

# NumPy and Pandas fundamentals for handling biological datasets

## Prerequisites

- Programming Fundamentals in Python
  - Basic Python syntax and data structures
  - Functions and control flow
  - File handling in Python
  - Experience with Python IDEs and Jupyter notebooks
- Basic Biology Knowledge
  - Basic genomics terminology
  - Familiarity with common bioinformatics file formats (FASTA, FASTQ)

## Who is the course for?

Bioinformaticians and genomics researchers who want to enhance their data analysis capabilities by mastering NumPy and Pandas for efficient processing of genomic datasets

## About the course

### Overall Course Objective

By the end of this course, students will be able to effectively utilize NumPy and Pandas libraries to manipulate, analyze, and process complex numerical and tabular data in Python, demonstrating proficiency in advanced array operations, data structures, and data manipulation techniques. Additionally, students will apply these skills to real-world bioinformatics problems, gaining practical experience in genomics data analysis and handling.

### Specific Learning Objectives

1. After completing the NumPy section and hands-on exercises, students will be able to:
  - Explain the purpose and advantages of using NumPy in scientific computing and data analysis
  - Create, manipulate, and efficiently implement NumPy arrays through advanced techniques including indexing, sorting, splitting, vectorized operations, and broadcasting
2. After completing the Pandas section and hands-on exercises, students will be able to:

- Understand the relationship between Pandas and NumPy, and effectively use Pandas Series and DataFrames for data analysis
- Perform advanced data manipulation techniques including indexing, filtering, handling missing data, and combining DataFrames through merging and concatenation

## Overall time schedule

Numpy for Bioinformatics	3 Hours
Pandas for Bioinformatics	3 Hours

## Lesson plan

### Overall objectives

#### ! Objectives

1. Understand the fundamentals of NumPy and its importance in scientific computing and bioinformatics
2. Develop proficiency in creating, manipulating, and performing operations on NumPy arrays
3. Apply NumPy's computational capabilities to solve common bioinformatics data manipulation tasks
4. Compare the efficiency and syntax advantages of NumPy versus standard Python for numerical computation

### Specific Objectives

By the end of this workshop, participants will be able to:

1. NumPy Foundations
  - Explain NumPy's purpose and advantages over standard Python lists
  - Describe how NumPy leverages contiguous memory allocation for improved performance
2. Array Creation and Structure
  - Create NumPy arrays of different dimensions from Python lists and other data sources
  - Examine array attributes such as `shape`, `ndim`, `size`, and `dtype`
3. Data Types
  - Contrast Python and NumPy data types for numerical computation
  - Select appropriate NumPy data types for optimizing memory usage and computational precision
  - Understand and manage type coercion in array operations
4. Indexing and Selection
  - Access and manipulate array elements using basic indexing

- Extract subsets of data using slicing operations in multiple dimensions
- Apply boolean masking and advanced filtering techniques to arrays

## 5. Array Operations

- Reshape and restructure arrays to better match analytical needs
- Combine arrays using concatenation and splitting operations
- Generate descriptive statistics using NumPy's built-in functions

## 6. Vectorization and Performance

- Implement vectorized operations to replace traditional Python loops
- Apply broadcasting to perform operations between arrays of different shapes
- Optimize calculations for working with large biological datasets

# Introduction to NumPy

## ! Objectives

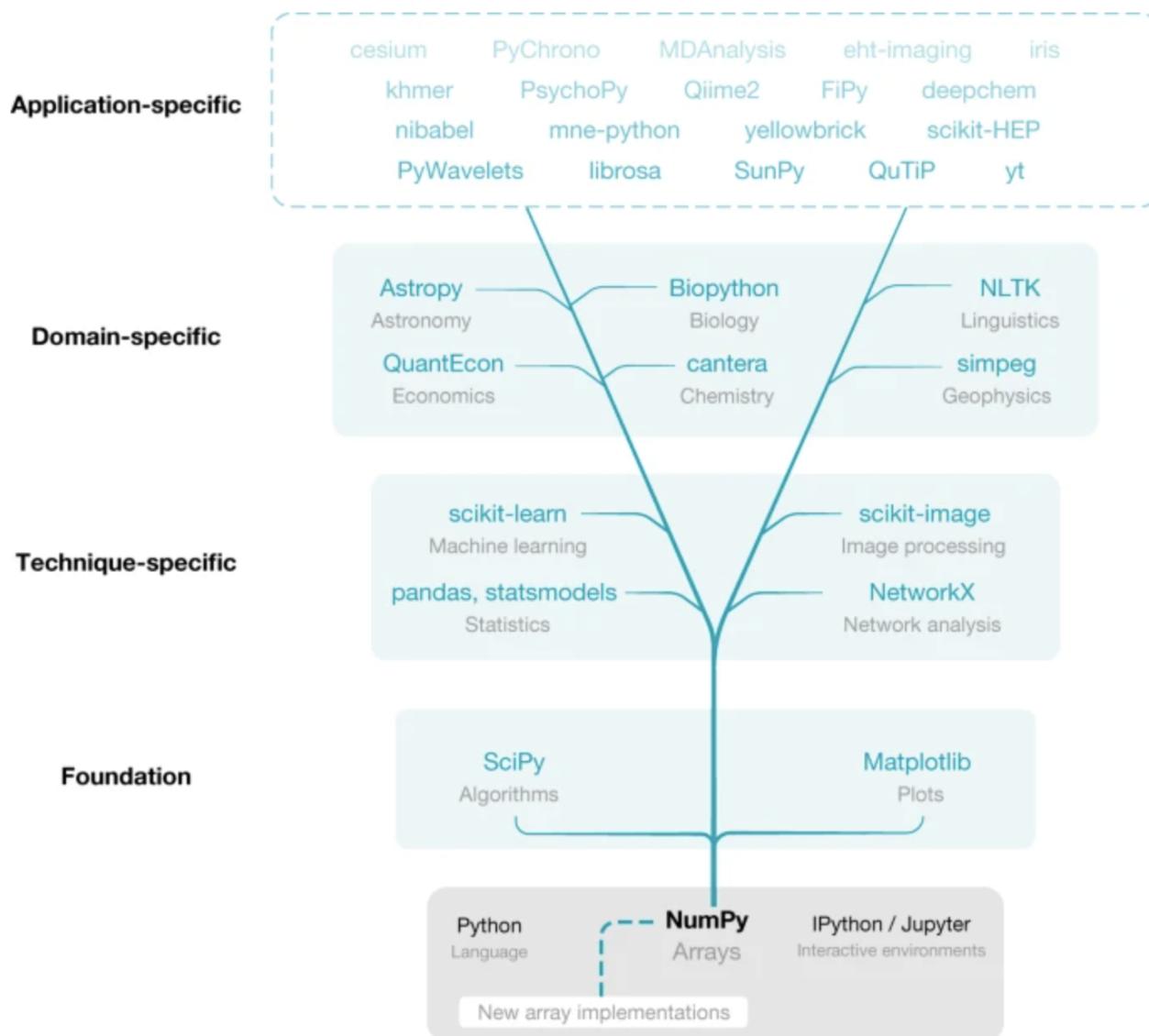
- What is NumPy and why it's important for bioinformatics
- Performance advantages over Python lists
- Foundation for other scientific libraries

## Instructor note

- Teaching : 10 min
- Demo: 10 min

## What is `numpy` ?

- `NumPy` is short for “Numerical Python”
- Core python library for scientific computing
- Useful for processing large quantities of same-type data
- Foundation for:
  - Data manipulation, analysis and visualization libraries (`Pandas`, `Matplotlib`, `scipy`)
  - Machine learning libraries (`scikit-learn`, `TensorFlow`, `PyTorch`)
- NumPy operations are written in compiled C, significantly speeding up mathematical operations



[Ref: Array programming with NumPy](#)

## Why NumPy is Essential for Bioinformatics

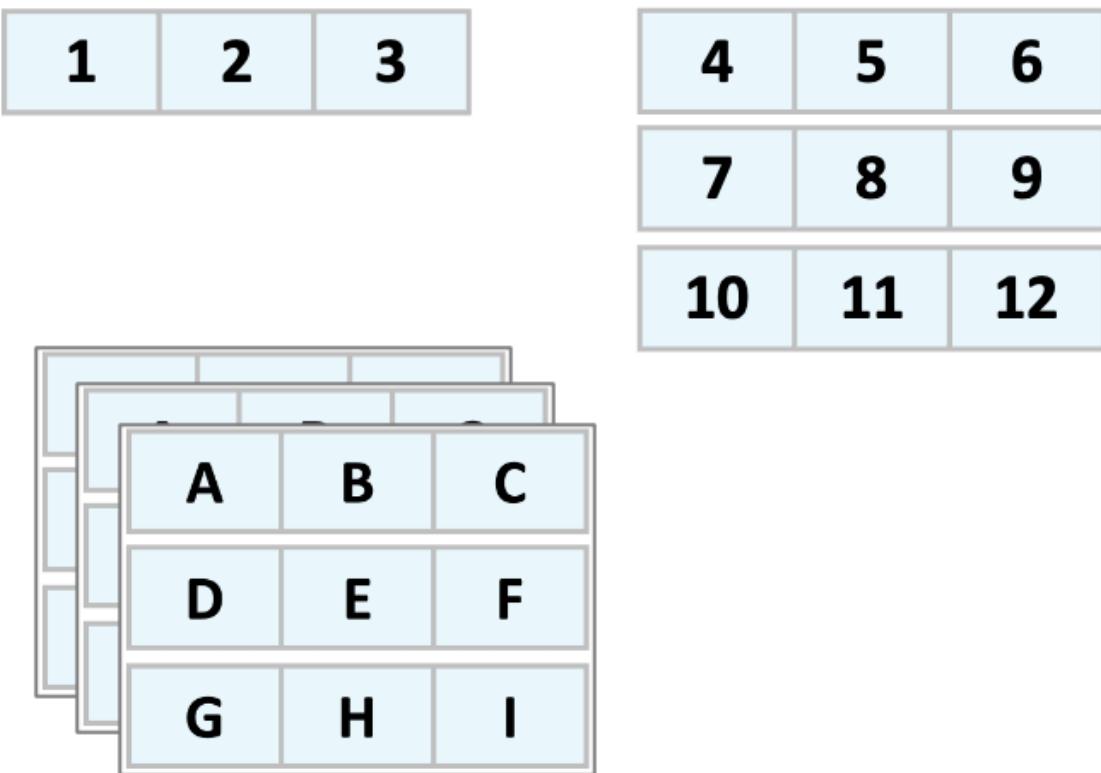
- Bioinformatics involves processing and analyzing vast amounts of biological data, from genomic sequences to protein structures
- NumPy's efficient N-dimensional arrays allow for fast and memory-efficient processing of these large datasets
  - C-optimized operations: NumPy's compiled C backend makes processing of big-data feasible without having C programming knowledge
  - Reduced memory footprint help optimize the big-data processing: [Accelerating Key Bioinformatics Tasks 100-fold by Improving Memory Access](#)
- Run statistical analysis/operations using Biological Data effectively (low barrier to entry)
- Numpy is essential for Python-based machine learning applications on biological datasets

### ! Note

In essence, NumPy bridges the gap between high-level Python programming and the performance requirements of modern bioinformatics, making it possible to analyze the increasingly large datasets generated by modern biological research techniques.

## NumPy Arrays vs Python Lists

- Lists are data structures used to store collections of elements
- NumPy arrays enforce a single data type for all elements
- Benefits of NumPy arrays:
  - Homogeneity removes need for type checking during operations
  - Contiguous memory allocation (faster than Python's scattered storage)
  - Vectorization allows operations on entire arrays without loops
  - Rich set of mathematical functions and operations



## Creating NumPy Arrays

### Demo

#### 1D Arrays from lists

```
import numpy as np

# Create from list
py_list = list(range(1,5))
np_array = np.array(py_list)
print(np_array) # Output: array([1, 2, 3, 4])
```

#### 2D Arrays (matrices)

```
# Create a 2D array
rows, cols = 3, 4
list_of_list = [[j for j in range(cols)] for i in range(rows)]
np_array = np.array(list_of_list)
print(np_array)
```

### ✓ Output:

```
[1 2 3 4]

array([[0, 1, 2, 3],
       [0, 1, 2, 3],
       [0, 1, 2, 3]])
```

## Creating arrays from scratch

### 👀 Demo

```
# Range of values
print("np.arange")
print(np.arange(1, 10, 2)) # <start,stop,step>, stop is not included in the array

# Arrays of zeros
print("np.zeros")
print(np.zeros((2, 2)))      # Array of zeros

# Arrays of ones
print("np.ones")
print(np.ones(5))           # Array of ones

# 2-D arrays
print("2-D arrays")
print(np.ones([5,2])) # 2-D array of ones
print(np.random.random((2, 2))) # 2-D array Random values between 0 and 1
```

### ✓ Output

```

np.arange
[1 3 5 7 9]
np.zeros
[[0. 0.]
 [0. 0.]]
np.ones
[1. 1. 1. 1. 1.]
2-D arrays
[[1. 1.]
 [1. 1.]
 [1. 1.]
 [1. 1.]
 [1. 1.]]
[[0.76528238 0.95473465]
 [0.81062275 0.14766793]]

```

## Examining numpy array structure and storage

- NumPy arrays come with several attributes that provide important information about their structure and data storage.

Attribute	Description	Example	Purpose
<code>shape</code>	A tuple of integers representing the size of each dimension of the array	(3, 4) (2D array with 3 rows and 4 columns)	Understands the layout and number of elements within the array.
<code>ndim</code>	An integer indicating the dimensionality of the array (number of dimensions)	2 (for a 2D array), 1 (for a vector)	Clarifies how many axes are used to access elements.
<code>size</code>	An integer representing the total number of elements within the array	12 (for a 2D array with shape (3, 4))	Provides a quick way to determine the total number of elements.

## 👀 Demo

```

print("2-D array")
np_2d = np.ones([5,2])
print("\tshape", np_2d.shape)
print("\tndim", np_2d.ndim)
print("\tsize", np_2d.size)

```

## ✓ Output

```

2-D array
    shape (5, 2)
    ndim 2
    size 10

```

## More info

- Additional notes: Exercise

## NumPy Data Types

### ! Objectives

- Explain the fundamental concept of data types and their importance in computing
- Compare and contrast Python's general data types with NumPy's specialized data types
- Identify the key NumPy data types relevant to bioinformatics applications
- Apply data type conversion techniques to optimize NumPy arrays
- Explore different NumPy data types for different bioinformatics use cases

### Instructor note

- Teaching : 15 min
- Demo: 10 min

## Introduction to Data Types

Data types are fundamental categories that define how computers interpret and store information in memory

### Data Types



#### Value Constraints

Defines the types of values a variable can hold.



#### Memory Allocation

Determines the amount of memory allocated for data storage.



#### Operations

Specifies the operations that can be performed on the data.



#### Binary Storage

Describes how data is stored at the binary level.

### Data types directly impact:

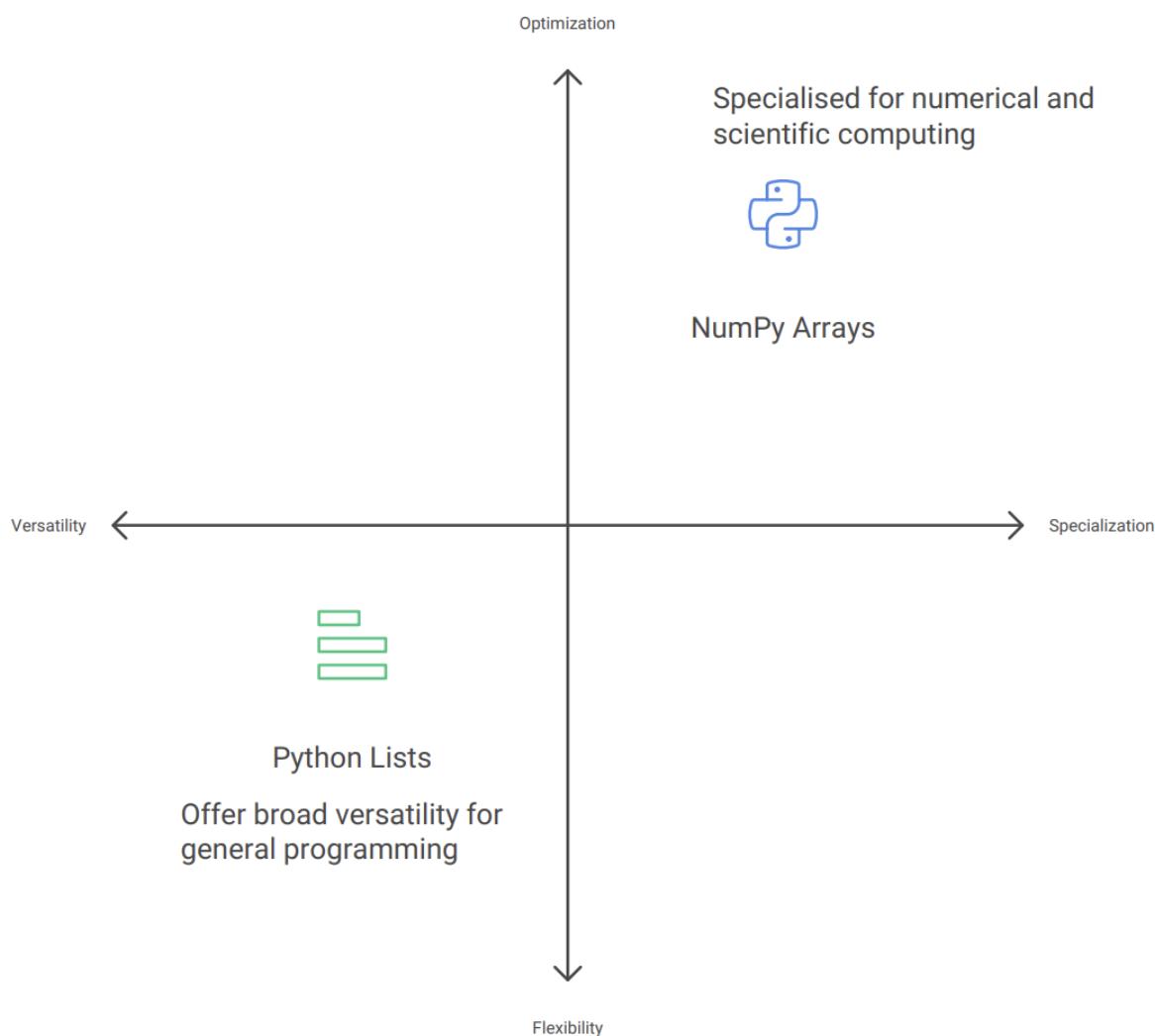
- Program correctness

- Inappropriate data types can lead to errors or unexpected behavior
- Computational performance
  - Different data types have different processing speeds
  - e.g., Choosing appropriate data types helps optimize memory usage

In scientific computing and bioinformatics specifically, where we often work with large datasets, choosing the right data type becomes even more critical for both accuracy and performance.

## Python vs NumPy Data Types

Python and NumPy both provide data type systems, but they serve different purposes and have important distinctions:



### Note

This specialization allows NumPy to provide exactly what's needed for scientific applications without unnecessary overhead. For example, summing a million numbers can be 10-100x faster using NumPy arrays compared to Python lists.

### More info

## Type Homogeneity

### 👀 Demo

```
# Python collections like lists can contain mixed types:  
mixed_list = [1, "DNA", True, 3.14] # Different types in one list  
print(type(mixed_list), type(mixed_list[0]), type(mixed_list[1]),  
      type(mixed_list[2]), type(mixed_list[3]))  
  
# NumPy arrays enforce type homogeneity:  
# All elements converted to the same type (float64)  
np_array = np.array([1, 2, 3.14, 4])  
print(np_array.dtype)
```

### ✓ Output

```
<class 'list'> <class 'int'> <class 'str'> <class 'bool'> <class 'float'>  
float64
```

This homogeneity enables:

- Predictable memory usage
- Optimized vectorized operations
- Simplified data processing logic

For bioinformatics applications, this homogeneity helps ensure consistency when processing large datasets of gene expression values, sequence reads, or alignment scores.

## Key NumPy Data Types

### Integer Types

- Stores whole numbers only, no decimals - Integer

`np.int32` & `np.int64` (64-bit signed integer):

- `np.int32` Range: -2,147,483,648 to 2,147,483,647
- `np.int64` Range: -9,223,372,036,854,775,808 to 9,223,372,036,854,775,807
- Primary uses in bioinformatics:
  - Storing chromosome positions
  - Indexing into large sequences

## 👀 Demo

```
# Storing chromosome positions for a set of genes
gene_positions = np.array([45123, 67845, 123456, 789012], dtype=np.int32)
print(gene_positions.dtype)

print(f"int8 range: {np.iinfo(np.int8).min} to {np.iinfo(np.int8).max}")
print(f"int16 range: {np.iinfo(np.int16).min} to {np.iinfo(np.int16).max}")
```

## ✓ Output

```
int32
int8 range: -128 to 127
int16 range: -32768 to 32767
```

## More info

- ▶ Additional notes: `np.uint8`

## Floating-Point Types

`np.float32` (Single precision); `np.float64` (double-precision float):

- `np.float32` (Single precision)
  - 32 bits of precision (~7 significant decimal digits)
- `np.float64` (double-precision float)
  - 64 bits of precision (~15-17 significant decimal digits)

## More info

- ▶ Additional notes: Inspect float-types
- ▶ Additional notes: Primary uses in bioinformatics

## Boolean Type

`np.bool_` (Boolean type):

- Values: True or False
- Primary uses in bioinformatics:
  - Creating masks for filtering data
  - Representing presence/absence of features
  - Storing binary outcomes from statistical tests
  - Marking regions of interest in genomic data

Boolean arrays in NumPy are extremely useful for data filtering and are more memory-efficient and faster than equivalent Python list comprehensions.

## String Types

<U# (Fixed-length string):

- Stores character data with fixed length
- Primary uses in bioinformatics:
  - Storing DNA/RNA sequences
  - Representing gene names, IDs, or annotations
  - Storing taxonomic information

### 👀 Demo

```
# Array of gene IDs
gene_ids = np.array(['BRCA1', 'TP53', 'EGFR', 'KRAS'])
print(gene_ids.dtype)

x = np.array(["1234567890", "12345678901234567890"])
print(x.dtype)

# Output
# dtype('<U20')
```

### ✓ Output

```
<U5
<U20
```

NumPy's string types are less flexible than Python strings but more memory-efficient when working with large collections of fixed-length identifiers.

External resources - [Working with Arrays of Strings And Bytes](#)

## Data Type Conversion and Specification

NumPy provides several ways to specify or convert data types:

### Explicit Type Declaration

```
# Create array with specific type
counts = np.array([1, 2, 3, 4], dtype=np.int32)

# Convert existing array to new type
float_counts = counts.astype(np.float64)
```

## Checking Data Types

```
# Check the data type of an array
data = np.array([1.0, 2.0, 3.0])
print(data.dtype) # Output: float64
```

## Automatic Type Inference

NumPy attempts to choose an appropriate type based on the data:

### 👀 Demo

```
np.array([1, 2, 3])           # Creates int64 array
np.array([1.0, 2.0, 3.0])     # Creates float64 array
np.array([True, False, True])  # Creates bool array
np.array(['A', 'C', 'G', 'T']) # Creates string array
```

## Practical Considerations for Bioinformatics

### More info

- ▶ Additional notes: Memory Optimization
- ▶ Additional notes: Performance Considerations

## Key Takeaways

### ❗ Keypoints

NumPy's specialized data types provide significant advantages for bioinformatics applications:

1. Efficiency - Both in terms of memory usage and computational performance
2. Precision - Control over numeric representation ensures accurate calculations
3. Compatibility - Designed to work well with other scientific computing libraries
4. Consistency - Type homogeneity helps prevent errors in large datasets

By choosing appropriate data types, bioinformaticians can:

- Process larger datasets in memory
- Run analyses faster
- Ensure computational accuracy
- Build more robust analysis pipelines

Understanding the distinctions between Python's general-purpose types and NumPy's specialized numeric types is essential for effective scientific programming in bioinformatics.

