Lists

PF2

Learning Objectives

1. Understand how to create and manipulate Python **lists**
2. Apply **indexing** and **slicing** to access items inside a list
3. Learn about **list methods** and how they can modify lists
4. Work with **nested lists**

Introduction

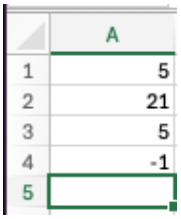
As explained in the introduction, Python natively contains many data structures for storing multiple values. However, what are the benefits of collecting your data points together? When working with related data points, such as multiple experimental recordings or sample IDs, handling each value individually becomes tedious. To address this, we use **data structures**, of which one is a **list**.

> **NOTE**
>
> Lists are a core object in Python with many of the learned components applying to other structures. You may therefore find that this section is quite lengthy. Subsequent sections that cover other data structures - namely **tuples**, **sets** and **strings** - will be shorter.

What are lists?

Lists are one of the most common data structures in Python, providing a flexible structure that can hold *mixed data types*. It is therefore important to understand how they work, how we can use them, and the features they offer to our advantage.

The easiest way to imagine how a simple 1-dimensional list works, is to think of it as a numbered list in your laboratory notebook. Each line can record a different measurement, observation or sample identifier, in sequential order. For instance, suppose you have four entries in your notebook, each recording different experimental values:



	A
1	5
2	21
3	5
4	-1
5	

The number of entries or **items** in a list determines its length. The above list of results has four entries; therefore it is said to have a length of 4.

KEY TERMS

Lists: One of the most common data structures in Python, providing a flexible structure that can hold mixed data types in square brackets `[]`, separated by commas.

Item / Element: An individual value stored within a data structure such as a list. Also referred to as an element.

FACT

If you have had any experience programming in other langauges, the term **array** is one that may be familiar. An array is a data structure that stores a collection of items, typically of the same data type, in an ordered and indexable sequence. We are introducing this term here, as it is one you may have encountered before. The term *array* is, in many ways, an overhang from older programming langauges, and is used to describe an ordered collection of items of the same type, but in Python it's not actually a built-in structure — lists serve a similar purpose, while true arrays are provided by libraries like **NumPy**, which we will encounter more in the next module.

NOTE

In addittion to lists, the Python ecosystem includes external packages, and one such popular package that we will use throughout our course, is **NumPy**. NumPy provides its own data structure type known as the **NumPy array**. NumPy arrays are especially useful for mathematical operations, as they support fast, element-wise computations and are optimised for performance. Unlike regular Python lists, NumPy arrays store data more efficiently and in a fixed type, making them well suited to numerical applications. However, a lot of the concepts behind lists are applicable to NumPy arrays. We will explore the differences between NumPy arrays and lists later in the Data Handling module of the course, but they are worth mentioning at this stage, due to their importance in mathematical and scientific computing.

Creating Lists

Lists store multiple items in square brackets `[]`, separated by commas. This can be created by placing square brackets `[]` around your comma-separated data or by using the `list()` function.

> **TIP**
>
> Using square brackets `[]` is the most common method when creating a new list. Alternatively, it is possible to force another data type into a list by feeding it into the round parentheses of an in-built class: `list()`. However, there is no official consenus that specifies that one way to create a list is preferable over the other.

```
# Storing measurements in a list:

exp_measurements = [2.3, 4.1, 3.8, 5.2, 2.9]
print(exp_measurements)
```

```
[2.3, 4.1, 3.8, 5.2, 2.9]
```

```
# A list type <class 'list'>

print(type(exp_measurements))
```

```
<class 'list'>
```

```
# Use this cell to practise creating your own list.
```

Run Code

```
Ready to run code!
```

PRACTICE EXERCISE

1.

Create a list called `fibonacci` with these numbers - 0, 1, 1, 2, 3, 5, 8, 13, 21, 34:

- Use both `[]` and `list()`

```
# Create your fibonacci list here
```

Run Code

```
Ready to run code!
```

List characteristics

Some programming languages insist that all items in a list must be of the same data type, but not in Python. We can mix strings, integers, floats. We can even have functions, other lists, and more. If it's an object in Python then it can be stored in a list.

```
# Lists can contain mixed data types - useful for sample metadata
sample_info = ['Patient_001', 25, 'Male', 68.5]  # ID, age, gender, weight_kg
print(sample_info)
```

```
['Patient_001', 25, 'Male', 68.5]
```

As shown when counting our list of entries, the number of items in your **list** determines its length. To find it programmatically we use the built-in function `len()`.

TIP

You may remember `len()` from the previous lesson being used to find the number of characters in a string. This is because `len()` can be used in multiple circumstances to find the length of an object, all that is required is the object must be a sequence or a collection (data structure).

FACT

What is an object in Python?

In Python, everything is an object, every piece of data you work with. An object is simply a container that holds data along with built-in capabilities (methods), which we'll explore later in this lesson. This **len()** works with all data structures - they're all objects that Python knows how to measure.

This is why you may hear of Python described as **Object-oriented programming**.

```
exp_recordings = [1.2, 4.6, 7.3, 9.2, 2.5, 2.4]
```

```
2
3 # Use len() to find the number of items in your data collection / list
4
5 print(len(exp_recordings))
```

```
6
```

As you can see in the cell above, the `len()` function will return an integer value, as it is a discrete count of the items in the list. This value will always be equal to, or greater than zero, with zero being returned for an empty list (a common occurrence!). This returned value can be stored in a variable to be used in the future, such as the mathematical operations, conditional statements or logical conditions you learned, previously.

```
1 # We can add the length of a new list of recordings to our first set of data
2
3 exp_recordings_2 = [1.3, 4.9]
4
5 exp_1_length = len(exp_recordings)
6 exp_2_length = len(exp_recordings_2)
7
8 print(exp_1_length + exp_2_length)
```

```
8
```

```
1 # We can check if we have enough data
2
3 print(exp_1_length > 5)
```

```
True
```

```
1 # Which can then be chained together with conditional statements to create a work f
2
3 if exp_1_length > 10:
4     print("10 recordings found, stop the experiment")
5 else:
6     print(f"Not enough data points, only {exp_1_length}, please continue")
```

```
Not enough data points, only 6, please continue
```

PRACTICE EXERCISE

2.

