hyperplanes.

[102]:
```
kernels = ['linear', 'rbf', 'poly']

xlabel = 'Petal length'
ylabel = 'Petal width'

for kernel in kernels:
    svc = svm.SVC(kernel=kernel).fit(X, y)
    plotSVC('kernel = ' + str(kernel), xlabel, ylabel)
```




kernel = rbf
Petal width
Petal length
0
1
2
3
2
4
6

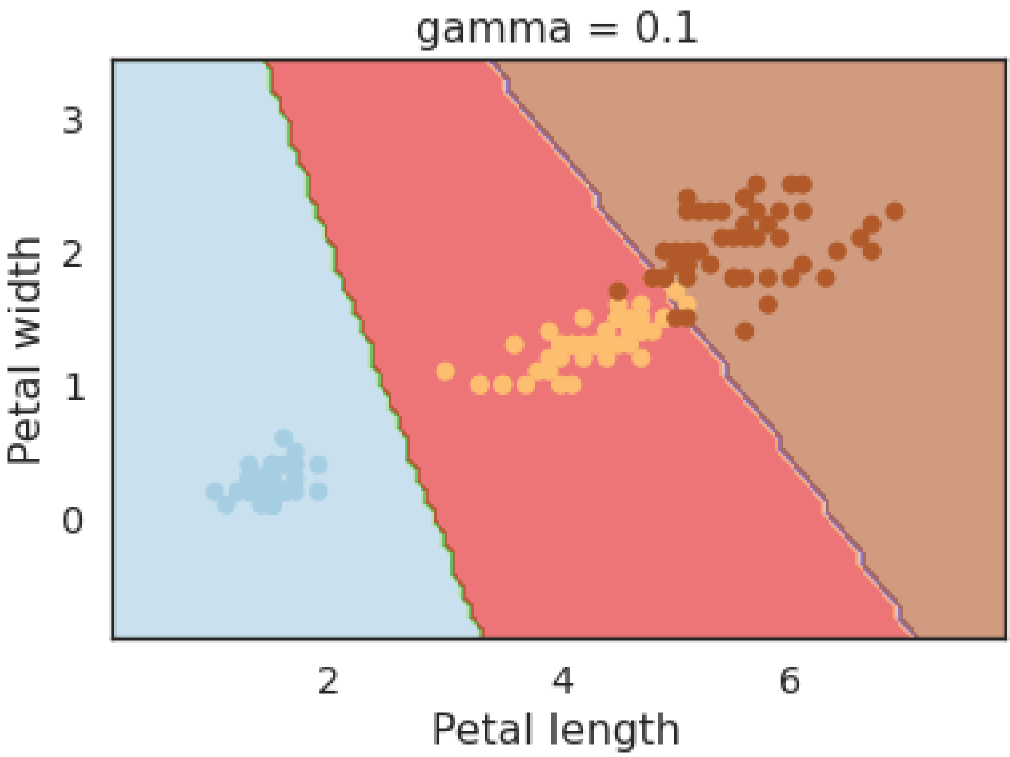

kernel = poly
Petal width
Petal length
0
1
2
3
2
4
6

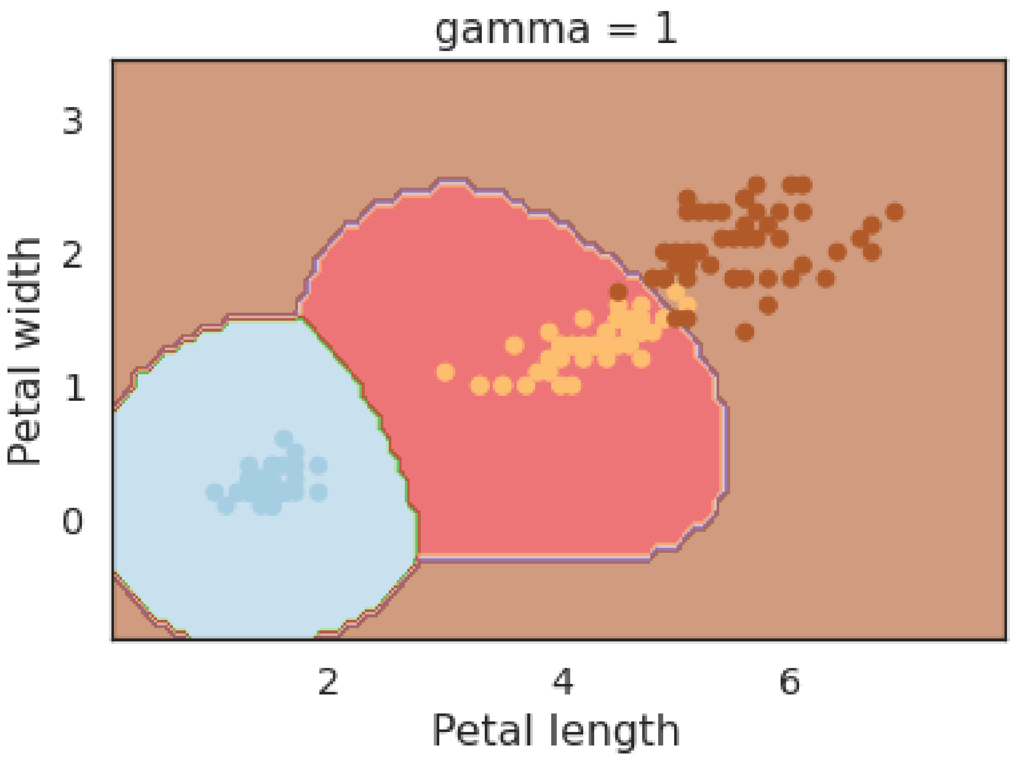
8.4 Vary gamma parameter

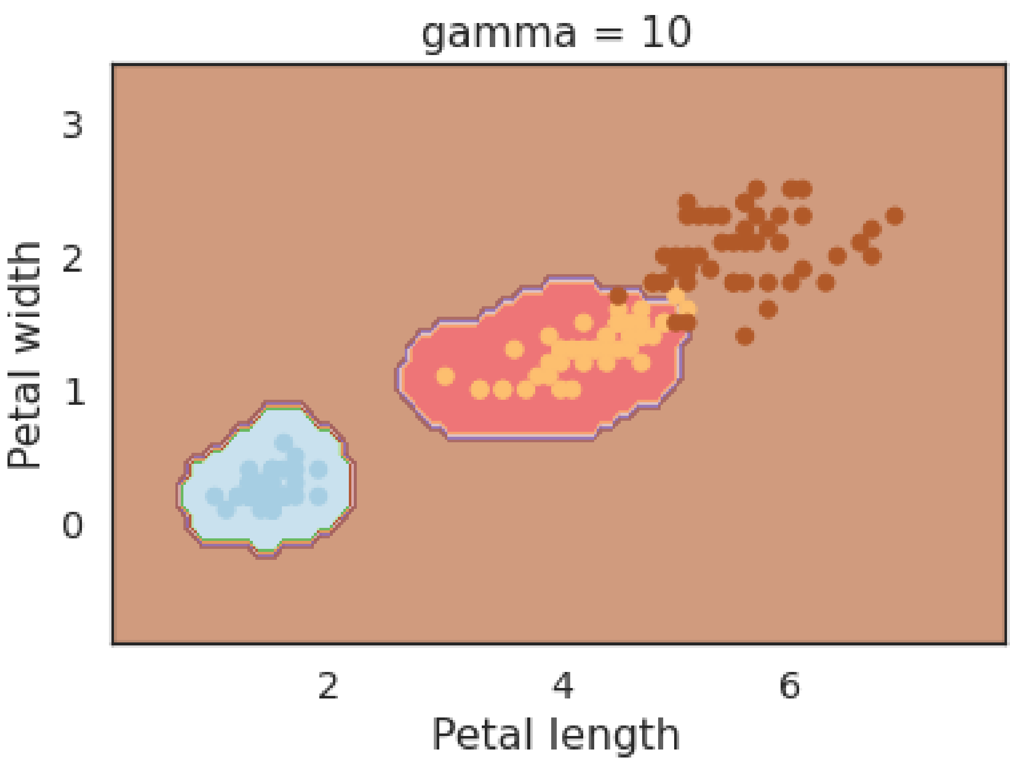
The gamma parameter is used for non linear hyperplanes. The higher the gamma value it tries to exactly fit the training data set.