## Array Indexing and Slicing

### ! Objectives

- Define and distinguish between indexing and slicing operations in NumPy arrays
- Demonstrate proper syntax for accessing individual elements in 1D and 2D arrays using indexing
- Extract ranges of elements using slicing techniques, including with negative indices and step parameters
- Recognize and avoid common pitfalls when working with arrays, such as off-by-one errors and unintended modifications to original data

### Instructor note

- Teaching : 10 min
- Demo: 5 min

## Introduction

### What is Indexing and Slicing?

- Indexing is the process of accessing specific individual elements within a data structure
  - Uses square brackets with a single index value: `array[0]`
  - Most programming languages use zero-based indexing (first element is at position 0)
- Slicing is the process of extracting a subset or range of elements
  - Uses square brackets with a range specification: `array[start:stop:step]`
  - Creates a view of the original data (changes to the slice affect the original array)

### Why Indexing Matters in Bioinformatics:

- Bioinformatics deals with large, complex biological datasets:
  - DNA/RNA sequences (can be millions of nucleotides long)
  - Protein sequences
  - Gene expression matrices (thousands of genes × dozens/hundreds of samples)
  - Phylogenetic trees
  - Molecular structures
- Efficient data access is crucial for:
  - Sequence alignment and comparison
  - Identifying motifs or patterns
  - Analyzing specific regions of interest (e.g., genes, domains, binding sites)
  - Processing large-scale genomic or proteomic data

- Statistical analysis across experimental conditions

## NumPy Arrays in Bioinformatics

- Common bioinformatics applications:
  - Storing sequence data as numeric arrays
  - Representing position weight matrices
  - Managing alignment scores
  - Handling gene expression matrices

## 1D Array Operations

### 👀 Demo

#### 1D Array Indexing

```
# Example: String sequence converted to numerical representation
# A=0, C=1, G=2, T=3
dna_seq = np.array([0, 1, 2, 3, 0, 0, 1, 2]) # "ACGTAACG"

# Single element access through indexing
print("Original array", dna_seq)
print("First element (0th index)", dna_seq[0])    # First nucleotide (0 = A)
print("Fourth element", dna_seq[3])    # Fourth nucleotide (3 = T)
print("Last element", dna_seq[-1])   # Last nucleotide (2 = G) using negative
indexing
```

### ✓ Output

```
Original array [0 1 2 3 0 0 1 2]
First element (0th index) 0
Fourth element 3
Last element 2
```

## 1D Array Slicing

```

print("Original array", dna_seq)

# Slicing * extracting subsequences
print("From second to fourth", dna_seq[1:4]) # From second to fourth nucleotide:
array([1, 2, 3]) = "CGT"
print("First three nucleotides", dna_seq[:3]) # First three nucleotides: array([0, 1,
2]) = "ACG"
print("From sixth nucleotide to the end", dna_seq[5:]) # From sixth nucleotide to the
end: array([0, 1, 2]) = "ACG"

# Slicing with negative indices
print("Last three nucleotides", dna_seq[-3:]) # Last three nucleotides: array([0, 1,
2]) = "ACG"

# Slicing with step
print("Every second nucleotide", dna_seq[::-2]) # Every second nucleotide: array([0, 2,
0, 1]) = "AGAC"

# Reverse array
print("Every second nucleotide", dna_seq[::-1])

```

## ✓ Solution

```

Original array [0 1 2 3 0 0 1 2]
From second to fourth [1 2 3]
First three nucleotides [0 1 2]
From sixth nucleotide to the end [0 1 2]
Last three nucleotides [0 1 2]
Every second nucleotide [0 2 0 1]
Every second nucleotide [2 1 0 0 3 2 1 0]

```

## Real-world significance in bioinformatics:

- Indexing:
  - Accessing specific nucleotide positions of interest
  - Retrieving expression values for particular genes
  - Referencing elements in position-specific scoring matrices
- Slicing:
  - Extracting specific regions like promoters, exons, or binding sites
  - Identifying sequence motifs (e.g., restriction sites, protein domains)
  - Analyzing k-mers (subsequences of length k)
  - Creating sliding windows along DNA/protein sequences

## More info

- ▶ Additional notes: 2D Array Operations

## Real-world significance in bioinformatics

- Indexing:

- Retrieving expression value for a specific gene in a specific condition
- Accessing specific positions in sequence alignments
- Finding interaction pairs in protein-protein interaction matrices
- Slicing:
  - Comparing gene expression profiles across different tissues or time points
  - Analyzing subsets of genes after clustering
  - Extracting data for specific experiments or replicates
  - Processing sections of alignment score matrices
  - Analyzing specific regions in protein contact maps
  - Extracting protein domains from structure coordinate arrays

## Additional exercises

- ▶ Additional notes: Exercises

## Key Takeaways

### ! Keypoints

- Efficient indexing and slicing are crucial for bioinformatics workflows
- Key takeaways:
  - Indexing for accessing individual elements
  - Slicing for extracting regions of interest
  - Leverage both for efficient data manipulation in matrices (gene × condition, position × sequence, etc.)
  - Combine with boolean operations for filtering
  - Remember zero-based indexing
- Common pitfalls:
  - Off-by-one errors (especially when converting between biology's 1-based and programming's 0-based systems)
  - Overlooking the exclusive upper bound in slicing (end index is not included)
  - Forgetting that modifying slices can modify the original array (use `.copy()` when needed)
  - Confusing row-major vs. column-major operations

## NumPy Boolean Masking and Filtering

### ! Objectives

1. Create boolean masks for array filtering using comparison operators
2. Apply boolean masks to select specific elements from arrays
3. Combine multiple conditions using logical operators (`&`, `|`, `~`)
4. Use `np.where()` to find indices where conditions are met
5. Apply `np.where()` for conditional value assignment
6. Implement `np.isin()` to check array membership

### Instructor note

- Teaching : 10 min
- Demo: 5 min

## Introduction to Advanced Indexing

When working with data, we often need to focus on specific elements that meet certain criteria. NumPy provides elegant and efficient ways to accomplish this through:

1. Boolean masking
2. The `np.where()` function
3. The `np.isin()` function

Let's explore each technique in detail.

### Boolean Masking: The Concept

Boolean masking is a fundamental technique in NumPy that allows us to filter arrays based on conditions. The process happens in two steps:

#### Step 1: Create a Boolean Mask:

- We apply a condition to an array
- This produces a new array of the same shape filled with `True` and `False` values
- Elements that satisfy our condition are marked as `True`
- Elements that don't satisfy our condition are marked as `False`

#### Step 2: Apply the Mask:

- We use this boolean array to index into our original array
- Only elements corresponding to `True` values are selected

Let's see this in action:

### Demo

```
import numpy as np

# Create a sample array
data = np.array([1, 4, 2, 5, 3])
print("Original array:", data)

# Create a boolean mask for elements greater than 3
mask = data > 3
print("Boolean mask (data > 3):", mask)
# This produces: [False, True, False, True, False]

# Apply the mask to select elements
selected_data = data[mask]
print("Selected elements:", selected_data)
# This produces: [4, 5]

## Elegant approach - mask array has the exact same shape as data array
## Each position containing information about whether that element meets our
criteria
```

## ✓ Output

```
Original array: [1 4 2 5 3]
Boolean mask (data > 3): [False  True False  True False]
Selected elements: [4 5]
```

## Combining Multiple Conditions

We can combine multiple conditions using logical operators:

- `&` for logical AND
- `|` for logical OR
- `~` for logical NOT

### Additional info

- ▶ Additional notes: Combining Multiple Conditions

**Important:** When combining conditions, always use parentheses around each individual condition to ensure proper precedence.

## Using `np.where()`: Finding Positions

The `np.where()` function gives us even more capabilities. In its simplest form, it returns the indices where a condition is True:

### 👀 Demo

```

# Create an array with a sequence
data = np.arange(0, 20, 3) # [0, 3, 6, 9, 12, 15, 18]
print("Original array:", data)

# Find indices where elements are even
indices = np.where(data % 2 == 0)
print("Indices of even elements:", indices[0])
# This produces: [0, 2, 4, 6]

# Use these indices to get the actual values
even_elements = data[indices]
print("Even elements:", even_elements)
# This produces: [ 0,  6, 12, 18]

```

## ✓ Output

```

Original array: [ 0  3  6  9 12 15 18]
Indices of even elements: [0 2 4 6]
Even elements: [ 0  6 12 18]

```

- The result of `np.where()` is a tuple of arrays, one for each dimension of the input array. Since we're working with a 1D array here, we access the first (and only) element of this tuple with `indices[0]`.

## Using `np.where()`: Conditional Assignment

The real power of `np.where()` comes from its three-argument form:

```
np.where(condition, x, y)
```

This works like a vectorized if-else statement:

- Where the condition is `True`, take values from `x`
- Where the condition is `False`, take values from `y`

### Additional info

- Additional notes: `np.where(cond, x, y)`

This is much more concise and efficient than using loops or other conditional constructs.

### `np.isin()` Function

- `np.isin()` useful when we have a specific set of values we're interested in.

## Additional info

- ▶ Additional notes: The `np.isin()` Function
- ▶ Additional notes: Practical Applications
- ▶ Additional notes: Exercise 2 & 3

## Key Takeaways

### ! Keypoints

- Boolean masking and `np.where()` operations are highly optimized in NumPy. They:
  - Avoid explicit loops in Python
  - Execute at C-speed under the hood
  - Allow vectorized operations on large datasets
- For large datasets, these techniques are drastically faster than traditional iteration.
- Boolean masking provides an intuitive way to filter arrays based on conditions
- `np.where()` in its single-argument form finds indices where conditions are true
- `np.where(condition, x, y)` acts as a vectorized if-else statement
- `np.isin()` lets us filter based on membership in a set of values

## Essential Array Operations with NumPy

### ! Objectives

1. Reshape arrays to transform data structures while preserving values
2. Combine arrays using concatenation operations along different axes
3. Generate descriptive statistics from arrays using NumPy's built-in functions
4. Apply the axis parameter correctly to perform row-wise and column-wise operations
5. Integrate reshaping, concatenation, and statistical functions to solve practical data problems

## Instructor note

- Teaching : 20 min
- Demo: 15 min

## Introduction

NumPy is the foundation of Python's data science ecosystem. At its core is the powerful ndarray object - an efficient, versatile container for large datasets. We'll explore three essential capabilities:

- Reshaping arrays to organize data differently

- Combining arrays using concatenation
- Generating summary statistics to understand our data

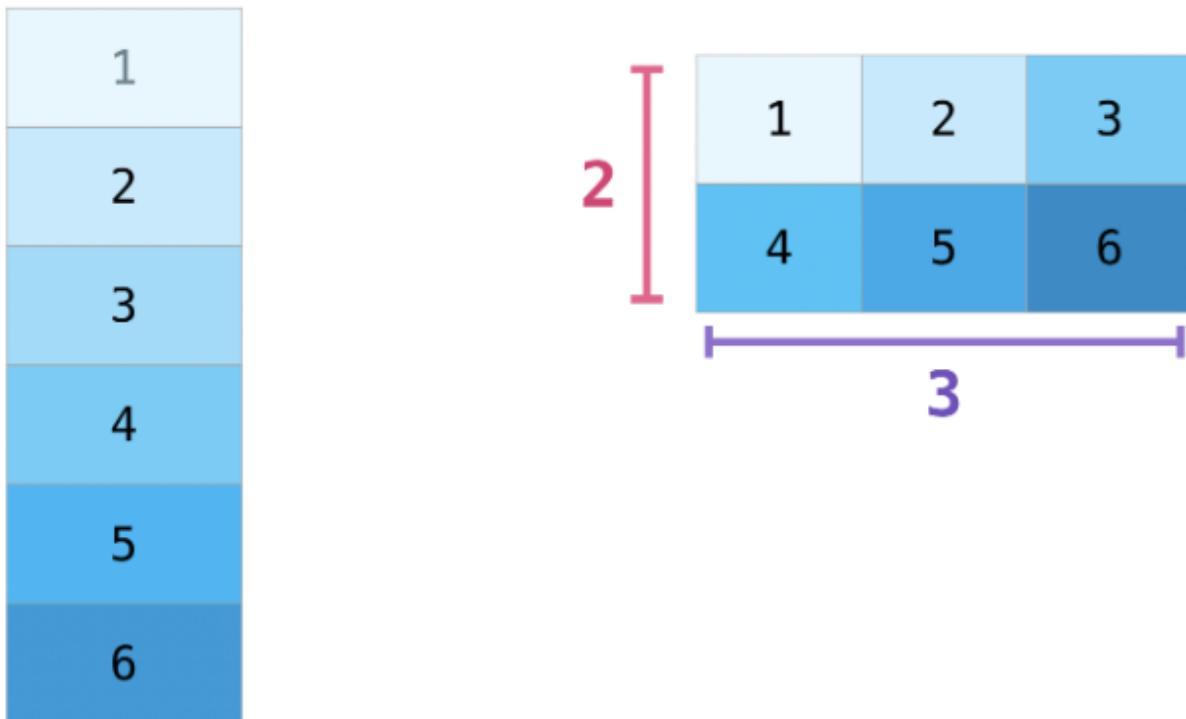
Let's dive into how these operations can transform the way we work with numerical data.

## Reshaping Arrays

### Understanding Array Dimensions

Arrays can have different dimensions:

- 1D arrays (vectors): Simple sequences of values
- 2D arrays (matrices): Tables with rows and columns
- 3D arrays and beyond: Multi-dimensional structures



The shape and dimension of an array tell us how data is organized:

#### 👀 Demo

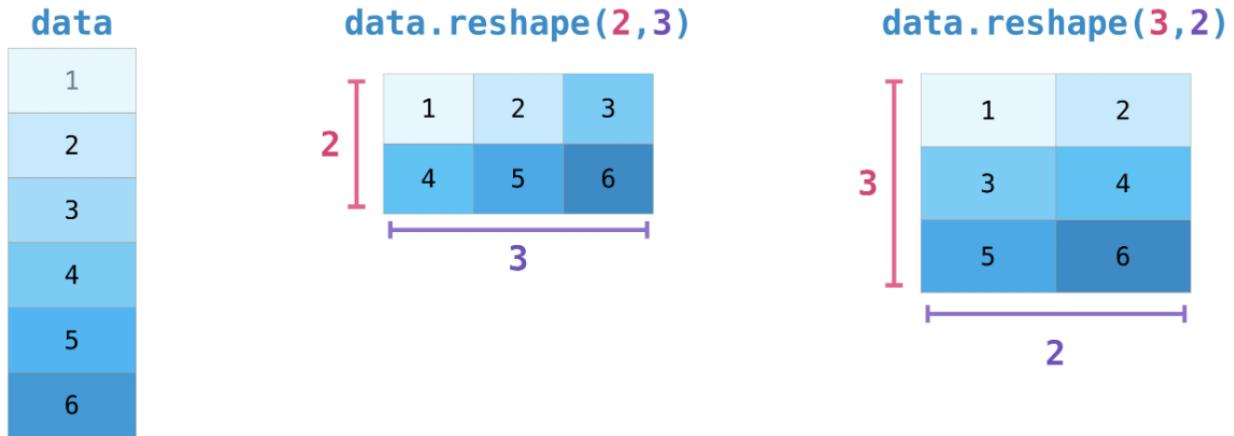
```
import numpy as np

# Create a simple 1D array
a = np.ones(6)
print("Original array:")
print(a)
print(f"Dimensions: {a.ndim}") # Number of dimensions
print(f"Shape: {a.shape}")      # Tuple showing size in each dimension
```

✓ Output:

```
Original array:  
[1. 1. 1. 1. 1. 1.]  
Dimensions: 1  
Shape: (6, )
```

## Reshaping Arrays using `reshape`



- Reshaping allows us to reorganize the same data into different dimensions
- The key rule: the total number of elements must remain the same

## 👀 Demo

```
a = np.array(range(1,7))  
# Reshape our 1D array with 6 elements into a 2D array (2 rows, 3 columns)  
b = a.reshape(2, 3)  
print("\nReshaped to 2x3 array:")  
print(b)  
print(f"Dimensions: {b.ndim}")  
print(f"Shape: {b.shape}")
```

## ✓ Output

```
Reshaped to 2x3 array:  
[[1 2 3]  
 [4 5 6]]  
Dimensions: 2  
Shape: (2, 3)
```

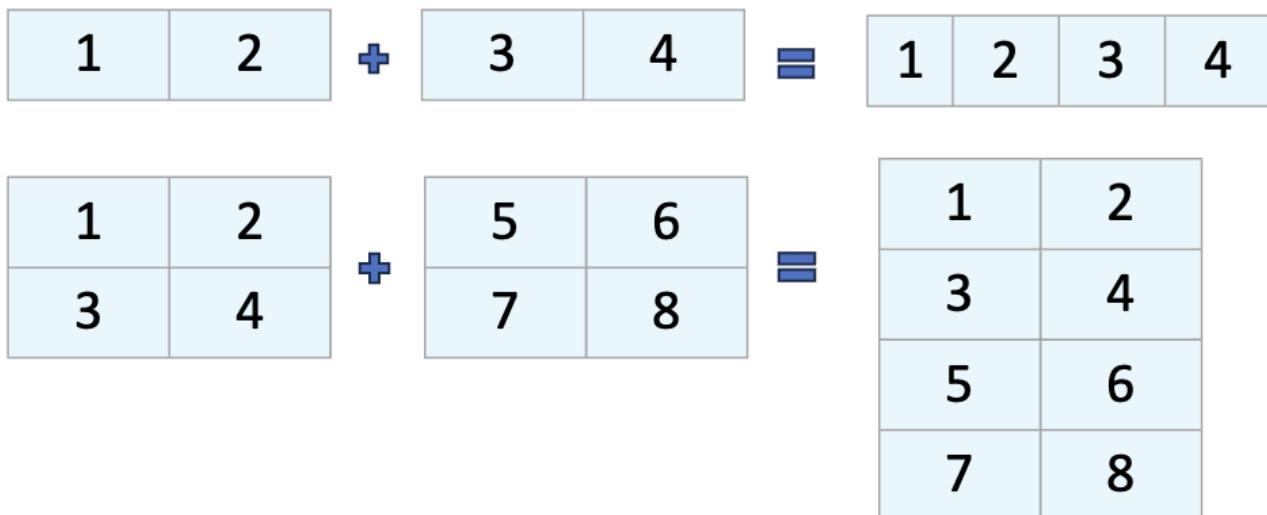
## More info

- ▶ Additional notes: example

## Array Concatenation

Concatenation lets us combine multiple arrays into a single larger array. This is essential when:

- Merging datasets
- Building up arrays piece by piece
- Combining results from different operations



### More info

- ▶ Additional notes: array concatenation

## Summary Statistics

NumPy provides efficient functions to calculate statistical measures across arrays. These are essential for:

- Data exploration and understanding
- Identifying patterns and outliers
- Summarizing large datasets

Function	Description
<code>np.sum()</code>	Sum of array elements
<code>np.min()</code>	Minimum value
<code>np.max()</code>	Maximum value
<code>np.mean()</code>	Arithmetic mean (average)
<code>np.median()</code>	Median value
<code>np.std()</code>	Standard deviation

Function	Description
np.var()	Variance

- axis=None (default): Operate on all elements (flattened array)
- axis=0: Collapse rows and operate along columns (down)
- axis=1: Collapse columns and operate along rows (across)

## 👀 Demo

```
# Create a 2D array
data = np.array([[1, 2, 3],
                [4, 5, 6]])

print("Our data:")
print(data)

# Sum of all elements
total = np.sum(data)
print(f"\nTotal sum: {total}") # 21

# Column sums (axis=0)
col_sums = np.sum(data, axis=0)
print(f"Column sums: {col_sums}") # [5 7 9]
## Collapse values in rows along the the column 0 and aggregate: [1, 4] = 5
## Collapse values in rows along the the column 1 and aggregate: [2, 5] = 7
## Collapse values in rows along the the column 2 and aggregate: [3, 6] = 9

# Row sums (axis=1)
row_sums = np.sum(data, axis=1)
print(f"Row sums: {row_sums}") # [6 15]
## Collapse values in columns along the the row 0 and aggregate: [1, 2, 3] = 6
## Collapse values in columns along the the row 1 and aggregate: [4, 5, 6] = 15
```

## ✓ Output

```
Our data:
[[1 2 3]
 [4 5 6]]

Total sum: 21
Column sums: [5 7 9]
Row sums: [ 6 15]
```

## ❗ Keypoints

- **Reshaping Arrays:** Maintain the total number of elements when reshaping; use -1 for automatic dimension calculation.

- **Concatenation of Arrays:** Combine arrays while matching dimensions, except along the concatenation axis.
- **Statistical Functions:** Utilize NumPy's statistical functions for data analysis, operating across different axes.
- **Error Handling:** Be aware of shape requirements for concatenation to avoid errors.

## Vectorized Operations in NumPy: Beyond Python Loops

### ! Objectives

By the end of this lecture, you will be able to:

- Understand and implement vectorized operations to replace traditional Python loops
- Apply broadcasting to perform operations between arrays of different shapes
- Optimize calculations for working with large biological datasets

### Instructor note

- Teaching : 15 min
- Demo: 20 min

## Introduction to Vectorized Operations

### What are Vectorized Operations?

Vectorized operations allow us to perform mathematical operations on entire arrays at once, rather than iterating through each element individually. This approach offers several key advantages:

- Performance and Efficiency:
  - Vectorized operations are significantly faster than Python loops, especially for large datasets
  - NumPy uses optimized C code under the hood, making calculations much more efficient
- Readability:
  - The code becomes more concise and often easier to understand

### The Speed Advantage: Loops vs. Vectorization

Let's see a simple example comparing a traditional Python loop with NumPy's vectorized approach:

### 👀 Demo

```

import numpy as np
import time

# Create a large array for testing
size = 100000000
data = np.random.random(size)

# Method 1: Traditional Python loop
start_time = time.time()
result_loop = []
for value in data:
    result_loop.append(value * 2 + 5)
loop_time = time.time() - start_time
print(f"Python loop time: {loop_time:.4f} seconds")

# Method 2: NumPy vectorized operation
start_time = time.time()
result_vectorized = data * 2 + 5
vector_time = time.time() - start_time
print(f"NumPy vectorized time: {vector_time:.4f} seconds")

# Calculate the speedup
speedup = loop_time / vector_time
print(f"Vectorized operations are {speedup:.1f}x faster!")

```

## ✓ Output

```

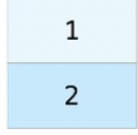
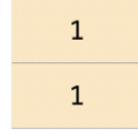
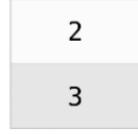
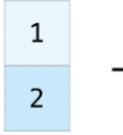
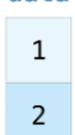
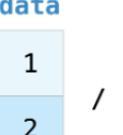
Python loop time: 1.0195 seconds
NumPy vectorized time: 0.0613 seconds
Vectorized operations are 16.6x faster!