You're analysing PCR amplification results from a 96-well plate experiment. You tested 12 different samples to check if your target DNA fragment is present. Each sample should produce a detectable PCR product if the target sequence is successfully amplified. The results are stored in a list: `pcr_products`.

1. Use the `len()` function to check how many PCR products you have
2. Write a conditional statement that prints "Run complete." if you have exactly 12 products, or "Incomplete run - missing samples." if you have fewer than 12

```
pcr_products = ['positive', 'positive', 'negative', 'positive', 'negative', 'positi
```

Run Code

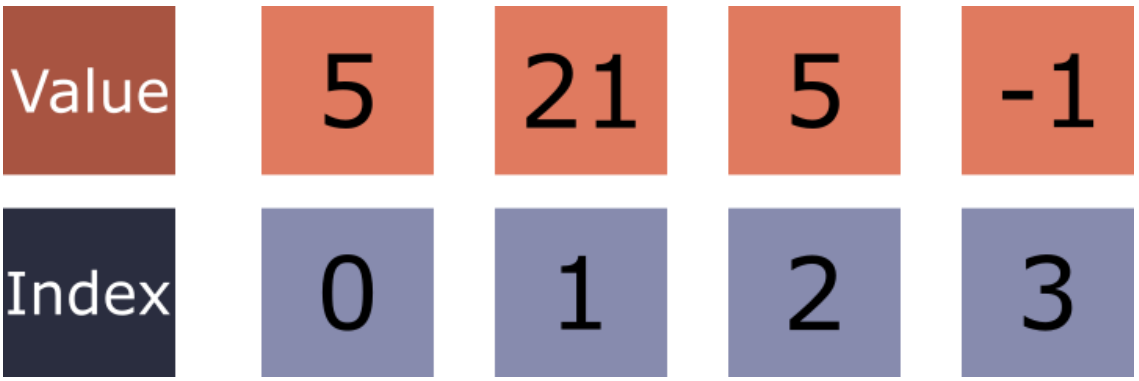
```
Ready to run code!
```

Indexing: accessing specific elements

The fundamentals

Now that we have our data inside a list, we might want to access individual or multiple items within our list.

Each item inside a list has a specific position, termed its **index**, which is a whole number or **integer**, starting with `0` which references the first position. Each subsequent character index then increases by a value of 1. We can visualise this as follows:



KEY TERMS

Index: The position of an element in a list. In Python, indexes are numbered starting from 0 for the first element.

FACT

Why `0` and not `1` for indexing?

This is because Python, as a coding language, uses **zero-based indexing** as the method for finding the first element. This was chosen due to its memory efficiency and continuation from other coding languages like **C**.

Now that we know the positional value (index) of each item, we can use that index to retrieve it from a list.

Given a list stored in the variable `my_list`, we can access an item by writing the variable name, followed by the index value, inside a pair of square brackets `[]`.

```
my_list = [5, 21, 5, -1]

# To retrieve the third item we use index 2:
print(my_list[2])
```

```
5
```

The retrieved item can then be saved to a new variable.

```
item = my_list[3]

print(item)
```

```
-1
```

Use the code cell below to experiment with indexing into the `my_list` list object:

```
# Have a play with indexing my_list
```

Run Code

```
Ready to run code!
```

> **NOTE**
>
> You cannot access values beyond the end of the list; this will result in an **error**. Python reports an `IndexError` if we attempt to access a value that doesn't exist. This kind of error is called a **runtime error**, as it is detected when the Python file is executed, not parsed.
>
> When a Python script runs, the first task that the interpreter performs, is **parsing** - which is where it checks through the entire structure of your code, making sure that there are no syntax errors raised. Once this stage has been successfully completed, the interpreter then runs the code, line by line: and it is at this stage when a runtime error (like `IndexError`) can be raised.

```
# Try running this cell to see the returned error

my_list[4]
```

Run Code

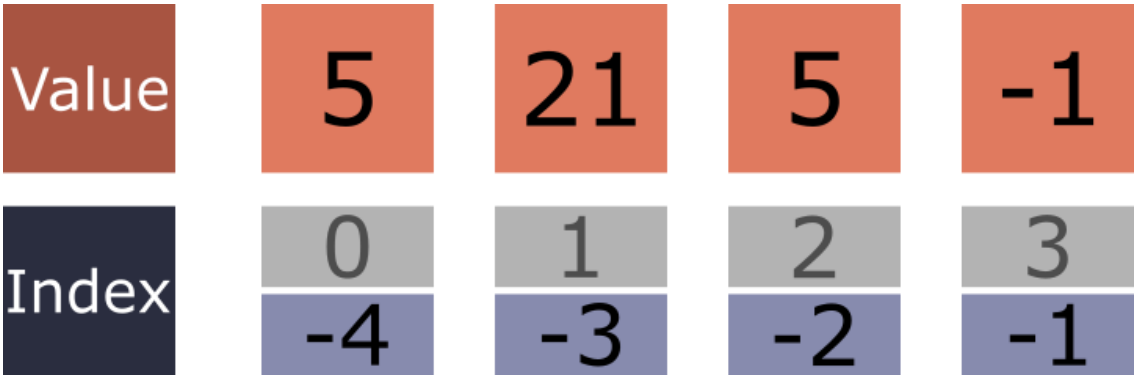
```
Ready to run code!
```

Negative indexing

In scenarios where you might have a long list and wish to access elements at, or near to, the end of that list, it is sometimes more convenient to index an array, backwards — that is, to reference the members from the end of the list, first. This is termed **negative indexing**.

