

Essential Computing for Bioinformatics

Lecture 3

High-level Programming with Python

Container Objects

MARC: Developing Bioinformatics Programs

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- Lecture 2 Homework
- Lists and Other Sequences
- Dictionaries and Sequence Translation
- Finding ORF's in sequences

Lecture 2 Homework: Finding Patterns Within Sequences

```
from string import *  
def searchPattern(dna, pattern):  
    'print all start positions of a pattern string inside a target string'  
    site = findDNAPattern (dna, pattern)  
    while site != -1:  
        print 'pattern %s found at position %d' % (pattern, site)  
        site = findDNApattern (dna, pattern, site + 1)
```

```
>>> searchPattern("acgctaggct","gc")  
pattern gc at position 2  
pattern gc at position 7  
>>>
```

What if DNA may contain unknown nucleotides 'X'?

Example from Pasteur Institute Bioinformatics Using Python

Lecture 2 Homework: One Approach

Write your own find function:

```
def findDNAPattern(dna, pattern, startPosition, endPosition):  
    'Finds the index of the first occurrence of DNA pattern within DNA sequence'  
    dna = dna.lower() # Force sequence and pattern to lower case  
    pattern = pattern.lower()  
    for i in xrange(startPosition, endPosition):  
        # Attempt to match pattern starting at position i  
        if (matchDNAPattern(dna[i:], pattern)):  
            return i  
    return -1
```

Top-Down Design: From **BIG** functions to small helper functions



Lecture 2 Homework: One Approach

Write your own find function:

```
def matchDNAPattern(sequence, pattern):  
    'Determines if DNA pattern is a prefix of DNA sequence'  
    i = 0  
    while ((i < len(pattern)) and (i < len(sequence))):  
        if (not matchDNANucleotides(sequence[i], pattern[i])):  
            return False  
        i = i + 1  
    return (i == len(pattern))
```



Lecture 2 Homework: One Approach

Write your own find function:

```
def matchDNANucleotides(base1, base2):  
    'Returns True is nucleotide bases are equal or one of them is unknown'  
    return (base1 == 'x' or  
            base2 == 'x' or  
            (isDNANucleotide(base1) and (base1 == base2)))
```



Lecture 2 Homework: One Approach

Using default parameters:

```
def findDNAPattern(dna, pattern, startPosition=0, endPosition=None):  
    'Finds the index of the first occurrence of DNA pattern within DNA sequence'  
    if (endPosition == None):  
        endPosition = len(dna)  
    dna = dna.lower() # Force sequence and pattern to lower case  
    pattern = pattern.lower()  
    for i in xrange(startPosition, endPosition):  
        # Attempt to match pattern starting at position i  
        if (matchDNAPattern(dna[i:], pattern)):  
            return i  
    return -1
```



Top Down Design: A Recursive Process

- Start with a high level problem
- Design a high-level function assuming existence of ideal lower level functions that it needs
- Recursively design each lower level function top-down



[10, 20, 30, 40]

['spam', 'bungee', 'swallow']

['hello', 2.0, 5, [10, 20]]

[]

The empty list

Lists can be
heterogeneous
and nested

Generating Integer Lists

```
>>> range(1,5)
```

```
[1, 2, 3, 4]
```

```
>>> range(10)
```

```
[0, 1, 2, 3, 4, 5, 6, 7, 8, 9]
```

```
>>> range(1, 10, 2)
```

```
[1, 3, 5, 7, 9]
```

In General

`range(first,last+1,step)`

Accessing List Elements

```
>> words=['hello', 'my', 'friend']
```

```
>> words[1]  
'my'
```

single element

```
>> words[1:3]  
['my', 'friend']
```

slices

```
>> words[-1]  
'friend'
```

negative
index

```
>> 'friend' in words  
True
```

Testing
List membership

```
>> words[0] = 'goodbye'
```

```
>> print words  
['goodbye', 'my', 'friend']
```

Lists are
mutable

```
>> numbers = range(1,5)
```

```
>> numbers[1:]
```

```
[1, 2, 3, 4]
```

```
>> numbers[:3]
```

```
[1, 2]
```

```
>> numbers[:]
```

```
[1, 2, 3, 4]
```

Slicing operator always returns a NEW list

Modifying Slices of Lists

```
>>> list = ['a', 'b', 'c', 'd', 'e', 'f']
```

```
>>> list[1:3] = ['x', 'y']
```

```
>>> print list
```

```
['a', 'x', 'y', 'd', 'e', 'f']
```

Replacing
slices

```
>>> list[1:3] = []
```

```
>>> print list
```

```
['a', 'd', 'e', 'f']
```

Deleting
slices

```
>>> list = ['a', 'd', 'f']
```

```
>>> list[1:1] = ['b', 'c']
```

```
>>> print list
```

```
['a', 'b', 'c', 'd', 'f']
```

Inserting
slices

```
>>> list[4:4] = ['e']
```

```
>>> print list
```

```
['a', 'b', 'c', 'd', 'e', 'f']
```

Traversing Lists (2 WAYS)

```
codons = ['cac', 'caa', 'ggg']
```

```
for codon in codons:  
    print codon
```

```
i = 0  
while (i < len(codons)):  
    codon = codons[i]  
    print codon  
    i = i + 1
```

Which one do you prefer? Why?