```

## Basic Vectorized Operations in NumPy

### Arithmetic Operations

NumPy enables element-wise arithmetic operations on arrays:

<b>data</b> 	<b>ones</b> 	$=$ 	<b>data</b> 	<b>ones</b> 	$=$ 
$\begin{matrix} \mathbf{data} & \mathbf{ones} \\ \begin{pmatrix} 1 \\ 2 \end{pmatrix} & \begin{pmatrix} 1 \\ 1 \end{pmatrix} \end{pmatrix} = \begin{pmatrix} 2 \\ 3 \end{pmatrix}$			$\begin{matrix} \mathbf{data} & \mathbf{ones} \\ \begin{pmatrix} 1 \\ 2 \end{pmatrix} & \begin{pmatrix} 1 \\ 1 \end{pmatrix} \end{pmatrix} = \begin{pmatrix} 0 \\ 1 \end{pmatrix}$		
<b>data</b> 	<b>data</b> 	$=$ 	<b>data</b> 	<b>data</b> 	$=$ 
$\begin{matrix} \mathbf{data} & \mathbf{data} \\ \begin{pmatrix} 1 \\ 2 \end{pmatrix} & \begin{pmatrix} 1 \\ 2 \end{pmatrix} \end{pmatrix} = \begin{pmatrix} 1 \\ 4 \end{pmatrix}$			$\begin{matrix} \mathbf{data} & \mathbf{data} \\ \begin{pmatrix} 1 \\ 2 \end{pmatrix} & \begin{pmatrix} 1 \\ 2 \end{pmatrix} \end{pmatrix} = \begin{pmatrix} 1 \\ 1 \end{pmatrix}$		

## 👀 Demo

```
import numpy as np

# Create two arrays
a = np.array([1, 2, 3, 4, 5])
b = np.array([10, 20, 30, 40, 50])

# Element-wise operations
addition = a + b
subtraction = b - a
multiplication = a * b
division = b / a

print(f"Addition: {addition}")
print(f"Subtraction: {subtraction}")
print(f"Multiplication: {multiplication}")
print(f"Division: {division}")
```

## ✓ Output

```
Addition: [11 22 33 44 55]
Subtraction: [ 9 18 27 36 45]
Multiplication: [ 10  40  90 160 250]
Division: [10. 10. 10. 10. 10.]
```

## Scalar Operations

You can perform operations between arrays and scalars (single values):

$$\begin{array}{c|c} 1 \\ \hline 2 \end{array} \quad * \quad \begin{matrix} \textcolor{blue}{1.6} \end{matrix} \quad = \quad \begin{array}{c|c} 1 \\ \hline 2 \end{array} \quad * \quad \begin{array}{c|c} \textcolor{blue}{1.6} \\ \hline 1.6 \end{array} \quad = \quad \begin{array}{c|c} 1.6 \\ \hline 3.2 \end{array}$$

## 👀 Demo

```
# Scalar operations
a = np.array([1, 2, 3, 4, 5])

plus_10 = a + 10
times_2 = a * 2
square = a ** 2
reciprocal = 1 / a

print(f"Plus 10: {plus_10}")
print(f"Times 2: {times_2}")
print(f"Squared: {square}")
print(f"Reciprocal: {reciprocal}")
```

## ✓ Output

```
Plus 10: [11 12 13 14 15]
Times 2: [ 2  4  6  8 10]
Squared: [ 1  4  9 16 25]
Reciprocal: [1.          0.5          0.33333333 0.25          0.2          ]
```

## Comparison Operations

Comparison operations create boolean masks that can be useful for filtering data:

### 👀 Demo

```
# Comparison operations
a = np.array([1, 2, 3, 4, 5])

greater_than_3 = a > 3
less_equal_to_2 = a <= 2
equal_to_3 = a == 3

print(f"a > 3: {greater_than_3}")
print(f"a <= 2: {less_equal_to_2}")
print(f"a == 3: {equal_to_3}")

# Using boolean masks for filtering
filtered_data = a[greater_than_3] # [4, 5]
print(f"Values greater than 3: {filtered_data}")
```

## ✓ Output

```
a > 3: [False False False True True]
a <= 2: [ True  True False False False]
a == 3: [False False  True False False]
Values greater than 3: [4 5]
```

## Aggregation Functions and Universal Functions

NumPy also provides functions to calculate aggregate statistics across arrays:

data  
1  
2 .max() = 3  
3

data  
1  
2 .min() = 1  
3

data  
1  
2 .sum() = 6  
3

## 👀 Demo

```
# Aggregation functions
a = np.array([1, 2, 3, 4, 5])

sum_a = np.sum(a)                      # Sum of all elements (15)
mean_a = np.mean(a)                    # Mean of all elements (3.0)
min_a = np.min(a)                     # Minimum value (1)
max_a = np.max(a)                     # Maximum value (5)
std_a = np.std(a)                      # Standard deviation (~1.41)

print(f"Sum: {sum_a}")
print(f"Mean: {mean_a}")
print(f"Min: {min_a}")
print(f"Max: {max_a}")
print(f"Standard deviation: {std_a}")
```

## ✓ Output

```
Sum: 15
Mean: 3.0
Min: 1
Max: 5
Standard deviation: 1.4142
```

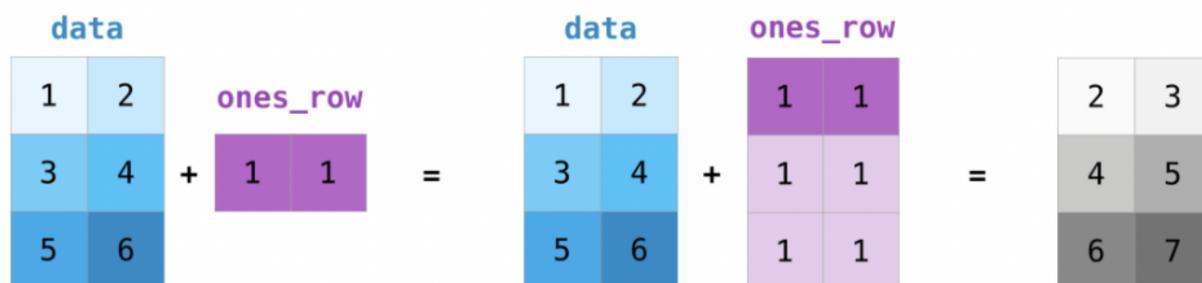
## More info

- ▶ Additional notes: Universal Functions
- ▶ Additional notes: Exercise

## 3. Broadcasting in NumPy

### What is Broadcasting?

Broadcasting is a powerful mechanism that allows NumPy to perform operations on arrays of different shapes. It automatically “broadcasts” the smaller array across the larger array so that they have compatible shapes.



### Broadcasting Rules

1. If the arrays don't have the same number of dimensions, the shape of the smaller array is padded with ones on the left
2. If the shape of the arrays doesn't match in any dimension, the array with shape equal to 1 in that dimension is stretched to match the other shape
3. If in any dimension the sizes disagree and neither is equal to 1, an error is raised

## Broadcasting Examples

### Example 1: Adding a scalar to an array

The simplest form of broadcasting:

#### Demo

```
# Adding a scalar to an array
a = np.array([1, 2, 3, 4, 5])
result = a + 10 # Scalar 10 is broadcast to array [10, 10, 10, 10, 10]
print(result) # [11, 12, 13, 14, 15]
```

#### Note

If the sizes along a dimension differ, the array with size 1 in that dimension is stretched to match the other size

#### More info

- ▶ Additional notes: Broadcasting with n-D arrays
- ▶ Additional notes: Array Splitting

## Best Practices

1. **Avoid Python Loops** when working with numerical data; use vectorized operations instead
2. **Use Broadcasting** wisely to make your code concise and efficient
3. **Pre-allocate Arrays** when you know their size in advance
4. **Leverage NumPy's Built-in Functions** for optimal performance
5. **Be Mindful of Memory Usage** when working with large biological datasets

Vectorized operations in NumPy are a powerful tool for data analysis in computational biology. By replacing traditional loops with vectorized operations, you can significantly improve the performance and readability of your code, making it easier to work with large biological datasets.

## Key Takeaways

## ! Keypoints

1. **Vectorized Operations** are much faster than Python loops for numerical computations
2. **Broadcasting** allows operations between arrays of different shapes
3. **NumPy's Universal Functions** provide efficient implementations of common mathematical operations
4. **Array Splitting** is useful for dividing data for analysis and machine learning

## Hands-on: RNA Expression Analysis - alternative method

### Objective

- Examine differential expression of immune-related genes between patient groups previously classified as immunologically strong ('`istrong`') and immunologically weak ('`iweak`')
- Apply an alternative analytical approach using Z-ratio methodology to complement standard differential expression tools like DESeq
- Ranks immune-related genes based on their relative expression differences between the patient groups

### Dataset description

- `test_data/Sample_group_info.csv`
  - Patients were divided into `istrong` (immunity-strong) and `iweak` (immunity-weak) groups based on their Immunity score
  - The Immunity score was calculated by averaging the gene expression values of the 17 identified immune-genes
- `test_data/count_matrix.csv`: Gene expression raw counts

### Steps

1. Data Loading and visualization
  1. Load sample group information (`iweak` vs `istrong`)
  2. Load gene expression count matrix
  3. Examine array information
2. Sample Identification
  1. Filter samples by group (`iweak` / `istrong`)
  2. Match count matrix columns with sample IDs
3. Data Preprocessing
  1. Convert count matrix to numeric values
  2. Apply log2 transformation:  $\log_2(\text{counts} + 1)$
4. Statistical Analysis
  1. Calculate mean and std for each gene within each group

2. Compute Z-scores within each sample group
3. Calculate Z-score differences between groups
4. Compute standard deviation of all differences
5. Ranking Genes
  1. Calculate Z-ratio: difference / std\_difference
  2. Rank genes by Z-ratio (highest to lowest)

**Workflow:**

```

    flowchart TD
    A[Load Sample Group Info] --> B{Filter by Group}
    B -->|iweak| C[Identify iweak samples]
    B -->|istrong| D[Identify istrong samples]

    E[Load Count Matrix] --> F[Match columns with samples]

    F --> G[Convert to numeric]
    G --> H[Log2 transformation]

    C --> F
    D --> F

    H --> I1[Calculate iweak mean & std]
    H --> I2[Calculate istrong mean & std]

    I1 --> J1[Compute Z-scores for iweak]
    I2 --> J2[Compute Z-scores for istrong]

    J1 --> K[Calculate Z-score difference]
    J2 --> K

    K --> L[Calculate standard deviation]

    L --> M[Compute Z-ratio]

    M --> N[Rank genes by Z-ratio]

    classDef dataNode fill:#f9f9f9,stroke:#aaa,stroke-width:2px;
    classDef processNode fill:#e1f5fe,stroke:#01579b,stroke-width:2px;
    classDef resultNode fill:#e8f5e9,stroke:#2e7d32,stroke-width:2px;

    class A,E dataNode;
    class B,C,D,F,G,H,I1,I2,J1,J2,K,L,M processNode;
    class N resultNode;
  
```

**Step 1: Loading and inspecting data**

```
import numpy as np
from urllib.request import urlopen

# Read the CSV file into a numpy array
## CSV file contains sample group information
sample_group_info_url = "https://coderefinery.github.io/intermediate-python-
ml/_downloads/b458a48eed87eb03931a8ce6efcdd351/Sample_group_info.csv"

data = np.genfromtxt(urlopen(sample_group_info_url), delimiter=',', dtype='str')
```

```
# Print the numpy array information

def print_array_info(array):
    # Get the shape of the array
    shape = array.shape

    # Get the number of dimensions of the array
    ndim = array.ndim

    # Get the data type of the array
    dtype = array.dtype

    # Get the number of elements in the array
    size = array.size

    print(f"Shape: {shape} \nNumber of dimensions: {ndim} \nData type: {dtype} \nSize:
{size}")
```

```
print_array_info(data)
```

```
Shape: (303, 2)
Number of dimensions: 2
Data type: <U12
Size: 606
```

```
# Read the CSV file into a numpy array with string dtype
## CSV file contains RNA count matrix

count_matrix_url = "https://coderefinery.github.io/intermediate-python-
ml/_downloads/ab7de98031b77441be14a9d7ba21466c/count_matrix.csv"

count_matrix = np.genfromtxt(urlopen(count_matrix_url), delimiter=',',
                           dtype='str')
print_array_info(count_matrix)
```

```
Shape: (81, 483)
Number of dimensions: 2
Data type: <U18
Size: 39123
```

```
# Remove sample names from the count matrix (cm) - Delete the first row
## Convert the cm to a float32 array
print(count_matrix[0:5, 0:5])
print("___")
cm = np.delete(count_matrix, 0, axis=0).astype("float32")
print(cm[0:5, 0:5])
```

```
[['SH_TS_BC_C1' 'SH_TS_BC_C11' 'SH_TS_BC_C15' 'SH_TS_BC_C3' 'SH_TS_BC01']
 ['25' '559' '231' '44' '23']
 ['173' '2475' '886' '320' '6']
 ['114' '8806' '2781' '537' '47']
 ['626' '7492' '2829' '564' '14']]
```

---

```
[[2.500e+01 5.590e+02 2.310e+02 4.400e+01 2.300e+01]
 [1.730e+02 2.475e+03 8.860e+02 3.200e+02 6.000e+00]
 [1.140e+02 8.806e+03 2.781e+03 5.370e+02 4.700e+01]
 [6.260e+02 7.492e+03 2.829e+03 5.640e+02 1.400e+01]
 [3.170e+02 5.949e+03 2.357e+03 2.750e+02 2.600e+01]]
```

## Step 2: Sample Identification

1. Filter samples by group (iweak/istrong)
2. Match count matrix columns with sample IDs

index	Sample	Group
0	SH_TS_BC111	iweak
1	SH_TS_BC112	iweak
2	SH_TS_BC113	iweak
3	SH_TS_BC119	istrong
4	SH_TS_BC133	iweak
5	SH_TS_BC134	iweak
6	SH_TS_BC139	iweak
7	SH_TS_BC141	iweak
8	SH_TS_BC146	iweak
9	SH_TS_BC147	iweak
10	SH_TS_BC150	istrong
11	SH_TS_BC151	istrong
12	SH_TS_BC152	iweak
13	SH_TS_BC153	istrong
14	SH_TS_BC154	iweak
15	SH_TS_BC155	iweak
16	SH_TS_BC160	iweak
17	SH_TS_BC161	iweak
18	SH_TS_BC163	iweak

```
# Print the first 5 rows and columns of the data
print(data[:5, :5])
```

```
[['SH_TS_BC111' 'iweak'],
 ['SH_TS_BC112' 'iweak'],
 ['SH_TS_BC113' 'iweak'],
 ['SH_TS_BC119' 'istrong'],
 ['SH_TS_BC133' 'iweak']]
```

```
# Access indices of the array where the second column is 'iweak'
iweak_index = np.where(data[:, 1] == 'iweak')
print(iweak_index)
print_array_info(iweak_index[0])
```

```
(array([  0,   1,   2,   4,   5,   6,   7,   8,   9,  12,  14,  15,  16,
       17,  18,  21,  24,  25,  27,  31,  33,  34,  35,  38,  39,  41,
       43,  45,  47,  49,  50,  51,  53,  54,  55,  56,  59,  60,  61,
       63,  64,  65,  67,  69,  71,  72,  73,  74,  75,  78,  80,  81,
       84,  86,  92,  93,  94,  97, 102, 106, 108, 111, 112, 114, 122,
      123, 126, 131, 132, 133, 139, 142, 145, 146, 148, 149, 150, 151,
      160, 161, 163, 164, 166, 168, 170, 171, 173, 176, 177, 180, 186,
      188, 192, 195, 196, 197, 200, 203, 206, 207, 212, 214, 215, 216,
      217, 219, 223, 225, 226, 227, 228, 230, 235, 244, 248, 249, 252,
      256, 258, 260, 262, 263, 265, 266, 269, 270, 271, 275, 276, 278,
      279, 280, 282, 283, 285, 286, 287, 288, 289, 291, 292, 293, 294,
      295, 296, 298, 299, 300, 302]),)
Shape: (149,)
Number of dimensions: 1
Data type: int64
Size: 149
```

```
# Access indices of the array where the second column is 'iweak'
iweak_index = np.where(data[:, 1] == 'iweak')[0]
print("Index\n", iweak_index[:5], "\nData\n", data[iweak_index][:5,:])
print_array_info(iweak_index)
```

```
Index
[0 1 2 4 5]
Data
[['SH_TS_BC111' 'iweak']
 ['SH_TS_BC112' 'iweak']
 ['SH_TS_BC113' 'iweak']
 ['SH_TS_BC133' 'iweak']
 ['SH_TS_BC134' 'iweak']]
Shape: (149,)
Number of dimensions: 1
Data type: int64
Size: 149
```

```
# View the first column of the count matrix where the sample group is 'iweak'
print(count_matrix[0:5, 0:5])
```

```
[['SH_TS_BC_C1' 'SH_TS_BC_C11' 'SH_TS_BC_C15' 'SH_TS_BC_C3' 'SH_TS_BC01']
 ['25' '559' '231' '44' '23']
 ['173' '2475' '886' '320' '6']
 ['114' '8806' '2781' '537' '47']
 ['626' '7492' '2829' '564' '14']]
```

```
# Create a boolean mask to find if the columns in the count matrix where the sample
group is 'iweak'
cm_iweak_mask = np.isin(count_matrix[0, :], data[iweak_index, 0])
print(cm_iweak_mask[:30])
```

```
[False False  
False False False False False False False False False False False  
False True True True False False]
```

```
# Find the indices of the columns in the count matrix where the sample group is 'iweak'  
cm_weak_cols = np.where(cm_iweak_mask)[0]  
print(cm_weak_cols)  
print_array_info(cm_weak_cols)
```

```
[ 25  26  27  36  37  38  40  41  42  46  48  49  51  52  53  56  64  65  
 67  71  73  74  75  79  80  83  85  88  91  93  94  95  97  98  99 100  
103 104 105 108 109 110 112 114 116 117 118 119 120 124 126 128 131 133]  
Shape: (54,)  
Number of dimensions: 1  
Data type: int64  
Size: 54
```

```
# Access indices of the array where the second column is 'istrong'  
## Assign the indices to a istrong_index (not the tuple returned by np.where)  
istrong_index = np.where(data[:, 1] == 'istrong')[0]  
print(istrong_index)  
print_array_info(istrong_index)
```

```
[ 3  10  11  13  19  20  22  23  26  28  29  30  32  36  37  40  42  44  
 46  48  52  57  58  62  66  68  70  76  77  79  82  83  85  87  88  89  
 90  91  95  96  98  99 100 101 103 104 105 107 109 110 113 115 116 117  
118 119 120 121 124 125 127 128 129 130 134 135 136 137 138 140 141 143  
144 147 152 153 154 155 156 157 158 159 162 165 167 169 172 174 175 178  
179 181 182 183 184 185 187 189 190 191 193 194 198 199 201 202 204 205  
208 209 210 211 213 218 220 221 222 224 229 231 232 233 234 236 237 238  
239 240 241 242 243 245 246 247 250 251 253 254 255 257 259 261 264 267  
268 272 273 274 277 281 284 290 297 301]  
Shape: (154,)  
Number of dimensions: 1  
Data type: int64  
Size: 154
```

```
# Find the indices of the columns in the count matrix where the sample group is 'istrong'  
cm_strong_cols = np.where(np.isin(count_matrix[0, :], data[istrong_index, 0]))[0]  
print(cm_strong_cols)  
print_array_info(cm_strong_cols)
```

```
[ 33  44  45  47  54  55  58  63  66  68  69  70  72  76  78  81  84  86
 89  92  96 101 102 107 111 113 115 121 122 125 129 130 132 134 136 137
138]
Shape: (37,)
Number of dimensions: 1
Data type: int64
Size: 37
```

```
count_matrix.shape
```

## Step 3: Data Preprocessing

- Convert count matrix to numeric values
- Apply log2 transformation:  $\log_2(\text{counts} + 1)$

```
# Remove sample names from the count matrix (cm) - Delete the first row
print(count_matrix[0:5, 0:5])
print("___")
## Convert the cm to a float32 array

cm = np.delete(count_matrix, 0, axis=0).astype("float32")
print(cm[0:5, 0:5])
```

```
[[ 'SH_TS_BC_C1' 'SH_TS_BC_C11' 'SH_TS_BC_C15' 'SH_TS_BC_C3' 'SH_TS_BC01']
 ['25' '559' '231' '44' '23']
 ['173' '2475' '886' '320' '6']
 ['114' '8806' '2781' '537' '47']
 ['626' '7492' '2829' '564' '14']]

[[2.500e+01 5.590e+02 2.310e+02 4.400e+01 2.300e+01]
 [1.730e+02 2.475e+03 8.860e+02 3.200e+02 6.000e+00]
 [1.140e+02 8.806e+03 2.781e+03 5.370e+02 4.700e+01]
 [6.260e+02 7.492e+03 2.829e+03 5.640e+02 1.400e+01]
 [3.170e+02 5.949e+03 2.357e+03 2.750e+02 2.600e+01]]
```

```
# Convert cm to log scale
cm = np.log2(cm + 1)
print(cm)
print_array_info(cm)
```

```
[[ 4.70044  9.129283  7.857981 ... 0.       6.5999126 7.936638 ]
 [ 7.4429436 11.273795  9.79279  ... 6.794416  9.865733 11.2842455]
 [ 6.84549  13.104435  11.441907 ... 9.187352  10.403012 11.279611 ]
 ...
 [10.675957 13.7911625 12.428099 ... 10.456354 11.276706 12.22581 ]
 [ 4.857981  8.169925  7.491853 ... 8.948367  4.5849624 8.204571 ]
 [ 9.432542  12.378024 10.899357 ... 10.82893  13.397273 14.26415 ]]
```

Shape: (80, 483)

Number of dimensions: 2

Data type: float32

Size: 38640

```
# Calculate mean and STD of each gene in iweak samples
iweak_mean = cm[:, cm_weak_cols].mean(1)      ## Mean of iweak samples
iweak_std = cm[:, cm_weak_cols].std(1)         ## STD of iweak samples
print("iweak_mean", iweak_mean[:5], iweak_mean.shape)
print("iweak_std", iweak_std[:5], iweak_std.shape)
```

```
iweak_mean [7.8603177 8.870119 8.839295 9.873015 8.818066] (80,)
iweak_std [1.9773906 1.5399547 2.0553062 1.1807643 2.1794095] (80,)
```

```
# Calculate mean and STD of each gene in istrong samples
istrong_mean = cm[:,cm_strong_cols].mean(1) ## Mean of istrong disease samples
istrong_std = cm[:,cm_strong_cols].std(1)    ## STD of istrong samples

print("istrong_mean", istrong_mean[:5], istrong_mean.shape)
print("istrong_std", istrong_std[:5], istrong_std.shape)
```

```
istrong_mean [ 6.9949713 6.953521 10.527761 9.192108 9.029262 ] (80,)
istrong_std [2.2878554 2.8049028 1.3030388 2.2123892 1.9921837] (80,)
```

## Step 4: Statistical Analysis

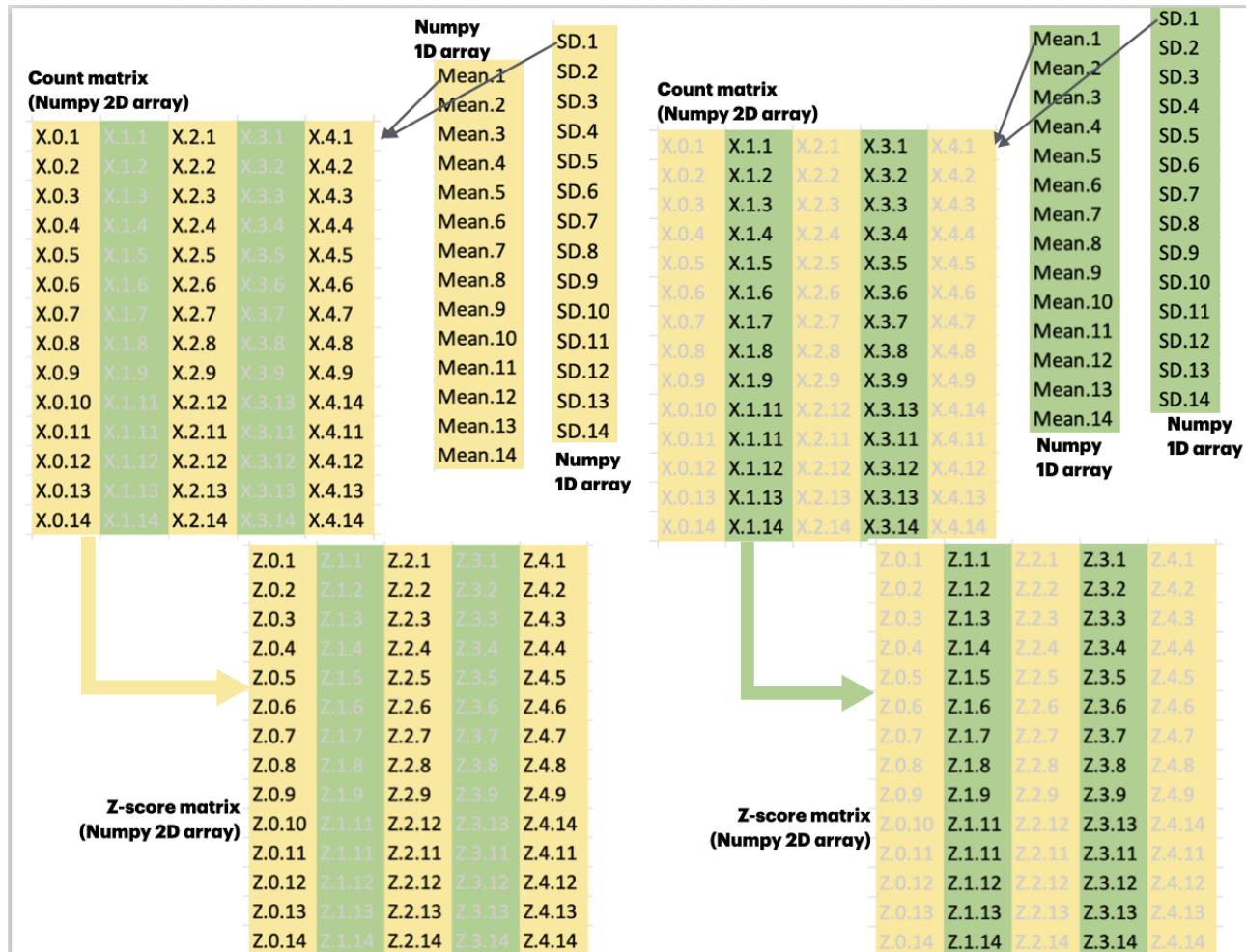
1. Calculate mean and std for each gene within each group
2. Compute Z-scores within each sample group
3. Calculate Z-score differences between groups
4. Compute standard deviation of all differences

### Z-scores:

- Gene expression measurements (counts) can have vastly different scales across different samples due to technical variations
- The Z-score transformation standardizes these measurements

$$\$ \$ Z_{\{G\}} = \frac{\text{Count}_G - \mu_{\{\text{Count}_{\{\text{group}\}}\}}}{\sigma_{\{\text{Count}_{\{\text{group}\}}\}}} \$ \$$$