For example, we could have automated sampling of data from an experiment, and it may be that you are only interested in the most recent recording to check that everything is running correctly. If your list is, say, 124 items in length, it might be cumbersome to access the list using `exp_data[123]`. In such example, using negative indexing provides a cleaner and easier way to access the last value: `exp_data[-1]`. It's easier to write than other alternatives such as `exp_data[len(exp_data) - 1]`, which relies on the `len()` function in order to retrieve the last item in the list.

The following diagram displays a list with numbers in it, and shows both the positive and negative index of each item.




```
codons = ['ATG', 'GCA', 'TTC', 'TAG']  # Start, Ala, Phe, Stop

print(f"Last codon: {codons[-1]}")      # -1 = last element
print(f"Second to last: {codons[-2]}")  # -2 = second from end
```

```
Last codon: TAG
Second to last: TTC
```

Use the following code cell to play around with positive and negative indexing:

```
# Have a play around with positive and negative indexing.
# Try accessing all items in `codons` with both.
```

Run Code

```
Ready to run code!
```

PRACTICE EXERCISE

3.

You have the following pH readings from a fermentation experiment: `[6.8, 6.5, 6.2, 5.9, 5.7, 5.4]`:

1. Print the first pH (using positive indexing)

2. Print the second to last pH (using negative indexing)

```
# Complete the PRACTICE EXERCISE here

ph_readings = [6.8, 6.5, 6.2, 5.9, 5.7, 5.4]
```

Run Code

```
Ready to run code!
```

Obtaining an item's index from its actual value

Often, you will be working with a large list: one where you cannot know the position of a particular value that you might be looking for. For this situation, where we know the value but not its index, we can use the method `.index()`.

KEY TERMS

Method: A method is a function that is attached to a specific object, and defines behaviour that is associated *with* that object. Methods are called using dot notation in Python, by typing a `.` directly after the object, followed by the method name with rounded brackets `()`. We'll encounter more methods further in this lesson.

```
# We have a long list of amino acids, but we're not sure where "Met" is

amino_acids = ['Ala', 'Gly', 'Val', 'Leu', 'Ile', 'Pro', 'Met', 'Phe', 'Trp', 'Pro'

# .index() returns the index integer

met_index = amino_acids.index('Met')

print(f"Index of Met: {met_index}")

print("Retrieving the amino acid:", amino_acids[met_index])
```

```
Index of Met: 6
Retrieving the amino acid: Met
```

In lists with duplicated values, if a value appears more than once, the index that is returned will correspond to that value's first occurence.

```
# Pro is present at index 5, as well as index 9
```

```
2
3 print(amino_acids.index('Pro'))
```

```
5
```

A handy feature of the `.index()` method is that it will raise a `ValueError` when the value does not exist in the `list`. You can use this as a method to query large lists for wanted information. These errors were also introduced in the **PF1** lesson.

```
1 # Run this cell to see the error message
2
3 print(amino_acids.index('Cys'))
```

Run Code

```
Ready to run code!
```

Slicing: accessing multiple specific elements

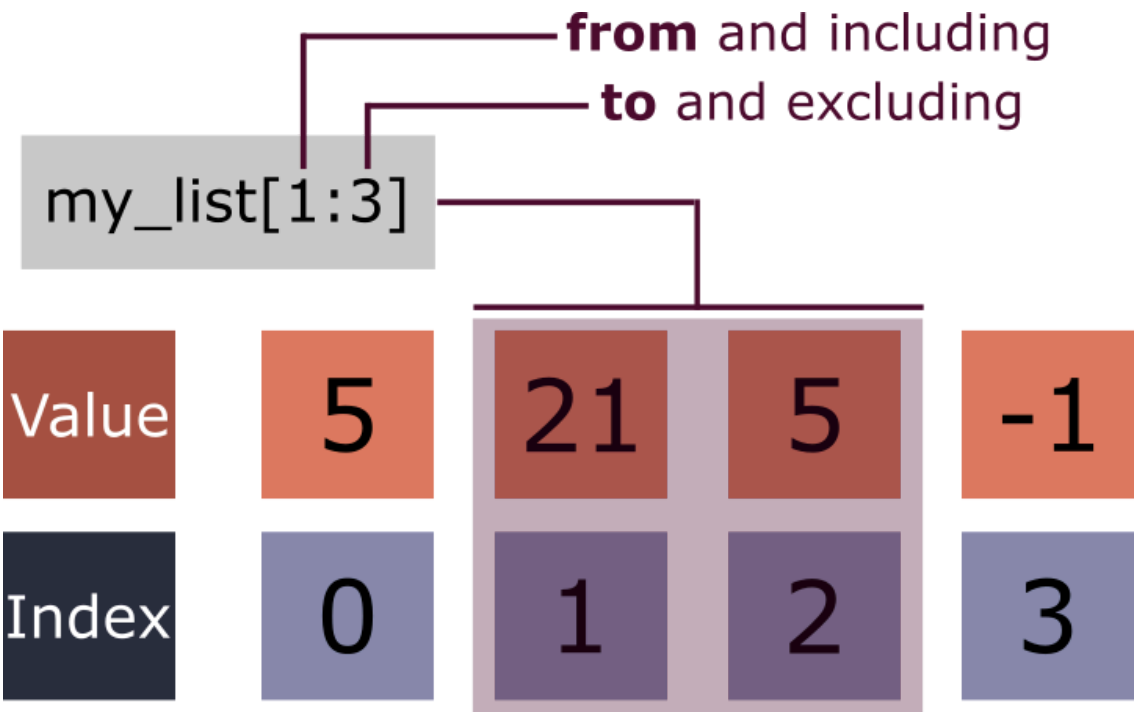
You can also retrieve more than one value from a `list` at a time, using a mechanism called **slicing**. To slice a list you use square brackets `[]` directly after the variable storing your list: `my_list[]`. Slicing extracts portions of lists using a `[start:end]` notation, where start and end are integers, separated by a colon.

