

Data Visualization III

Download the Iris flower dataset or any other dataset into a DataFrame. (eg <https://archive.ics.uci.edu/ml/datasets/Iris>). Scan the dataset and give the inference as:

1. How many features are there and what are their types (e.g., numeric, nominal)?
2. Create a histogram for each feature in the dataset to illustrate the feature distributions.
3. Create a boxplot for each feature in the dataset.

```
In [33]: import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
```

Loading the dataset, checking for null values and preprocessing data

```
In [34]: iris = pd.read_csv('/content/drive/MyDrive/TE/Colab Notebooks/Datasets/Iris (1).csv')
iris
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
0	1	5.1	3.5	1.4	0.2	Iris-setosa
1	2	4.9	3.0	1.4	0.2	Iris-setosa
2	3	4.7	3.2	1.3	0.2	Iris-setosa
3	4	4.6	3.1	1.5	0.2	Iris-setosa
4	5	5.0	3.6	1.4	0.2	Iris-setosa
...
145	146	6.7	3.0	5.2	2.3	Iris-virginica
146	147	6.3	2.5	5.0	1.9	Iris-virginica
147	148	6.5	3.0	5.2	2.0	Iris-virginica
148	149	6.2	3.4	5.4	2.3	Iris-virginica
149	150	5.9	3.0	5.1	1.8	Iris-virginica

150 rows × 6 columns

```
In [35]: """col_names = ['Sepal_Length','Sepal_Width','Petal_Length','Petal_Width','Species']
iris = pd.read_csv('/content/drive/MyDrive/TE/Colab Notebooks/Datasets/Iris (1).csv',
iris[col_names]"""
```

```
Out[35]: "col_names = ['Sepal_Length','Sepal_Width','Petal_Length','Petal_Width','Species']\niris = pd.read_csv('/content/drive/MyDrive/TE/Colab Notebooks/Datasets/Iris (1).csv',
names = col_names)\niris[col_names]"
```

```
In [36]: iris.shape
```

Out[36]: (150, 6)

In [37]: `iris.describe()`

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm
count	150.000000	150.000000	150.000000	150.000000	150.000000
mean	75.500000	5.843333	3.054000	3.758667	1.198667
std	43.445368	0.828066	0.433594	1.764420	0.763161
min	1.000000	4.300000	2.000000	1.000000	0.100000
25%	38.250000	5.100000	2.800000	1.600000	0.300000
50%	75.500000	5.800000	3.000000	4.350000	1.300000
75%	112.750000	6.400000	3.300000	5.100000	1.800000
max	150.000000	7.900000	4.400000	6.900000	2.500000

In [38]: `iris.head()`

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
0	1	5.1	3.5	1.4	0.2	Iris-setosa
1	2	4.9	3.0	1.4	0.2	Iris-setosa
2	3	4.7	3.2	1.3	0.2	Iris-setosa
3	4	4.6	3.1	1.5	0.2	Iris-setosa
4	5	5.0	3.6	1.4	0.2	Iris-setosa

In [39]: `iris.tail()`

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
145	146	6.7	3.0	5.2	2.3	Iris-virginica
146	147	6.3	2.5	5.0	1.9	Iris-virginica
147	148	6.5	3.0	5.2	2.0	Iris-virginica
148	149	6.2	3.4	5.4	2.3	Iris-virginica
149	150	5.9	3.0	5.1	1.8	Iris-virginica

In [40]: `iris.isnull().sum()`

Out[40]:

Id	0
SepalLengthCm	0
SepalWidthCm	0
PetalLengthCm	0
PetalWidthCm	0
Species	0
dtype:	int64

How many features are there and what are their types (e.g., numeric, nominal)?

```
In [43]: column = len(list(iris))
column
```

```
Out[43]: 6
```

```
In [44]: iris.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 6 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   Id               150 non-null    int64  
 1   SepalLengthCm   150 non-null    float64 
 2   SepalWidthCm    150 non-null    float64 
 3   PetalLengthCm   150 non-null    float64 
 4   PetalWidthCm    150 non-null    float64 
 5   Species          150 non-null    object  
dtypes: float64(4), int64(1), object(1)
memory usage: 7.2+ KB
```

```
In [45]: iris.columns
```

```
Out[45]: Index(['Id', 'SepalLengthCm', 'SepalWidthCm', 'PetalLengthCm', 'PetalWidthCm',
               'Species'],
               dtype='object')
```

```
In [46]: iris.columns.values
```

```
Out[46]: array(['Id', 'SepalLengthCm', 'SepalWidthCm', 'PetalLengthCm',
               'PetalWidthCm', 'Species'], dtype=object)
```

```
In [47]: print("Features and Types:\n")
iris.dtypes
```

Features and Types:

```
Out[47]: Id           int64
SepalLengthCm  float64
SepalWidthCm   float64
PetalLengthCm  float64
PetalWidthCm   float64
Species        object
dtype: object
```

Ans. There are 6 features namely:

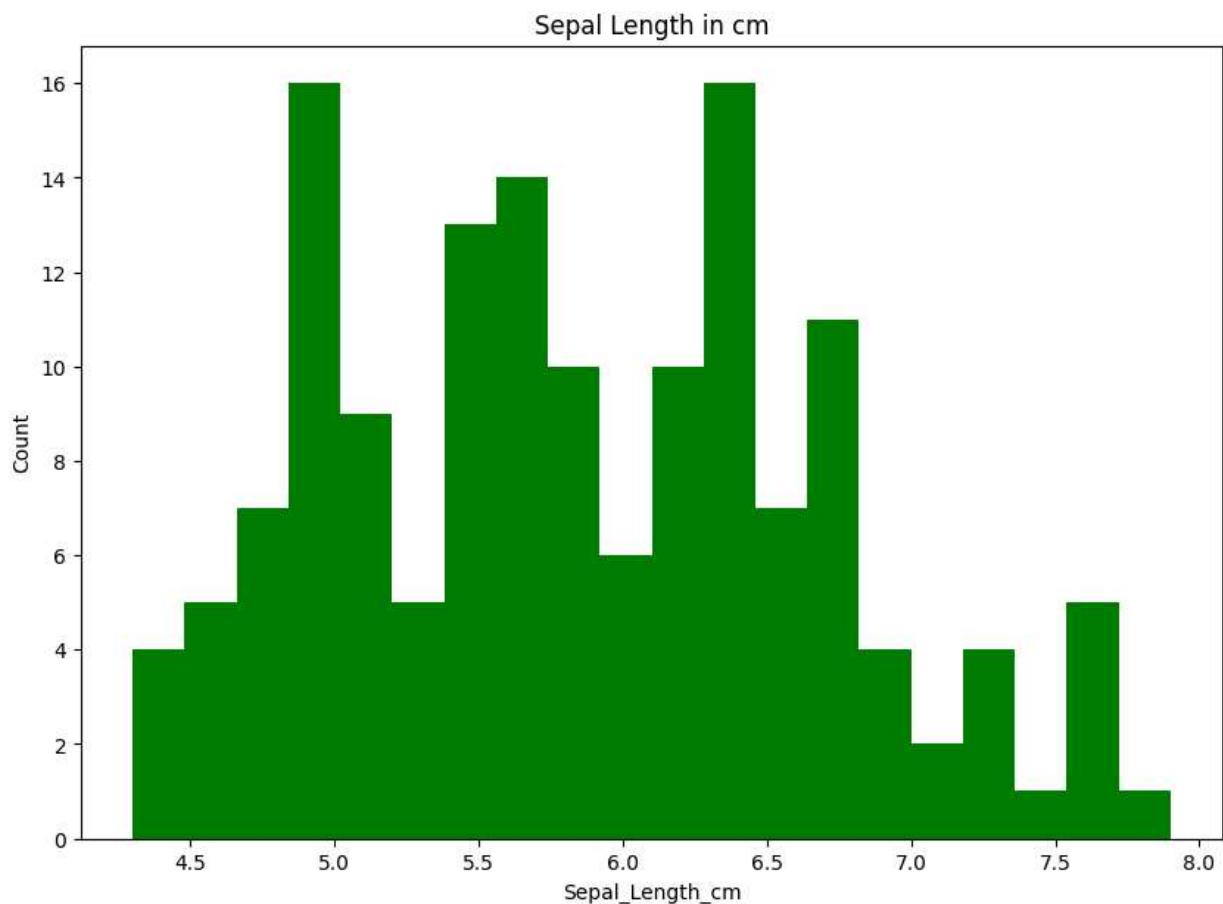
- Id, datatype = int64
- Sepal_Length, datatype = float64
- Sepal_Width, datatype = float64
- Petal_Length, datatype = float64
- Petal_Width, datatype = float64
- Species, datatype = object

Create a histogram for each feature in the dataset to illustrate the feature distributions.

