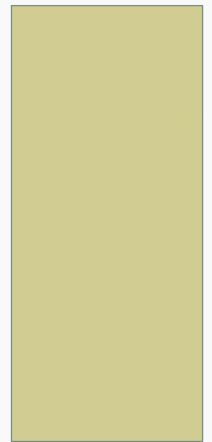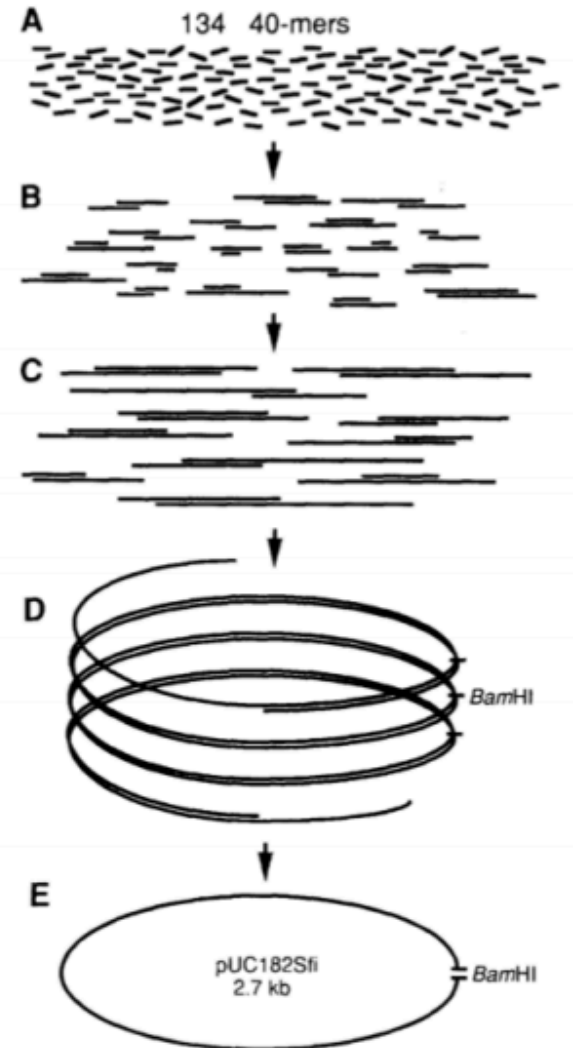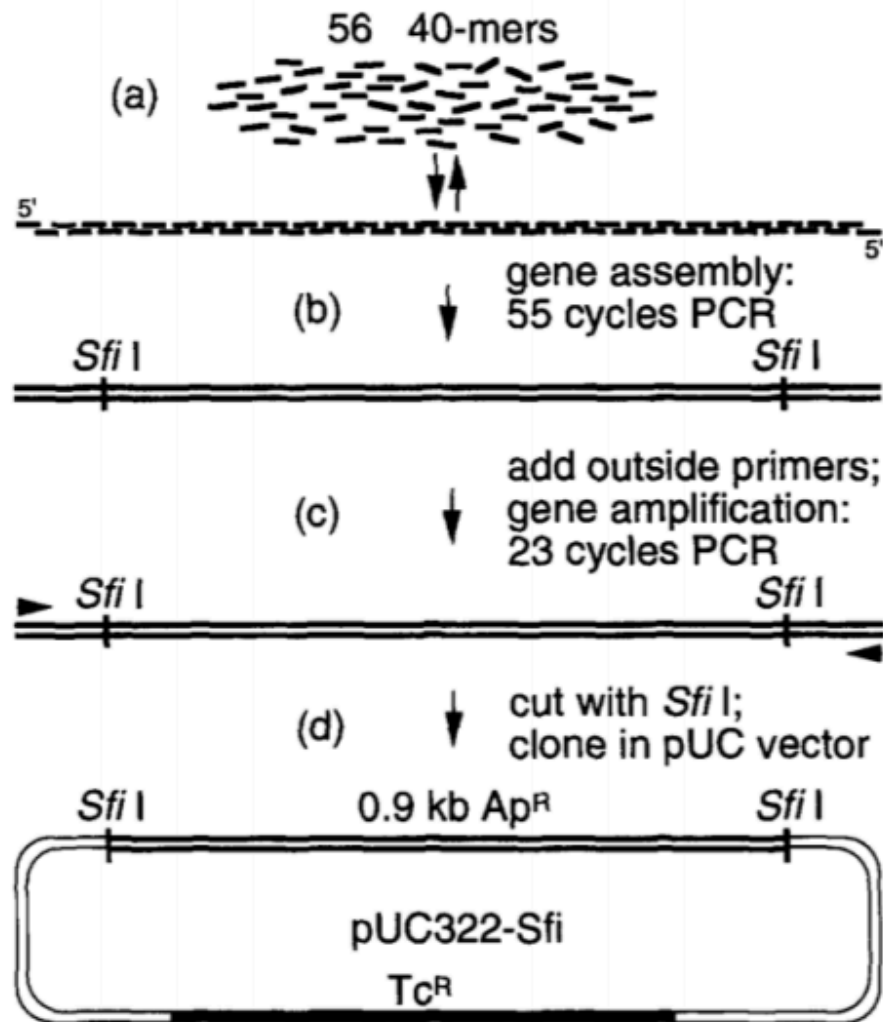# ASSIGNMENT 6

SYNTHETIC BIOLOGY

Gene Synthesis

Stemmer, Gene 164 (1995)

GOAL OF ASSIGNMENT

- Design primers to synthetically construct a novel peptide.

