



# *File Handling*

**Akhil Kaushik**  
Asstt. Prof., CE Deptt.,  
TIT Bhiwani



## *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

localhost:8888/notebooks/Untitled.ipynb

ML Basics Research Basics NLP ABSA WE Gmail Scholar PCA-C19 YT Studio Confs Attendance Inter

jupyter Untitled Last Checkpoint: 5 minutes ago (unsaved changes)

File Edit View Insert Cell Kernel Widgets Help

Code

```
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

File Edit Format View Help

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

Li 100% Windows (CRLF) UTF-8



## *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 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'

## *Random Access - File*

- There is no need to access the records of file sequentially.
- To random access the files, there are 3 functions:
  - `f.seek()`
  - `f.tell()`

## *Random Access - Files*

- It is used to seek pointer position in file at specified byte. Its syntax is->

**seek(offset, from = SEEK\_SET)**

- Changes the file position to offset bytes, in reference to from (start, current, end).
- **f.tell()** – It returns value of current position in file. The value is count from beginning of file. Its syntax-

**f.tell()**

## *Other Functions*

- **fileno()** - Returns an integer number (file descriptor) of the file.
- **flush()** – Flushes the write buffer of the file stream.
- **seekable()** - Returns True if the file stream supports random access.
- **truncate(size=None)** - Resizes the file stream to size bytes. If size is not specified, resizes to current location.
- **writable()** - Returns True if the file stream can be written to.

## *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\nline 8\n\nThis is line 9\n\nThis is line 10\n\n'
```

```
In [8]: 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.

```
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:-
- Write from Colab:-



```
from google.colab import files  
upload = files.upload()
```



Browse...

No files selected.

Cancel upload



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



Go to this URL in a browser: <https://accounts.google.com>

Enter your authorization code:

.....

Mounted at /mntDrive



# THANK YOU !!!

## CONTACT ME AT:



Akhil Kaushik



[akhilkaushik05@gmail.com](mailto:akhilkaushik05@gmail.com)



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