```
In [49]: plt.figure(figsize = (10, 7))
x = iris["SepalLengthCm"]
```

```
plt.hist(x, bins = 20, color = "green")
plt.title("Sepal Length in cm")
plt.xlabel("Sepal_Length_cm")
plt.ylabel("Count")
```

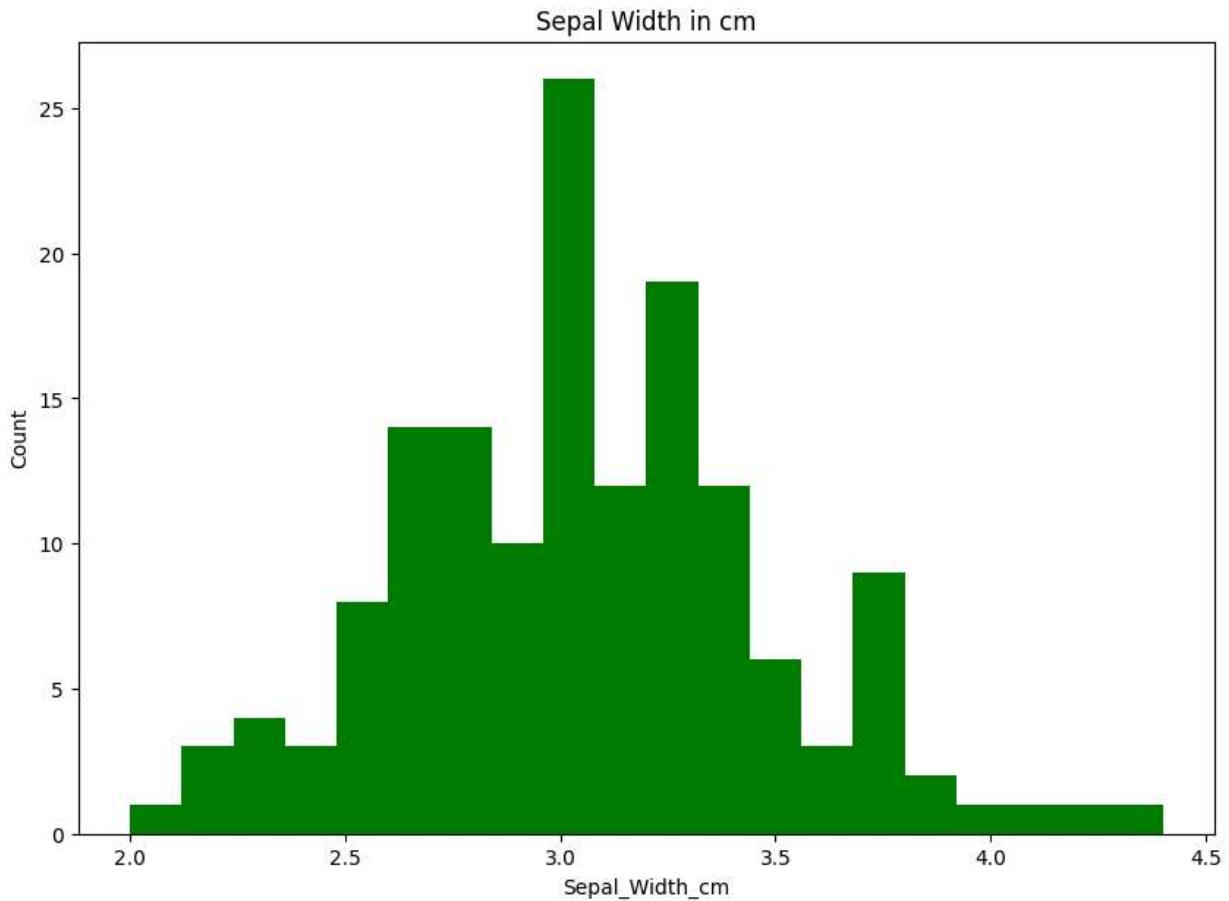
```
Out[49]: Text(0, 0.5, 'Count')
```



