

```
# Alineamiento de secuencias
from google.colab import drive
drive.mount("/content/drive")
```

```
with open ("/content/drive/MyDrive/examen.fasta/sequence (1).txt", "r") as archivo:
    secuencia = archivo.read ()
    print (secuencia)
```

```
Mounted at /content/drive
>lcl|MG674053.1_cds_AXR85408.1_1 [protein=beta-tubulin] [frame=3] [protein_id=AXR85408.1] [location=join(<1..13,127..168
GCTGCTTTCTGGCAGCAGATCTCAGGCGAGCACGGCCTGGACAGCAATGGCGTGACACGGCACGTCGG
AGCTCCAGCTGGAGCGCATGAGCGTCTACTTCAACGAGGCTTCTGGCAACAAGTACGTCCCGCGTGCTGT
CCTGGTCGATCTCGAGCCCGGTACCATGGACGCCGTCCGCGCCGGTCTTTCGGCCAGCTTTCCGCCCC
GACAACTTTGTCTTCGGCCAGTCGGGTGCTGGCAACAAGTGGGCCAAGGTCTAC
```

```
from google.colab import drive
drive.mount("/content/drive")
```

```
with open ("/content/drive/MyDrive/examen.fasta/sequence (2).txt", "r") as archivo:
    secuencia = archivo.read ()
    print (secuencia)
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=True)
>MZ436942.1 Harringtonia aguacate isolate C2964 large subunit ribosomal RNA gene, partial sequence
CAATAAGCGGAGGAAAGAAACCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAACAGCTCAAA
TTTGAAATCTGGCCCCCGCGGGCCCGAGTTGTACTTTGGAGAGGACGCTTCTGGCGCGGCGCCGGCCGA
GTGCCCTGGAACGGGCGCGGAGAGGGTGAGAGCCCGTACGGCCGGCCGCTAGCCTCTGCGAAGCTC
CTTCGACGAGTCGAGTAGTTTGGAATGCTGCTCAAAATGGGAGGTAAATTTCTTCTAAAGCTAAATACC
GGCCAGAGACCGATAGCCGACAAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGGGTTAAACA
GTACGTGAAATTGCTGAAAGGGAAGCGCCTGTGGCCAGACTTGCGCCCGCGGACCAACCGGCGCCGCGG
CCGGGGCAGCCGCGGGGCGCAGGCCAGCATCGGCTCTCCAGGGGGACAAAGGCCGCGGGAACGTAGCG
CCCTCGGGCGTGTTACAGCCCGCGGCCCATGCCCTGGGGGGCCGAGG
```

```
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
```

```
y_values_random = np.random.randn(19)
y_values_sequence = np.array([2.0, 2.5, 3.0, 3.8, 4.2, 4.8, 5.1, 6.0, 6.3, 7.0, 7.5, 8.2, 8.0, 8.7, 9.5, 10.0, 9.8, 10.5, 11
y_values = y_values_random + y_values_sequence
```

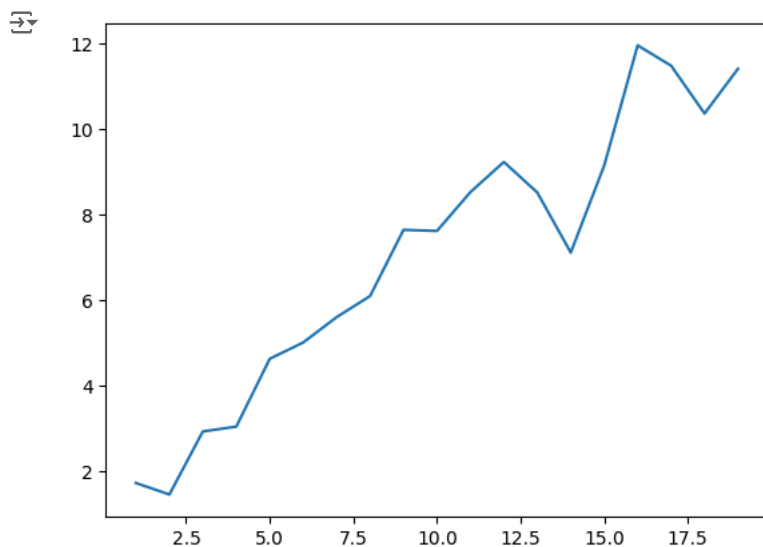
```
df = pd.DataFrame({"x_values": range(1, 20), "y_values": y_values})
```

```
print(df)
```

```

x_values  y_values
0         1  1.711591
1         2  1.444180
2         3  2.919367
3         4  3.032061
4         5  4.619543
5         6  5.001370
6         7  5.595208
7         8  6.089322
8         9  7.639043
9        10  7.612865
10        11  8.522435
11        12  9.228150
12        13  8.511664
13        14  7.107254
14        15  9.143976
15        16 11.956725
16        17 11.481612
17        18 10.361603
18        19 11.409991
```

```
plt.plot("x_values", "y_values", data=df, linestyle="solid")
plt.show()
```

