File Handling

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What is a File?

- A **file** represents a sequence of bytes on disk, where a group of related data is stored.

- File is ready-made structure.

- File is created for permanent data storage (HDD).

- Syntax: file_object = open("filename", "mode")

File Modes

- **r** – opens a file in reading mode.
- **w** – opens/ creates a file in writing mode.
- **x** - opens a file for exclusive creation. If the file already exists, the operation fails.
- **a** - opens a file in append mode.
- **t** - opens in text mode. (default)
- **b** - opens in binary mode.
- **+** - opens a file for updating (reading and writing)

File Modes

- In '**append mode**', previous contents of file remain & we can write more data after it (if file exists).

- In '**write mode**', previous contents are cleared & user writes from scratch(if file exists).

- A '**Binary File**' is similar to text file. It deals with non-text files like images or executable files..

Opening Files in Python

- Python has a built-in **open() function** to open a file.

- This function returns a file object, also called a **handle**, as it is used to read or modify the file accordingly.

- Ex: f = open("test.txt")   #file in current directory

- f = open("C:/Python38/README.txt") # specifying full path of file

Opening Files in Python

- f = open("raw.txt")   # equivalent to 'r' or 'rt'

- f = open("raw.txt",'w') # write in text mode

- f = open("img.png",'r+b') # read and write in binary mode

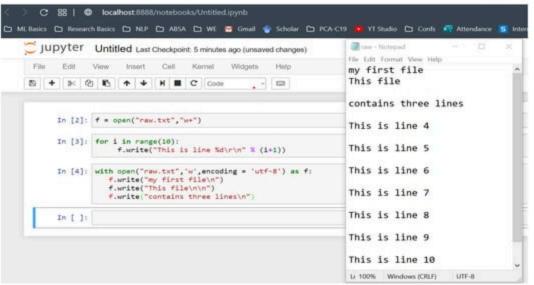- f= open("raw.txt","w+") #read and write permissions

Create a Text File

- f = open("raw.txt","w+")
- Here, f is a variable to open a file.
- open() function is used here.
- raw.txt is a text file that has name 'raw'.
- Permission is read and write.
- If file does not exist, file will be created.

Writing in a File


```
In [2]: f = open("raw.txt","w+")

In [3]: for i in range(10):
            f.write("This is line %d\r\n" % (i+1))

In [4]: with open("raw.txt",'w',encoding = 'utf-8') as f:
            f.write("my first file\n")
            f.write("This file\n\n")
            f.write("contains three lines\n")

In [ ]:
```

raw - Notepad

```
my first file
This file

contains three lines

This is line 4

This is line 5

This is line 6

This is line 7

This is line 8

This is line 9

This is line 10
```

Reading from a File

- f = open("raw.txt", 'r', encoding = 'utf-8')

- f.read(4)   # read the first 4 data

- f.read(4)   # read the next 4 data

- f.read()   # read in the rest till end of file

- f.readline()   #read individual lines of a file

Reading from a File

```
In [5]: f = open("raw.txt",'r',encoding = 'utf-8')
        f.read(4)
```

Out[5]: 'my f'

```
In [6]: f.read(4)
```

Out[6]: 'irst'

```
In [7]: f.read()
```

Out[7]: ' file\nThis file\n\ncontains three lines\n\nThis is line 4\n\nThis is line 5\n\nThis is line 6\n\nThis is line 7\n\nThis is li ne 8\n\nThis is line 9\n\nThis is line 10\n\n'

Reading from a File

In [1]:
```
f = open("input.txt", "r")
print(f.readline())
print(f.readline())
```

DNA is Deoxyribonucleic Acid has four

nitrogen bases named Adenine (A), Thymine (T),

In [2]:
```
print(f.readline())
```

Cytosine(C) and Guanine (G). It is a double helix

In [3]:
```
print(f.readline())
```

in its structure and it has the information carrier in

---

input - Notepad

File Edit Format View Help

DNA is Deoxyribonucleic Acid has four
nitrogen bases named Adenine (A), Thymine (T),
Cytosine(C) and Guanine (G). It is a double helix
in its structure and it has the information
carrier in
human body to any living organism. It plays a
vital
role in human structure. It determines the
characteristic of a human. In a double helix DNA,
each type of nucleotide base paired with their
complementary bases. It is called as
complementary base pairing. The nucleotide'A'
pairs with 'T' and 'C' pairs with 'G'. It is a
proven

Reading from a File

Read the whole file line by line:

```
In [4]: f = open("input.txt", "r")
        for x in f:
          print(x)
```

DNA is Deoxyribonucleic Acid has four

nitrogen bases named Adenine (A), Thymine (T),

Cytosine(C) and Guanine (G). It is a double helix

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complementary base pairing. The nucleotide'A'

Close a File

- When we are done with performing operations on the file, we need to properly close the file.

- Closing a file will free up the resources that were tied with the file. It is done using the **close() method** available in Python.

- Python has a garbage collector to clean up unreferenced objects but we must not rely on it to close the file.

Close a File

In [7]: `f.read()`

Out[7]: `' file\nThis file\n\ncontains three lines\n\nThis is line 4\n\nThis is line 5\n\n`
`ne 8\n\nThis is line 9\n\nThis is line 10\n\n'`

In [8]:
```python
f = open("raw.txt", encoding = 'utf-8')
# perform file operations
f.close()
```

In [ ]:

Close a File

- This method is not entirely safe.

- If an exception occurs when we are performing some operation with the file, the code exits without closing the file.

- A safer way is to use a try...finally block.

```python
try:
    f = open("test.txt", encoding = 'utf-8')
    # perform file operations
finally:
    f.close()
```

Close a File

- This way, we are guaranteeing that the file is properly closed even if an exception is raised that causes program flow to stop.

- The best way to close a file is by using the **with statement**.

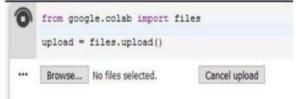- We don't need to explicitly call the close() method. It is done internally.

```
with open("test.txt", encoding = 'utf-8') as f:
    # perform file operations
```

File Handling using Colab

- **Upload the file:-**

```
from google.colab import files

upload = files.upload()
```

Browse... No files selected.   Cancel upload

- **Write from Colab:-**

```
1 from google.colab import drive
2 drive.mount('/mntDrive')
```

Go to this URL in a browser: https://accounts.google.co

Enter your authorization code:
....
Mounted at /mntDrive