IMPORTANT BOX

A slicing behaviour that is very important to note is:

- A **`start`** index is **inclusive** (the value at that position is included).
- An **`end`** index is **exclusive** (the value at that position is not included).

The diagram below helps to visualise this for more clarity:




```
my_list = [5, 21, 5, -1]
```

```
Code executed successfully (no output)
```

```
my_slice = my_list[1:3]

print(my_slice)
```

```
[21, 5]
```

If we want to retrieve all the values *from* the first index, it can be written in either of two ways: `my_list[0:3]` or `my_list[:3]` with the latter being more commonly used. The start index (`0`, in this case) is done away with entirely, with Python's interpreter implicitly treating this as meaning 'all elements up to' to the stop index.

```
# Including the zero when slicing from the first index is not necessary

# With zero
print(my_list[0:3])

# Without, starting with just the :
print(my_list[:3])

# They return the same slice
print(my_list[0:3] == my_list[:3])
```

```
[5, 21, 5]
[5, 21, 5]
True
```

The same is also true in reverse, when you wish to return all the values from a certain point in your list, all the way to end of that list. Namely, the start index is given, and the end value is left out.

```
# Slicing to the end
print(my_list[2:])
```

```
[5, -1]
```

These principles can also be applied to negative indices, resulting in negative slicing, as follows:

```
# Combining with negative slicing can produce the same result
print(my_list[-2:])
```

```
[5, -1]
```

In the code cell below, feel free to experiment with slicing into lists.

```
# Have a play with slicing lists here
```

Run Code

```
Ready to run code!
```

NOTE

Python also provides a `slice()` function that creates reusable slice objects. This is particularly useful when you need to apply the same slice pattern to multiple lists or when the slice parameters need to be calculated programmatically.

```
my_slice = slice(1, 3) # Retrieves items 2 and 3 in the list. Index 3 is exclusive,

print(my_list[my_slice])
```

```
[21, 5]
```

As well as a start and end index (given as integers), you can also give it a third input argument: `step`. This directs `slice()` to skip values, only returning every 2 or 3 values in your slice, for example.

Let's create a new list, with a few more items in it, and slice into this using the `slice()` function, to obtain the first 6 items in this list:

```
my_2nd_list = [1, 2, 3, 4, 5, 6, 7, 8, 9]

my_2nd_list[slice(0, 6)]
```

Run Code

```
Ready to run code!
```

And now run the cell below, which operates over the same 6 elements, but skips every second item from its returned output, by the provision of `2` as the **step** argument:

```
my_2nd_list[slice(0, 6, 2)]
```

Run Code

```
Ready to run code!
```

PRACTICE EXERCISE

4.

You're studying bacterial growth over time and have collected optical density measurements at regular intervals. The data shows the classic bacterial growth curve with different phases. Your growth data is stored in the cell below as `growth_data`:

1. Extract the early phase (first 4 measurements)
2. Extract the late phase (last 3 measurements)
3. Extract the exponential phase (measurements 3-7)

```
# Complete the PRACTICE EXERCISE here
```

```
2
3 growth_data = [0.1, 0.2, 0.4, 0.8, 1.6, 3.2, 6.4, 12.8, 25.6, 51.2]
```

Run Code

```
Ready to run code!
```

Mutability

A key property to consider in differing data structures is their **mutability**; that is, the capability of that data structure being changed, once it has been created. Lists are an example of a **mutable** data structure, and can therefore be modified *in situ* (in place) by adding, removing, and altering the items stored within them. This is done *via* built-in Python methods associated with list objects.

KEY TERMS

mutable: a data type that can be changed after creation. You can modify the contents directly without creating a new object.

We can reassign an item in a `list` through indexing, and casting a new value using hte assignment operator: `=`

```
1 # We notice an item is incorrect
2
3 amino_acids = ['Ala', 'Gly', 'Va']
4
5 # Using the index of the item of interest we reassign it the correct value
6
7 amino_acids[2] = 'Val'
8
9 print(amino_acids)
```

```
['Ala', 'Gly', 'Val']
```

It is also possible to perform the reassignment over a slice containing any number of values. The replacement values must be of the **same length** as the slice they are replacing.

```
1 # We've decided to change the last two amino acids in our list
2 # Have a play with this one
3
4 amino_acids[1:] = ['Pro', 'Met']
```

```
5
6 print(amino_acids)
```

Run Code

```
Ready to run code!
```

Mutability of list members

As discussed at the start of this lesson, **lists** can contain any Python object. Each object will have a data type, and a useful feature of Python lists is that they can contain **multiple data types** within a single list. As a result, each type will be subject to its own properties and mutability.

Methods

As we briefly mentioned earlier, **methods** are special functions associateed with an object using **dot notation**. Each specific data type in Python will have its own suite of methods available to it. You can think of a method as a tool that is permanently attached to a particular type of object, such as a *list*, *string* or an *integer*.

