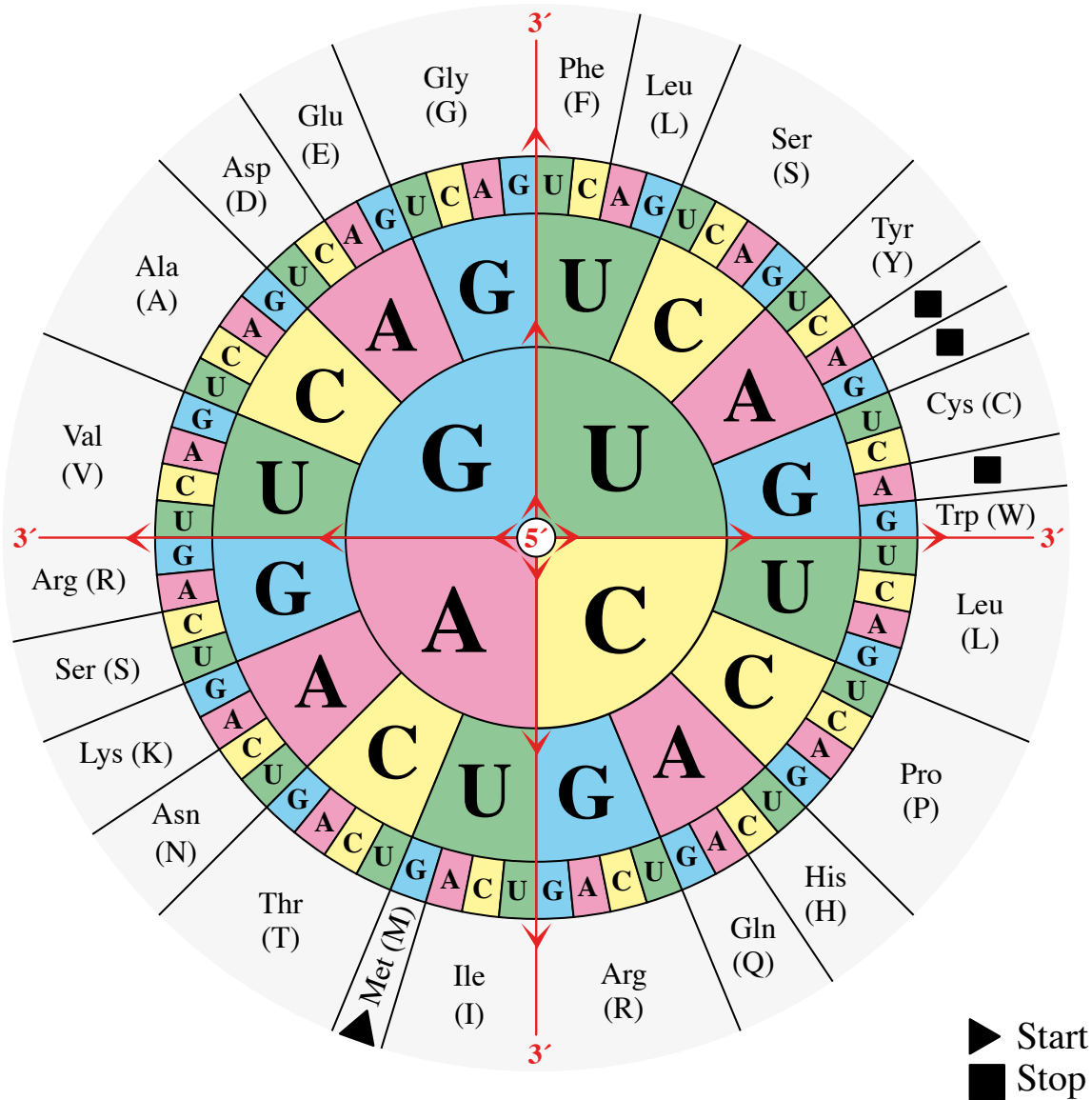


# Lab 05 - String Operations, Using a Map, on DNA / RNA

100pts each part (2 parts), 200 pts total.

Amino Acid Coding Table



Information that you need for this lab is in the lecture notes. <https://github.com/Univ-Wyo-Education/S22-1010/blob/main/class/lect/Lect-11/Lect-11.html.pdf>

## Part 1

Create a new file `conv_t_to_u.py`.

Write a python function that will:

1. Convert the input parameter to all lower case
2. Change all the t's to u's
3. Return the converted string.

This is very close to the example in class.

Use the `example-conv_t_to_u.py` as a starting point.

Link on github.com: [https://github.com/Univ-Wyo-Education/S22-1010/blob/main/homework/04/example-conv\\_t\\_to\\_u.py](https://github.com/Univ-Wyo-Education/S22-1010/blob/main/homework/04/example-conv_t_to_u.py)

Input Example: aaTggTaaa

Output Example: aaugguaaa

Implement a test that verifies that this works. See `example-conv_t_to_u.py` for testing code as well.

## Part 2

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Create a new file `rna_lookup.py`.

Implement a function that uses a dictionary to lookup the amino acid that corresponds to a set of 3 RNA letters. The lookup takes in a 3 letter codon string and returns a single letter amino acid. If the three letter is not found then return '!'

Example Input: "ccu"

Example Output: "P"

For starts codons, "aug", it returns 'M' for stop, "uaa", "uag", "uga" it returns ''

Call the function `rna_to_amino_acid` . Passing the 3 letter amino sequence.

Return the single letter coding for the amino acid as a string.

Use the `example-rna_lookup.py` as a starting point. It has the dictionary in it and some of the other code. You will need to implement some test cases. Look at the previous code and copy, then modify the tests to be appropriate for this.

Link on github.com: [https://github.com/Univ-Wyo-Education/S22-1010/blob/main/homework/04/example-rna\\_lookup.py](https://github.com/Univ-Wyo-Education/S22-1010/blob/main/homework/04/example-rna_lookup.py)

## Part 3

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Download `amino.py` from <https://github.com/Univ-Wyo-Education/S22-1010/blob/main/homework/04/amino.py>.

Run the file `amino.py` that imports the functions from Part 1 and Part 2 and calls them in order to produce the amino acid sequence.

Expected Output:

```
RYPQPARPPGSDLRRTVLRLQSTTEICAEDNAAPPSRCSPGLC
```

Make sure you have all the files in the same folder.

# Turn in

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Your 2 python files `conv_t_to_u.py` and `rna_lookup.py`.