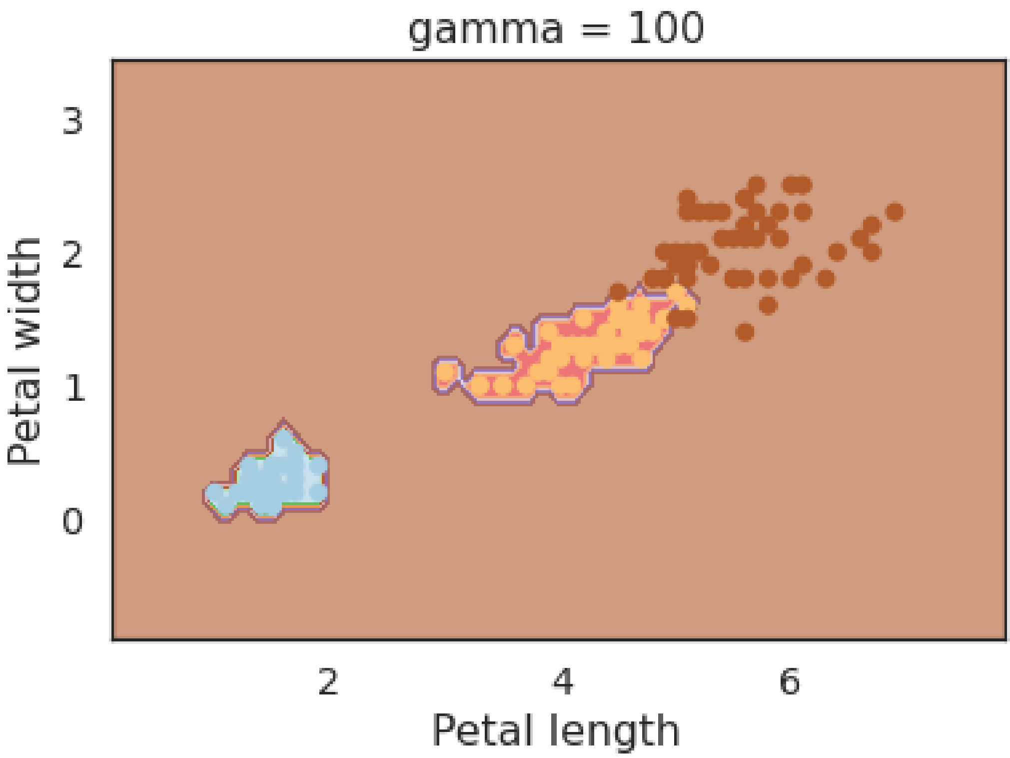
As we can see, increasing gamma leads to **overfitting** as the classifier tries to perfectly fit the training data.

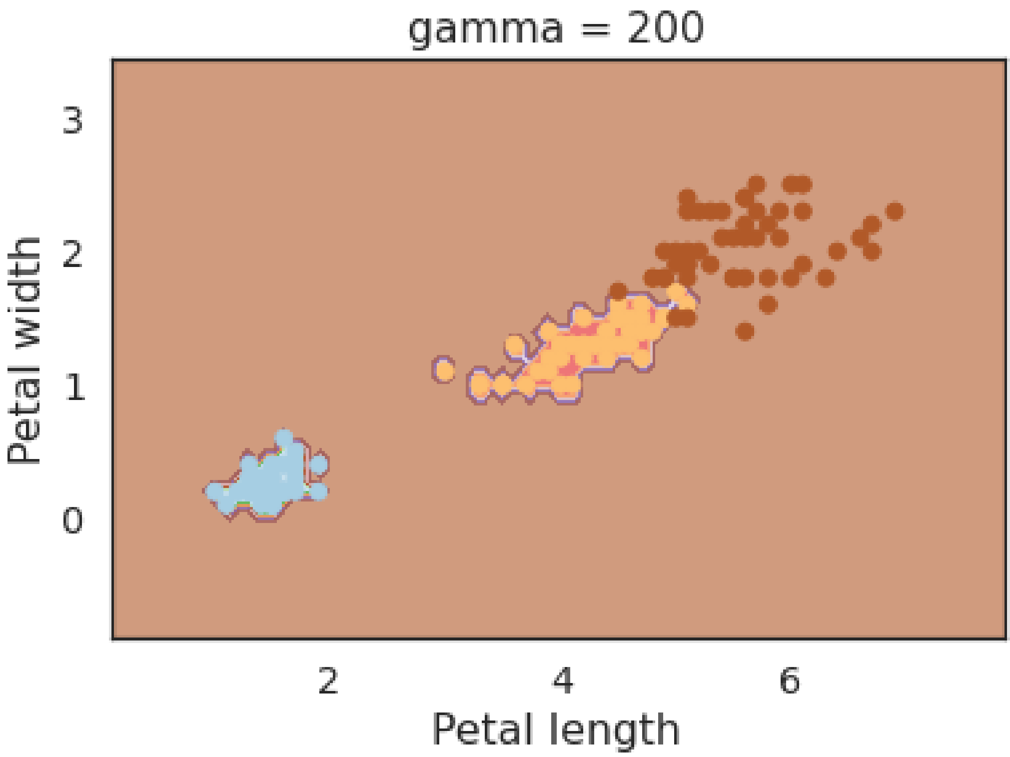
[106]:
```
gammas = [0.1, 1, 10, 100, 200]

xlabel = 'Petal length'
ylabel = 'Petal width'

for gamma in gammas:
    svc = svm.SVC(kernel='rbf', gamma=gamma).fit(X, y)
    plotSVC('gamma = ' + str(gamma), xlabel, ylabel)
```