IMPORTANT BOX

The key difference when comparing methods to functions is that `methods` are *dependent on their object*; they **cannot be called independently**. To call a method, we use dot notation `.` in Python, appending the method to the object using its name. I.e. `my_list.append(5)`, `my_list.index(3)`.

Types of methods

Methods can be separated into two general categories:

1. Operations that *return* a result **without** modifying the original object.

2. Operations that **modify** the original object, but *do not return* anything.

Adding to (and combining) lists

One useful feature of **lists** is the ability to add new items to them. There are two common built-in Python methods for this `.append()` and `.insert()`. Both of these methods operate *in situ*, modifying the original *list*.

As with two strings, the `+` operator can also be used to add one list to another *via* a process called **concatenation**.

`.append()` The Python method `.append()` can be used to add items to the *end* of a `list`. If that item is a collection like another `list`, the entire collection is added as a *single element*, rather than merging its contents.

> **NOTE**
>
> When you have a list stored within another list as an item or element, we call the outer list a **nested list**. The inner list is referred to as a **sublist**, and will appear as a comma-separated element inside the outer list, and will be wrapped in square brackets `[]`.

```
amino_acids = ['Ala', 'Gly', 'Val', 'Leu', 'Ile']

amino_acids.append('Met')

print("Appending a single value with .append():", amino_acids)

amino_acids.append(['Phe', 'Trp'])

print("Appending a list using .append():", amino_acids)
```

```
Appending a single value with .append(): ['Ala', 'Gly', 'Val', 'Leu',
'Ile', 'Met']
Appending a list using .append(): ['Ala', 'Gly', 'Val', 'Leu', 'Ile',
'Met', ['Phe', 'Trp']]
```

The method `.insert()` gives you more control than `.append()`, allowing you to dictate the index position you want the new value to be. Due to this, the method takes two arguments, the first being the index, and the second the value.

```
amino_acids.insert(2, 'new AA at index 2')

print(amino_acids)
```

```
['Ala', 'Gly', 'new AA at index 2', 'Val', 'Leu', 'Ile', 'Met', ['Phe',
'Trp']]
```

Adding a new item one at a time for multiple items can be time consuming and inefficient. If you have lots of new data, it is most efficient to add all the new data in one go, combining one list with another, or **concatenating** them. For this you can use the `+` operator, which will return a new object unlike the previous methods.

```
amino_acids_2 = ['Met', 'Phe', 'Trp', 'Pro', 'Ser']

```

```
new_amino_acids = amino_acids + amino_acids_2 # Concatenate two lists using `+`.

print("Original list:", amino_acids)

print("Concatenated lists:", new_amino_acids)
```

```
Original list: ['Ala', 'Gly', 'new AA at index 2', 'Val', 'Leu', 'Ile',
'Met', ['Phe', 'Trp']]
Concatenated lists: ['Ala', 'Gly', 'new AA at index 2', 'Val', 'Leu',
'Ile', 'Met', ['Phe', 'Trp'], 'Met', 'Phe', 'Trp', 'Pro', 'Ser']
```

PRACTICE EXERCISE

5.

You're recording behaviours observed during a primate study. You have a list of morning behaviours saved to the variable `morning_behaviours`:

1. Use `.append()` to add 'vocalising' to the end of the list
2. Use `.insert()` to add 'socialising' at position 1 (second position)
3. Create a new list called `afternoon_behaviours` containing `['playing', 'territorial_display']`
4. Use the `+` operator to combine `morning_behaviours` and `afternoon_behaviours` into a new list called `all_behaviours`

```
morning_behaviours = ['foraging', 'grooming', 'resting']
```

Run Code

```
Ready to run code!
```

Removing items from a list

It is also necessary to remove items from a list, from time to time. For example you might want to drop a feature from your dataset. As with `.append()`, we have two options depending on our needs: `.remove()` and `.pop()`. Both operate *in situ*, modifying the `list`.

```
# Let's remove those items we added that don't fit the theme

amino_acids.remove('new AA at index 2')

print(amino_acids)
```

```
['Ala', 'Gly', 'Val', 'Leu', 'Ile', 'Met', ['Phe', 'Trp']]
```

The method `.pop()` does the same, but instead of only acting *in situ* it will also return the value too. Rather than giving the value, `.pop()` takes the index position.

```
# Store the popped value in a new variable

unwanted_item = amino_acids.pop(-1)

print("Item that is popped:", unwanted_item)

print("Original list:", amino_acids)
```

```
Item that is popped: ['Phe', 'Trp']
Original list: ['Ala', 'Gly', 'Val', 'Leu', 'Ile', 'Met']
```

There is also a third method to remove an item `DEL`. Although it is not commonly used.

```
print("Before:", amino_acids)

del amino_acids[0]

print("After:", amino_acids)
```

```
Before: ['Ala', 'Gly', 'Val', 'Leu', 'Ile', 'Met']
After: ['Gly', 'Val', 'Leu', 'Ile', 'Met']
```

PRACTICE EXERCISE

6.