##  $Z_{\{G\}}$  : Z-score\ for\ a\ gene\ G## ## Count\_G: Log10\ count\ of\ gene\ G\ in\ a\ given\ sample## ##  $\mu_{\{\text{Count}_{\{\text{group}\}}\}}$ : The\ overall\ average\ across\ all\ samples\ in\ the\ given\ group\ for\ each\ gene## ##  $\sigma_{\{\text{Count}_{\{\text{group}\}}\}}$ : Standard\ deviation\ all\ samples\ in\ the\ given\ group\ for\ each\ gene##



```
# Calculate Z-scores of each gene in iweak samples (vectorized)
print(cm.shape, iweak_mean.shape, iweak_std.shape)

## use .reshape(-1, 1) to convert the mean and std to column vectors
## This is necessary for vectorized operations to work correctly
cm_iweak_z = (cm[:, cm_weak_cols] - iweak_mean.reshape(-1, 1)) / iweak_std.reshape(-1, 1)
## The reshape is necessary because you want to subtract/divide row-wise, but NumPy's
## default broadcasting for 1D arrays applies column-wise.
print("cm_iweak_z", cm_iweak_z[:5, :5])
print_array_info(cm_iweak_z)
```

```
(80, 483) (80,) (80,)
cm_iweak_z [[-0.8058757 -0.7423927 -0.9294824  0.4624626 -0.95228404]
 [-1.1998737 -2.0764856  0.16326085  0.22980079 -5.1106176 ]
 [-4.3007193  0.31064132 -0.57465094  0.26697835 -1.5138254 ]
 [-1.1198412 -1.3803278  0.17033552  1.1318417 -2.3681269 ]
 [-4.04608 -0.28826228 -0.18751603  0.5879035 -1.0315684 ]]
Shape: (80, 54)
Number of dimensions: 2
Data type: float32
Size: 4320
```

```
# Calculate Z-scores of each gene in istrong samples (vectorized)
cm_istrong_z = (cm[:, cm_strong_cols] - istrong_mean.reshape(-1, 1)) /
istrong_std.reshape(-1, 1)
print("cm_istrong_z", cm_istrong_z[:5, :5])
print_array_info(cm_istrong_z)
```

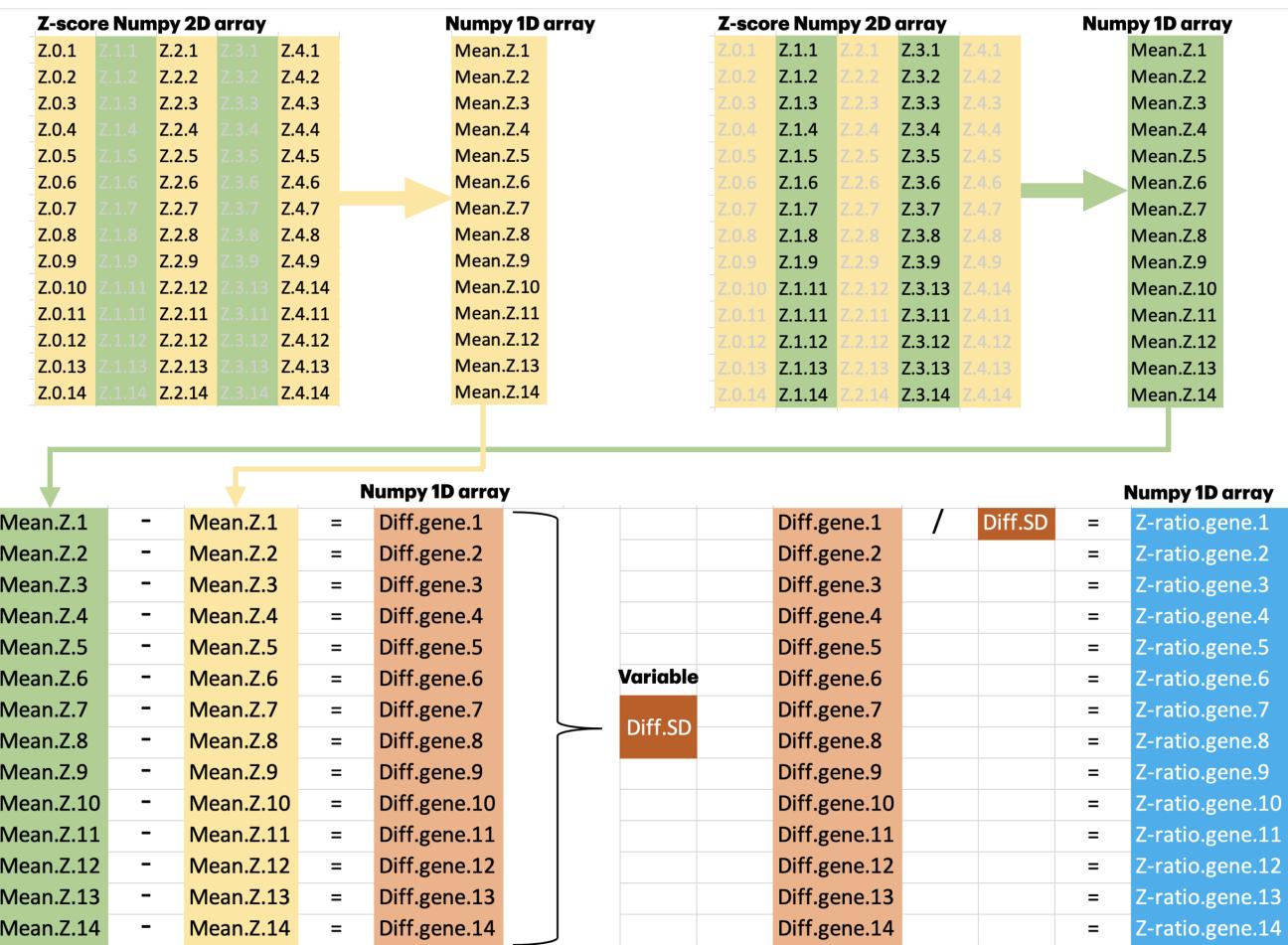
```
cm_istrong_z [[ 0.2545867   0.7559668   0.47983187  1.1538492   0.3143879 ]
 [ 0.97684896 -0.04753883  0.8586477   1.0635368   0.32466918]
 [ 0.13716765  0.28922623  1.1129626   1.229808    0.77283007]
 [ 0.4442336   0.6031446   0.74163324  0.75332576  0.71388024]
 [ 0.29755822  1.1648388   1.0060126   0.3692481   -0.07359705]]
Shape: (80, 37)
Number of dimensions: 2
Data type: float32
Size: 2960
```

### Z-ratio = Z-score difference (per gene):

- The Z-ratio provides a standardized measure of the difference between conditions for each gene
- This accounts for the overall variability in the experiment
- A gene showing a difference of, say, 0.5 in average Z-score
  - might be highly significant if most genes show very little difference (small Z-score difference - SD),
  - but not significant if many genes show large differences (large Z-score difference - SD)
- It puts the individual gene's change in the context of the overall experimental variation

$\text{Z.score}_{\{\text{Diff}_{\{\text{gene}\}}\}} = \bar{Z}_{\{\text{Gene}, \text{istrong}\}} - \bar{Z}_{\{\text{Gene}, \text{iweak}\}}$

$\text{Z}_{\{\text{Ratio}, \text{Gene}\}} = \frac{\text{Z.score}_{\{\text{Diff}_{\{\text{gene}\}}\}}}{\text{SD}_{\{\text{Z.score}_{\{\text{Diff}_{\{\text{gene}\}}\}}\}}} \quad \text{Z-score}$



```

diff_z_scores = cm_istrong_z.mean(1) - cm_iweak_z.mean(1)
std_diff = diff_z_scores.std()

### z-score ratio for each gene
## Divide Z-Ratio differences by the Z-Ratio differences SD
z_score_ratios = diff_z_scores / std_diff
print_array_info(z_score_ratios)
print(z_score_ratios[:10])

```

```

Shape: (80,)
Number of dimensions: 1
Data type: float32
Size: 80
[-0.43179178 -1.5044755   1.247218    0.22787355  0.64381164  0.83408666
 0.96931595  2.2225075   2.1141531   0.49432233]

```

## Step5: Rank genes according to the Z score ratio:

- Sort z\_score\_ratio in descending order and access indices
- Rank genes using indices

```
gene_list = ["ACTR3B", "ANLN", "APOBEC3G", "AURKA", "BAG1", "BCL2", "BIRC5", "BLVRA",
"CCL5", "CCNB1", "CCNE1", "CCR2", "CD2", "CD27", "CD3D", "CD52", "CD68", "CDC20",
"CDC6", "CDH3", "CENPF", "CEP55", "COR01A", "CTSL2", "CXCL9", "CXXC5", "EGFR", "ERBB2",
"ESR1", "EX01", "FGFR4", "FOXA1", "FOXC1", "GAPDH", "GPR160", "GRB7", "GSTM1", "GUSB",
"GZMA", "GZMK", "HLA-DMA", "IL2RG", "KIF2C", "KRT14", "KRT17", "KRT5", "LCK", "MAPT",
"MDM2", "MELK", "MIA", "MKI67", "MLPH", "MMP11", "MRPL19", "MYBL2", "MYC", "NAT1",
"NDC80", "NUF2", "ORC6", "PGR", "PHGDH", "PRKCB", "PSMC4", "PTPRC", "PTTG1", "RRM2",
"SCUBE2", "SF3A1", "SFRP1", "SH2D1A", "SLC39A6", "TFRC", "TMEM45B", "TP53", "TYMS",
"UBE2C", "UBE2T", "VEGFA"]
```

```
### `np.argsort()` returns indices of the array that would sort in ascending order
### slicing syntax [start:stop:step] with step -1 returns a reversed array

gene_ranks = np.argsort(z_score_ratios)[::-1]
print("Genes ranked according to Z-score ratio:")
print(np.array(gene_list)[gene_ranks])
```

```
Genes ranked according to Z-score ratio:
['PSMC4' 'FOXC1' 'TP53' 'BLVRA' 'CCL5' 'CD68' 'PTPRC' 'GRB7' 'APOBEC3G'
'MRPL19' 'CENPF' 'BIRC5' 'UBE2C' 'PHGDH' 'ERBB2' 'TFRC' 'BCL2' 'GUSB'
'MDM2' 'KRT5' 'BAG1' 'FOXA1' 'CCNB1' 'KRT17' 'CEP55' 'KRT14' 'NDC80'
'AURKA' 'CXCL9' 'TMEM45B' 'SLC39A6' 'GZMK' 'PTTG1' 'GPR160' 'IL2RG'
'GZMA' 'MYC' 'EX01' 'MKI67' 'TYMS' 'PGR' 'SH2D1A' 'CD27' 'PRKCB' 'CCR2'
'NUF2' 'RRM2' 'MIA' 'MELK' 'ESR1' 'SF3A1' 'UBE2T' 'EGFR' 'CCNE1' 'MAPT'
'KIF2C' 'MMP11' 'HLA-DMA' 'NAT1' 'CTSL2' 'MLPH' 'CXXC5' 'CD2' 'ACTR3B'
'COR01A' 'SFRP1' 'FGFR4' 'CD3D' 'ORC6' 'LCK' 'CD52' 'CDH3' 'GSTM1'
'VEGFA' 'SCUBE2' 'CDC6' 'ANLN' 'MYBL2' 'CDC20' 'GAPDH']
```

## Lesson plan

### ! Objectives

- 1. Understand the Basics:** Familiarize participants with the fundamentals of the Pandas library and its relationship with NumPy.
- 2. Data Handling:** Equip participants with the skills to import and export various data formats using Pandas, facilitating easy data manipulation and analysis.
- 3. Data Manipulation Skills:** Provide practical techniques for data manipulation, including selection, addition, removal, and handling of missing values within DataFrames.
- 4. Indexing Proficiency:** Enable participants to effectively index and select data from DataFrames using various methods, enhancing their data exploration capabilities.
- 5. Data Analysis Techniques:** Introduce advanced data transformation, grouping, and aggregation techniques, enabling participants to perform in-depth data analysis and summarization.

## Specific Objectives

- Introduction to Pandas
  - Explain the relationship between Pandas and NumPy, highlighting when to use each library effectively.
  - Define and differentiate between Series and DataFrame data structures in Pandas.
  - Demonstrate the creation of Pandas objects from NumPy arrays, solidifying foundational knowledge.
- Data Import and Export
  - Illustrate how to read data from various formats, including CSV, Excel, and JSON, into Pandas.
  - Show how to export DataFrames to different formats, ensuring participants can save their analyses.
  - Utilize data inspection methods (head, info, describe) to gain an understanding of data structure and content.
- DataFrame Manipulation & Sorting
  - Demonstrate effective techniques for selecting specific rows and from DataFrames.
  - Equip participants with skills to add and remove columns within a DataFrame.
  - Implement sorting methods by values, by index, and perform multiple column sorting with custom orders.
- Indexing, Selection & Slicing
  - Differentiate between label-based and position-based indexing and apply each method appropriately.
  - Use Boolean indexing to filter data based on specific conditions, connecting concepts from NumPy.
  - Apply .loc, .iloc, and .at selection methods to extract desired data, and employ multi-level slicing techniques.
- Handling Missing Data
  - Identify missing values in DataFrames using isna() and notna() methods.
  - Strategize the filling of missing values with fillna() and interpolation methods tailored to scenario needs.
  - Demonstrate how to drop missing data with dropna() and discuss various strategies for handling missing data.
- Merging DataFrames
  - Illustrate how to concatenate DataFrames using pd.concat() and understand its applications.
  - Explain database-style joins with the merge() function and illustrate the different join types (inner, outer, left, \* right).
  - Address challenges faced with duplicate columns and indexes during merging operations.
- Summary Statistics & Aggregations
  - Calculate basic statistics (mean, median, min, max) to summarize and analyze data.
  - Develop custom aggregation functions for specific needs in data analysis.
  - Apply GroupBy operations effectively, utilizing the Split-Apply-Combine pattern to derive insights from grouped data.
- Advanced Data Transformation
  - Utilize apply() and map() functions for advanced data transformation on DataFrames.

- Perform string and datetime operations effectively using Pandas functionality.
- Construct pivot tables and crosstabs to summarize data visually and contextually.
- Practical Exercises and Q&A
  - Execute practical exercises using real-world datasets to reinforce concepts learned during the workshop.
  - Connect concepts from both NumPy and Pandas to solidify understanding through application.
  - Engage in a Q&A session to clarify doubts, deepen understanding, and discuss challenges faced during practical sessions

## Introduction to Pandas

### ! Objectives

- Explain the relationship between Pandas and NumPy, highlighting when to use each library effectively.
- Define and differentiate between Series and DataFrame data structures in Pandas.
- Demonstrate the creation of Pandas objects from NumPy arrays, solidifying foundational knowledge.

### Instructor note

- Teaching : 10 min
- Demo: 10 min

## What is Pandas?

- A powerful Python library for data manipulation and analysis
- Built on top of NumPy (which you're already familiar with)
- Essential tool in data science, machine learning, and analytics
- Name comes from “panel data” - economic term for multidimensional data

### ! Note

- “Pandas is to data analysis what NumPy is to numerical computing.”
- “If you’ve ever used Excel or SQL, Pandas will feel somewhat familiar.”
- “Today we’ll see how the NumPy skills you’ve learned provide the foundation for Pandas.”

## Pandas vs NumPy Relationship

### Key Differences:

NumPy	Pandas
Homogeneous arrays	Heterogeneous data

NumPy	Pandas
Numerical focus	Tabular data focus
Unlabeled axes	Labeled axes
Fast mathematical operations	Data manipulation operations
Memory efficient	Feature rich

## 👀 Demo

```

import numpy as np
import pandas as pd

# Try to put mixed types in NumPy - notice what happens
mixed_numpy = np.array([1, 'string', 3.14])
print(f"Mixed NumPy array: {mixed_numpy}")
print(f"Mixed array dtype: {mixed_numpy.dtype}") # Converts to common type

# Pandas Series - can handle mixed types
pandas_series = pd.Series([1, 'string', 3.14])
print("\nPandas Series with mixed types:")
print(pandas_series)

```

## ✓ Output

```

NumPy array: [1 2 3 4 5]
NumPy data type: int64
Mixed NumPy array: ['1' 'string' '3.14']
Mixed array dtype: <U32 # Unicode string with a maximum length of 32 characters

Pandas Series with mixed types:
0      1
1    string
2      3.14
dtype: object

```

## 👀 Demo

```

print([type(i) for i in mixed_numpy])
print([type(i) for i in pandas_series])

```

## ✓ Output

```
[<class 'numpy.str_>, <class 'numpy.str_>, <class 'numpy.str_>]
# NumPy converts everything to strings when faced with mixed types

[<class 'int'>, <class 'str'>, <class 'float'>]
# Pandas preserves the original types using an 'object' dtype
```

## DataFrame Data Structures

- Pandas introduces two new data structures
  - Series: A labeled one-dimensional array
  - DataFrames: Labeled Tables for Powerful Data Analysis

## Pandas Series

- 1D labeled array capable of holding any data type
- Like a cross between a list and a dictionary
- Has an Index (labels) and values (data)
- Built on NumPy, so supports vectorized operations

### 👀 Demo

```
# Creating a Series
s = pd.Series([10, 20, 30, 40], index=['a', 'b', 'c', 'd'])
print("Pandas Series with custom index:")
print(s)
print(f"The index: {s.index}")
print(f"The values: {s.values}") # Notice this returns a NumPy array

# Dictionary-like access
print(f"\nValue at index 'b': {s['b']}")
print(f"Values at indices 'a' and 'c': {s[['a', 'c']]}")

# NumPy-like operations
print(f"\nAdding 5 to all values: \n{s + 5}")
print(f"Values greater than 25: \n{s > 25}")
```

### ✓ Output

```
Pandas Series with custom index:  
a    10  
b    20  
c    30  
d    40  
dtype: int64  
The index: Index(['a', 'b', 'c', 'd'], dtype='object')  
The values: [10 20 30 40]  
  
Value at index 'b': 20  
Values at indices 'a' and 'c': a    10  
c    30  
dtype: int64  
  
Adding 5 to all values:  
a    15  
b    25  
c    35  
d    45  
dtype: int64  
Values greater than 25:  
a    False  
b    False  
c    True  
d    True  
dtype: bool
```

## More info

- ▶ Additional notes: Why uses labels?

## The Pandas DataFrame

- 2D labeled data structure with columns of potentially different types
- Think: spreadsheet or SQL table
- Collection of Series objects that share the same index
- Primary data structure you'll use in data analysis

## 👀 Demo

```

# Creating a DataFrame
data = {
    'Name': ['Alice', 'Bob', 'Charlie'],
    'Age': [25, 30, 35],
    'City': ['New York', 'Boston', 'Chicago']
}
df = pd.DataFrame(data)
print("Pandas DataFrame:")
print(df)

# DataFrame info
print(f"\nDataFrame shape: {df.shape}")
print(f"DataFrame columns: {df.columns}")
print(f"DataFrame index: {df.index}")

# Accessing a column (returns a Series)
print("\nAccessing the Age column:")
print(df['Age'])
print(f"Type of column: {type(df['Age'])}")

```

## ✓ Output

```

Pandas DataFrame:
   Name  Age      City
0   Alice  25  New York
1     Bob  30    Boston
2  Charlie  35   Chicago

DataFrame shape: (3, 3)
DataFrame columns: Index(['Name', 'Age', 'City'], dtype='object')
DataFrame index: RangeIndex(start=0, stop=3, step=1)

Accessing the Age column:
0    25
1    30
2    35
Name: Age, dtype: int64
Type of column: <class 'pandas.core.series.Series'>

```

## More info

- ▶ Additional notes: Pandas data structures

## Creating Pandas Objects from NumPy Arrays

- Pandas objects can be created directly from NumPy arrays
- Indexes can be automatically generated or custom-defined
- The underlying NumPy array is still accessible
- Pandas adds powerful indexing and data manipulation features

## Numpy array to Pandas series

## ❖ Demo

```
# NumPy array to Pandas Series
numpy_data = np.array([100, 200, 300, 400])
s1 = pd.Series(numpy_data)
print("Series with default index:")
print(s1)

s2 = pd.Series(numpy_data, index=['w', 'x', 'y', 'z'])
print("\nSeries with custom index:")
print(s2)
```

## ✓ Output

```
Series with default index:
```

```
0    100
1    200
2    300
3    400
dtype: int64
```

```
Series with custom index:
```

```
w    100
x    200
y    300
z    400
dtype: int64
```

```
print("Original Pandas Series (s2):")
print(s2)
print("\nIndex of the Pandas Series (s2.index):")
print(s2.index)

# Convert the Pandas Series to a NumPy array
numpy_array_from_s2 = s2.to_numpy()

print("\nNumPy Array created from s2 (s2.to_numpy()):")
print(numpy_array_from_s2)

# There's no explicit index in the NumPy array, it's implicitly 0, 1, 2, ...
# You can demonstrate accessing elements using numerical indices in the NumPy
array
print("\nAccessing elements in the NumPy array (numerical indexing):")
print(f"numpy_array_from_s2[0]: {numpy_array_from_s2[0]}")
print(f"numpy_array_from_s2[2]: {numpy_array_from_s2[2]}")
```

## ✓ Output

```
Original Pandas Series (s2):  
w    100  
x    200  
y    300  
z    400  
dtype: int64  
  
Index of the Pandas Series (s2.index):  
Index(['w', 'x', 'y', 'z'], dtype='object')  
  
NumPy Array created from s2 (s2.to_numpy()):  
[100 200 300 400]  
  
Accessing elements in the NumPy array (numerical indexing):  
numpy_array_from_s2[0]: 100  
numpy_array_from_s2[2]: 300
```

## More info

- ▶ Additional notes: Pandas dataframe from Numpy 2D array
- ▶ Additional notes: Other ways to create Pandas DataFrames

## More info

- ▶ Additional notes: Exercises

## Key Takeaways

### ! Keypoints

1. **Building on NumPy:** Pandas uses NumPy under the hood, adding labels and mixed-type support
2. **Series:** 1D labeled array similar to a dictionary + array hybrid
3. **DataFrame:** 2D labeled structure, like a collection of Series sharing an index
4. **Labels Matter:** Named axes make your data self-documenting and easier to work with
5. **Data Types:** Pandas handles mixed types better than NumPy, crucial for real-world data

## Data Import and Export in Pandas

### ! Objectives

- Illustrate how to read data from various formats, including CSV, Excel, and JSON, into Pandas.
- Show how to export DataFrames to different formats, ensuring participants can save their analyses.

- Utilize data inspection methods (head, info, describe) to gain an understanding of data structure and content.

### Instructor note

- Teaching : 10 min
- Demo: 20 min

## Introduction to Data Import and Export

- Real-world data analysis starts with getting data into Pandas
- Pandas supports many file formats natively
- The process: Import → Inspect → Manipulate → Export

## Reading Data from Various Formats

### Reading Data - Main Methods

Function	Purpose	Common Parameters
<code>pd.read_csv()</code>	Read CSV files	<code>filepath_or_buffer</code> , <code>sep</code> , <code>header</code> , <code>index_col</code>
<code>pd.read_excel()</code>	Read Excel files	<code>io</code> , <code>sheet_name</code> , <code>header</code> , <code>index_col</code>
<code>pd.read_json()</code>	Read JSON files	<code>path_or_buf</code> , <code>orient</code> , <code>typ</code>
<code>pd.read_sql()</code>	Read SQL query/table	<code>sql</code> , <code>con</code> , <code>index_col</code>
<code>pd.read_html()</code>	Read HTML tables	<code>io</code> , <code>match</code> , <code>flavor</code>

## Reading CSV Data

### 👀 Demo

```

import pandas as pd
from urllib.request import urlopen

# Basic CSV reading

sample_data_csv_url = "https://coderefinery.github.io/NumPy-and-Pandas-
fundamentals-for-handling-biological-
datasets/_downloads/4c11eeffe234e7bc729008f767fe631a/sample_data.csv"

df_csv = pd.read_csv(urlopen(sample_data_csv_url))
# df_csv = pd.read_csv('test_data/sample_data.csv')

print("Basic CSV import:")
print(df_csv.head()) # Show first 3 rows

# Customizing CSV import
df_csv_custom = pd.read_csv(urlopen(sample_data_csv_url),
                            sep=',',           # Delimiter (comma is default)
                            header=0,          # Row to use as column names (0 is
default)
                            index_col='ID',    # Column to set as index
                            usecols=['ID', 'Name', 'Value'], # Only import specific
columns
                            nrows=5)           # Only read first 5 rows
print("\nCustomized CSV import:")
print(df_csv_custom)

```

## ✓ Output

Basic CSV import:

	ID	Name	Age	City	Value	Category	Date
0	1	Person_1	22	Chicago	34.61	B	2023-01-01
1	2	Person_2	52	Phoenix	47.46	A	2023-01-02
2	3	Person_3	38	Phoenix	48.85	D	2023-01-03
3	4	Person_4	27	Houston	75.10	A	2023-01-04
4	5	Person_5	34	Houston	47.88	B	2023-01-05

Customized CSV import:

ID	Name	Value
1	Person_1	34.61
2	Person_2	47.46
3	Person_3	48.85
4	Person_4	75.10
5	Person_5	47.88

## Reading Excel Data

### 👀 Demo

```

# Basic Excel reading

import requests
from io import BytesIO

## Read XLSX file directly from a URL
# sample_data_xls_url = "https://coderefinery.github.io/NumPy-and-Pandas-fundamentals-for-handling-biological-datasets/_downloads/04c10398f323fcf8ff5ec474e4b22205/sample_data.xlsx"

# response = requests.get(sample_data_xls_url)
# df_excel = pd.read_excel(BytesIO(response.content))

df_excel = pd.read_excel('test_data/sample_data.xlsx')
print("Basic Excel import:")
print(df_excel.head())

# Reading specific sheet
df_excel_sheet2 = pd.read_excel('test_data/sample_data.xlsx',
                                sheet_name='Sheet 1 - sample_data',
                                skiprows=1)      # Skip first row
print("\nReading specific Excel sheet:")
print(df_excel_sheet2.head())

# List all sheets in workbook
xl = pd.ExcelFile('test_data/sample_data.xlsx')
print(f"\nAll sheets in workbook: {xl.sheet_names}")

```

## ✓ Output

```

Basic Excel import:
sample_data Unnamed: 1 Unnamed: 2 Unnamed: 3 Unnamed: 4 Unnamed: 5 Unnamed: 6
0          ID     Name    Age      City   Value Category     Date
1          1 Person_1    22 Chicago  34.61      B 2023-01-01
2          2 Person_2    52 Phoenix  47.46      A 2023-01-02
3          3 Person_3    38 Phoenix  48.85      D 2023-01-03
4          4 Person_4    27 Houston  75.10      A 2023-01-04

Reading specific Excel sheet:
      ID     Name  Age      City  Value Category     Date
0    1 Person_1  22 Chicago  34.61      B 2023-01-01
1    2 Person_2  52 Phoenix  47.46      A 2023-01-02
2    3 Person_3  38 Phoenix  48.85      D 2023-01-03
3    4 Person_4  27 Houston  75.10      A 2023-01-04
4    5 Person_5  34 Houston  47.88      B 2023-01-05

All sheets in workbook: ['Sheet 1 - sample_data']

```

## More info

- Additional notes: Reading JSON Data

## ! Note

- Notice that all these different file formats are loaded into the same DataFrame structure.
- Each import function has many parameters for fine-tuning the import process.
- The defaults work well in many cases, but customization gives you control over exactly what data gets loaded and how.
- For real-world data, you'll often need to use these parameters to handle messy or improperly formatted files.