gamma = 1
Petal width
Petal length
0
1
2
3
2
4
6


gamma = 10
Petal width
Petal length
0
1
2
3
2
4
6


gamma = 100
3
2
1
0
Petal width
2
4
6
Petal length

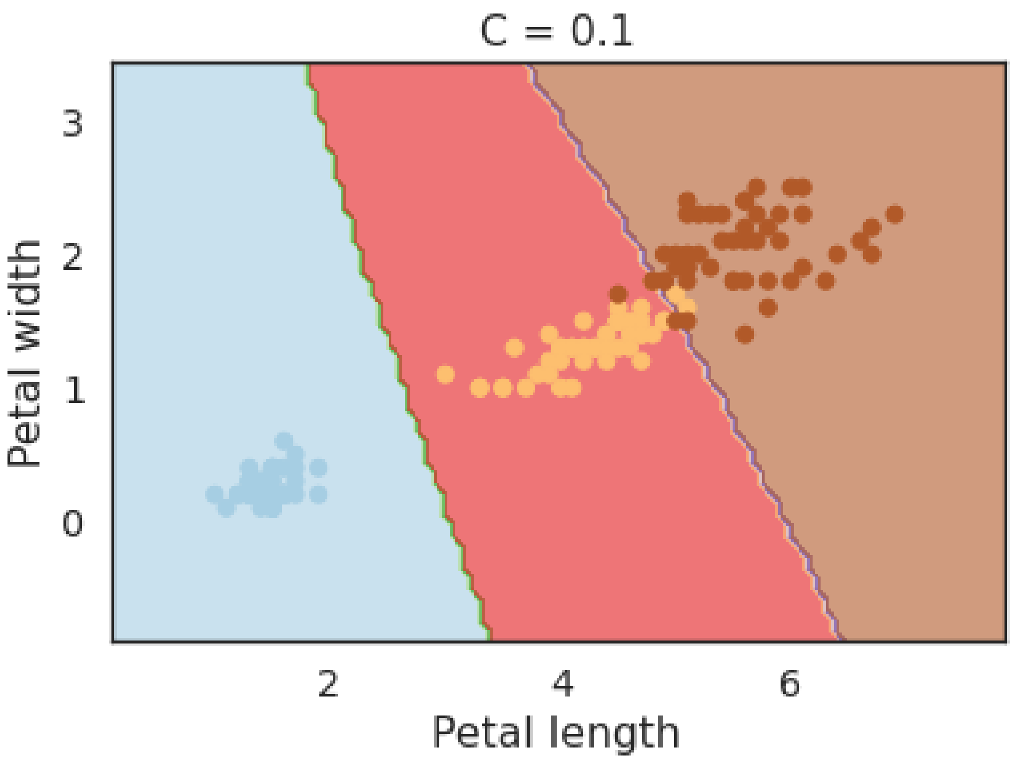

gamma = 200
3
2
1
0
Petal width
2
4
6
Petal length

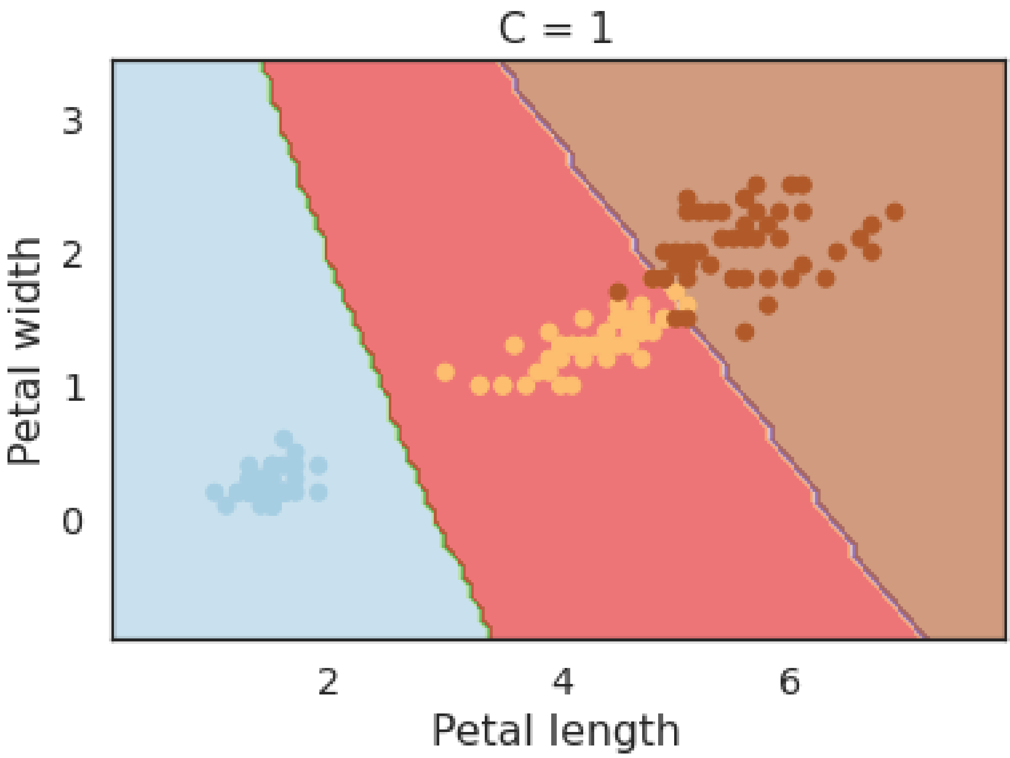
8.5 Vary C parameter

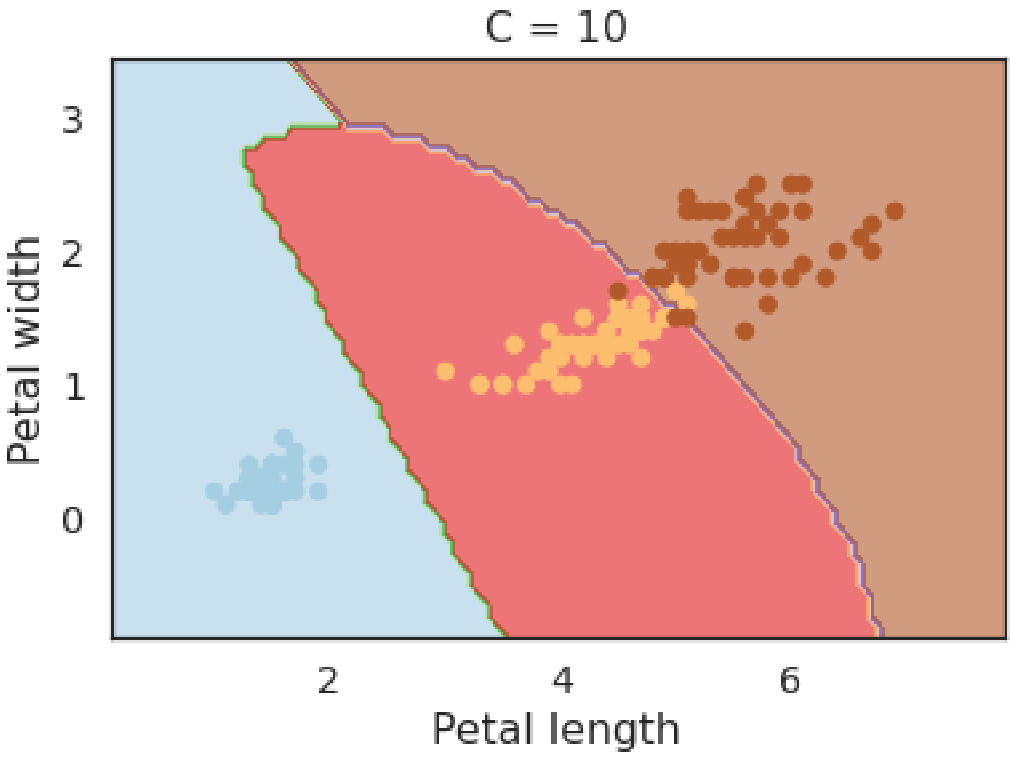
The C parameter is the **penalty** of the error term. It controls the trade off between smooth decision boundary and classifying the training points correctly.