```
In [50]: plt.figure(figsize = (10, 7))
x = iris.SepalWidthCm
```

```
plt.hist(x, bins = 20, color = "green")
plt.title("Sepal Width in cm")
plt.xlabel("Sepal_Width_cm")
plt.ylabel("Count")
```

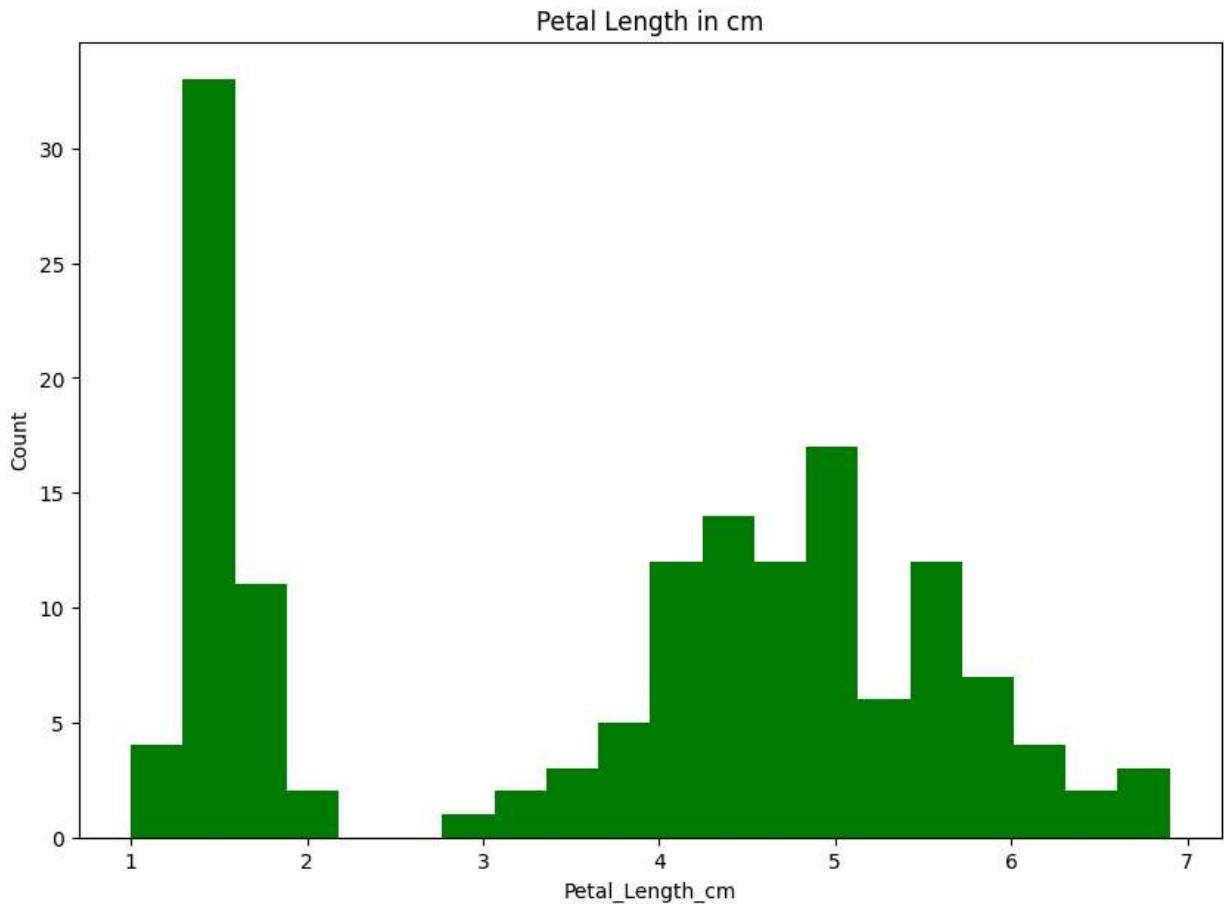
```
plt.show()
```



```
In [51]: plt.figure(figsize = (10, 7))
x = iris.PetalLengthCm

plt.hist(x, bins = 20, color = "green")
plt.title("Petal Length in cm")
plt.xlabel("Petal_Length_cm")
plt.ylabel("Count")