## Writing Data to Files

### Writing Data - Main Methods

Function	Purpose	Common Parameters
<code>to_csv()</code>	Write to CSV	<code>path_or_buf</code> , <code>index</code> , <code>header</code> , <code>sep</code>
<code>to_excel()</code>	Write to Excel	<code>excel_writer</code> , <code>sheet_name</code> , <code>index</code> , <code>header</code>
<code>to_json()</code>	Write to JSON	<code>path_or_buf</code> , <code>orient</code> , <code>lines</code>
<code>to_sql()</code>	Write to SQL table	<code>name</code> , <code>con</code> , <code>if_exists</code> , <code>index</code>
<code>to_html()</code>	Write to HTML	<code>buf</code> , <code>columns</code> , <code>header</code> , <code>index</code>

### Writing to Different Formats

#### Demo

```
# Create a small DataFrame to export
data = {
    'Name': ['Alex', 'Beth', 'Charlie', 'Diana'],
    'Department': ['Sales', 'HR', 'Tech', 'Finance'],
    'Salary': [55000, 60000, 75000, 70000],
    'Hire_Date': ['2020-01-15', '2019-07-10', '2021-03-22', '2018-11-05']
}
df = pd.DataFrame(data)
print("DataFrame to export:")
print(df)

# Export to CSV
df.to_csv('employees.csv', index=False)
print("\nExported to CSV (employees.csv)")

# Export to Excel
df.to_excel('employees.xlsx', sheet_name='Employees', index=False)
print("Exported to Excel (employees.xlsx)")
```

#### More info

- Additional notes: Export to JSON

## Note

- Writing data is even simpler than reading it, since Pandas already knows the structure.
- Setting `index=False` is common when exporting, to avoid having an extra column.
- Different export formats are useful in different contexts:
  - CSV is universal but loses data types
  - Excel preserves formatting but requires Excel to open
  - JSON is great for metadata

## Data Inspection Methods

### Key Inspection Methods

Method	Purpose	What It Shows
<code>head()</code> / <code>tail()</code>	View first/last n rows	A preview of the data
<code>info()</code>	Summary of DataFrame	Data types, non-null counts, memory usage
<code>describe()</code>	Statistical summary	Count, mean, std, min, 25%, 50%, 75%, max
<code>dtypes</code>	Column data types	Data type of each column
<code>shape</code>	Dimensions	(rows, columns)
<code>columns</code>	Column names	Index of column names
<code>value_counts()</code>	Count unique values	Frequency of each unique value

## Demo

### Inspection Methods

```
# Let's inspect a more interesting dataset
import numpy as np

# Create a sample dataset with different data types
np.random.seed(42) # For reproducibility
data = {
    'Category': np.random.choice(['A', 'B', 'C', 'D'], size=1000),
    'Value': np.random.normal(100, 20, size=1000),
    'Count': np.random.randint(1, 100, size=1000),
    'Date': pd.date_range(start='2023-01-01', periods=1000),
    'Flag': np.random.choice([True, False], size=1000)
}
df = pd.DataFrame(data)

# Add some missing values
df.loc[10:20, 'Value'] = np.nan
df.loc[500:510, 'Category'] = None

# Now let's inspect
print("First 5 rows with head():")
print(df.head())

print("\nLast 3 rows with tail(3):")
print(df.tail(3))

print("\nDataFrame information with info():")
df.info()

print("\nStatistical summary with describe():")
print(df.describe())

print("\nInclude all columns in describe (even non-numeric):")
print(df.describe(include='all'))

print("\nData types of each column:")
print(df.dtypes)

print("\nShape (rows, columns):", df.shape)

print("\nValue counts for 'Category':")
print(df['Category'].value_counts())
```

## ✓ Output

First 5 rows with head():

	Category	Value	Count	Date	Flag
0	C	106.835120	72	2023-01-01	False
1	D	137.523417	49	2023-01-02	False
2	A	119.008477	79	2023-01-03	True
3	C	88.461927	17	2023-01-04	True
4	C	82.031707	60	2023-01-05	False

Last 3 rows with tail(3):

	Category	Value	Count	Date	Flag
997	D	87.885702	77	2025-09-24	True
998	D	114.841907	59	2025-09-25	False
999	C	105.985852	47	2025-09-26	False

DataFrame information with info():

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1000 entries, 0 to 999
Data columns (total 5 columns):
 #   Column      Non-Null Count  Dtype  
--- 
 0   Category    989 non-null    object  
 1   Value       989 non-null    float64 
 2   Count       1000 non-null    int64   
 3   Date        1000 non-null    datetime64[ns]
 4   Flag        1000 non-null    bool    
dtypes: bool(1), datetime64[ns](1), float64(1), int64(1), object(1)
memory usage: 32.4+ KB
```

Statistical summary with describe():

	Value	Count	Date
count	989.000000	1000.000000	1000
mean	100.858217	49.007000	2024-05-14 12:00:00
min	42.074892	1.000000	2023-01-01 00:00:00
25%	87.503628	24.000000	2023-09-07 18:00:00
50%	100.811834	48.000000	2024-05-14 12:00:00
75%	113.637830	73.000000	2025-01-19 06:00:00
max	161.577616	99.000000	2025-09-26 00:00:00
std	20.024572	28.269703	NaN

Include all columns in describe (even non-numeric):

	Category	Value	Count	Date	Flag
count	989	989.000000	1000.000000	1000	1000
unique	4	NaN	NaN	NaN	2
top	D	NaN	NaN	NaN	True
freq	277	NaN	NaN	NaN	512
mean	NaN	100.858217	49.007000	2024-05-14 12:00:00	NaN
min	NaN	42.074892	1.000000	2023-01-01 00:00:00	NaN
25%	NaN	87.503628	24.000000	2023-09-07 18:00:00	NaN
50%	NaN	100.811834	48.000000	2024-05-14 12:00:00	NaN
75%	NaN	113.637830	73.000000	2025-01-19 06:00:00	NaN
max	NaN	161.577616	99.000000	2025-09-26 00:00:00	NaN
std	NaN	20.024572	28.269703	NaN	NaN

Data types of each column:

```
Category          object
Value            float64
Count            int64
Date            datetime64[ns]
Flag             bool
dtype: object
```

Shape (rows, columns): (1000, 5)

Value counts for 'Category':

```
Category
D    277
A    254
C    229
B    229
Name: count, dtype: int64
```

## ! Note

- “These inspection methods are critical to understanding your data before analysis.”
- “Always start data exploration with these methods - they quickly reveal dataset characteristics and potential issues.”
- “`info()` shows missing values and data types - crucial for cleaning strategies.”
- “`describe()` gives statistical summaries - great for spotting outliers or distribution patterns.”
- “Real data is messy - these tools help you understand what needs to be cleaned.”

## More info

- ▶ Additional notes: Exercises

## Key Takeaways

### ! Keypoints

1. **Data Import Flexibility:** Pandas can read data from virtually any structured data format
2. **Customized Reading:** Parameters let you control exactly how data is imported
3. **Easy Export:** Writing data is straightforward with similar syntax across formats
4. **Always Inspect First:** `head()`, `info()`, and `describe()` should be your first steps with any new dataset
5. **Real-World Ready:** These tools prepare you for working with messy, real-world data

## DataFrame Manipulation & Sorting

### ! Objectives

- Demonstrate effective techniques for selecting specific rows and from DataFrames.
- Equip participants with skills to add and remove columns within a DataFrame.
- Implement sorting methods by values, by index, and perform multiple column sorting with custom orders.

## Instructor note

- Teaching : 15 min
- Demo: 25 min

## ⚠ Note

- Now that we can import data, we need to reshape and manipulate it for analysis
- In real-world data analysis, you'll spend about 80% of your time cleaning and manipulating data, and only 20% on actual analysis
- The skills we're covering in this session form the backbone of data wrangling in Python
- Think of these operations as transforming raw data into analysis-ready information

## Column and Row Selection

Different Ways to Select Data:

Selection Type	Purpose	Example Syntax
Single column	Get one variable	<code>df['column_name']</code> or <code>df.column_name</code>
Multiple columns	Get specific variables	<code>df[['col1', 'col2']]</code>
Row by index	Get specific observation	<code>df.loc['index_label']</code>
Row by position	Get nth observation	<code>df.iloc[n]</code>
Row and column	Get specific value(s)	<code>df.loc['index', 'column']</code>
Slicing	Get ranges of data	<code>df.loc['idx1':'idx2', 'col1':'col2']</code>

## Basic Selection

### 👀 Demo

```
import pandas as pd
import numpy as np

# Create a sample dataset
data = {
    'Name': ['Alice', 'Bob', 'Charlie', 'David', 'Eva'],
    'Age': [24, 30, 35, 42, 28],
    'City': ['New York', 'Boston', 'Chicago', 'Seattle', 'Miami'],
    'Salary': [65000, 72000, 85000, 92000, 70000],
    'Department': ['HR', 'Sales', 'Tech', 'Tech', 'Finance']
}
df = pd.DataFrame(data)
df.index = ['emp001', 'emp002', 'emp003', 'emp004', 'emp005'] # Custom index
print("Original DataFrame:")
print(df)
```

## More info

- Additional notes: Dataframe set\_index

## 👀 Demo

```
# Single column selection - two methods
print("\n1. Single column as Series:")
print(df['Age']) # Returns a Series

print("\n2. Alternative syntax for columns without spaces:")
print(df.Age) # Also returns a Series, but only works if column name has no spaces

# Multiple column selection
print("\n3. Selecting multiple columns:")
print(df[['Name', 'Salary']]) # Returns a DataFrame

# Row selection by index label using .loc
print("\n4. Selecting row by index label:")
print(df.loc['emp003']) # Returns a Series representing the row

# Row selection by position using .iloc
print("\n5. Selecting row by position (third row):")
print(df.iloc[2]) # Also returns a Series

# Selecting a subset of rows
print("\n6. Selecting multiple rows by position:")
print(df.iloc[1:4]) # Row indices 1, 2, and 3 (not including 4)

# Selecting specific cells
print("\n7. Selecting specific value (cell):")
print(df.loc['emp002', 'Salary']) # Returns the value (72000)

# Selecting a subset of rows and columns
print("\n8. Selecting subset of rows and columns:")
print(df.loc['emp001':'emp003', ['Name', 'Age', 'Salary']])
## df.iloc[0:3, [0,1,3]] == df.loc['emp001':'emp003', ['Name', 'Age', 'Salary']]
```

## ✓ Output

Original DataFrame:

	Name	Age	City	Salary	Department
emp001	Alice	24	New York	65000	HR
emp002	Bob	30	Boston	72000	Sales
emp003	Charlie	35	Chicago	85000	Tech
emp004	David	42	Seattle	92000	Tech
emp005	Eva	28	Miami	70000	Finance

1. Single column as Series:

```
emp001    24
emp002    30
emp003    35
emp004    42
emp005    28
Name: Age, dtype: int64
```

2. Alternative syntax for columns without spaces:

```
emp001    24
emp002    30
emp003    35
emp004    42
emp005    28
Name: Age, dtype: int64
```

3. Selecting multiple columns:

	Name	Salary
emp001	Alice	65000
emp002	Bob	72000
emp003	Charlie	85000
emp004	David	92000
emp005	Eva	70000

4. Selecting row by index label:

```
Name      Charlie
Age       35
City     Chicago
Salary    85000
Department Tech
Name: emp003, dtype: object
```

5. Selecting row by position (third row):

```
Name      Charlie
Age       35
City     Chicago
Salary    85000
Department Tech
Name: emp003, dtype: object
```

6. Selecting multiple rows by position:

	Name	Age	City	Salary	Department
emp002	Bob	30	Boston	72000	Sales
emp003	Charlie	35	Chicago	85000	Tech
emp004	David	42	Seattle	92000	Tech

7. Selecting specific value (cell):

```
72000
```

8. Selecting subset of rows and columns:

	Name	Age	Salary
emp001	Alice	24	65000
emp002	Bob	30	72000
emp003	Charlie	35	85000

## ⚠ Note

- Notice that selecting a single column returns a Series, while selecting multiple columns maintains the DataFrame structure
- The `.loc` accessor is used for label-based indexing, while `.iloc` is for position-based indexing

## Advanced Selection with Conditions

## 👀 Demo

```
# Boolean selection - rows where Age > 30
print("\n9. Boolean selection - employees over 30:")
print(df[df['Age'] > 30])

# Multiple conditions using & (and) and | (or)
print("\n10. Multiple conditions - Tech department with salary > 80000:")
print(df[(df['Department'] == 'Tech') & (df['Salary'] > 80000)])

# Using .query() method for cleaner syntax
## .query() method allows you to use and/or
## print("\n11. Using query method - same condition:")
## print(df.query("Department == 'Tech' and Salary > 80000"))

# Row selection with .isin()
print("\n12. Using .isin() - employees in HR or Finance:")
print(df[df['Department'].isin(['HR', 'Finance'])])
```

## ✓ Output

```
9. Boolean selection - employees over 30:
      Name  Age     City   Salary Department
emp003  Charlie  35  Chicago    85000      Tech
emp004    David  42  Seattle    92000      Tech

10. Multiple conditions - Tech department with salary > 80000:
      Name  Age     City   Salary Department
emp003  Charlie  35  Chicago    85000      Tech
emp004    David  42  Seattle    92000      Tech

11. Using query method - same condition:
      Name  Age     City   Salary Department
emp003  Charlie  35  Chicago    85000      Tech
emp004    David  42  Seattle    92000      Tech

12. Using .isin() - employees in HR or Finance:
      Name  Age     City   Salary Department
emp001   Alice  24  New York   65000        HR
emp005     Eva  28    Miami    70000    Finance
```

## ! Note

- Boolean selection is incredibly powerful - it lets you filter data based on specific conditions
- These selection methods can be combined in powerful ways to extract exactly the data you need

## More info

- ▶ Additional notes: Exercise

## Adding and Removing Columns/Rows

### Modifying DataFrame Structure:

Operation	Method	Example
Add column	Direct assignment	<code>df['new_col'] = values</code>
Add column	From existing columns	<code>df['new_col'] = df['col1'] + df['col2']</code>
Add column	Using apply/lambda	<code>df['new_col'] = df.apply(lambda x: func(x), axis=1)</code>
Remove column	Using drop	<code>df.drop('column', axis=1)</code>
Remove row	Using drop	<code>df.drop('index_label')</code>
Add row	Using loc	<code>df.loc['new_index'] = values</code>
Add row	Using append/concat	<code>pd.concat([df, new_row])</code>

## Adding and Removing Columns

- Adding new column with
  - a scalar value
  - a list of values
  - a calculated values in a pandas series
  - a column with conditional values
- Removing
  - a single column
  - multiple columns
  - columns in-place

## OO Demo

```

# Create a sample dataset
data = {
    'Name': ['Alice', 'Bob', 'Charlie', 'David', 'Eva'],
    'Age': [24, 30, 35, 42, 28],
    'City': ['New York', 'Boston', 'Chicago', 'Seattle', 'Miami'],
    'Salary': [65000, 72000, 85000, 92000, 70000],
    'Department': ['HR', 'Sales', 'Tech', 'Tech', 'Finance']
}
df = pd.DataFrame(data)
df.index = ['emp001', 'emp002', 'emp003', 'emp004', 'emp005'] # Custom index
print("Original DataFrame:")
print(df)

# 1. Adding a new column with scalar value
df['Active'] = True
print("\n1. Adding 'Active' column with same value for all rows:")
print(df)

# 2. Adding a column with a list of values
df['Performance'] = [4.5, 4.0, 3.8, 4.7, 4.2]
print("\n2. Adding 'Performance' column with different values:")
print(df)

# 3. Adding a calculated column
df['Bonus'] = df['Salary'] * df['Performance'] / 100
print("\n3. Adding calculated 'Bonus' column:")
print(df)

# 4. Adding a column with conditional values
df['Experience'] = np.where(df['Age'] > 30, 'Senior', 'Junior')
print("\n4. Adding conditional 'Experience' column:")
print(df)

# 5. Removing a single column
df_no_city = df.drop('City', axis=1)
print("\n5. Removing 'City' column:")
print(df_no_city)

# 6. Removing multiple columns
df_minimal = df.drop(['Active', 'Performance', 'Bonus'], axis=1)
print("\n6. Removing multiple columns:")
print(df_minimal)

# 7. Remove columns in-place
df.drop(['City', 'Active'], axis=1, inplace=True)
print("\n7. Removing multiple columns (inplace=True):")
print(df)

```

## ✓ Output

Original DataFrame:

	Name	Age	City	Salary	Department
emp001	Alice	24	New York	65000	HR
emp002	Bob	30	Boston	72000	Sales
emp003	Charlie	35	Chicago	85000	Tech
emp004	David	42	Seattle	92000	Tech
emp005	Eva	28	Miami	70000	Finance

1. Adding 'Active' column with same value for all rows:

	Name	Age	City	Salary	Department	Active
emp001	Alice	24	New York	65000	HR	True
emp002	Bob	30	Boston	72000	Sales	True
emp003	Charlie	35	Chicago	85000	Tech	True
emp004	David	42	Seattle	92000	Tech	True
emp005	Eva	28	Miami	70000	Finance	True

2. Adding 'Performance' column with different values:

	Name	Age	City	Salary	Department	Active	Performance
emp001	Alice	24	New York	65000	HR	True	4.5
emp002	Bob	30	Boston	72000	Sales	True	4.0
emp003	Charlie	35	Chicago	85000	Tech	True	3.8
emp004	David	42	Seattle	92000	Tech	True	4.7
emp005	Eva	28	Miami	70000	Finance	True	4.2

3. Adding calculated 'Bonus' column:

	Name	Age	City	Salary	Department	Active	Performance	Bonus
emp001	Alice	24	New York	65000	HR	True	4.5	2925.0
emp002	Bob	30	Boston	72000	Sales	True	4.0	2880.0
emp003	Charlie	35	Chicago	85000	Tech	True	3.8	3230.0
emp004	David	42	Seattle	92000	Tech	True	4.7	4324.0
emp005	Eva	28	Miami	70000	Finance	True	4.2	2940.0

4. Adding conditional 'Experience' column:

	Name	Age	City	Salary	Department	Active	Performance	Bonus	Experience
emp001	Alice	24	New York	65000	HR	True	4.5	2925.0	Junior
emp002	Bob	30	Boston	72000	Sales	True	4.0	2880.0	Junior
emp003	Charlie	35	Chicago	85000	Tech	True	3.8	3230.0	Senior
emp004	David	42	Seattle	92000	Tech	True	4.7	4324.0	Senior
emp005	Eva	28	Miami	70000	Finance	True	4.2	2940.0	Junior

5. Removing 'City' column:

	Name	Age	Salary	Department	Active	Performance	Bonus	Experience
emp001	Alice	24	65000	HR	True	4.5	2925.0	Junior
emp002	Bob	30	72000	Sales	True	4.0	2880.0	Junior
emp003	Charlie	35	85000	Tech	True	3.8	3230.0	Senior
emp004	David	42	92000	Tech	True	4.7	4324.0	Senior
emp005	Eva	28	70000	Finance	True	4.2	2940.0	Junior

6. Removing multiple columns:

	Name	Age	City	Salary	Department	Experience
emp001	Alice	24	New York	65000	HR	Junior
emp002	Bob	30	Boston	72000	Sales	Junior
emp003	Charlie	35	Chicago	85000	Tech	Senior
emp004	David	42	Seattle	92000	Tech	Senior
emp005	Eva	28	Miami	70000	Finance	Junior

7. Removing multiple columns (inplace=True):

Name	Age	Salary	Department	Performance	Bonus
------	-----	--------	------------	-------------	-------

emp001	Alice	24	65000	HR	4.5	2925.0
emp002	Bob	30	72000	Sales	4.0	2880.0
emp003	Charlie	35	85000	Tech	3.8	3230.0
emp004	David	42	92000	Tech	4.7	4324.0
emp005	Eva	28	70000	Finance	4.2	2940.0

## Adding and Removing Rows

- Removing
  - a row by index label
  - multiple rows
- Adding a new row
  - with `.loc`
  - with a Series

### 👀 Demo

```
data = {
    'Name': ['Alice', 'Bob', 'Charlie', 'David', 'Eva'],
    'Age': [24, 30, 35, 42, 28],
    'City': ['New York', 'Boston', 'Chicago', 'Seattle', 'Miami'],
    'Salary': [65000, 72000, 85000, 92000, 70000],
    'Department': ['HR', 'Sales', 'Tech', 'Tech', 'Finance']
}
df = pd.DataFrame(data)
df.index = ['emp001', 'emp002', 'emp003', 'emp004', 'emp005'] # Custom index

# 1. Removing a row by index label
df_no_bob = df.drop('emp002')
print("\n1. DataFrame without Bob (emp002):")
print(df_no_bob)

# 2. Removing multiple rows
df_reduced = df.drop(['emp001', 'emp005'])
print("\n2. DataFrame without emp001 and emp005:")
print(df_reduced)

# 3. Adding a new row with .loc
# Create a copy to avoid SettingWithCopyWarning
df_new = df.copy()
df_new.loc['emp006'] = ['Frank', 38, 'Dallas', 88000, 'Sales']
print("\n3. DataFrame with new employee:")
print(df_new)

# 4. Adding a row with a Series
new_employee = pd.Series({
    'Name': 'Grace', 'Age': 27, 'City': 'Denver', 'Salary': 67000, 'Department':
    'HR',
}, name='emp007')

df_newer = pd.concat([df_new, new_employee.to_frame().T])
print("\n4. DataFrame with another new employee:")
print(df_newer)
```

## ✓ Output

1. DataFrame without Bob (emp002):

	Name	Age	City	Salary	Department
emp001	Alice	24	New York	65000	HR
emp003	Charlie	35	Chicago	85000	Tech
emp004	David	42	Seattle	92000	Tech
emp005	Eva	28	Miami	70000	Finance

2. DataFrame without emp001 and emp005:

	Name	Age	City	Salary	Department
emp002	Bob	30	Boston	72000	Sales
emp003	Charlie	35	Chicago	85000	Tech
emp004	David	42	Seattle	92000	Tech

3. DataFrame with new employee:

	Name	Age	City	Salary	Department
emp001	Alice	24	New York	65000	HR
emp002	Bob	30	Boston	72000	Sales
emp003	Charlie	35	Chicago	85000	Tech
emp004	David	42	Seattle	92000	Tech
emp005	Eva	28	Miami	70000	Finance
emp006	Frank	38	Dallas	88000	Sales

4. DataFrame with another new employee:

	Name	Age	City	Salary	Department
emp001	Alice	24	New York	65000	HR
emp002	Bob	30	Boston	72000	Sales
emp003	Charlie	35	Chicago	85000	Tech
emp004	David	42	Seattle	92000	Tech
emp005	Eva	28	Miami	70000	Finance
emp006	Frank	38	Dallas	88000	Sales
emp007	Grace	27	Denver	67000	HR

## ⚠ Note

- Notice that we can add columns based on calculations from other columns - this is ideal for metrics and KPIs
- The `drop()` function is powerful but doesn't modify the original DataFrame unless you specify `inplace=True`
- Adding rows is less common but useful for simulation, testing, or creating summary rows
- Always be careful with the `axis` parameter - `axis=0` is for rows, `axis=1` is for columns

## More info

- ▶ Additional notes: Additional info and exercise

## DataFrame Sorting

### Sorting functions

Method	Description	Key Parameters
<code>sort_values()</code>	Sort by column values	<code>by</code> , <code>ascending</code> , <code>inplace</code> , <code>na_position</code>
<code>sort_index()</code>	Sort by index	<code>ascending</code> , <code>inplace</code>
Multi-column sorting	Sort by multiple columns	<code>by=['col1', 'col2']</code>
Custom sorting	Sort with custom orders	<code>by=col</code> , <code>key=function</code>

## Basic Sorting

- Sorting by a single column - ascending and descending
- Sorting by index
- Sorting by multiple columns
- Sorting with different directions for each column

### Demo