Using the `list` you created in an earlier **PRACTICE EXERCISE**, `morning_behaviours`:

1. Use `.remove()` to remove 'vocalising' from the list
2. Use `.pop()` to remove 'territorial_display', and save it as a new variable

```
# Write your code here
```

Run Code

```
Ready to run code!
```

Other useful methods

Python's `list` type has many helpful methods beyond just adding and removing items. Below are some other commonly used methods used on lists:

Count specific values: The `.count()` method tells us how many times a particular value appears in a list. This is particularly useful for analysing the frequency of an item in your data.

```
# Count frequency of PCR results
pcr_results = ['positive', 'negative', 'positive', 'positive', 'negative', 'positive

positive_count = pcr_results.count('positive')
negative_count = pcr_results.count('negative')

print(f'Positive results: {positive_count}')
print(f'Negative results: {negative_count}')
```

```
Positive results: 4
Negative results: 2
```

Extending lists: The `.extend()` method adds all items from one list to another, and retains the item designation in the destination list. For instance, unlike `.append()` which adds the entire list as a single element, using `.extend()` adds all items to the list *as individual items*. And unlike using the `+` operator, `.extend()`, modifies the original list *in situ*.

```
morning_samples = ['A1', 'A2', 'A3']
evening_samples = ['B1', 'B2', 'B3']

# Create a copy and extend it
morning_samples.extend(evening_samples)

print('All samples:', morning_samples)
```

```
All samples: ['A1', 'A2', 'A3', 'B1', 'B2', 'B3']
```

Sorting lists: The `.sort()` method sorts items in *ascending* order, by default. Use the optional argument and set its value to `reverse=True`, for *descending* order.

```
concentrations = [2.5, 1.2, 4.8, 3.1, 0.9, 5.2]

# Sort ascending (lowest to highest)
concentrations.sort()
print('Ascending:', concentrations)

# Sort descending (highest to lowest)
concentrations.sort(reverse=True)
print('Descending:', concentrations)
```

```
Ascending: [0.9, 1.2, 2.5, 3.1, 4.8, 5.2]
Descending: [5.2, 4.8, 3.1, 2.5, 1.2, 0.9]
```

```
# Practice: Try using .count(), .extend(), and .sort() with your own data
```

Run Code

```
Ready to run code!
```

PRACTICE EXERCISE

7.

You're analysing enzyme activity data from multiple assays. Your data contains some duplicate readings that you want to count, and you need to sort the results. Using the `enzyme_activities` list:

1. Count how many times `85` appears in the data
2. Create a sorted version (ascending) of the data
3. Create a reversed version of your original list

```
enzyme_activities = [92, 78, 85, 91, 85, 73, 88, 85, 79, 94]
```

Run Code

```
Ready to run code!
```

Membership testing

Often we need to check whether a specific value exists in our dataset. Python provides the **membership operator keyword** `in` for membership testing, which returns the boolean `True` if a value is found in the list, and `False` if not.

```
genes_of_interest = ['BRCA1', 'TP53', 'EGFR', 'MYC', 'KRAS']

# Check if specific genes are in our list
print('BRCA1 in list:', 'BRCA1' in genes_of_interest)
print('BRAF in list:', 'BRAF' in genes_of_interest)
```

```
BRCA1 in list: True
BRAF in list: False
```

We can also use `not in` to check if a value is **not** present in the list:

```
# Check what's missing from our gene panel
```

```
target_genes = ['BRCA1', 'BRCA2', 'TP53']

if 'BRCA2' not in genes_of_interest:
    print('BRCA2 is missing from our gene panel')
else:
    print('BRCA2 is included in our gene panel')
```

```
BRCA2 is missing from our gene panel
```

Membership testing also works with conditional statements, making it easy to create decision logic based on your data:

```
# Checking experimental conditions
valid_conditions = ['control', 'treated', 'inhibitor', 'activator']
current_condition = 'treated'

if current_condition in valid_conditions:
    print(f'Condition {current_condition} is valid - proceeding with analysis')
else:
    print(f'Error: {current_condition} is not a valid experimental condition')
```

```
Condition treated is valid - proceeding with analysis
```

NOTE

Case Sensitivity: Remember that string comparisons in Python are *case-sensitive*. 'Gene' and 'gene' are considered different values. This is particularly important when working with biological nomenclature where case often matters (e.g., gene symbols vs. protein names).

```
# Practice: Given a list of randomly generated peptide sequences, `peptides`. Deter
# Try combining your test with finding the index of the value

peptides = [
  'FAEKE', 'DMSGG', 'CMGFT', 'HVEFW', 'DCYFH', 'RDFDM', 'RTYRA',
  'PVTEQ', 'WITFR', 'SWANQ', 'PFELC', 'KSANR', 'EQKVL', 'SYALD',
  'FPNCF', 'SCDYK', 'MFRST', 'KFMII', 'NFYQC', 'LVKVR', 'PQKTF',
  'LTWFQ', 'EFAYE', 'GPCCQ', 'VFDYF', 'RYSAY', 'CCTCG', 'ECFMY',
  'CPNLY', 'CSMFW', 'NNVSR', 'SLNKF', 'CGRHC', 'LCQCS', 'AVERE',
  'MDKHQ', 'YHKTQ', 'HVRWD', 'YNFQW', 'MGCLY', 'CQCCL', 'ACQCL'
  ]
```

Run Code

```
Ready to run code!
```

References and copies

One of the most important concepts when working with mutable objects like lists is understanding the difference between **references** (also called aliases) and **copies**. This becomes crucial when you want to preserve your original data whilst performing modifications. It's good practice in data exploration/analysis to keep your original data unmodified in a variable for easy access.

KEY TERMS

reference: An alias created when you assign one list variable to another using `=`. Both variables point to the same list object in memory, so modifying one affects the other. For example, if `backup_data = original_data`, then `backup_data` is a reference to `original_data`, not a separate list.

copy: An independent duplicate of a list created using methods like `.copy()` or slice notation `[:]`. Changes made to a copy do not affect the original list, making it essential for preserving experimental data whilst performing modifications. For example, `treated_samples = control_samples.copy()` creates a true copy that can be modified independently.