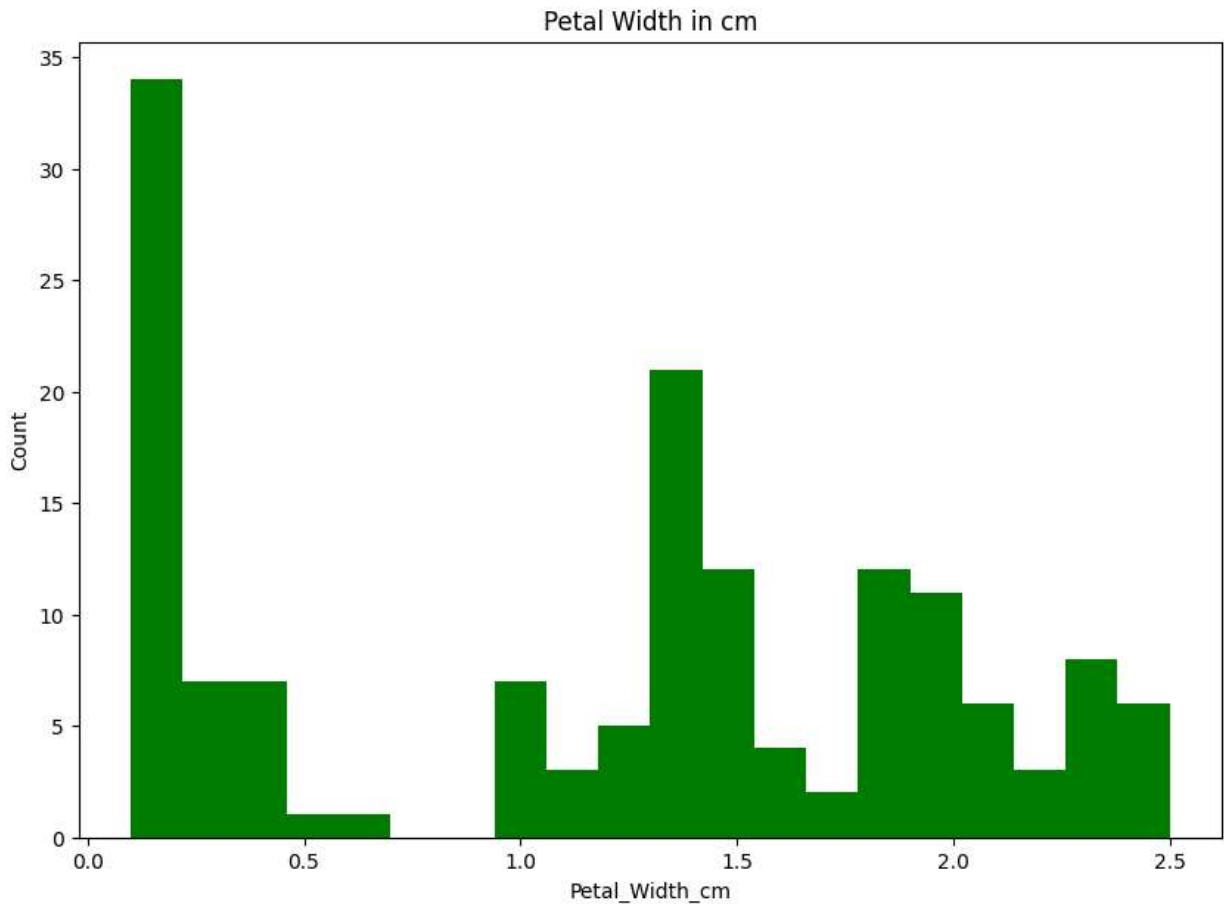
plt.show()
```



```
In [53]: plt.figure(figsize = (10, 7))
x = iris.PetalWidthCm

plt.hist(x, bins = 20, color = "green")
plt.title("Petal Width in cm")
plt.xlabel("Petal_Width_cm")
plt.ylabel("Count")

plt.show()
```



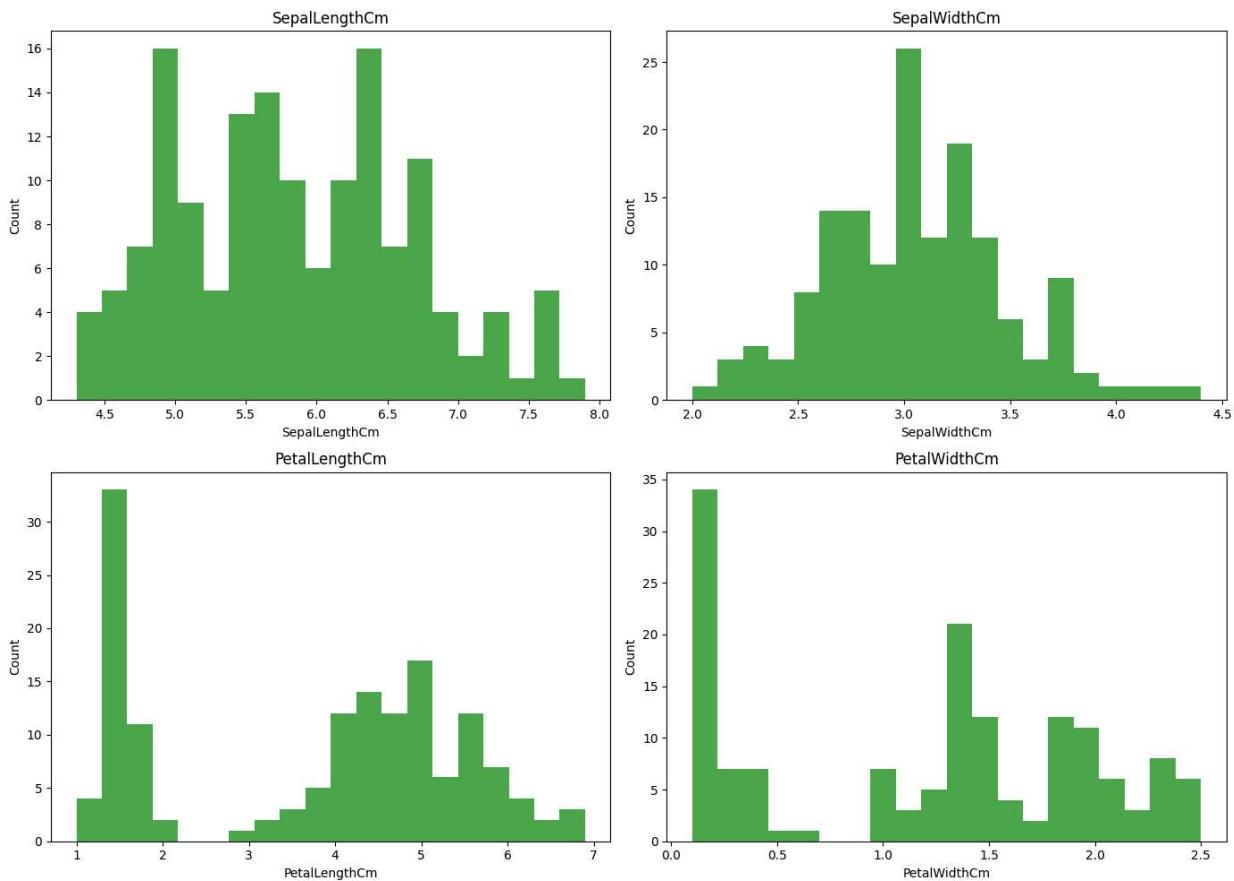
```
In [54]: import matplotlib.pyplot as plt