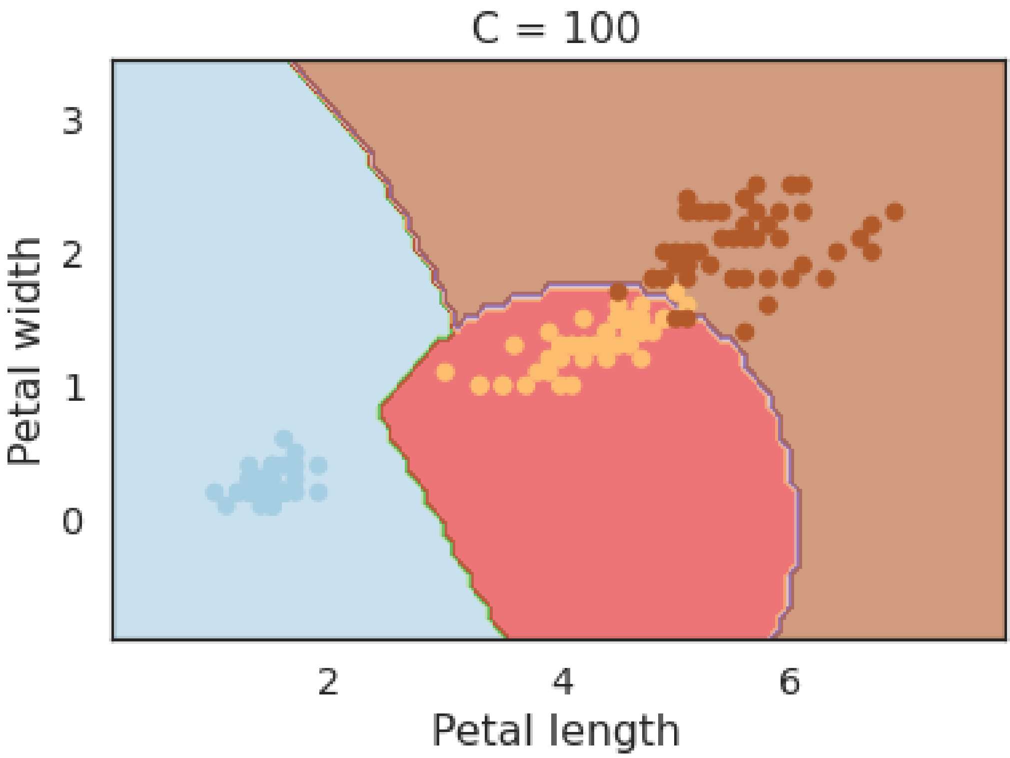
But be careful: to high C values may lead to **overfitting** the training data.

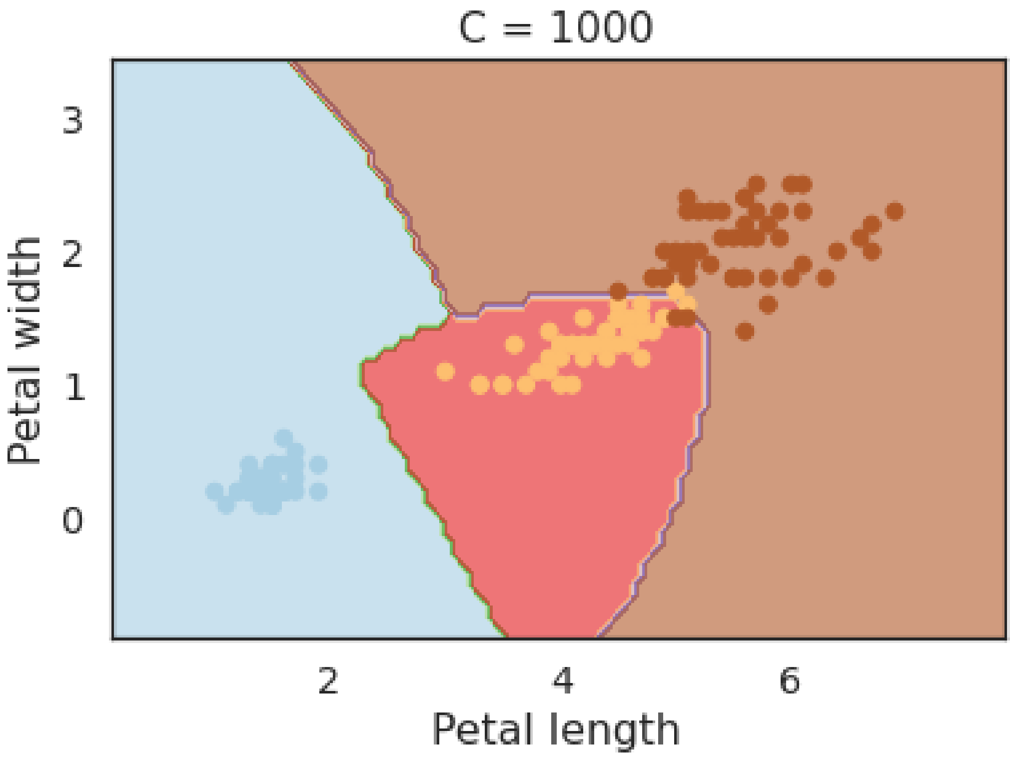
[108]:
```
cs = [0.1, 1, 10, 100, 1000, 10000]

xlabel = 'Petal length'
ylabel = 'Petal width'

for c in cs:
    svc = svm.SVC(kernel='rbf', C=c).fit(X, y)
    plotSVC('C = ' + str(c), xlabel, ylabel)
```

