

## You

In DNA strings, symbols “A” and “T” are complements of each other, as “C” and “G”. Your function receives one side of the DNA (string, except for Haskell); you need to return the other complementary side. DNA strand is never empty or there is no DNA at all (again, except for Haskell).

## Copilot

Sure, I can help with that. Here is a Python function that takes a DNA string as input and returns its complementary string:

```
def DNA_strand(dna):  
    # create a dictionary that maps each nucleotide to its complement  
    complements = {'A': 'T', 'T': 'A', 'C': 'G', 'G': 'C'}  
  
    # use a list comprehension to replace each nucleotide in the dna string with its complement  
    complement_dna = ''.join([complements[nucleotide] for nucleotide in dna])  
  
    return complement_dna
```

You can use this function like so:

```
print(DNA_strand("ATTGC")) # returns "TAACG"  
print(DNA_strand("GTAT")) # returns "CATA"
```

This function works by creating a dictionary that maps each nucleotide to its complement. It then uses a list comprehension to replace each nucleotide in the DNA string with its complement. The resulting list of complement nucleotides is then joined back into a string and returned. Please let me know if you need help with another programming language!