```

data = {
    'Name': ['Alice', 'Bob', 'Charlie', 'David', 'Eva'],
    'Age': [24, 30, 35, 42, 28],
    'City': ['New York', 'Boston', 'Chicago', 'Seattle', 'Miami'],
    'Salary': [65000, 72000, 85000, 92000, 70000],
    'Department': ['HR', 'Sales', 'Tech', 'Tech', 'Finance']
}
df = pd.DataFrame(data)
df.index = ['emp001', 'emp002', 'emp003', 'emp004', 'emp005'] # Custom index

# Continuing with our employee DataFrame
print("Original DataFrame:")
print(df)

# 1. Sorting by a single column (ascending by default)
df_by_age = df.sort_values('Age')
print("\n1. Sorted by Age (ascending):")
print(df_by_age)

# 2. Sorting by a single column (descending)
df_by_salary_desc = df.sort_values('Salary', ascending=False)
print("\n2. Sorted by Salary (descending):")
print(df_by_salary_desc)

# 3. Sorting by index
df_by_index = df.sort_index()
print("\n3. Sorted by index:")
print(df_by_index)

# 4. Sorting by multiple columns
df_multi_sort = df.sort_values(['Department', 'Salary'])
print("\n4. Sorted by Department, then by Salary within each department:")
print(df_multi_sort)

# 5. Sorting with different directions for each column
df_complex = df.sort_values(['Department', 'Salary'],
                             ascending=[True, False])
print("\n5. Sorted by Department (asc), then by Salary (desc) within each department:")
print(df_complex)

```

## ✓ Output

Original DataFrame:

	Name	Age	City	Salary	Department
emp001	Alice	24	New York	65000	HR
emp002	Bob	30	Boston	72000	Sales
emp003	Charlie	35	Chicago	85000	Tech
emp004	David	42	Seattle	92000	Tech
emp005	Eva	28	Miami	70000	Finance

1. Sorted by Age (ascending):

	Name	Age	City	Salary	Department
emp001	Alice	24	New York	65000	HR
emp005	Eva	28	Miami	70000	Finance
emp002	Bob	30	Boston	72000	Sales
emp003	Charlie	35	Chicago	85000	Tech
emp004	David	42	Seattle	92000	Tech

2. Sorted by Salary (descending):

	Name	Age	City	Salary	Department
emp004	David	42	Seattle	92000	Tech
emp003	Charlie	35	Chicago	85000	Tech
emp002	Bob	30	Boston	72000	Sales
emp005	Eva	28	Miami	70000	Finance
emp001	Alice	24	New York	65000	HR

3. Sorted by index:

	Name	Age	City	Salary	Department
emp001	Alice	24	New York	65000	HR
emp002	Bob	30	Boston	72000	Sales
emp003	Charlie	35	Chicago	85000	Tech
emp004	David	42	Seattle	92000	Tech
emp005	Eva	28	Miami	70000	Finance

4. Sorted by Department, then by Salary within each department:

	Name	Age	City	Salary	Department
emp005	Eva	28	Miami	70000	Finance
emp001	Alice	24	New York	65000	HR
emp002	Bob	30	Boston	72000	Sales
emp003	Charlie	35	Chicago	85000	Tech
emp004	David	42	Seattle	92000	Tech

5. Sorted by Department (asc), then by Salary (desc) within each department:

	Name	Age	City	Salary	Department
emp005	Eva	28	Miami	70000	Finance
emp001	Alice	24	New York	65000	HR
emp002	Bob	30	Boston	72000	Sales
emp004	David	42	Seattle	92000	Tech
emp003	Charlie	35	Chicago	85000	Tech

## More info

- Additional notes: Additional note

## Key Takeaways

## ! Keypoints

1. **Flexible Selection:** Pandas provides multiple ways to select, filter, and extract data
2. **Structure Modification:** Adding and removing columns/rows enables dataset evolution
3. **Meaningful Sorting:** Proper sorting is essential for analysis and presentation
4. **Custom Orders:** Categorical data types allow you to enforce domain-specific ordering
5. **Combined Operations:** The real power comes from combining these techniques

## Indexing, Selection & Slicing in Pandas

## ! Objectives

- Differentiate between label-based and position-based indexing and apply each method appropriately.
- Use Boolean indexing to filter data based on specific conditions, connecting concepts from NumPy.
- Apply `.loc`, `.iloc`, and `.at` selection methods to extract desired data, and employ multi-level slicing techniques.

## Instructor note

- Teaching : 5 min
- Demo: 25 min

## ! Note

- In the previous session, we introduced some basic ways to select data. Now we'll dive deeper into Pandas' powerful indexing systems.
- Think of these techniques as the surgical tools that let you precisely extract exactly the data you need.
- Understanding the differences between these indexing methods will make your code more efficient and help you avoid common errors.
- These concepts build directly on your NumPy knowledge, but with added capabilities for labeled data.

- Precise data access is the foundation of efficient data analysis
- Pandas offers multiple ways to access data, each with specific use cases

## Label vs. Position-based Indexing

- Two Fundamental Indexing Approaches

Indexing Type	Method	Use Case	NumPy Equivalent
Label-based	<code>.loc[]</code>	When you know the labels	N/A (NumPy is position-based)
Position-based	<code>.iloc[]</code>	When you know the positions	Standard NumPy indexing
Mixed	Direct <code>[]</code>	Simple selection (but less explicit)	N/A

## Creating a DataFrame with Meaningful Indices

### 👀 Demo

```
# Create a DataFrame with custom indices
import pandas as pd

# Create a genetic dataset
genetic_data = {
    'Gene': ['BRCA1', 'TP53', 'APOE', 'PTEN', 'BRAF', 'KRAS',
             'BRCA2', 'EGFR', 'TNF', 'IL6'],
    'Chromosome': ['Chr17', 'Chr17', 'Chr19', 'Chr10', 'Chr7', 'Chr12',
                   'Chr13', 'Chr7', 'Chr6', 'Chr7'],
    'Study': ['Study1', 'Study2', 'Study1', 'Study3', 'Study2', 'Study3',
              'Study1', 'Study2', 'Study3', 'Study1'],
    'PValue': [0.0001, 0.0050, 0.0200, 0.0150, 0.0300, 0.0400,
               0.0005, 0.0250, 0.0100, 0.0450],
    'EffectSize': [2.5, 1.8, 3.2, 2.1, 1.5, 1.2, 2.7, 1.9, 2.3, 1.1]
}

genetic_df = pd.DataFrame(genetic_data)
print("Genetic DataFrame:")
print(genetic_df)

# Set a meaningful index from an existing column
genetic_df.set_index('Gene', inplace=True)
print("DataFrame with 'Gene' as index:")
print(genetic_df)

# Reset index to return to default integer indexing
df_reset = genetic_df.reset_index()
print("\nDataFrame with default integer index:")
print(df_reset)
```

### ✓ Output

Genetic DataFrame:

	Gene	Chromosome	Study	PValue	EffectSize
0	BRCA1	Chr17	Study1	0.0001	2.5
1	TP53	Chr17	Study2	0.0050	1.8
2	APOE	Chr19	Study1	0.0200	3.2
3	PTEN	Chr10	Study3	0.0150	2.1
4	BRAF	Chr7	Study2	0.0300	1.5
5	KRAS	Chr12	Study3	0.0400	1.2
6	BRCA2	Chr13	Study1	0.0005	2.7
7	EGFR	Chr7	Study2	0.0250	1.9
8	TNF	Chr6	Study3	0.0100	2.3
9	IL6	Chr7	Study1	0.0450	1.1

DataFrame with 'Gene' as index:

Gene	Chromosome	Study	PValue	EffectSize
BRCA1	Chr17	Study1	0.0001	2.5
TP53	Chr17	Study2	0.0050	1.8
APOE	Chr19	Study1	0.0200	3.2
PTEN	Chr10	Study3	0.0150	2.1
BRAF	Chr7	Study2	0.0300	1.5
KRAS	Chr12	Study3	0.0400	1.2
BRCA2	Chr13	Study1	0.0005	2.7
EGFR	Chr7	Study2	0.0250	1.9
TNF	Chr6	Study3	0.0100	2.3
IL6	Chr7	Study1	0.0450	1.1

DataFrame with default integer index:

	Gene	Chromosome	Study	PValue	EffectSize
0	BRCA1	Chr17	Study1	0.0001	2.5
1	TP53	Chr17	Study2	0.0050	1.8
2	APOE	Chr19	Study1	0.0200	3.2
3	PTEN	Chr10	Study3	0.0150	2.1
4	BRAF	Chr7	Study2	0.0300	1.5
5	KRAS	Chr12	Study3	0.0400	1.2
6	BRCA2	Chr13	Study1	0.0005	2.7
7	EGFR	Chr7	Study2	0.0250	1.9
8	TNF	Chr6	Study3	0.0100	2.3
9	IL6	Chr7	Study1	0.0450	1.1

## Use Label and Position-based Indexing

- Label-based indexing with `.loc`
- Select multiple rows by label
- Select rows and columns by label
- Slicing dataframe using labels
- Position-based indexing with `.iloc`
- Select multiple rows by position
- Slicing dataframe using indices (Select rows and columns by position)

### 👀 Demo

```

# Using the genetic_df with 'Gene' as the index

# 1. Label-based indexing with .loc
print("\n1.1. Label-based selection (.loc):")
print("Data for 'BRCA1':")
print(genetic_df.loc['BRCA1'])

# Select multiple rows by label
print("\n1.2. Data for 'TP53' and 'APOE':")
print(genetic_df.loc[['TP53', 'APOE']])

# Select rows and columns by label
print("\n1.3. Chromosome and PValue for 'BRAF' and 'KRAS':")
print(genetic_df.loc[['BRAF', 'KRAS'], ['Chromosome', 'PValue']])

# Slicing dataframe using labels
print("\n1.4. All the rows of Chromosome and PValue columns:")
print(genetic_df.loc[:, ['Chromosome', 'PValue']])
gene_set = ["BRCA1", "BRCA2", "TP53"]
print("\n1.5. row indices in gene_set array and column indices - Study, EffectSize:")
print(genetic_df.loc[['BRCA1', 'BRAF'], ['Study', 'EffectSize']])

# 2. Position-based indexing with .iloc
print("\n2.1. Position-based selection (.iloc):")
print("Third row (index position 2):")
print(genetic_df.iloc[2])

# Select multiple rows by position
print("\n2.2. First and fourth rows (positions 0 and 3):")
print(genetic_df.iloc[[0, 3]])

# Slicing dataframe using indices - Select rows and columns by position
print("\n2.3. Rows 1-3, columns 0-1:")
print(genetic_df.iloc[1:4, 0:2])

# 3. Mixed indexing (direct [])
# Mixing approaches (not recommended but sometimes seen)
# print("\nFirst two rows of 'Study' column:")
# print(genetic_df['Study'][0:2]) # Chained indexing - can lead to issues

```

## ✓ Output

```

1.1. Label-based selection (.loc):
Data for 'BRCA1':
Chromosome      Chr17
Study          Study1
PValue         0.0001
EffectSize      2.5
Name: BRCA1, dtype: object

1.2. Data for 'TP53' and 'APOE':
   Chromosome  Study  PValue  EffectSize
Gene
TP53      Chr17  Study2    0.005       1.8
APOE      Chr19  Study1    0.020       3.2

1.3. Chromosome and PValue for 'BRAF' and 'KRAS':
   Chromosome  PValue
Gene
BRAF        Chr7     0.03
KRAS        Chr12    0.04

1.4. All the rows of Chromosome and PValue columns:
   Chromosome  PValue
Gene
BRCA1      Chr17  0.0001
TP53       Chr17  0.0050
APOE       Chr19  0.0200
PTEN       Chr10  0.0150
BRAF       Chr7   0.0300
KRAS       Chr12  0.0400
BRCA2      Chr13  0.0005
EGFR       Chr7   0.0250
TNF        Chr6   0.0100
IL6        Chr7   0.0450

1.5. row indices in gene_set array and column indices - Study, EffectSize:
   Study  EffectSize
Gene
BRCA1  Study1        2.5
BRAF   Study2        1.5

2.1. Position-based selection (.iloc):
Third row (index position 2):
Chromosome      Chr19
Study          Study1
PValue         0.02
EffectSize      3.2
Name: APOE, dtype: object

2.2. First and fourth rows (positions 0 and 3):
   Chromosome  Study  PValue  EffectSize
Gene
BRCA1      Chr17  Study1  0.0001       2.5
PTEN       Chr10  Study3  0.0150       2.1

2.3. Rows 1-3, columns 0-1:
   Chromosome  Study
Gene
TP53      Chr17  Study2
APOE      Chr19  Study1
PTEN       Chr10  Study3

```

## ! Note

- The key distinction is that `.loc` uses labels, while `.iloc` uses integer positions.
- Think of `.loc` as looking up data in a dictionary by key, and `.iloc` as accessing a list by position.
- Label-based indexing is more intuitive when working with real-world data that has meaningful labels.
- Position-based indexing connects directly to your NumPy knowledge and is useful for algorithms that need specific positions.
- Using the direct `[]` approach is convenient but can be ambiguous and lead to unexpected behavior.
  - `df[mask]` can be thought as shorthand for `df.loc[mask, :]`
  - Using `.loc` is more explicit and makes your intentions clearer - you're specifically asking for label-based indexing
- When filtering data with conditions, particularly with missing values, `.loc` is generally safer.
  - `.loc` generally handles missing values more gracefully. If your mask involves columns containing NaN values, direct indexing might raise unexpected errors while `.loc` will typically handle them correctly

## Boolean Indexing

### Boolean Indexing and Filtering:

Concept	Description	Connection to NumPy
Boolean masks	Arrays of True/False values	Direct equivalent in NumPy
Comparison operators	<code>&gt;, &lt;, ==, !=, &gt;=, &lt;=</code>	Same as NumPy
Compound conditions	Combined with `&,	, ~`
<code>query()</code> method	SQL-like filtering	Pandas-specific, no NumPy equivalent

## 👀 Demo

- Simple boolean mask
- Using the mask to filter rows
- Inline boolean indexing
- Multiple conditions with & (and), | (or)

### Creating and Using Boolean Masks:

```

# Reset example
genetic_df = pd.DataFrame(genetic_data)
genetic_df.set_index('Gene', inplace=True)
print("Original DataFrame:")
print(genetic_df)

# 1. Simple boolean mask
low_pvalue_mask = genetic_df['PValue'] < 0.01
print("\n1. Boolean mask for low P-values:")
print(low_pvalue_mask)

# Using the mask to filter rows
print("\nGenes with low P-values:")
print(genetic_df[low_pvalue_mask])

# 2. Inline boolean indexing
print("\n2. Genes on Chromosome 7:")
print(genetic_df[genetic_df['Chromosome'] == 'Chr7'])

# 3. Multiple conditions with & (and), | (or)
print("\n3a. Genes from Study1 with large effect size:")
multi_cond_and = (genetic_df['Study'] == 'Study1') & (genetic_df['EffectSize'] > 2.5)
print(genetic_df[multi_cond_and]) # print(genetic_df.loc[multi_cond_and, :])

print("\n3b. Genes with either very low P-value or large effect size:")
multi_cond_or = (genetic_df['PValue'] < 0.005) | (genetic_df['EffectSize'] > 3.0)
print(genetic_df[multi_cond_or]) # print(genetic_df.loc[multi_cond_or, :])

# 4. Using .loc with boolean masks
print("\n4.a Using .loc with boolean mask:")
chr17_genes = (genetic_df['Chromosome'] == 'Chr17')
col_list = ['Study', 'EffectSize']
print(genetic_df.loc[chr17_genes, col_list])
print("\n4.b Using .loc with boolean mask:")
print(genetic_df.loc[multi_cond_and, col_list])

```

## ✓ Output

Original DataFrame:

	Chromosome	Study	PValue	EffectSize
Gene				
BRCA1	Chr17	Study1	0.0001	2.5
TP53	Chr17	Study2	0.0050	1.8
APOE	Chr19	Study1	0.0200	3.2
PTEN	Chr10	Study3	0.0150	2.1
BRAF	Chr7	Study2	0.0300	1.5
KRAS	Chr12	Study3	0.0400	1.2
BRCA2	Chr13	Study1	0.0005	2.7
EGFR	Chr7	Study2	0.0250	1.9
TNF	Chr6	Study3	0.0100	2.3
IL6	Chr7	Study1	0.0450	1.1

1. Boolean mask for low P-values:

Gene	
BRCA1	True
TP53	True
APOE	False
PTEN	False
BRAF	False
KRAS	False
BRCA2	True
EGFR	False
TNF	False
IL6	False

Name: PValue, dtype: bool

Genes with low P-values:

Gene	Chromosome	Study	PValue	EffectSize
BRCA1	Chr17	Study1	0.0001	2.5
TP53	Chr17	Study2	0.0050	1.8
BRCA2	Chr13	Study1	0.0005	2.7

2. Genes on Chromosome 7:

Gene	Chromosome	Study	PValue	EffectSize
BRAF	Chr7	Study2	0.030	1.5
EGFR	Chr7	Study2	0.025	1.9
IL6	Chr7	Study1	0.045	1.1

3a. Genes from Study1 with large effect size:

Gene	Chromosome	Study	PValue	EffectSize
APOE	Chr19	Study1	0.0200	3.2
BRCA2	Chr13	Study1	0.0005	2.7

3b. Genes with either very low P-value or large effect size:

Gene	Chromosome	Study	PValue	EffectSize
BRCA1	Chr17	Study1	0.0001	2.5
APOE	Chr19	Study1	0.0200	3.2
BRCA2	Chr13	Study1	0.0005	2.7

4.a Using .loc with boolean mask:

Gene	Study	EffectSize
BRCA1	Study1	2.5
TP53	Study2	1.8

4.b Using .loc with boolean mask:

Gene	Study	EffectSize
BRCA1	Study1	2.5
TP53	Study2	1.8

APOE	Study1	3.2
BRCA2	Study1	2.7

## Key Takeaways

### ! Keypoints

- 1. Selection Toolkit:** Different indexing methods are optimized for different tasks
- 2. Label vs. Position:** `.loc` uses labels, `.iloc` uses positions - choose based on what you know
- 3. Boolean Filtering:** Powerful way to extract data matching specific conditions

### More info

- Additional notes: Advanced Boolean Indexing

### More info

- Additional notes: Homework

## Summary Statistics & Aggregations in Pandas

### ! Objectives

- We've learned how to load, clean, and combine data in Pandas, now we'll explore how to extract insights from that data.
- Explore the use of summary statistics and aggregation operations to transform raw data into actionable information
- Implement methods with Pandas' intuitive syntax.

### Instructor note

- Teaching : 5 min
- Demo: 25 min

- Data collection and cleaning are just the beginning
- The real value comes from extracting meaningful insights
- Summary statistics reduce complex data into understandable metrics
- Aggregations allow us to analyze data at different levels of granularity
- These operations form the foundation of data analysis (these methods connect directly to statistical concepts)
- i.e., These techniques allow us to answer questions like
  - 'What's the average customer spending?' or

- ‘How do sales compare across different regions?’”

## Basic Descriptive Statistics

### Built-in Statistical Methods

Method	Purpose	Returns
<code>describe()</code>	Comprehensive summary	DataFrame with count, mean, std, min, quartiles, max
<code>mean()</code> , <code>median()</code>	Central tendency	Series or scalar
<code>min()</code> , <code>max()</code>	Range boundaries	Series or scalar
<code>std()</code> , <code>var()</code>	Dispersion/spread	Series or scalar
<code>quantile([0.25, 0.75])</code>	Distribution points	Series or DataFrame
<code>count()</code>	Non-null count	Series or scalar
<code>sum()</code>	Sum of values	Series or scalar

### Basic Statistical Methods:

#### 👀 Demo

- Comprehensive statistical summary
- Include all columns (even non-numeric)
- Basic statistical methods
  - Mean, Median, Minimum, Maximum, Standard deviation

```

import pandas as pd
import numpy as np

# Create a sample gene expression DataFrame
np.random.seed(42) # For reproducibility

# Generate 15 sample genes
data = {
    'Gene_ID': [f'GENE{i:03d}' for i in range(1, 16)],
    'Expression_Level': np.random.lognormal(4, 1, 15).round(2), # Draw random samples Log-normal distribution for expression values
    'Log2_Fold_Change': np.random.normal(0, 2, 15).round(2), # Draw random samples from normal distribution for log2 fold changes
    'P_Value': np.random.beta(1, 10, 15).round(4), # Draw random samples Beta distribution for p-values
    'Tissue_Type': np.random.choice(['Brain', 'Liver', 'Kidney', 'Heart', 'Lung'], 15),
    'Chromosome': np.random.choice(['chr1', 'chr2', 'chr3', 'chr4', 'chrX', 'chrY'], 15)
}

df = pd.DataFrame(data)

# Add some missing values for realism
df.loc[4, 'P_Value'] = None
df.loc[9, 'Log2_Fold_Change'] = None

# Add a column for significance based on P_Value and Log2_Fold_Change
df['Is_Significant'] = ((df['P_Value'] < 0.05) & (abs(df['Log2_Fold_Change']) > 1))

print("Sample Gene Expression DataFrame:")
print(df)

# 1. Comprehensive statistical summary
print("\n1. Comprehensive statistical summary with describe():")
print(df.describe())

# 2. Include all columns (even non-numeric)
print("\n2. Describing all columns (including non-numeric):")
print(df.describe(include='all'))

# 3. Basic statistical methods
print("\n3. Basic statistical methods:")
print(f"Mean expression level: {df['Expression_Level'].mean():.2f}")
print(f"Median log2 fold change: {df['Log2_Fold_Change'].median():.2f}")
print(f"Minimum p-value: {df['P_Value'].min():.4f}")
print(f"Number of significant genes: {df['Is_Significant'].sum()}")
print(f"Standard deviation of expression: {df['Expression_Level'].std():.2f}")

# 4. Multiple statistics at once
print("\n4. Multiple statistics for Expression Level:")
print(df['Expression_Level'].agg(['min', 'max', 'mean', 'median', 'std']))

# 5. Quantiles/percentiles
print("\n5. Expression level quartiles:")
print(df['Expression_Level'].quantile([0, 0.25, 0.5, 0.75, 1.0]))

```

## ✓ Output

### Sample Gene Expression DataFrame:

	Gene_ID	Expression_Level	Log2_Fold_Change	P_Value	Tissue_Type	Chromosome
	Is_Significant					
0	GENE001	89.72	-1.12	0.1445	Lung	chr4
False						
1	GENE002	47.55	-2.03	0.0038	Kidney	chrY
True						
2	GENE003	104.34	0.63	0.0458	Brain	chrX
False						
3	GENE004	250.39	-1.82	0.0555	Lung	chrX
False						
4	GENE005	43.20	-2.82	NaN	Liver	chr3
False						
5	GENE006	43.20	2.93	0.0073	Kidney	chrX
True						
6	GENE007	264.86	-0.45	0.0067	Brain	chr4
False						
7	GENE008	117.62	0.14	0.2418	Liver	chrX
False						
8	GENE009	34.14	-2.85	0.0479	Liver	chr3
True						
9	GENE010	93.93	NaN	0.0076	Heart	chr3
False						
10	GENE011	34.35	0.22	0.1132	Lung	chrY
False						
11	GENE012	34.27	-2.30	0.1041	Kidney	chr4
False						
12	GENE013	69.54	0.75	0.0723	Brain	chr2
False						
13	GENE014	8.06	-1.20	0.0268	Heart	chr2
True						
14	GENE015	9.73	-0.58	0.0947	Lung	chrX
False						

### 2. Describing all columns (including non-numeric):

	Gene_ID	Expression_Level	Log2_Fold_Change	P_Value	Tissue_Type
	Chromosome	Is_Significant			
count	15	15.000000	14.000000	14.000000	15
15		15			
unique	15	NaN	NaN	NaN	5
5		2			
top	GENE001	NaN	NaN	NaN	Lung
chrX		False			
freq	1	NaN	NaN	NaN	4
5		11			
mean	NaN	82.993333	-0.750000	0.069429	NaN
NaN		NaN			
std	NaN	78.207700	1.611707	0.066835	NaN
NaN		NaN			
min	NaN	8.060000	-2.850000	0.003800	NaN
NaN		NaN			
25%	NaN	34.310000	-1.977500	0.012400	NaN
NaN		NaN			
50%	NaN	47.550000	-0.850000	0.051700	NaN
NaN		NaN			
75%	NaN	99.135000	0.200000	0.101750	NaN
NaN		NaN			
max	NaN	264.860000	2.930000	0.241800	NaN
NaN		NaN			

### 3. Basic statistical methods:

Mean expression level: 82.99

Median log2 fold change: -0.85

Minimum p-value: 0.0038