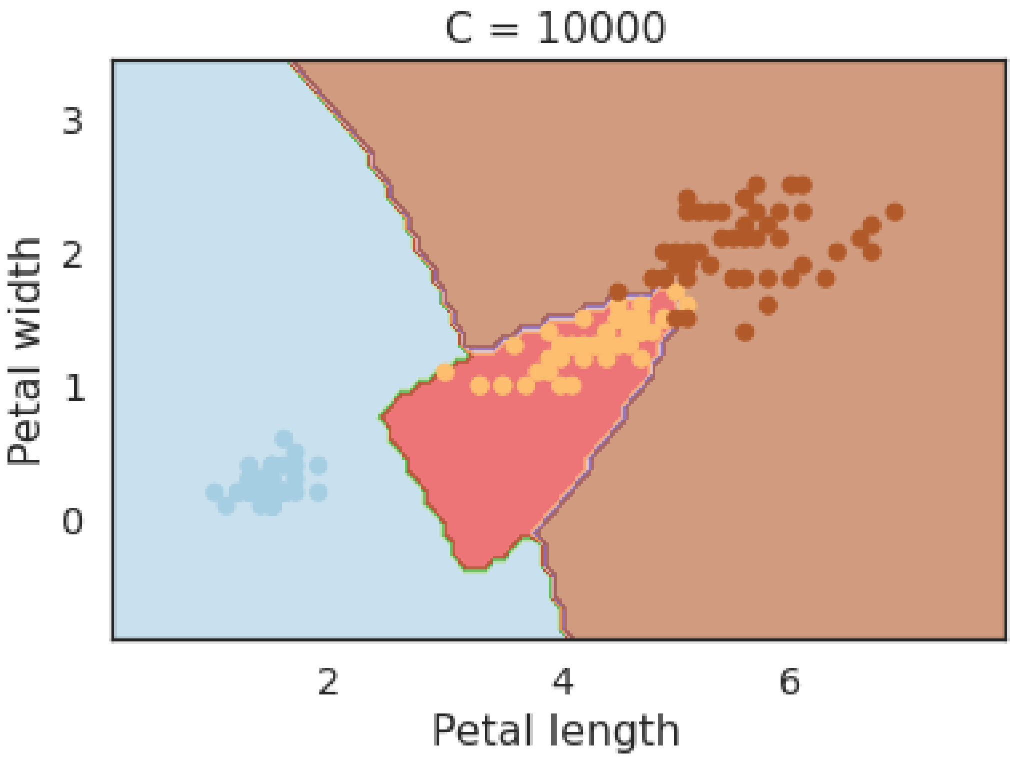



C = 1
Petal width
3
2
1
0
2
4
6
Petal length


C = 10
Petal width
3
2
1
0
2
4
6
Petal length


C = 100
Petal width
3
2
1
0
2
4
6
Petal length


C = 1000
Petal width
3
2
1
0
2
4
6
Petal length

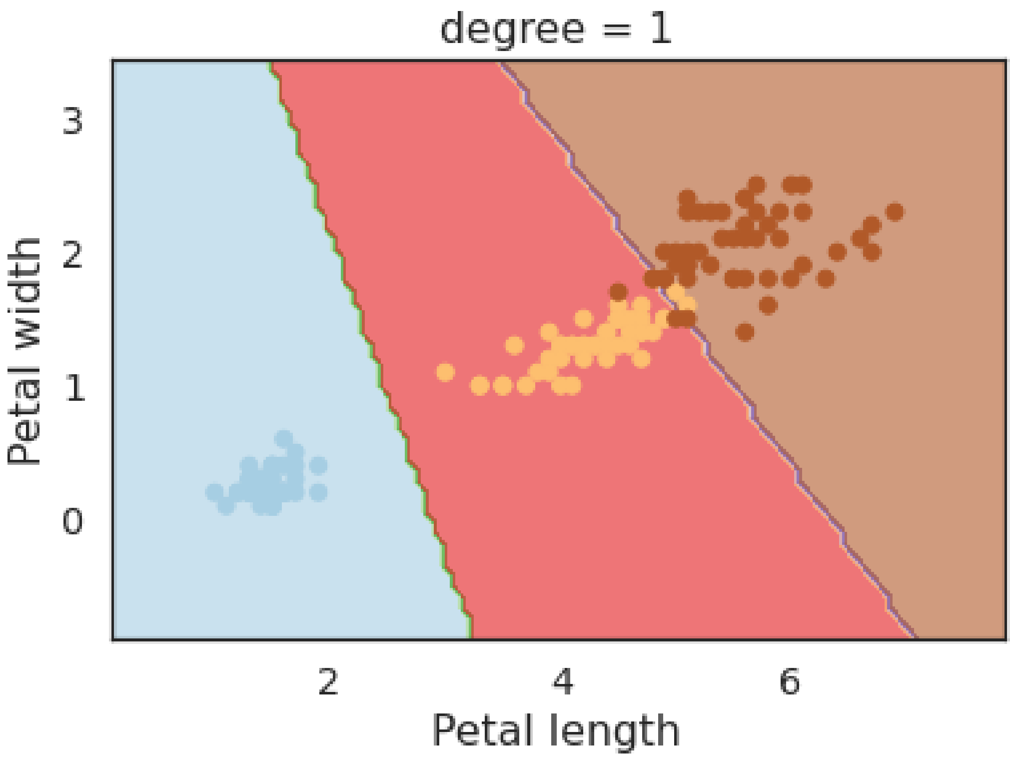


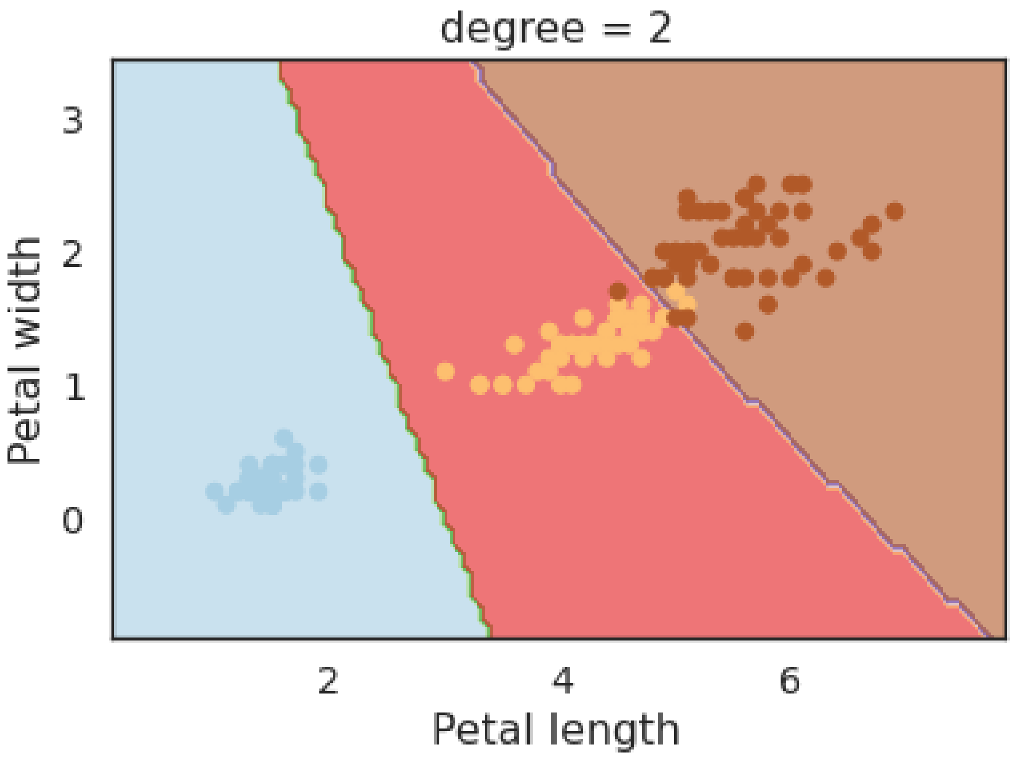
8.6 Vary degree parameter

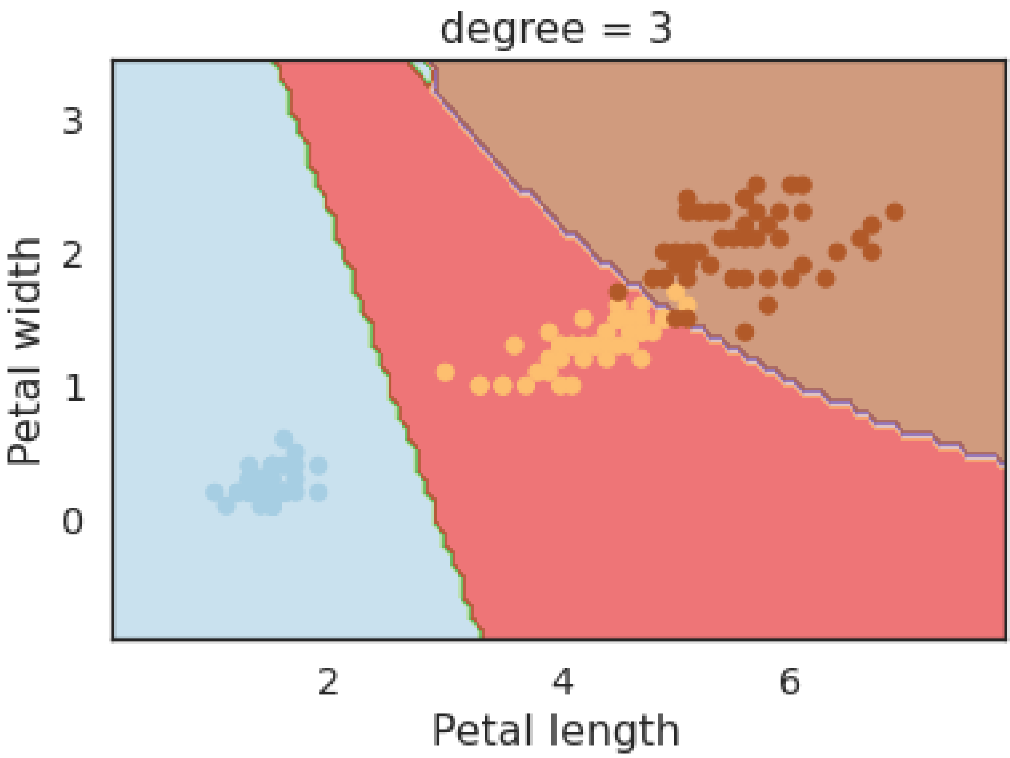
The degree parameter is used when the kernel is set to poly. It's basically the **degree of the polynomial** used to find the hyperplane to split the data.