Why does Python provide both `for` and `while`?

String $\leftrightarrow$ List Conversion

```
def stringToList(theString):  
    'Returns the input string as a list of characters'  
    result = []  
    for element in theString:  
        result = result + [element]  
    return result  
  
def listToString(theList):  
    'Returns the input list of characters as a string'  
    result = ""  
    for element in theList:  
        result = result + element  
    return result
```

Complementing Sequences: Utilities

```
DNANucleotides='acgt'
DNAComplements='tgca'

def isDNANucleotide(nucleotide):
    'Returns True when n is a DNA nucleotide'
    return (type(nucleotide) == type("")) and
            len(nucleotide)==1 and
            nucleotide.lower() in DNANucleotides)

def isDNASequence(sequence):
    'Returns True when sequence is a DNA sequence'
    if type(sequence) != type(""):
        return False;
    for base in sequence:
        if (not isDNANucleotide(base.lower())):
            return False
    return True
```



Complementing Sequences

```
def getComplementDNANucleotide(n) :  
    'Returns the DNA Nucleotide complement of n'  
    if (isDNA Nucleotide(n)) :  
        return(DNAComplements[find(DNANucleotides,n.lower())])  
    else:  
        raise Exception ("getComplementDNA Nucleotide: Invalid DNA  
                           sequence: " + n)  
  
def getComplementDNASequence(sequence) :  
    'Returns the complementary DNA sequence'  
    if (not isDNA Sequence(sequence)) :  
        raise Exception("getComplementRNA Sequence: Invalid DNA  
                           sequence: " + sequence)  
  
    result = ""  
    for base in sequence:  
        result = result + getComplementDNA Nucleotide(base)  
    return result
```



Complementing a List of Sequences

```
def getComplementDNASequences(sequences):  
    'Returns a list of the complements of list of DNA sequences'  
    result = []  
    for sequence in sequences:  
        result = result + [getComplementDNASequence(sequence)]  
    return result
```

```
>>> getComplementDNASequences(['acg', 'ggg'])  
  
['tgc', 'ccc']  
  
>>>
```



Python Sequence Types

Type	Description	Elements	Mutable
StringType	Character string	Characters only	no
UnicodeType	Unicode character string	Unicode characters only	no
ListType	List	Arbitrary objects	yes
TupleType	Immutable List	Arbitrary objects	no
XRangeType	return by xrange()	Integers	no
BufferType Buffer	return by buffer()	arbitrary objects of one type	yes/no

Operations on Sequences

Operator/Function	Action	Action on Numbers
[], (), ''	creation	
s + t	concatenation	addition
s * n	repetition n times	multiplication
s[i]	indexation	
s[i:k]	slice	
x in s	membership	
x not in s	absence	
for a in s	traversal	
len(s)	length	
min(s)	return smallest element	
max(s)	return greatest element	

Design and implement Python functions to satisfy the following contracts:

- Return the list of codons in a DNA sequence for a given reading frame
- Return the lists of restriction sites for an enzyme in a DNA sequence
- Return the list of restriction sites for a list of enzymes in a DNA sequence
- Find all the ORF's of length $\geq n$ in a sequence

Dictionaries are mutable unordered collections which may contain objects of different sorts. The objects can be accessed using a key.