References (Aliases) When you assign one list variable to another using `=`, you're creating a reference, not a copy. Both variables point to the same list in memory:

```
original_samples = ['Sample_A', 'Sample_B', 'Sample_C']

# This creates a reference, not a copy
samples_alias = original_samples

print('Original:', original_samples)
print('Alias:', samples_alias)
print('Are they the same object?', original_samples is samples_alias)
```

```
Original: ['Sample_A', 'Sample_B', 'Sample_C']
Alias: ['Sample_A', 'Sample_B', 'Sample_C']
Are they the same object? True
```

If we were to modify a new reference, the original will also be changed.

```
# Modifying the alias affects the original!
samples_alias.append('Sample_D')

print('After modifying alias:')
print('Original:', original_samples)
```

```
print('Alias:', samples_alias)
```

```
After modifying alias:
Original: ['Sample_A', 'Sample_B', 'Sample_C', 'Sample_D']
Alias: ['Sample_A', 'Sample_B', 'Sample_C', 'Sample_D']
```

Creating True Copies To preserve your original data, you need to create a proper copy. Python provides two main methods:

```
control_data = [12.5, 13.1, 12.8, 13.0, 12.9]

# Method 1: Using .copy()
treatment_data = control_data.copy()

# Method 2: Using slice notation [:]
backup_data = control_data[:]

print('Original:', control_data)
print('Copy method:', treatment_data)
print('Slice method:', backup_data)
print('Are they the same object?', control_data is treatment_data)
```

```
Original: [12.5, 13.1, 12.8, 13.0, 12.9]
Copy method: [12.5, 13.1, 12.8, 13.0, 12.9]
Slice method: [12.5, 13.1, 12.8, 13.0, 12.9]
Are they the same object? False
```

Now modifications to one list won't affect the others:

```
# Modify the copy - original stays unchanged
treatment_data[0] = 15.2  # Simulate treatment effect

print('After modifying copy:')
print('Original control:', control_data)
print('Modified treatment:', treatment_data)
```

```
After modifying copy:
Original control: [12.5, 13.1, 12.8, 13.0, 12.9]
Modified treatment: [15.2, 13.1, 12.8, 13.0, 12.9]
```

```
# Practice: Create references and copies to understand the difference
```

Run Code

```
Ready to run code!
```

NOTE

The aforementioned versions of copy are called **shallow copies**. A shallow copy creates a *new list*, but the items in the new list are still *references* to the original items. If those items are mutable, such as being a list itself, then changing them in the copy will affect the original.

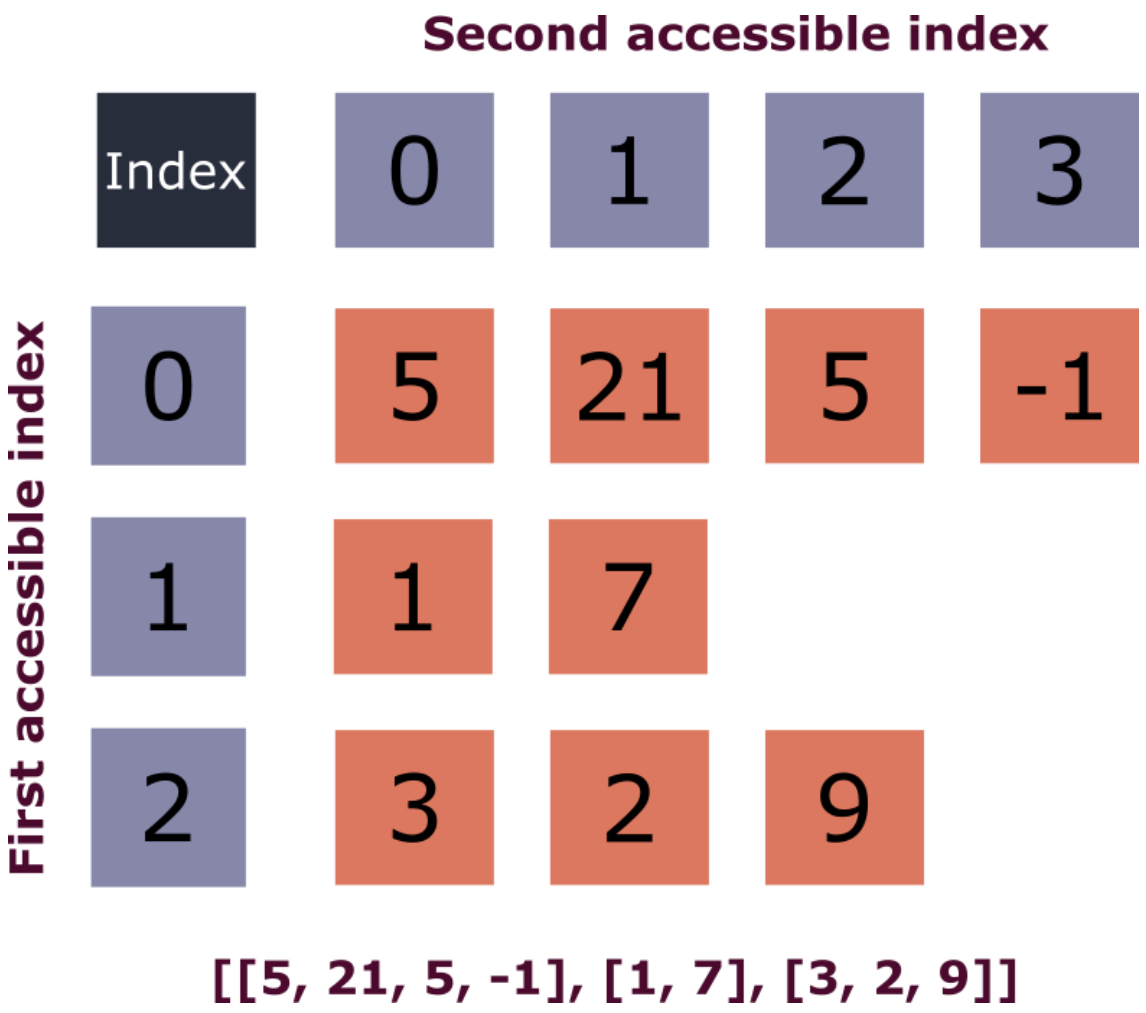
A true **deep copy** requires use of the `copy.deepcopy()` function from the copy module.