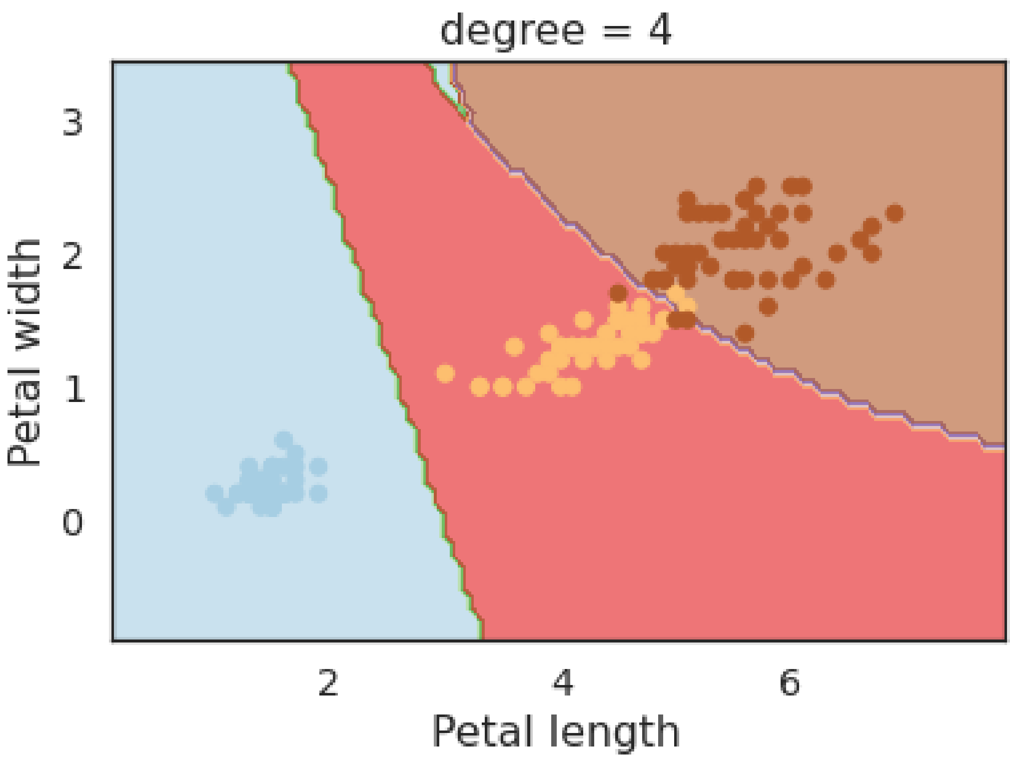
Using degree = 1 is the same as using a linear kernel. Also, increasing this parameters leads to **higher training times**.

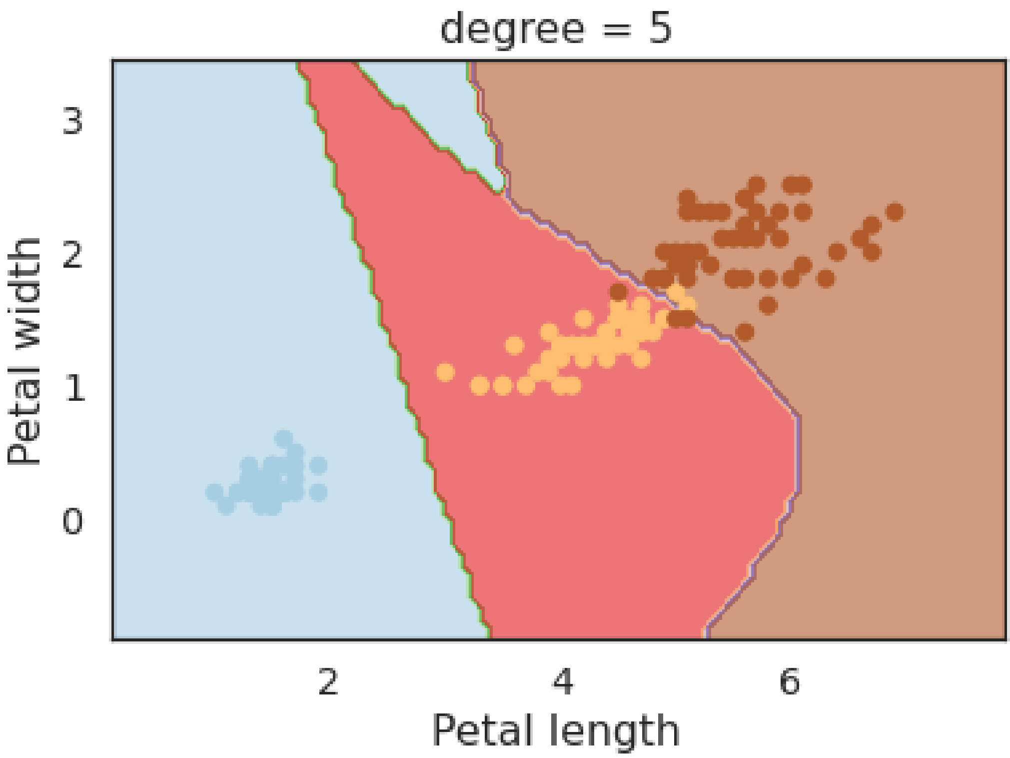
[113]:
```
degrees = [1, 2, 3, 4, 5, 6, 7, 8, 9, 10]

xlabel = 'Petal length'
ylabel = 'Petal width'

for degree in degrees:
    svc = svm.SVC(kernel='poly', degree=degree).fit(X, y)
    plotSVC('degree = ' + str(degree), xlabel, ylabel)
```