```
Number of significant genes: 4  
Standard deviation of expression: 78.21
```

#### 4. Multiple statistics for Expression Level:

```
min      8.060000  
max     264.860000  
mean    82.993333  
median   47.550000  
std     78.207700  
Name: Expression_Level, dtype: float64
```

#### 5. Expression level quartiles:

```
0.00    8.060  
0.25   34.310  
0.50   47.550  
0.75   99.135  
1.00  264.860  
Name: Expression_Level, dtype: float64
```

## ! Note

- The `describe()` method gives you a quick overview of your data's distribution.
- Notice how Pandas handles missing values in statistical calculations - they're automatically excluded.
- You can compute multiple statistics at once with the `agg()` method, which we'll explore further.
- Statistical methods can be combined with grouping to compare metrics across categories.
- Remember that these methods only make sense for numerical data - Pandas will ignore or handle non-numeric data differently.

## Aggregation Functions

- Aggregation functions help perform beyond Built-in Statistics

Approach	Use Case	Method
Built-in aggregations	Common statistics	<code>.agg(['mean', 'median'])</code>
Lambda functions	Simple custom calculations	<code>.agg(lambda x: x.max() - x.min())</code>
Named functions	Complex custom calculations	<code>.agg(custom_function)</code>
Dictionary approach	Different aggs per column	<code>.agg({'A': 'sum', 'B': 'mean'})</code>
Multiple aggregations	Comprehensive analysis	<code>.agg(['count', 'mean', custom_func])</code>

## 👀 Demo

- Define a custom function and use `agg`

- Different aggregations for different columns

```

# Create a sample gene expression DataFrame
np.random.seed(42) # For reproducibility

# Generate 15 sample genes
data = {
    'Gene_ID': [f'GENE{i:03d}' for i in range(1, 16)],
    'Expression_Level': np.random.lognormal(4, 1, 15).round(2), # Log-normal for
expression values
    'Log2_Fold_Change': np.random.normal(0, 2, 15).round(2), # Normal distribution
for log2 fold changes
    'P_Value': np.random.beta(1, 10, 15).round(4), # Beta distribution for p-
values
    'Tissue_Type': np.random.choice(['Brain', 'Liver', 'Kidney', 'Heart', 'Lung'],
15),
    'Chromosome': np.random.choice(['chr1', 'chr2', 'chr3', 'chr4', 'chrX',
'chrY'], 15)
}

df = pd.DataFrame(data)
print("Original dataframe")
print(df)

# 1. Simple custom aggregation with custom function

# Define a custom function
def get_range(x):
    """Get range"""
    return x.max() - x.min()

def range_ratio(x):
    """Calculate the ratio of max to min value"""
    return x.max() / x.min()

range_calc = df['Expression_Level'].agg(get_range)
print("\n1. Expression Level range using lambda function:")
print(f"{range_calc:.2f}")

print("\n2. Expression Level max/min ratio using custom function:")
print(f"{df['Expression_Level'].agg(range_ratio):.2f}")

# 3. Different aggregations for different columns
print("\n3. Different aggregations per column:")
mixed_aggs = df.agg({
    'Expression_Level': ['min', 'max', 'mean'],
    'Log2_Fold_Change': ['median', 'std'],
    'P_Value': ['min', 'mean'],
    'Is_Significant': 'sum'
})
print(mixed_aggs)

# 4. Genomics-specific custom aggregation
def differential_expression_score(x):
    """Calculate a custom score based on fold change magnitude and significance"""
    # Higher absolute fold change and lower p-values yield higher scores
    return x.abs().mean() * (-np.log10(df['P_Value'].dropna().mean()))

print("\n4. Custom differential expression score:")
print(f"{df['Log2_Fold_Change'].agg(differential_expression_score):.2f}")

```

## ✓ Output

1. Expression Level range using lambda function:  
256.80

2. Expression Level max/min ratio using custom function:  
32.86

3. Different aggregations per column:

	Expression_Level	Log2_Fold_Change	P_Value	Is_Significant
min	8.060000	NaN	0.003800	NaN
max	264.860000	NaN	NaN	NaN
mean	82.993333	NaN	0.069429	NaN
median	NaN	-0.850000	NaN	NaN
std	NaN	1.611707	NaN	NaN
sum	NaN	NaN	NaN	4.0

4. Custom differential expression score:  
1.64

## Custom Aggregations with GroupBy

- The `groupby()` function allows us to split data into groups based on some criteria
- We can apply a function to each group independently, and combine the results
- Think of it as a “split-apply-combine” strategy

## Basic GroupBy Concept

### Group dataframes on columns

```

# Create a genetic dataset
import pandas as pd
import numpy as np

genetic_data = {
    'Gene': ['BRCA1', 'TP53', 'APOE', 'PTEN', 'BRAF', 'KRAS',
              'BRCA2', 'EGFR', 'TNF', 'IL6'],
    'Chromosome': ['Chr17', 'Chr17', 'Chr19', 'Chr10', 'Chr7', 'Chr12',
                    'Chr13', 'Chr7', 'Chr6', 'Chr7'],
    'Study': ['Study1', 'Study2', 'Study1', 'Study3', 'Study2', 'Study3',
              'Study1', 'Study2', 'Study3', 'Study1'],
    'PValue': [0.0001, 0.0050, 0.0200, 0.0150, 0.0300, 0.0400,
               0.0005, 0.0250, 0.0100, 0.0450],
    'EffectSize': [2.5, 1.8, 3.2, 2.1, 1.5, 1.2, 2.7, 1.9, 2.3, 1.1]
}

genetic_df = pd.DataFrame(genetic_data)
print("Genetic DataFrame:")
print(genetic_df)

# Group by Chromosome
chromosome_groups = genetic_df.groupby('Chromosome')

# View the groups
print("Available groups:")
print(list(chromosome_groups.groups.keys()))

# Access a specific group
print("\nGenes on Chr17:")
print(chromosome_groups.get_group('Chr17'))

```

## ✓ Output

```

Genetic DataFrame:
   Gene Chromosome  Study  PValue  EffectSize
0  BRCA1      Chr17  Study1  0.0001        2.5
1   TP53      Chr17  Study2  0.0050        1.8
2   APOE      Chr19  Study1  0.0200        3.2
3   PTEN      Chr10  Study3  0.0150        2.1
4   BRAF       Chr7  Study2  0.0300        1.5
5   KRAS      Chr12  Study3  0.0400        1.2
6  BRCA2      Chr13  Study1  0.0005        2.7
7   EGFR       Chr7  Study2  0.0250        1.9
8    TNF       Chr6  Study3  0.0100        2.3
9    IL6       Chr7  Study1  0.0450        1.1

Available groups:
['Chr10', 'Chr12', 'Chr13', 'Chr17', 'Chr19', 'Chr6', 'Chr7']

Genes on Chr17:
   Gene Chromosome  Study  PValue  EffectSize
0  BRCA1      Chr17  Study1  0.0001        2.5
1   TP53      Chr17  Study2  0.0050        1.8

```

## 👀 Demo

### Aggregations - The Core of GroupBy:

After grouping, we typically want to perform calculations on each group.

## Basic Aggregation Functions

```
# Calculate mean effect size and p-value for each chromosome
chromosome_stats = genetic_df.groupby('Chromosome').agg({
    'PValue': 'mean',
    'EffectSize': 'mean'
})

print("Mean statistics by chromosome:")
print(chromosome_stats)
```

### ✓ Output

```
Mean statistics by chromosome:
      PValue  EffectSize
Chromosome
Chr10      0.015000     2.10
Chr12      0.040000     1.20
Chr13      0.000500     2.70
Chr17      0.002550     2.15
Chr19      0.020000     3.20
Chr6       0.010000     2.30
Chr7       0.033333     1.50
```

### More info

- ▶ Additional notes: Multiple Aggregations

### More info

- ▶ Additional notes: Homework

## Key Takeaways

### ❶ Keypoints

- 1. Descriptive Statistics:** Pandas provides comprehensive methods for calculating summary statistics on your data
- 2. Custom Aggregations:** When built-in statistics aren't enough, you can create custom aggregation functions
- 3. GroupBy Power:** The split-apply-combine pattern enables sophisticated analyses across subsets of your data
- 4. Multiple Dimensions:** You can group by multiple columns to create hierarchical analyses

# Hands-on: RNA Expression Analysis - alternative method

## Objectives

- Examine differential expression of immune-related genes between patient groups previously classified as immunologically strong ('istrong') and immunologically weak ('iweak')
- Apply an alternative analytical approach using Z-ratio methodology to complement standard differential expression tools like DESeq
- Ranks immune-related genes based on their relative expression differences between the patient groups

## RNA Expression Analysis Steps:

### 1. Data Loading and visualization

- Load sample group information (iweak vs istrong)
- Load gene expression count matrix
- View first few rows/columns
- View basic info

### 2. Sample Identification

- Filter samples by group (iweak/istrong)
- Match count matrix columns with sample IDs

### 3. Data Preprocessing

- Convert count matrix to numeric values
- Apply log2 transformation:  $\log_2(\text{counts} + 1)$

### 4. Statistical Analysis

- Calculate mean and std for each gene within each group
- Compute Z-scores within each sample group
- Calculate Z-score differences between groups
- Compute standard deviation of all differences

### 5. Ranking Genes

- Calculate Z-ratio: difference / std\_difference
- Rank genes by Z-ratio (highest to lowest)

This workflow standardizes the comparison between sample groups by accounting for the overall variability in gene expression across the entire experiment.

```
import pandas as pd
import numpy as np
```

### 1. Data Loading and visualization

- Load sample group information (iweak vs istrong)
- Load gene expression count matrix

- View first few rows/columns
- View basic info

## Load sample group information (iweak vs istrong)

```
sample_info = pd.read_csv(
    "test_data/Sample_group_info.csv", header=None, names=["Sample", "Group"]
)
print("Samples and Groups:\n", sample_info.head())
print("Dataframe info:\n", sample_info.info())
print("\nNumber of samples in each group:")
print(sample_info.groupby(by="Group").size())
```

Samples and Groups:

	Sample	Group
0	SH_TS_BC111	iweak
1	SH_TS_BC112	iweak
2	SH_TS_BC113	iweak
3	SH_TS_BC119	istrong
4	SH_TS_BC133	iweak

<class 'pandas.core.frame.DataFrame'>  
RangeIndex: 303 entries, 0 to 302  
Data columns (total 2 columns):  
# Column Non-Null Count Dtype   
--- --   
0 Sample 303 non-null object   
1 Group 303 non-null object   
dtypes: object(2)  
memory usage: 4.9+ KB  
Dataframe info:  
None

Number of samples in each group:

Group	Count
istrong	154
iweak	149

dtype: int64

## Load gene expression count matrix

```
count_matrix = pd.read_csv(
    "test_data/count_matrix_with_row_indices.csv", header=0, index_col=0, sep=";" )
print("Count matrix:\n", count_matrix.iloc[:, :5].head())
print("Dataframe info:\n", count_matrix.info())
print(
    "Descriptive statistics (First 5 samples):\n", count_matrix.iloc[:, :5].describe()
)
```

```

Count matrix:
      SH_TS_BC_C1  SH_TS_BC_C11  SH_TS_BC_C15  SH_TS_BC_C3  SH_TS_BC01
Gene
ACTR3B          25           559          231          44          23
ANLN           173          2475          886         320           6
APOBEC3G        114          8806         2781         537          47
AURKA          626          7492         2829         564          14
BAG1           317          5949         2357         275          26
<class 'pandas.core.frame.DataFrame'>
Index: 80 entries, ACTR3B to VEGFA
Columns: 483 entries, SH_TS_BC_C1 to UNC_TGS_BC_Y90_R1
dtypes: int64(483)
memory usage: 302.5+ KB
Dataframe info:
None
Descriptive statistics (First 5 samples):
      SH_TS_BC_C1  SH_TS_BC_C11  SH_TS_BC_C15  SH_TS_BC_C3  SH_TS_BC01
count    80.000000    80.000000    80.000000    80.000000    80.000000
mean    1118.700000  20114.175000  6846.137500  1403.150000  126.212500
std     2627.440095  42620.73209  13895.968032  2411.549117  329.326881
min     1.000000     13.000000     6.000000     0.000000     0.000000
25%    58.500000    1758.50000    692.500000   207.000000    3.750000
50%    265.000000   5481.00000    1903.500000   529.000000   22.000000
75%    849.500000  15620.50000    5396.750000  1142.000000  100.250000
max   15912.000000 239031.00000  79955.000000 12397.000000 2352.000000

```

---

```

print("Number of NaN values in each column:", count_matrix.isna().sum())
print("Number of NaN values in the dataframe:", count_matrix.isna().sum().sum())

```

```

Number of NaN values in each column: SH_TS_BC_C1          0
SH_TS_BC_C11        0
SH_TS_BC_C15        0
SH_TS_BC_C3          0
SH_TS_BC01          0
.
.
UNC_TGS_BC_9m        0
UNC_TGS_BC_Y23       0
UNC_TGS_BC_Y23_R1    0
UNC_TGS_BC_Y90       0
UNC_TGS_BC_Y90_R1    0
Length: 483, dtype: int64
Number of NaN values in the dataframe: 0

```

## 2. Sample Identification

- Filter samples by group (iweak/istrong)
- Match count matrix columns with sample IDs

### Filter samples and match count matrix - iweak

```

# Display info about iweak samples
iweak_samples = sample_info[sample_info["Group"] == "iweak"]
print("iweak samples:")
print(iweak_samples.head())
print("Number of iweak samples:", len(iweak_samples))
# Display info about iweak samples
print("iweak samples:")
print(iweak_samples.info())

```

```

iweak samples:
   Sample  Group
0  SH_TS_BC111  iweak
1  SH_TS_BC112  iweak
2  SH_TS_BC113  iweak
4  SH_TS_BC133  iweak
5  SH_TS_BC134  iweak
Number of iweak samples: 149
iweak samples:
<class 'pandas.core.frame.DataFrame'>
Index: 149 entries, 0 to 302
Data columns (total 2 columns):
 #   Column  Non-Null Count  Dtype  
---  --   --   --   --   --   --   -- 
 0   Sample   149 non-null    object 
 1   Group    149 non-null    object 
dtypes: object(2)
memory usage: 3.5+ KB
None

```

```

# Identify columns that match iweak sample IDs
print("Samples in count matrix (first 10):\n", count_matrix.columns[:10])
print("Data Type of count_matrix.columns:", type(count_matrix.columns))

## `pandas.core.indexes.base.Index` is not a NumPy ndarray, but it is built on top of
## NumPy arrays.
## In other words, while a Pandas Index can store data in a way that is compatible with
## NumPy
## `pandas.core.indexes.base.Index` it is a separate object that provides additional
## functionality specific to indexing and more complex operations suited for Pandas

```

```

Samples in count matrix (first 10):
Index(['SH_TS_BC_C1', 'SH_TS_BC_C11', 'SH_TS_BC_C15', 'SH_TS_BC_C3',
       'SH_TS_BC01', 'SH_TS_BC010_1', 'SH_TS_BC010_2', 'SH_TS_BC02',
       'SH_TS_BC04', 'SH_TS_BC05'],
      dtype='object')
Data Type of count_matrix.columns: <class 'pandas.core.indexes.base.Index'>

```

```

iweak_cols = count_matrix.columns.isin(iweak_samples["Sample"])
print("iweak column mask (first 10):")
print(iweak_cols[:10])
print("Number of iweak columns in iweak column mask:", iweak_cols.sum())
# print("Number of iweak columns in count matrix:", len(iweak_cols[iweak_cols]))
print("\niweak column mask (first 30):", iweak_cols[:30])
print(
    f"First 30 columns of iweak: {count_matrix.columns[iweak_cols][:30]} \\" 
    "\n Total number of iweak columns: {len(count_matrix.columns[iweak_cols])}"
)

```

```

iweak column mask (first 10):
[False False False False False False False False False]
Number of iweak columns in iweak column mask: 54

iweak column mask (first 30): [False False False False False False False False False
False False False
False False False False False False False False False False
False True True True False False]
First 30 columns of iweak: Index(['SH_TS_BC111', 'SH_TS_BC112', 'SH_TS_BC113',
'SH_TS_BC133',
'SH_TS_BC134', 'SH_TS_BC139', 'SH_TS_BC141', 'SH_TS_BC146',
'SH_TS_BC147', 'SH_TS_BC152', 'SH_TS_BC154', 'SH_TS_BC155',
'SH_TS_BC160', 'SH_TS_BC161', 'SH_TS_BC163', 'SH_TS_BC169',
'SH_TS_BC172', 'SH_TS_BC173', 'SH_TS_BC176', 'SH_TS_BC181',
'SH_TS_BC183', 'SH_TS_BC184', 'SH_TS_BC185', 'SH_TS_BC196',
'SH_TS_BC198', 'SH_TS_BC200', 'SH_TS_BC203', 'SH_TS_BC207',
'SH_TS_BC210', 'SH_TS_BC212'],
dtype='object')
Total number of iweak columns: 54

```

## Filter samples and match count matrix - istrong

```

# Display info about istrong samples
istrong_samples = sample_info[sample_info["Group"] == "istrong"]
print("\nistrong samples:")
print(istrong_samples.head())
print("Number of iweak samples:", len(istrong_samples))
# Display info about iweak samples
print("iweak samples:")
print(istrong_samples.info())

```

```

istrong samples:
      Sample   Group
3  SH_TS_BC119  istrong
10 SH_TS_BC150  istrong
11 SH_TS_BC151  istrong
13 SH_TS_BC153  istrong
19 SH_TS_BC165  istrong
Number of iweak samples: 154
iweak samples:
<class 'pandas.core.frame.DataFrame'>
Index: 154 entries, 3 to 301
Data columns (total 2 columns):
 #   Column  Non-Null Count  Dtype  
---  -- 
 0   Sample   154 non-null    object 
 1   Group    154 non-null    object 
dtypes: object(2)
memory usage: 3.6+ KB
None

```

```

istrong_cols = count_matrix.columns.isin(istrong_samples["Sample"])
print("istrong column mask (first 10):")
print(istrong_cols[:10])
print("Number of istrong columns in istrong column mask:", istrong_cols.sum())

print("\nistrong column mask (first 30):", istrong_cols[:30])
print(
    f"First 30 columns of istrong: {count_matrix.columns[istrong_cols][:30]} \n"
    f"Total number of istrong columns: {len(count_matrix.columns[istrong_cols])}"
)

```

```

istrong column mask (first 10):
[False False False False False False False False False]
Number of istrong columns in istrong column mask: 37

istrong column mask (first 30): [False False False False False False False False False
False False False False False False False False False
False False False False False False False False False
False False False False False False]
First 30 columns of istrong: Index(['SH_TS_BC119', 'SH_TS_BC150', 'SH_TS_BC151',
'SH_TS_BC153',
'SH_TS_BC165', 'SH_TS_BC166', 'SH_TS_BC170', 'SH_TS_BC171',
'SH_TS_BC175', 'SH_TS_BC177', 'SH_TS_BC178', 'SH_TS_BC180',
'SH_TS_BC182', 'SH_TS_BC188', 'SH_TS_BC193', 'SH_TS_BC199',
'SH_TS_BC202', 'SH_TS_BC204', 'SH_TS_BC209', 'SH_TS_BC211',
'SH_TS_BC219', 'SH_TS_BC233', 'SH_TS_BC235', 'SH_TS_BC240',
'SH_TS_BC249', 'SH_TS_BC252', 'SH_TS_BC255', 'SH_TS_BC265',
'SH_TS_BC266', 'SH_TS_BC272'],
dtype='object')
Total number of istrong columns: 37

```

### 3. Data Preprocessing

- Convert count matrix to numeric values
- Apply log2 transformation:  $\log_2(\text{counts} + 1)$

Convert cm to log scale:

- Gene expression count data often contains zeros (genes that weren't detected)
- Since  $\log_2(0)$  is mathematically undefined (negative infinity), we add 1 to every value
- This is called a “pseudo-count” approach, creating what's known as “ $\log_2(\text{counts}+1)$ ”
- Differences in log space correspond to fold changes in original space
  - A difference of 1 in  $\log_2$  space = a 2-fold change in original counts
  - A difference of 2 in  $\log_2$  space = a 4-fold change in original counts

## Convert count matrix to numeric values

```
# Convert count matrix to numeric values
count_matrix = count_matrix.astype(float, errors="raise")
count_matrix.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 80 entries, ACTR3B to VEGFA
Columns: 483 entries, SH_TS_BC_C1 to UNC_TGS_BC_Y90_R1
dtypes: float64(483)
memory usage: 302.5+ KB
```

```
print("Counts of zeros in each column:")
print(count_matrix.apply(lambda x: x == 0, axis=0).sum(axis=0))
print(
    "Total zeros in count matrix:",
    count_matrix.apply(lambda x: x == 0, axis=0).sum(axis=0).sum(),
)
```

```
Counts of zeros in each column:
SH_TS_BC_C1          0
SH_TS_BC_C11         0
SH_TS_BC_C15         0
SH_TS_BC_C3          3
SH_TS_BC01           5
...
UNC_TGS_BC_9m          1
UNC_TGS_BC_Y23         4
UNC_TGS_BC_Y23_R1       9
UNC_TGS_BC_Y90          2
UNC_TGS_BC_Y90_R1        3
Length: 483, dtype: int64
Total zeros in count matrix: 3150
```

```
np_matrix = np.array(count_matrix.iloc[:, :])
print("NumPy matrix shape:", np_matrix.shape)
print("Counts of zeros in each column:", (np_matrix == 0).sum(axis=0))
print("Total Counts of zeros in matrix:", (np_matrix == 0).sum(axis=0).sum())
```

```

NumPy matrix shape: (80, 483)
Counts of zeros in each column: [ 0  0  0  3  5  4  3  2  6  6  6  2  4  4  4  1  4  0  0
8  0 16  1  0  1
 3 37  2  4  2  4  4  1  2  2  3  3  2  6 17 10 11  5  8  2  3  0  1  1
 5 3 4  2  2  4  1  1 18  2  4  1  8  0  0  3  1  1  5  6  2  3  6  4
 6 24 15  4  7 36  3 18 10 28  2 20  2  7  3  3  2  9 18  3  3  4  8  1
11 3 5 13  6 20  6 16 17  3 17  2  6  2  5 18  9  3 14  2 13  2  0  0
 0 1 3  8 11  1  8 17  2  4  6 17 19 12  5 21  3 36  2  1  2  5 32  1
 0 1 0  1  0  7  2  1  1  6 11  1  1  0  3  7  0  2  9 11  6  5  4  1
16 6 6  1  1  1  2  2  3  1  3  0  2  1  3  1  1  2  3  6  4  2 34  1
 1 2 2 12 24 20  3 2 13  2  2 21 10  1  8  3 18 19  4 23 35  1  2  3
10 1 0  0  6  8  0  0  1  1  0  1  1  1  1  2 15  4  6  2 12  3 11
 3 3 17  8  8  1 14  6 18  7  0  1 16  8 16  3  7  6  6 13 24 15  3  6
15 1 0  2  1 16  1  9  2  1  1  0  0  2  9  0  0  4  1  0 11  1 10  3
 0 7 0  3  0 2 24  2  8  1  2  0 18  4 17 26 22  9 20 21  1  7 10  2
13 1 23  5 17  8  7 19 13 28  25 24 21 11  4  4  3 15  9  2 12 11 16  1
 0 8 7  9 11 12  6 5  0  7 14 12  7 22  4  7 13 19 13  6  0  3  2 15
11 6 1 11  0  8  9  3  9 19  1  5  5  7  1  4  6  5  7  2  3  2  5  7
13 17 0  1  6  4  0  0  1  2  3  9  2  8 11  2 36  7  1  0  3  8  2  0
 2 24  4  6 10  2  1  3 12  8  7  6 23  1 10  3  0 15  3 12  3  6  2  8
 8 26 21 13  8  5 16 18 19  9  2  3  2  4  3  2  2  9  1  1  0 21  1  1
 1 0 0  1  2  1  1  6  1  1  0  6  5  2  2  8  1  4  2  4  2  4  1  4
 9 2  3]

```

Total Counts of zeros in matrix: 3150

## Apply log2 transformation: `log2(counts + 1)`