Genetic Code As Python Dictionary

```
GeneticCode =  
{ 'ttt': 'F', 'tct': 'S', 'tat': 'Y', 'tgt': 'C',  
  'ttc': 'F', 'tcc': 'S', 'tac': 'Y', 'tgc': 'C',  
  'tta': 'L', 'tca': 'S', 'taa': '*', 'tga': '*',  
  'ttg': 'L', 'tcg': 'S', 'tag': '*', 'tgg': 'W',  
  'ctt': 'L', 'cct': 'P', 'cat': 'H', 'cgt': 'R',  
  'ctc': 'L', 'ccc': 'P', 'cac': 'H', 'cgc': 'R',  
  'cta': 'L', 'cca': 'P', 'caa': 'Q', 'cga': 'R',  
  'ctg': 'L', 'ccg': 'P', 'cag': 'Q', 'cgg': 'R',  
  'att': 'I', 'act': 'T', 'aat': 'N', 'agt': 'S',  
  'atc': 'I', 'acc': 'T', 'aac': 'N', 'agc': 'S',  
  'ata': 'I', 'aca': 'T', 'aaa': 'K', 'aga': 'R',  
  'atg': 'M', 'acg': 'T', 'aag': 'K', 'agg': 'R',  
  'gtt': 'V', 'gct': 'A', 'gat': 'D', 'ggt': 'G',  
  'gtc': 'V', 'gcc': 'A', 'gac': 'D', 'ggc': 'G',  
  'gta': 'V', 'gca': 'A', 'gaa': 'E', 'gga': 'G',  
  'gtg': 'V', 'gcg': 'A', 'gag': 'E', 'ggg': 'G'  
}
```

```
cds = '''atgagtgaacgtctgagcattaccccgctggggccgtatatcggcgcacaaa  
tttcgggtgcccacctgacgcgcccggttaagcgataatcagtttgaacagctttaccatgcggtg  
ctgcgccatcaggtggtggtttctacgcgatcaagctattacgccgcagcagcaacgcgcgctggc  
ccagcgtttttggcgaattgcatattcacctgtttacccgcatgccgaaggggttgacgagatca  
tcgtgctggatacccataacgataatccgccagataacgacaactggcataccgatgtgacattt  
attgaaacgccaccccgaggggcgattctggcagctaaagagttaccttcgaccggcggtgatac  
gctctggaccagcggtattgcggcctatgaggcgctctctgttcccttcgccagctgctgagtg  
ggctgcgtgcggagcatgatttccgtaaatacgttcccgggaatacaataaccgcaaaaccgaggag  
gaacatcaacgctggcgcgagggcggtcgcgaaaaacccgccgttgctacatccggtggtgcgaac  
gcatccggtgagcggtaaacaggcgctgtttgtgaatgaaggctttactacgcgaattgttgatg  
tgagcgagaaagagagcggaagccttgtttaagttttttgtttgcccatacaccaaaccggagttt  
caggtgcgctggcgctggcaaccaaatagatattgcgatttgggataaccgcgtgaccagcacta  
tgccaatgccgattacctgccacagcgacggataatgcatcggggcgacgatccttgggggataaac  
cgtttttatcgggcgggggttaa'''.replace('\n', '').lower()
```

CDS Sequence -> Protein Sequence

```
def translatedDNASequence (dna) :  
    if (not isDNASequence(dna)):  
        raise Exception('translatedDNASequence: Invalid DNA sequence')  
    prot = ""  
    for i in range(0,len(dna),3):  
        codon = dna[i:i+3]  
        prot = prot + GeneticCode[codon]  
    return prot
```

```
>>> translatedDNASequence(cds)
```

```
'MSERLSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQAITPQQQ  
RALAQRFGE LHIHPVYPHAEGVDEIIIVLDTHNDNPPDNDNWHTDVTFIETPPAGAILA  
AKELPSTGGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFP EYKYRKTEEEHQ R  
WREAVAKNPPLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALLSFLFAHITK  
PEFQVRWRWQPNDIAIWDNRVTQHYANADYLPQRRIMHRATILGDKPFYRAG*'
```

```
>>>
```

Dictionary Methods and Operations

Method or Operation	Action
d[key]	Get the value of the entry with key key in d
d[key] = val	Set the value of entry with key key to val
del d[key]	Delete entry with key key
d.clear()	Removes all entries
len(d)	Number of items
d.copy()	Makes a shallow copy
d.has_key(key)	Returns 1 if key exists, 0 otherwise
d.keys()	Gives a list of all keys
d.values()	Gives a list of all values
d.items()	Returns a list of all items as tuples (key, value)
d.update(new)	Adds all entries of dictionary new to d
d.get(key[, otherwise])	Returns value of the entry with key key if it exists Otherwise returns to otherwise
d.setdefault(key [, val])	Same as d.get(key), but if key does not exist, sets d[key] to val
d.popitem()	Removes a random item and returns it as tuple

```
def findDNAORFPos(sequence, minLen, startCodon, stopCodon, startPos, endPos):  
    'Finds the position and length of the first ORF in sequence'  
    while (startPos < endPos):  
        startCodonPos = find(sequence, startCodon, startPos, endPos)  
        if (startCodonPos >= 0):  
            stopCodonPos = find(sequence, stopCodon, startCodonPos, endPos)  
            if (stopCodonPos >= 0):  
                if ((stopCodonPos - startCodonPos) > minLen):  
                    return [startCodonPos + 3, (stopCodonPos - startCodonPos) - 3]  
                else:  
                    startPos = startPos + 3  
            else:  
                return [-1,0] # Finished the sequence without finding stop codon  
        else:  
            return [-1,0] # Could not find any more start codons
```



```
def extractDNAORF(sequence, minLen, startCodon, stopCodon, startPos, endPos):  
    'Returns the first ORF of length >= minLen found in sequence'  
    ORFPos = findDNAORFPos(sequence, minLen, startCodon, stopCodon, startPos, endPos)  
    startPosORF = ORFPos[0]  
    endPosORF = startPosORF + ORFPos[1]  
    if (startPosORF >= 0):  
        return sequence[ORFPos[0]: ORFPos[0]+ORFPos[1]]  
    else:  
        return ""
```



- Design an ORF extractor to return the list of all ORF's within a sequence together with their positions



- Handling files containing sequences and alignments

