# Tasks (use NumPy only):

# 1. Create Arrays

- A 1D array of 20 random integers from 1 to 100
- A 5×5 matrix with values from 1 to 25

# 2. Reshape and Slicing

- o Reshape the 1D array into a 4×5 matrix
- Extract the 2nd and 4th columns

# 3. Mathematical Operations

- o Find the mean, median, max, and standard deviation of your matrix
- o Replace all values divisible by 5 with -1

### 4. Boolean Masking

- o Get all values greater than the matrix mean
- o Count how many values are less than 10

#### **Section 2: Pandas**

Use iris.csv

# • Tasks:

### 1. Load & Explore

- Load the dataset using pd.read\_csv()
- Show: .head(), .info(), .describe()

# 2. Selection & Filtering

- Select only columns 'sepal\_length' and 'species'
- Filter rows where petal\_width > 1.0 and species == 'setosa'

# 3. Group & Aggregate

- o Group by species and calculate the average of sepal\_length
- o Count how many records per species

### 4. Missing Values

o Inject missing values in some rows

- o Fill missing sepal\_length with column mean
- o Drop rows where species is missing

#### 5. Sorting & Value Counts

- Sort the DataFrame by petal\_length in descending order
- o Find top 2 most frequent species

# Section 3: Matplotlib

# Tasks (use Matplotlib & optionally Pandas plots):

### 1. Line Plot

o Plot the average sepal length for each species

#### 2. Bar Plot

Count of each species as a bar plot (.value\_counts().plot(kind='bar'))

#### 3. Scatter Plot

Plot sepal\_length vs petal\_length, color by species

# 4. Histogram

Plot histogram of sepal\_width with 10 bins

#### 5. Customization

- o Add title, xlabel, ylabel, grid, and legend to each plot
- 1. Plot a **boxplot** comparing sepal\_length across different species.
- 2. Use df.corr() and .heatmap() from seaborn (if allowed).
- 3. Export your cleaned DataFrame to CSV.

# **Submission Guidelines**

- Submit as a .ipynb (Jupyter Notebook) or .py script
- Include markdown/text for short explanations
- Use comments to explain steps