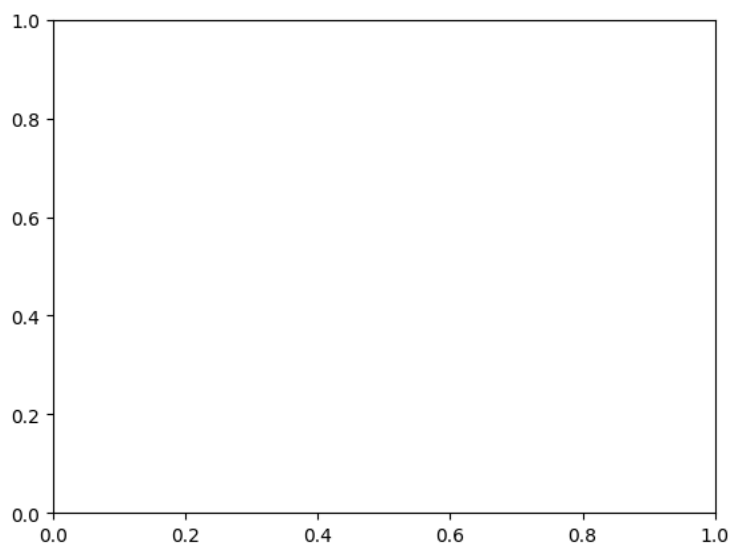


```
plt.plot("x_values", "y_values", data=df, linestyle="none", show="o")
plt.show()
```

```
-----
AttributeError                                Traceback (most recent call last)
<ipython-input-48-2c95d792b1e4> in <cell line: 1>()
----> 1 plt.plot("x_values", "y_values", data=df, linestyle="none", show="o")
      2 plt.show()
```

```
-----
10 frames
/usr/local/lib/python3.10/dist-packages/matplotlib/artist.py in _update_props(self, props, errfmt)
    1195         func = getattr(self, f"set_{k}", None)
    1196         if not callable(func):
-> 1197             raise AttributeError(
    1198                 errfmt.format(cls=type(self), prop_name=k))
    1199         ret.append(func(v))
```

**AttributeError:** Line2D.set() got an unexpected keyword argument 'show'



Pasos siguientes: [Explicar error](#)

!pip install biopython

```
Collecting biopython
  Downloading biopython-1.84-cp310-cp310-manylinux_2_17_x86_64.manylinux2014_x86_64.whl.metadata (12 kB)
Requirement already satisfied: numpy in /usr/local/lib/python3.10/dist-packages (from biopython) (1.26.4)
Downloading biopython-1.84-cp310-cp310-manylinux_2_17_x86_64.manylinux2014_x86_64.whl (3.2 MB)
-----
3.2/3.2 MB 26.6 MB/s eta 0:00:00
Installing collected packages: biopython
Successfully installed biopython-1.84
```

```
from Bio import pairwise2
from Bio.Seq import Seq
from Bio.pairwise2 import format_alignment
```

Empieza a programar o a crear código con IA.