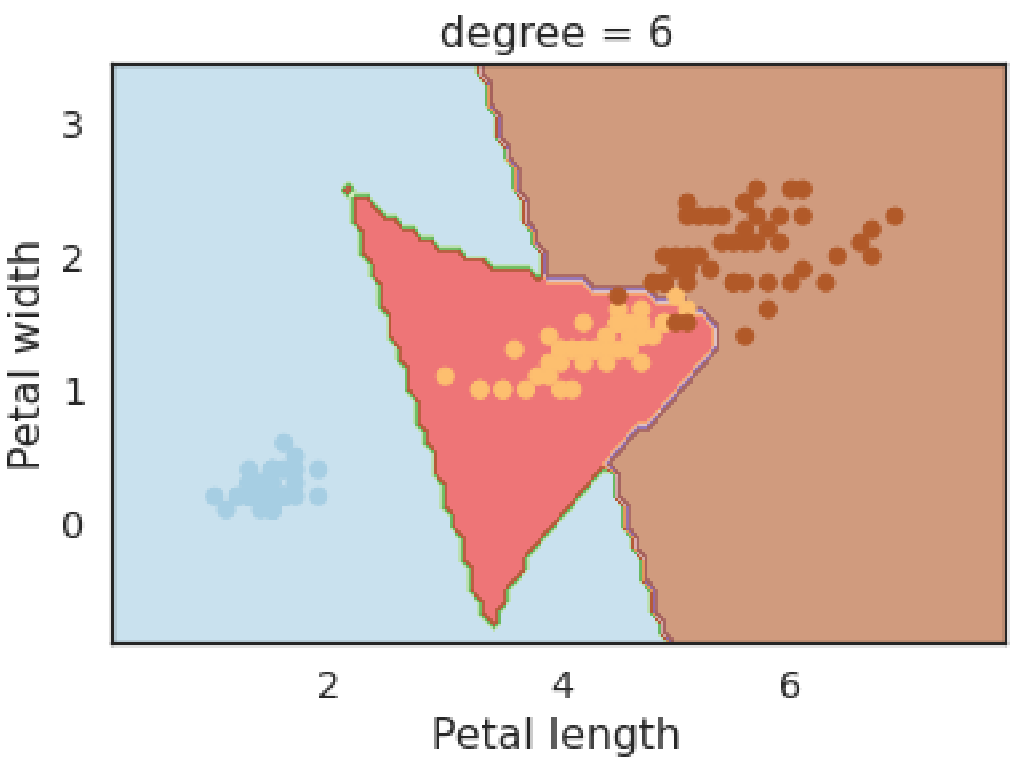

degree = 1
Petal width
Petal length
0
1
2
3
2
4
6

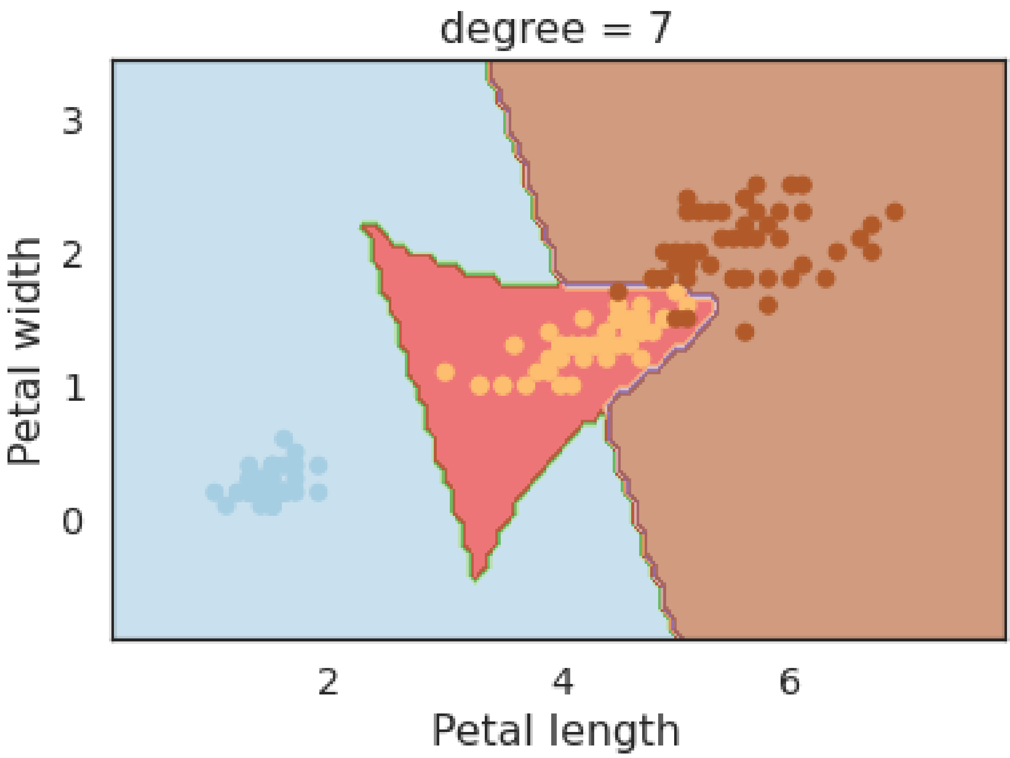

degree = 2
Petal width
Petal length
0
1
2
3
2
4
6

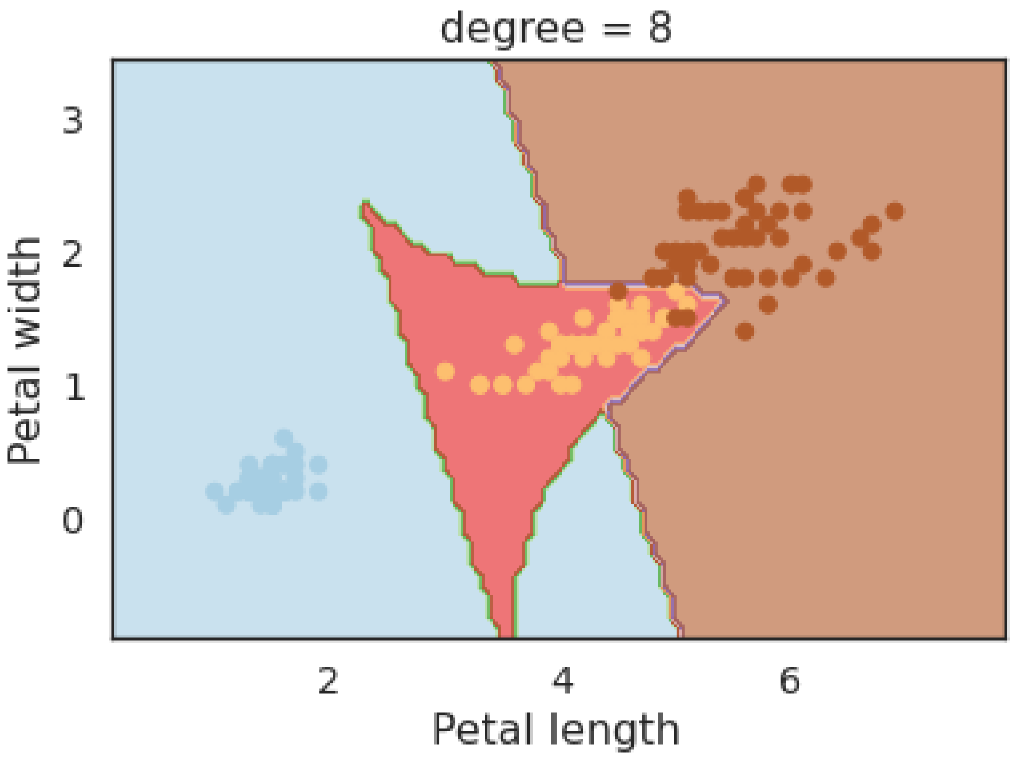

degree = 3
Petal width
Petal length
0
1
2
3
2
4
6

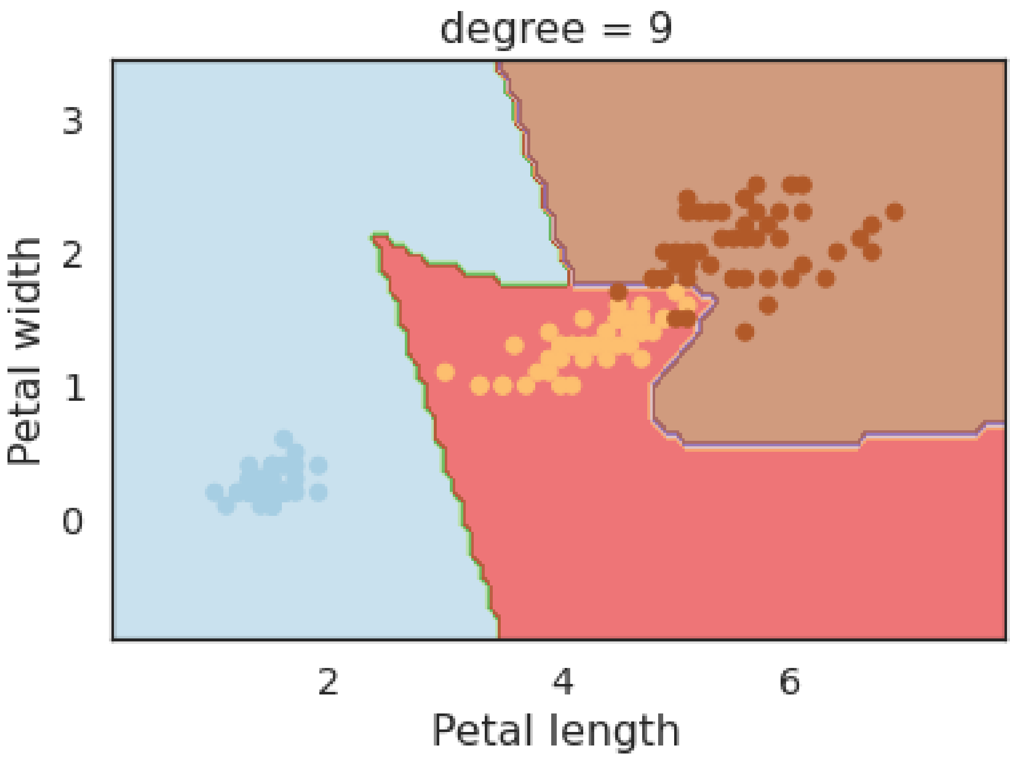

degree = 4
Petal width
Petal length
0
1
2
3
2
4
