```python
 1 import matplotlib.pyplot as plt
 2
 3 def plot_gc_skew(sequence):
 4     gc_skew = [0]
 5     gc_count = 0
 6
 7     for base in sequence:
 8         if base == 'G':
 9             gc_count += 1
10         elif base == 'C':
11             gc_count -= 1
12
13         gc_skew.append(gc_count)
14
15     # Plotting
16     x_values = range(len(sequence) + 1)
17     plt.plot(x_values, gc_skew, label='G-C Skew')
18
19     plt.title('G-C Skew Plot')
20     plt.xlabel('Position in Sequence')
21     plt.ylabel('G-C Skew')
22     plt.legend()
23     plt.show()
24
25 fasta_filename = r'C:\Users\Ahir\Downloads\sequence (
   3).fasta'
26
27 try:
28     with open(fasta_filename, 'r') as file:
29         # Read the FASTA file (assuming one sequence
   in the file)
30         lines = file.readlines()[1:]
31         dna_sequence = ''.join([line.strip() for line
    in lines])
32
33         # Plot the G-C skew
34         plot_gc_skew(dna_sequence)
35
36 except FileNotFoundError:
37     print(f"Error: File '{fasta_filename}' not found
   .")
```

```
38 except Exception as e:
39     print(f"An error occurred: {e}")
40
41
42
```