# Define the features you want to plot
features = ["SepalLengthCm", "SepalWidthCm", "PetalLengthCm", "PetalWidthCm"]

# Set figure size
plt.figure(figsize=(14, 10))

# Loop through each feature and create a histogram
for i, feature in enumerate(features, start=1):
    plt.subplot(2, 2, i)
    x = iris[feature]
    plt.hist(x, bins=20, color='green', alpha=0.7)
    plt.title(feature)
    plt.xlabel(feature)
    plt.ylabel("Count")

plt.tight_layout()
plt.show()
```



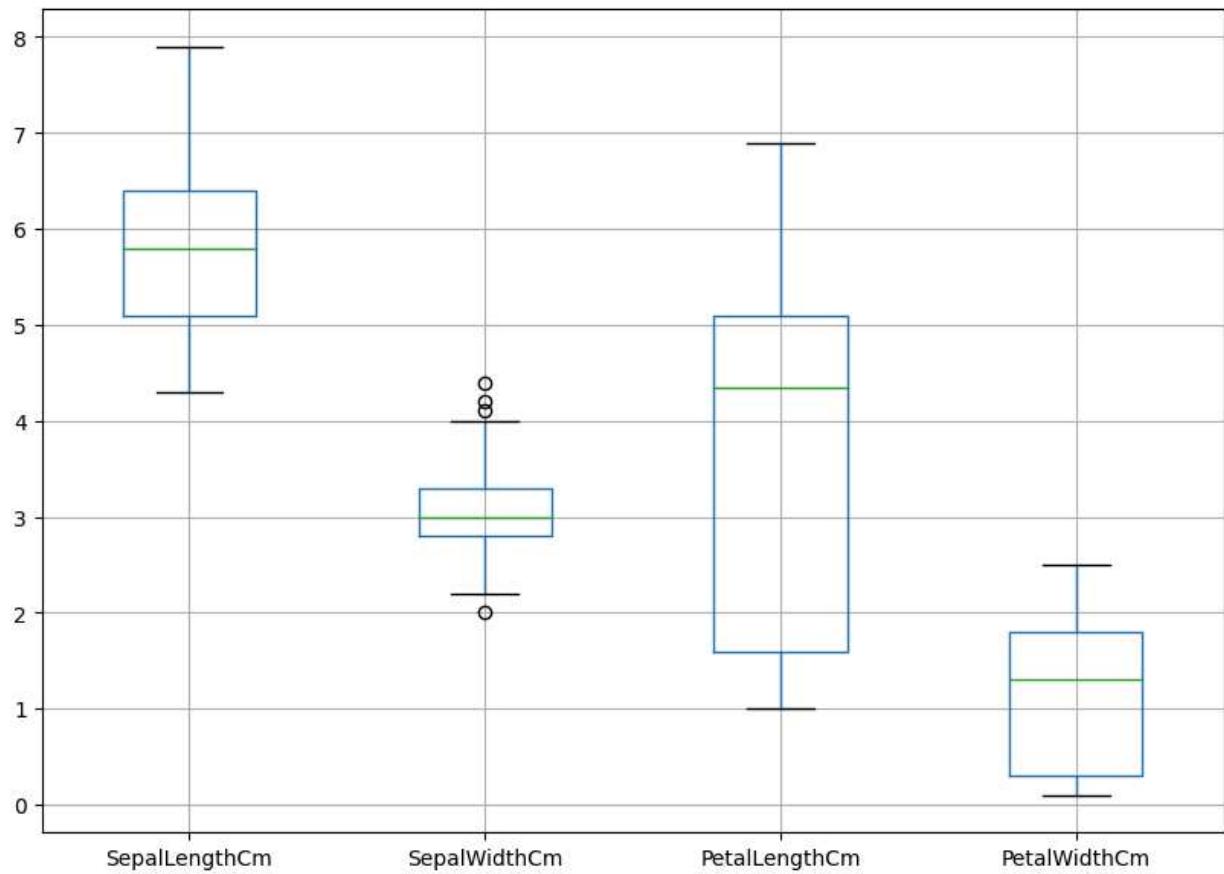
Create a boxplot for each feature in the dataset.