6

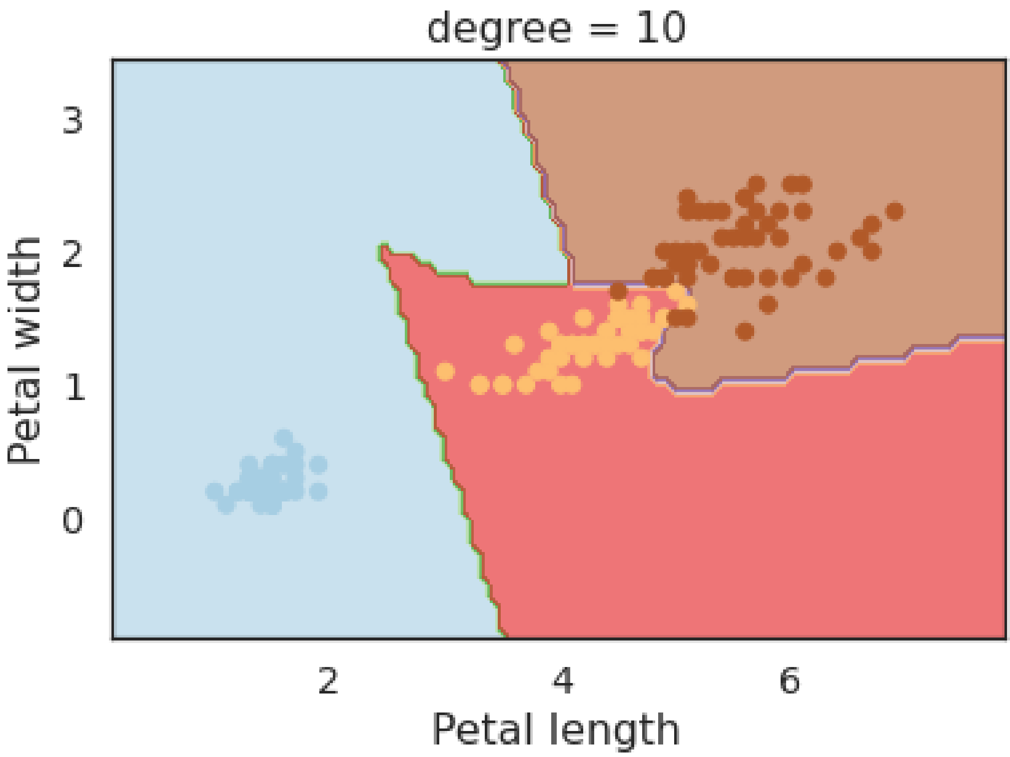

degree = 5
Petal width
Petal length
3
2
1
0
2
4
6


degree = 6
Petal width
Petal length
3
2
1
0
2
4
6


degree = 7
Petal width
Petal length
3
2
1
0
2
4
6


degree = 8
Petal width
Petal length
3
2
1
0
2
4
6


degree = 9
Petal width
0
1
2
3
2
4
6
Petal length


degree = 10
Petal width
0
1
2
3
2
4
6
Petal length

```
[ ]:
```