- Use Recursive Function to generate primer sequences
  - The process of repeating some action until you arrive at an answer. At least one of the steps calls for a new instance of the procedure.

- 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.
  - When you are using a while loop you are running until the statement becomes False.

BOOLEANS EXAMPLES

>>> A==1

if A==1: (evaluates to True)

- Do something

else: (above was False)

- Do something else

>>> A==10

while A>5: (Evaluates to True when A is 10,9,8,7,6) (False when A=5)

- Print(A)
- A=A-1

>>> A==1
A==2 evaluates to False
A>1 evaluates to False
A<1 evaluates to False
0<A evaluates to True
True and True evaluates to True
True and False evaluates to False
False and False evaluates to False
True and True evaluates to True
not False evaluates to True
not True evaluates to False
False or True evaluates to True
False or False evaluates to False
True or True evaluates to True

CODON TABLE

- Since some AAs have multiple codon sequences, the code must be able to generate all combination of sequences possible.

Second Base

First Base	U	C	A	G	Third Base
U	UUU ⎤ Phenyl- UUC ⎦ alanine F UUA ⎤ UUG ⎦ Leucine L	UCU ⎤ UCC ⎥ UCA ⎥ Serine S UCG ⎦	UAU ⎤ Tryosine Y UUC ⎦ UAA Stop codon UAG Stop codon	UGU ⎤ Cysteine C UGC ⎦ UGA Stop codon UGG Tryptophan W	U C A G
C	CUU ⎤ CUC ⎥ Leucine L CUA ⎥ CUG ⎦	CCU ⎤ CCC ⎥ Proline P CCA ⎥ CCG ⎦	CAU ⎤ Histidine H CAC ⎦ CAA ⎤ Glutamine Q CAG ⎦	CGU ⎤ CGC ⎥ Arginine R CGA ⎥ CGG ⎦	U C A G
A	AUU ⎤ AUC ⎥ Isoleucine I AUA ⎦ AUG Methionine M start codon	ACU ⎤ ACC ⎥ Threonine T ACA ⎥ ACG ⎦	AAU ⎤ Aspargine N AAC ⎦ AAA ⎤ Lysine K AAG ⎦	AGU ⎤ Serine S AGC ⎦ AGA ⎤ Arginine R AGG ⎦	U C A G
G	GUU ⎤ GUC ⎥ Valine V GUA ⎥ GUG ⎦	GCU ⎤ GCC ⎥ Alanine A GCA ⎥ GCG ⎦	GAU ⎤ Aspartic D GAC ⎦ acid GAA ⎤ Glutamic E GAG ⎦ acid	GGU ⎤ GGC ⎥ Glycine G GGA ⎥ GGG ⎦	U C A G

CHECK IF AN ELEMENT EXISTS (R.ENZYMES)
Using Any and All

```
>>> colors1=['blue','green','purple']
>>> colors2=['pink','purple','orange']
>>> 'pink' in colors1
False
>>> 'blue' in colors1
True
```

```
>>> for color in colors1:
...     color in colors2
...
False
False
True
```

```
>>> any(color in colors2 for color in colors1)
True
>>> all(color in colors2 for color in colors1)
False
```

```
>>> my_seq='AGCTACATA'
>>> my_search=['AG','CT','CG']
>>> 'AG' in my_seq
True
>>> 'CG' in my_seq
False
```

```
>>> for dinuc in my_search:
...     dinuc in my_seq
...
True
True
False
```

```
>>> any(dinuc in my_seq for dinuc in my_search)
True
>>> all(dinuc in my_seq for dinuc in my_search)
False
```

- 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.
- Any easy to remember this is anytime a True is in an "or" statement the whole statement will evaluate to True and anytime a False is in an "and" statement the whole statement will evaluate to False.

MELTING TEMPERATURE

- MT = 64.9 + (41.0 * (#G + #C - 16.4) / Length of oligo)
- All primers must be withing 0.5degrees of 58.0 degrees Celsius!
- Recommend writing another function that checks for this:
  - ie. def meltingtemp(DNA_seq):

YOUR ASSIGNMENT

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

- Given 3 AA sequences, you need to find nucleotides 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.

  - Consider making your code so that in can take any number of inputs.

REQUIREMENTS

- Due Wednesday (3/2/16) before class.
- Your submission folder should contain:
  - A modified Polk.py script (can take in either 2 or more arguments)
  - A README.txt file with instructions on how to run your program and a table of the DNA strings and temperatures for each AA inputted.
    - Should print Primer sequences and Melting Temperature
  - Remember to comment your script!