Nested Lists

As you have seen throughout this section, lists can contain any data type and even mixed data types. This extends to other data structures, such as lists themselves. A list that includes at least one item that is, itself, a list is referred to as a **nested list**. The inner list, stored within the nested list, is referred to as a **sublist**.

KEY TERMS

Nested: A data structure that contains other data structures of the same type within it. In the context of lists, a nested list is a list that contains other lists as its elements, creating a multi-dimensional structure similar to a table with rows and columns. The diagram below helps to visualise this concept.



Creating nested lists Think of nested lists as being like a table with rows and columns, where each row is a separate list:

```
# Experimental data: [sample_id, pH, temperature, growth_rate]
experiment_data = [
    ['Sample_1', 7.2, 37.0, 0.85],
    ['Sample_2', 6.8, 42.0, 0.73],
    ['Sample_3', 7.5, 37.0, 0.91]
]

print(experiment_data)
```

```
[['Sample_1', 7.2, 37.0, 0.85], ['Sample_2', 6.8, 42.0, 0.73],
['Sample_3', 7.5, 37.0, 0.91]]
```

Accessing elements in a nested list To access elements in nested lists, use multiple square brackets `[]`. The first index selects the row, the second selects the column:

```
# Access specific elements
print('First sample data:', experiment_data[0])  # First row
print('First sample ID:', experiment_data[0][0])  # First row, first column
print('Second sample temperature:', experiment_data[1][2])  # Second row, third colu
```

```
print('All growth rates:', [row[3] for row in experiment_data])  # All fourth colum
```

```
First sample data: ['Sample_1', 7.2, 37.0, 0.85]
First sample ID: Sample_1
Second sample temperature: 42.0
All growth rates: [0.85, 0.73, 0.91]
```

Modifying nested lists You can modify elements in nested lists just like regular lists:

```
# Update a specific measurement
print('Before update:', experiment_data[1])

# Correct a temperature reading
experiment_data[1][2] = 41.5  # Second sample, temperature column

print('After update:', experiment_data[1])
```

```
Before update: ['Sample_2', 6.8, 42.0, 0.73]
After update: ['Sample_2', 6.8, 41.5, 0.73]
```

PRACTICE EXERCISE

8.

You're analysing gene expression data from a cancer research study. The data is organised as a nested list where each row contains `[gene_name, control_expression, treatment_1_expression, treatment_2_expression]`. Using the gene_expression data provided:

1. Print the expression levels for the TP53 gene (second row)
2. Calculate and `print` the fold change for MYC gene comparing `treatment_1` to control (`treatment_1` ÷ `control`)
3. Update the BRCA1 `treatment_2` value to 2.1 (it was incorrectly recorded)
4. Add a new gene `'EGFR'` with expression levels `[3.5, 5.2, 1.8]` to the end of the list

```
# Gene expression matrix: [gene_name, control, treatment_1, treatment_2]
gene_expression = [
```

```
    ['BRCA1', 2.3, 4.1, 1.8],
    ['TP53', 1.9, 3.7, 2.1],
    ['MYC', 3.2, 1.4, 2.9]
]

# Complete the tasks above here
```

Run Code

```
Ready to run code!
```

Nested lists as matrices

A list where at least one of the items is not a list, is considered a one-dimensional (1-D) list. A list can be considered two-dimensional (2-D) when all of its items are lists of another data collection type, themselves. If the internal data lists are all of different sizes, it is called a **jagged list**. The opposite, where all lists are of the same size, would be called a **matrix**.

Matrices are important structures in mathematics and machine learning, as they provide a standardised way to represent and manipulate data in tabular form. Their rectangular structure allows for efficient mathematical operations such as matrix multiplication, transposition, and element-wise calculations. It is therefore important that we introduce them, early on.

The implementation of a matrix is identical to other nested arrays. However, there is a visually appealing way to do so by offsetting the outer brackets of the list:

```
matrix = [
  [1, 2, 3],
  [4, 5, 6],
  [7, 8, 9]
  ]

print(matrix)
```

```
[[1, 2, 3], [4, 5, 6], [7, 8, 9]]
```

```
# Play around with indexing and slicing the matrix

```

Run Code

```
Ready to run code!
```

In future modules we would create this matrix using a `NumPy` array, a list-like object made specifically for numerical calculations using the popular mathematical / scientific Python library, `NumPy`.

Summary

In this section, we learned about Python **lists**, one of the most fundamental and versatile data structures for storing collections of data. We explored how to **create lists** using square brackets `[]` and their key characteristics: they are **mutable**, can hold **mixed data types**, and use **zero-based indexing**.

Lists are the backbone of many data analytics pipelines, so understanding how to get the most out of them is crucial for future learning. Although there is a lot to learn, try to remember roughly some of the possible methods and operations, in the interest of facilitating you looking these up, later on. As with much of the course, please consider this a valuable reference material for your Python programming journey, going forward.

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