```
In [56]: # removing Id column
new_data = iris[["SepalLengthCm", "SepalWidthCm", "PetalLengthCm", "PetalWidthCm"]]
print(new_data.head())
```

	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm
0	5.1	3.5	1.4	0.2
1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2
3	4.6	3.1	1.5	0.2
4	5.0	3.6	1.4	0.2

```
In [65]: plt.figure(figsize = (10, 7))
new_data.boxplot()
```

```
Out[65]: <Axes: >
```



Compare distributions and identify outliers: If we observe closely. for the box 2, interquartile distance is roughly around 0.75 hence the values lying beyond this range of (third quartile + interquartile distance) i.e. roughly around 4.05 will be considered as outliers. Similarly outliers with other boxplots can be found.**bold text**

```
In [68]: !jupyter nbconvert --to html /content/drive/MyDrive/Colab Notebooks/DSBDAL-10.ipynb
```

[NbConvertApp] WARNING | pattern '/content/drive/MyDrive/Colab' matched no files
 [NbConvertApp] WARNING | pattern 'Notebooks/DSBDAL-10.ipynb' matched no files
 This application is used to convert notebook files (*.ipynb)
 to various other formats.

WARNING: THE COMMANDLINE INTERFACE MAY CHANGE IN FUTURE RELEASES.

Options

=====

The options below are convenience aliases to configurable class-options,
 as listed in the "Equivalent to" description-line of the aliases.
 To see all configurable class-options for some <cmd>, use:
 <cmd> --help-all

--debug

set log level to logging.DEBUG (maximize logging output)
 Equivalent to: [--Application.log_level=10]

--show-config

Show the application's configuration (human-readable format)
 Equivalent to: [--Application.show_config=True]

--show-config-json

Show the application's configuration (json format)
 Equivalent to: [--Application.show_config_json=True]

--generate-config

generate default config file
 Equivalent to: [--JupyterApp.generate_config=True]

-y

Answer yes to any questions instead of prompting.
 Equivalent to: [--JupyterApp.answer_yes=True]

--execute

Execute the notebook prior to export.
 Equivalent to: [--ExecutePreprocessor.enabled=True]

--allow-errors

Continue notebook execution even if one of the cells throws an error and include
 the error message in the cell output (the default behaviour is to abort conversion).
 This flag is only relevant if '--execute' was specified, too.

Equivalent to: [--ExecutePreprocessor.allow_errors=True]

--stdin

read a single notebook file from stdin. Write the resulting notebook with default
 basename 'notebook.*'

Equivalent to: [--NbConvertApp.from_stdin=True]

--stdout

Write notebook output to stdout instead of files.

Equivalent to: [--NbConvertApp.writer_class=StdoutWriter]

--inplace

Run nbconvert in place, overwriting the existing notebook (only
 relevant when converting to notebook format)

Equivalent to: [--NbConvertApp.use_output_suffix=False --NbConvertApp.export_form
 at=notebook --FilesWriter.build_directory=]

--clear-output

Clear output of current file and save in place,
 overwriting the existing notebook.

Equivalent to: [--NbConvertApp.use_output_suffix=False --NbConvertApp.export_form
 at=notebook --FilesWriter.build_directory= --ClearOutputPreprocessor.enabled=True]

--no-prompt

Exclude input and output prompts from converted document.

Equivalent to: [--TemplateExporter.exclude_input_prompt=True --TemplateExporter.e
 xclude_output_prompt=True]

--no-input

Exclude input cells and output prompts from converted document.

This mode is ideal for generating code-free reports.

Equivalent to: [--TemplateExporter.exclude_output_prompt=True --TemplateExporter.exclude_input=True --TemplateExporter.exclude_input_prompt=True]
--allow-chromium-download
Whether to allow downloading chromium if no suitable version is found on the system.

Equivalent to: [--WebPDFExporter.allow_chromium_download=True]
--disable-chromium-sandbox
Disable chromium security sandbox when converting to PDF..

Equivalent to: [--WebPDFExporter.disable_sandbox=True]
--show-input
Shows code input. This flag is only useful for dejavu users.

Equivalent to: [--TemplateExporter.exclude_input=False]
--embed-images
Embed the images as base64 dataurls in the output. This flag is only useful for the HTML/WebPDF/Slides exports.

Equivalent to: [--HTMLExporter.embed_images=True]
--sanitize-html
Whether the HTML in Markdown cells and cell outputs should be sanitized..

Equivalent to: [--HTMLExporter.sanitize_html=True]
--log-level=<Enum>
Set the log level by value or name.
Choices: any of [0, 10, 20, 30, 40, 50, 'DEBUG', 'INFO', 'WARN', 'ERROR', 'CRITICAL']
Default: 30
Equivalent to: [--Application.log_level]
--config=<Unicode>
Full path of a config file.
Default:
Equivalent to: [--JupyterApp.config_file]
--to=<Unicode>
The export format to be used, either one of the built-in formats
['asciidoc', 'custom', 'html', 'latex', 'markdown', 'notebook', 'pdf', 'python', 'rst', 'script', 'slides', 'webpdf']
or a dotted object name that represents the import path for an
`Exporter` class
Default:
Equivalent to: [--NbConvertApp.export_format]
--template=<Unicode>
Name of the template to use
Default:
Equivalent to: [--TemplateExporter.template_name]
--template-file=<Unicode>
Name of the template file to use
Default: None
Equivalent to: [--TemplateExporter.template_file]
--theme=<Unicode>
Template specific theme(e.g. the name of a JupyterLab CSS theme distributed as prebuilt extension for the lab template)
Default: 'light'
Equivalent to: [--HTMLExporter.theme]
--sanitize_html=<Bool>
Whether the HTML in Markdown cells and cell outputs should be sanitized.This should be set to True by nbviewer or similar tools.
Default: False
Equivalent to: [--HTMLExporter.sanitize_html]
--writer=<DottedObjectName>
Writer class used to write the results of the conversion
Default: 'FileWriter'

