Assignment 13: Synthetic Gene Assembly

April 19th, 2019
Gene Synth

Tell me the truth...

am I stuck in a
LASER
DOG BARK
FART RUT?

Gene Belcher
Bob's Burgers
Gene Synthesis

Fig. 1. Protocol for 5′-gene synthesis by oligo shuffling. (a) Oligo synthesis. (b) Gene assembly: 55 cycles PCR. (c) Add outside primers; gene amplification: 23 cycles PCR. (d) Cut with Sfi I; clone in pUC vector.
Goal of Assignment

- Design primers to synthetically construct a novel peptide.
  - Use Recursive Function to generate primer sequences

- Narrow down primers based on preferred annealing temperatures and by avoiding particular restriction sites.
  - Booleans are a data type with two values, True and False in python.
  - When you are using an “if” statement you are really evaluating whether a statement is True or False.
Assignment

You are given a function (Polk.py) that converts amino acid sequences to all possible nucleotide sequences.

- Given 3 AA sequences, you need to find nucleotide outputs based within a certain temperature range with sequence restrictions.
- Your code will take AA sequence(s) and melting temperature (Tm) as input and output all nucleotide sequences meeting the criteria.
- Don’t forget to disqualify cloning sites
- Consider making your code so that it can take any number of inputs.
Codons

Since some AAs have multiple codon sequences, the code must be able to generate all combinations of sequences possible.
Booleans: Any and All

Any and All allow you to see if a string appears in another string or list or dictionary.

- Any acts as an “or” so False or False or True evaluates to True.
- All acts as an “and” so False and False and True evaluates to False.

*Anytime a True is in an “or” statement, whole statement is True.

*Anytime a False is in an “and” statement, whole statement is False.
Melting Temperature

MT = 64.9 + (41.0 * (#G + #C - 16.4)/ length)

Melting temp is critical for primer design and PCR

Generated primers must be within 0.5C of specified temp

Can write function to check this?
RECURSIVE FUNCTIONS
def check_combinations(dna_string, aa_string):
    # Write a Doc string for this####
    # if this code is confusing to you, uncomment the print statement
    # print("Input DNA is:",dna_string,"Remaining AAs are:", aa_string, sep='\t')

    ### What's going on here###
    if len(aa_string) == 0:
        print(dna_string)

    ### What's going on here###
    else:
        ### What's going on here###
        current_AA = aa_string[0];

        ### What's going on here###
        for single_codon in aa_to_codons[current_AA]:
            ### What's going on here###
            new_dna_string = dna_string + single_codon

            ### What's going on here###
            check_combinations(new_dna_string, aa_string[1:])

    # Main Script

check_combinations("", sys.argv[1] )
Recursive function

def check_combinations(dna_string, aa_string):
    # Write a Doc string for this#
    # if this code is confusing to you, uncomment the print statement
    # print("Input DNA is:", dna_string,"Remaining AAs are:", aa_string, sep='\t')

    ### What's going on here###
    if len(aa_string) == 0:
        print(dna_string)

    else:
        ### What's going on here###
        current_AA = aa_string[0];

        ### What's going on here###
        for single_codon in aa_to_codons[current_AA]:
            ### What's going on here###
            new_dna_string = dna_string + single_codon

            ### What's going on here###
            check_combinations(new_dna_string, aa_string[1:])

    # Main Script
    check_combinations("", sys.argv[1])
Submission

Due Wednesday (3/22/16) before class.

Your submission folder should contain:

1. modified Polk.py script (can take in either 2 or more arguments)
2. README.txt file with instructions on how to run your program and a table of the DNA strings and temperatures for each AA inputted.
3. Should print Primer sequences and Melting Temperature

Remember to comment your script!