```

# Convert count_matrix to log2
count_matrix_log2 = count_matrix.apply(lambda x: np.log2(x + 1), axis=0)
print(
    "Log2 transformed count matrix (first 5 rows & columns):\n",
    count_matrix_log2.iloc[:5, :5],
)
print("Log2 transformed count matrix info:\n", count_matrix_log2.info())
print(
    "Log2 transformed count matrix descriptive statistics (first 5 samples):\n",
    count_matrix_log2.iloc[:, :5].describe(),
)

```

Log2 transformed count matrix (first 5 rows & columns):

Gene	SH_TS_BC_C1	SH_TS_BC_C11	SH_TS_BC_C15	SH_TS_BC_C3	SH_TS_BC01
ACTR3B	4.700440	9.129283	7.857981	5.491853	4.584963
ANLN	7.442943	11.273796	9.792790	8.326429	2.807355
APOBEC3G	6.845490	13.104435	11.441907	9.071462	5.584963
AURKA	9.292322	12.871328	11.466586	9.142107	3.906891
BAG1	8.312883	12.538674	11.203348	8.108524	4.754888

```

<class 'pandas.core.frame.DataFrame'>
Index: 80 entries, ACTR3B to VEGFA
Columns: 483 entries, SH_TS_BC_C1 to UNC_TGS_BC_Y90_R1
dtypes: float64(483)
memory usage: 302.5+ KB
Log2 transformed count matrix info:
None
Log2 transformed count matrix descriptive statistics (first 5 samples):
   SH_TS_BC_C1  SH_TS_BC_C11  SH_TS_BC_C15  SH_TS_BC_C3  SH_TS_BC01
count  80.000000  80.000000  80.000000  80.000000  80.000000
mean   7.777790  12.376603  10.938512  8.774008  4.519537
std    2.917182  2.540082  2.458104  2.686284  2.755204
min    1.000000  3.807355  2.807355  0.000000  0.000000
25%   5.894663  10.780910  9.436778  7.698564  2.241446
50%   8.049386  12.419880  10.895191  9.049684  4.523562
75%   9.732161  13.931187  12.398038  10.158550  6.661454
max   13.957918  17.866844  16.286919  13.597820  11.200286

```

## 4. Statistical Analysis

- Calculate mean and std for each gene within each group
- Compute Z-scores within each sample group
- Calculate Z-score differences between groups & SD of the Z-score difference

```

print(
    f"iweak_cols mask: {iweak_cols[:10]} \
\nstrong_cols mask: {strong_cols[:10]} \
\nTotal number of iweak columns: {len(count_matrix_log2.columns[iweak_cols])} \
\nTotal number of strong columns:
{len(count_matrix_log2.columns[strong_cols])}"
)

```

```

iweak_cols mask: [False False False False False False False False False]
strong_cols mask: [False False False False False False False False False]
Total number of iweak columns: 54
Total number of strong columns: 37

```

### Calculate mean and std for each gene within each group

```

# Mean log2 value for iweak and strong samples
mean_iweak = count_matrix_log2.iloc[:, iweak_cols].mean(axis=1)
mean_istrong = count_matrix_log2.iloc[:, strong_cols].mean(axis=1)
print("Mean log2 value for iweak samples (first 5 rows):\n", mean_iweak.head())
print("Mean log2 value for strong samples (first 5 rows):\n", mean_istrong.head())

```

```
Mean log2 value for iweak samples (first 5 rows):
Gene
ACTR3B      7.860318
ANLN        8.870121
APOBEC3G    8.839295
AURKA       9.873015
BAG1        8.818064
dtype: float64
Mean log2 value for istrong samples (first 5 rows):
Gene
ACTR3B      6.994971
ANLN        6.953521
APOBEC3G   10.527763
AURKA       9.192108
BAG1        9.029261
dtype: float64
```

```
# Mean log2 value for iweak and istrong samples
std_iweak = count_matrix_log2.iloc[:, iweak_cols].std(axis=1)
std_istrong = count_matrix_log2.iloc[:, istrong_cols].std(axis=1)
print(
    "Standard deviation log2 value for iweak samples (first 5 rows):\n",
    std_iweak.head(),
)
print(
    "Standard deviation log2 value for istrong samples (first 5 rows):\n",
    std_istrong.head(),
)
```

```
Standard deviation log2 value for iweak samples (first 5 rows):
Gene
ACTR3B      1.995958
ANLN        1.554415
APOBEC3G    2.074605
AURKA       1.191852
BAG1        2.199874
dtype: float64
Standard deviation log2 value for istrong samples (first 5 rows):
Gene
ACTR3B      2.319413
ANLN        2.843593
APOBEC3G    1.321013
AURKA       2.242906
BAG1        2.019663
dtype: float64
```

```
print(count_matrix_log2.shape, mean_iweak.shape)
```

```
(80, 483) (80, )
```

## Compute Z-scores within each sample group

```

# Calculate Z-scores for iweak samples
## Numpy like operations
z_iweak = (
    count_matrix_log2.iloc[:, iweak_cols] - mean_iweak.values.reshape(-1, 1)
) / std_iweak.values.reshape(-1, 1)
print("Z-scores for iweak samples (first 5 rows):\n")
print(z_iweak.iloc[:5, :5])

```

Z-scores for iweak samples (first 5 rows):

	SH_TS_BC111	SH_TS_BC112	SH_TS_BC113	SH_TS_BC133	SH_TS_BC134
Gene					
ACTR3B	-0.798379	-0.735487	-0.920836	0.458160	-0.943426
ANLN	-1.188713	-2.057170	0.161741	0.227662	-5.063077
APOBEC3G	-4.260712	0.307752	-0.569305	0.264495	-1.499743
AURKA	-1.109424	-1.367487	0.168751	1.121313	-2.346097
BAG1	-4.008440	-0.285580	-0.185771	0.582435	-1.021972

Z-score calculation using pandas built-in `sub` and `div` functions:

`sub()` and `div()`:

- `.sub()`: is pandas' method to perform element-wise subtraction
- `.div()`: is pandas' method to perform element-wise division
- Accepts a value, series, dataframe to subtract
- `axis=` - specify the axis along which to perform the operation
- This is the preferred method as it is more readable and less error-prone

**Note:** When you perform operations like subtraction using the `sub()` method, pandas typically follows its broadcasting rules to align indices. This can sometimes lead to unintended behavior if the shapes of the Series or DataFrames don't match.

```

# Calculate Z-scores for iweak samples, using `sub` and `div`

z_iweak = (
    count_matrix_log2.iloc[:, iweak_cols].sub(mean_iweak, axis=0).div(std_iweak,
axis=0)
)
print("Z-scores for iweak samples (first 5 rows):\n", z_iweak.iloc[:5, :5])
print(
    "\n Z-scores for iweak samples Rows (Genes) and Columns (samples):", z_iweak.shape
)

```

```
Z-scores for iweak samples (first 5 rows):
      SH_TS_BC111  SH_TS_BC112  SH_TS_BC113  SH_TS_BC133  SH_TS_BC134
Gene
ACTR3B     -0.798379   -0.735487   -0.920836    0.458160   -0.943426
ANLN      -1.188713   -2.057170    0.161741    0.227662   -5.063077
APOBEC3G   -4.260712    0.307752   -0.569305    0.264495   -1.499743
AURKA     -1.109424   -1.367487    0.168751    1.121313   -2.346097
BAG1      -4.008440   -0.285580   -0.185771    0.582435   -1.021972
```

Z-scores for iweak samples Rows (Genes) and Columns (samples): (80, 54)

```
# Calculate Z-scores for istrong samples, using `sub` and `div`

z_istrong = (
    count_matrix_log2.iloc[:, istrong_cols]
    .sub(mean_istrong, axis=0)
    .div(std_istrong, axis=0)
)
print("Z-scores for iweak samples (first 5 rows):\n", z_istrong.iloc[:5, :5])
print(
    "\n Z-scores for iweak samples Rows (Genes) and Columns (samples):",
    z_istrong.shape
)
```

```
Z-scores for iweak samples (first 5 rows):
      SH_TS_BC119  SH_TS_BC150  SH_TS_BC151  SH_TS_BC153  SH_TS_BC165
Gene
ACTR3B     0.251123   0.745681   0.473303    1.138150   0.310111
ANLN      0.963558   -0.046892   0.846965    1.049066   0.320252
APOBEC3G   0.135300   0.285290   1.097819    1.213074   0.762314
AURKA     0.438189   0.594938   0.731543    0.743076   0.704167
BAG1      0.293509   1.148990   0.992325    0.364224   -0.072595
```

Z-scores for iweak samples Rows (Genes) and Columns (samples): (80, 37)

## Calculate Z-score differences between groups & SD of the Z-score difference

1. Calculate mean z-score for each gene in two groups
2. Calculate z-score difference of each group
3. Calculate the SD

```
# Calculate mean z-score for each gene in two groups
# Calcualte z-score difference of each group

z_diff = z_istrong.mean(axis=1) - z_iweak.mean(axis=1)
print("Shape of z_diff:", z_diff.shape)
print("Z-score difference (istrong - iweak) (first 5 rows):\n", z_diff.head())
```

```
Shape of z_diff: (80, )
Z-score difference (istrong - iweak) (first 5 rows):
 Gene
ACTR3B      1.345857e-15
ANLN       -1.994845e-17
APOBEC3G    -7.123653e-16
AURKA      -4.685386e-16
BAG1        1.760576e-15
dtype: float64
```

```
# SD of z-score difference
z_diff_std = z_diff.std()
print("Type of z_diff_std:", type(z_diff_std))
print("Standard deviation of z-score difference:", z_diff_std)
```

```
Type of z_diff_std: <class 'numpy.float64'>
Standard deviation of z-score difference: 1.4956431674223958e-15
```

## 5. Ranking Genes

- Calculate Z-ratio: difference / std\_difference
- Rank genes by Z-ratio (highest to lowest)

### Calculate Z-ratio: Z-score difference / std\_difference

```
z_score_ratios = z_diff / z_diff_std
print("Shape of z_score_ratios:", z_score_ratios.shape)
print("Z-score ratios (istrong - iweak) (first 5 rows):\n", z_score_ratios.head())
```

```
Shape of z_score_ratios: (80, )
Z-score ratios (istrong - iweak) (first 5 rows):
 Gene
ACTR3B      0.899852
ANLN       -0.013338
APOBEC3G    -0.476294
AURKA      -0.313269
BAG1        1.177136
dtype: float64
```

### Rank genes by Z-ratio (highest to lowest)

```
z_score_ratios.sort_values(ascending=False)
```

```

import matplotlib.pyplot as plt
z_score_ratios.sort_values(ascending=False).plot(
    kind="bar",
    figsize=(20, 5),
    title="Z-score ratios (istrong - iweak)",
    xlabel="Genes",
    ylabel="Z-score ratios",
)

```

## Bonus Lesson 1: Handling Missing Data in Pandas

### ! Objectives

- Identify missing values in DataFrames using `isna()` and methods.
- Strategize the filling of missing values with `fillna()` and interpolation methods tailored to scenario needs.
- Demonstrate how to drop missing data with `dropna()` and discuss various strategies for handling missing data.

### Instructor note

- This lesson is not intended to cover in live session
- Lesson material is available only for the course participants to follow on their own time

- Missing data is ubiquitous in real-world datasets
- Pandas represents missing values as `NaN` (Not a Number)
- Proper handling of missing values is critical for accurate analysis
- We'll focus on the three most essential operations: detecting, filling, and dropping missing data

## Detecting Missing Values

### Key Methods for Finding Missing Data

Method	Returns	Purpose
<code>isna()</code> & <code>isnull()</code>	Boolean mask (True where missing)	Identify missing values
<code>notna()</code> & <code>notnull()</code>	Boolean mask (True where not missing)	Identify non-missing values
<code>isna().sum()</code>	Count of missing values per column	Quantify missing data
<code>isna().any()</code>	Whether any value is missing per column	Quick presence check

### Detecting Missing Values:

## 👀 Demo

- Detect missing values with `isna()`
  - consistent interface for detecting missing values with `isna()` and `notna()`
- Count missing values per column
- Count total missing values

```
import pandas as pd
import numpy as np

# Create a DataFrame with different types of missing values
data = {
    'A': [1, 2, np.nan, 4, 5, 8],
    'B': [6, np.nan, 8, 9, np.nan, 15],
    'C': [10, 11, 12, np.nan, 14, 20],
    'D': [np.nan, np.nan, np.nan, np.nan, np.nan, 15],
    'E': ['a', 'b', None, 'd', 'e', 'h'] # None also represents missing value
}
df = pd.DataFrame(data)
print("DataFrame with missing values:")
print(df)

# Detect missing values with isna()
print("\n1. Boolean mask of missing values:")
print(df.isna()) # True where values are missing

# Count missing values per column
print("\n2. Count of missing values per column:")
print(df.isna().sum(axis=0))

# Count total missing values
total_missing = df.isna().sum().sum()
print(f"\n3. Total missing values in DataFrame: {total_missing}")

# Filter rows with any missing value
rows_with_missing = df.isna().any(axis=1)
rows_with_any_missing = df.loc[rows_with_missing]
print("\n4. Rows with any missing value:")
print(rows_with_any_missing)

# Filter rows with no missing values
## Boolean masks generated by `isna()` or `notna()` can be used directly for filtering
row_without_missing = df.notna().all(axis=1)
complete_rows = df.loc[row_without_missing]
print("\n5. Rows with no missing values:")
print(complete_rows)
```

## ✓ Output

```
1. Boolean mask of missing values:  
     A      B      C      D      E  
0  False  False  False  True  False  
1  False  True  False  True  False  
2  True  False  False  True  True  
3  False  False  True  True  False  
4  False  True  False  True  False  
5  False  False  False  False  False
```

```
2. Count of missing values per column:  
A    1  
B    2  
C    1  
D    5  
E    1  
dtype: int64
```

```
3. Total missing values in DataFrame: 10
```

```
4. Rows with any missing value:  
     A      B      C      D      E  
0  1.0   6.0  10.0  NaN    a  
1  2.0   NaN  11.0  NaN    b  
2  NaN   8.0  12.0  NaN  None  
3  4.0   9.0  NaN  NaN    d  
4  5.0   NaN  14.0  NaN    e
```

```
5. Rows with no missing values:  
     A      B      C      D      E  
5  8.0  15.0  20.0  15.0  h
```

## Filling Missing Values

### Most Common Fill Strategies:

Method	Purpose	Key Parameters
<code>fillna(value)</code>	Replace with specific value	<code>value</code> , <code>inplace</code>
<code>ffill()</code>	Forward fill (use previous value)	
<code>bfill()</code>	Backward fill (use next value)	

### Basic Fill Methods

#### Demo

- Fill all missing values with a single value `fillna(value)`
- Fill with different values for each column `fillna(dict)`

```

data = {
    'A': [1, 2, np.nan, 4, 5, 8],
    'B': [6, np.nan, 8, 9, np.nan, 15],
    'C': [10, 11, 12, np.nan, 14, 20],
    'D': [np.nan, np.nan, np.nan, np.nan, np.nan, 15],
    'E': ['a', 'b', None, 'd', 'e', 'h'] # None also represents missing value
}
df = pd.DataFrame(data)

# Original DataFrame
print("Original DataFrame:")
print(df)

# 1. Fill all missing values with a single value
df_filled = df.fillna(0)
print("\n1. Fill all missing values with 0:")
print(df_filled)

# 2. Fill numeric columns with their means
df_mean = df.copy()
df_mean.fillna(df_mean.select_dtypes(include=['number']).mean(), inplace=True)
print("\n2. Fill numeric columns with their means:")
print(df_mean)

## The select_dtypes() method is specifically designed to filter columns based on
## their data types
## The parameter include=['number'] tells pandas to keep only columns whose data
## type falls under the "number" category,
## which encompasses both integers and floating-point numbers

## Thefillna() method replaces all NaN/missing values in the dataframe
## When you pass a Series as its argument (which is what we're doing with the
## means),
## pandas does something clever: it matches column names between the dataframe
## and the Series,
## and only fills values in columns that exist in both.

## String columns remain untouched since no means will be calculated for them
## df_mean["E"] = df_mean["E"].ffill() # Fills string column

```

## ✓ Output

#### Original DataFrame:

```
A      B      C      D      E
0  1.0   6.0  10.0    NaN    a
1  2.0   NaN  11.0    NaN    b
2  NaN   8.0  12.0    NaN  None
3  4.0   9.0   NaN    NaN    d
4  5.0   NaN  14.0    NaN    e
5  8.0  15.0  20.0  15.0    h
```

#### 1. Fill all missing values with 0:

```
A      B      C      D      E
0  1.0   6.0  10.0    0.0    a
1  2.0   0.0  11.0    0.0    b
2  0.0   8.0  12.0    0.0    0
3  4.0   9.0   0.0    0.0    d
4  5.0   0.0  14.0    0.0    e
5  8.0  15.0  20.0  15.0    h
```

#### 2. Fill numeric columns with their means:

```
A      B      C      D      E
0  1.0   6.0  10.0  15.0    a
1  2.0   9.5  11.0  15.0    b
2  4.0   8.0  12.0  15.0  None
3  4.0   9.0  13.4  15.0    d
4  5.0   9.5  14.0  15.0    e
5  8.0  15.0  20.0  15.0    h
```

## More info

### ► Additional info

## ! Note

- The choice of fill method should be based on the nature of your data and the analysis you're conducting.
- Forward fill and backward fill are especially useful for time series when you want to carry values forward or backward.
- Statistical measures like mean, median, or mode are common choices for filling numeric data.
- Remember that filling is modifying your data - it's important to document your approach and consider its impact on analysis.
- For categorical data, consider whether a missing value has meaning before deciding how to fill it.

## Dropping Missing Data

### Key Parameters for dropna():

Parameter	Purpose	Values
<code>axis</code>	Specify rows or columns	0 for rows, 1 for columns
<code>how</code>	Condition for dropping	'any' (default) or 'all'
<code>thresh</code>	Minimum non-NaN values to keep	integer
<code>subset</code>	Columns to consider	list of column names

## 👀 Demo

### Dropping Rows and Columns:

- Drop rows with any missing values (any missing values)
- Drop columns with any missing values
- Drop columns where all values are missing
- Keep rows with at least `n` non-NaN values
- Drop rows with missing values in specific columns

```

data = {
    'A': [1, 2, np.nan, 4, 5],
    'B': [6, np.nan, 8, 9, np.nan],
    'C': [10, 11, 12, np.nan, 14],
    'D': [np.nan, np.nan, np.nan, np.nan, np.nan],
    'E': ['a', 'b', None, 'd', 'e'], # None also represents missing value
}
df = pd.DataFrame(data)

# Original DataFrame
print("Original DataFrame:")
print(df)

# 1. Drop rows with any missing values
df_drop_rows = df.dropna()
print("\n1. After dropping rows with any missing values:")
print(df_drop_rows)

# 2. Drop columns with any missing values
## In filtering/dropping, axis=0 means "operate on the 0-axis (rows)"
df_drop_cols = df.dropna(axis=1)
print("\n2. After dropping columns with any missing values:")
print(df_drop_cols)
## In aggregations: axis specifies the axis to collapse/operate along

# 3. Drop columns where all values are missing
df_drop_all_na_cols = df.dropna(axis=1, how='all')
print("\n3. After dropping columns where all values are missing:")
print(df_drop_all_na_cols)

# 4. Keep rows with at least 3 non-NaN values
df_thresh = df.dropna(thresh=3)
print("\n4. Keep rows with at least 3 non-NaN values:")
print(df_thresh)

# 5. Drop rows with missing values in specific columns
df_subset = df.dropna(subset=['A', 'C'])
print("\n5. Drop rows with NaN in columns A or C:")
print(df_subset)

```

## ✓ Output

```
Original DataFrame:  
     A      B      C      D      E  
0   1.0    6.0   10.0    NaN    a  
1   2.0    NaN   11.0    NaN    b  
2   NaN    8.0   12.0    NaN  None  
3   4.0    9.0    NaN   NaN    d  
4   5.0    NaN   14.0    NaN    e
```

2. After dropping columns with any missing values:

```
Empty DataFrame  
Columns: []  
Index: [0, 1, 2, 3, 4, 5]
```

3. After dropping columns where all values are missing:

```
     A      B      C      E  
0   1.0    6.0   10.0    a  
1   2.0    NaN   11.0    b  
2   NaN    8.0   12.0  None  
3   4.0    9.0    NaN    d  
4   5.0    NaN   14.0    e
```

4. Keep rows with at least 3 non-NaN values:

```
     A      B      C      D      E  
0   1.0    6.0   10.0  NaN    a  
1   2.0    NaN   11.0  NaN    b  
3   4.0    9.0    NaN   NaN    d  
4   5.0    NaN   14.0  NaN    e
```

5. Drop rows with NaN in columns A or C:

```
     A      B      C      D      E  
0   1.0    6.0   10.0  NaN    a  
1   2.0    NaN   11.0  NaN    b  
4   5.0    NaN   14.0  NaN    e
```

## More info

- Additional info

## Key Takeaways

### Keypoints

- 1. Always detect first:** Understand the pattern and extent of missing values before taking action
- 2. Choose the right strategy:**
  - Fill when you can reasonably infer values or need to preserve data
  - Drop when missing data is minimal or would introduce bias if filled
- 3. Document your approach:** Your handling choices affect analysis results

## Bonus Lesson 2: Merging DataFrames in Pandas

### Objectives

- Illustrate how to concatenate DataFrames using `pd.concat()` and understand its applications.
- Explain database-style joins with the `merge()` function and illustrate the different join types (inner, outer, left, \* right).

### Instructor note

- This lesson is not intended to cover in live session
- Lesson material is available only for the course participants to follow on their own time

- In real-world data analysis, you rarely have all the data you need in a single file or table.
- Combining data from multiple sources is a fundamental data wrangling skill.
- Pandas gives us two main approaches: stacking data (concatenation) and joining data on common keys (merging)
- **Concatenation:** Stacking similar datasets (vertically or horizontally)
- **Merging/Joining:** Combining related datasets based on common keys

## Concatenation with `pd.concat()`

Parameter	Purpose	Common Values
<code>objs</code>	List of DataFrames	<code>[df1, df2, ...]</code>
<code>axis</code>	Direction	<code>0</code> (vertical, default), <code>1</code> (horizontal)

### 👀 Demo

- Vertical concatenation (stacking)
- Horizontal concatenation (side by side)

```

import pandas as pd

# Create sample DataFrames
df1 = pd.DataFrame({
    'A': ['A0', 'A1', 'A2'],
    'B': ['B0', 'B1', 'B2']
}, index=['K0', 'K1', 'K2'])

df2 = pd.DataFrame({
    'A': ['A3', 'A4', 'A5'],
    'B': ['B3', 'B4', 'B5']
}, index=['K3', 'K4', 'K5'])

df3 = pd.DataFrame({
    'C': ['C6', 'C7', 'C8'],
    'D': ['D6', 'D7', 'D8']
}, index=['K6', 'K7', 'K8'])

# Vertical concatenation (stacking)
result1 = pd.concat([df1, df2])
print("1. Vertical concatenation (stacking)")
print(result1)

# Horizontal concatenation (side by side)
result2 = pd.concat([df1, df3], axis=1)
print("2. Horizontal concatenation (side by side)")
print(result2)

```

## ✓ Output

```

1. Vertical concatenation (stacking)
     A   B
K0  A0  B0
K1  A1  B1
K2  A2  B2
K3  A3  B3
K4  A4  B4
K5  A5  B5

2. Horizontal concatenation (side by side)
      A   B   C   D
K0  A0  B0  NaN  NaN
K1  A1  B1  NaN  NaN
K2  A2  B2  NaN  NaN
K6  NaN  NaN  C6  D6
K7  NaN  NaN  C7  D7
K8  NaN  NaN  C8  D8

```

## ! Note

- Concatenation is like stacking datasets either vertically (axis=0) or horizontally (axis=1).
- Vertical concatenation is useful when you have data from different dataframes in the same format.

- Horizontal concatenation is useful when you have different features for the same observations
- Use `ignore_index=True` when original indices aren't meaningful after combining
  - e.g., `pd.concat([df1, df2], ignore_index=True)`

## More info

- ▶ Additional info

## More info

- ▶ Additional info

## Key Takeaways

### ! Keypoints

#### 1. Concatenation vs. Merging:

- Use concatenation for stacking similar data
- Use merging for combining related data on keys

## Datasets

- [Download Test dataset 1: Sample\\_group\\_info.csv](#)
- [Download Test dataset 2: count\\_matrix.csv](#)
- [Download Test dataset 3: sample\\_data.csv](#)
- [Download Test dataset 4: sample\\_data.xlsx](#)
- [Download Test dataset 5: sample\\_data.json](#)

## Dependencies

- All Python dependencies are listed in the `requirements.txt` file
- [Download requirements.txt](#)

## Setup Python environment

Follow installation instructions in document [linked here](#).

## Credits

- [BioNT - The Bio Network for Training](#)
- [Norwegian AI Cloud](#)
- [Scientific Computing Services, Department Informatics, University of Oslo](#)