```

Equivalent to: [--NbConvertApp.writer_class]
--post=<DottedOrNone>
    PostProcessor class used to write the
                                results of the conversion
    Default: ''
    Equivalent to: [--NbConvertApp.postprocessor_class]
--output=<Unicode>
    overwrite base name use for output files.
        can only be used when converting one notebook at a time.
    Default: ''
    Equivalent to: [--NbConvertApp.output_base]
--output-dir=<Unicode>
    Directory to write output(s) to. Defaults
                                to output to the directory of each notebook. To rec
over
                                previous default behaviour (outputting to the curre
nt
                                working directory) use . as the flag value.
    Default: ''
    Equivalent to: [--FileWriter.build_directory]
--reveal-prefix=<Unicode>
    The URL prefix for reveal.js (version 3.x).
    This defaults to the reveal CDN, but can be any url pointing to a copy
of reveal.js.
    For speaker notes to work, this must be a relative path to a local
copy of reveal.js: e.g., "reveal.js".
    If a relative path is given, it must be a subdirectory of the
current directory (from which the server is run).
    See the usage documentation
        (https://nbconvert.readthedocs.io/en/latest/usage.html#reveal-js-html-sli
deshow)
        for more details.
    Default: ''
    Equivalent to: [--SlidesExporter.reveal_url_prefix]
--nbformat=<Enum>
    The nbformat version to write.
        Use this to downgrade notebooks.
    Choices: any of [1, 2, 3, 4]
    Default: 4
    Equivalent to: [--NotebookExporter.nbformat_version]
```

Examples

The simplest way to use nbconvert is

```
> jupyter nbconvert mynotebook.ipynb --to html
```

Options include ['asciidoc', 'custom', 'html', 'latex', 'markdown', 'notebook', 'pdf', 'python', 'rst', 'script', 'slides', 'wevpdf'].

```
> jupyter nbconvert --to latex mynotebook.ipynb
```

Both HTML and LaTeX support multiple output templates. LaTeX includes 'base', 'article' and 'report'. HTML includes 'basic', 'lab' and 'classic'. You can specify the flavor of the format used.

```
> jupyter nbconvert --to html --template lab mynotebook.ipynb
```

You can also pipe the output to stdout, rather than a file

```
> jupyter nbconvert mynotebook.ipynb --stdout  
PDF is generated via latex  
> jupyter nbconvert mynotebook.ipynb --to pdf  
You can get (and serve) a Reveal.js-powered slideshow  
> jupyter nbconvert myslides.ipynb --to slides --post serve  
Multiple notebooks can be given at the command line in a couple of  
different ways:  
> jupyter nbconvert notebook*.ipynb  
> jupyter nbconvert notebook1.ipynb notebook2.ipynb  
or you can specify the notebooks list in a config file, containing::  
c.NbConvertApp.notebooks = ["my_notebook.ipynb"]  
> jupyter nbconvert --config mycfg.py  
To see all available configurables, use `--help-all`.
```