BIOINFORMATICS
SESSION 2 PRACTICE

2023-09-11

Working with the molecules of life in the computer

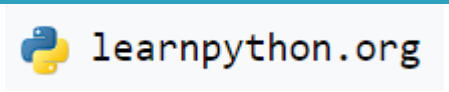
Contents

1. **How to use jupyter notebook**
2. **Basic python programming**; **strings, loops, dictionary**

- **DNA sequence as string**
    - **inferring products of DNA replication**
    - **inferring RNA products of trascription**
    - **inferring protein products of translation**

3. **Exercise & Assignment**

Python tutorial



https://www.learnpython.org/

Hello, World!

Python is a very simple language, and has a very straightforward syntax. It encourages programmers to program without boilerplate (prepared) code. The simplest directive in Python is the "print" directive - it simply prints out a line (and also includes a newline, unlike in C).

There are two major Python versions, Python 2 and Python 3. Python 2 and 3 are quite different. This tutorial uses Python 3, because it more semantically correct and supports newer features.

For example, one difference between Python 2 and 3 is the `print` statement. In Python 2, the "print" statement is not a function, and therefore it is invoked without parentheses. However, in Python 3, it is a function, and must be invoked with parentheses.

To print a string in Python 3, just write:

```
script.py                          IPython Shell
1  print("This line will be printed.")   In [1]:
```

Run

Powered by DataCamp

Chapters

Python tutorial

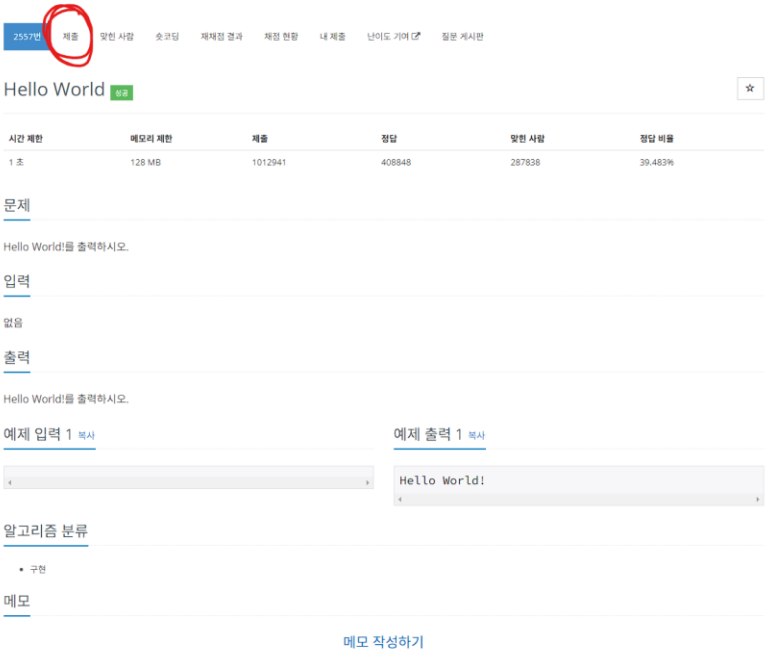
BAE/KJOON>
ONLINE JUDGE

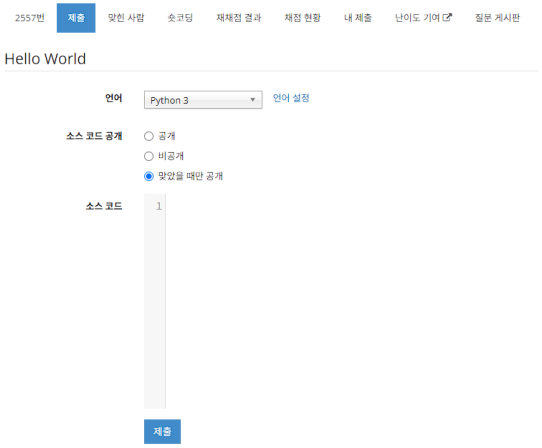
https://www.acmicpc.net/

단계	제목
1	입출력과 사칙연산
2	조건문
3	반복문
4	1차원 배열
5	문자열
6	심화 1
7	2차원 배열
8	일반 수학 1
9	약수, 배수와 소수
10	기하: 직사각형과 삼각형
11	시간 복잡도
12	브루트 포스
13	정렬
14	집합과 맵
15	약수, 배수와 소수 2
16	스택, 큐, 덱
17	==== 절취선 ====

단계	문제 번호	제목
1	2557	Hello World
Hello World!을 화면에 출력하는 문제 (예제 출력과 똑같이 출		
2	1000	A+B
두 수를 입력받고 합을 출력하는 문제		
3	1001	A-B
두 수를 입력받고 뺄셈을 한 결과를 출력하는 문제		
4	10998	A×B
곱셈 문제		
5	1008	A/B
나눗셈 문제. 이 문제에는 "스페셜 저지" 표시가 붙어 있는데,		
6	10869	사칙연산
모든 연산 문제		
7	10926	?!!
입출력을 응용하는 문제?!!		
8	18108	1998년생인 내가 태국에서는
식을 직접 세워서 계산하는 문제		
9	10430	나머지
네 개의 계산식을 계산하는 문제. 이 문제를 푼 다음에는 직접		
10	2588	곱셈
빈 칸에 들어갈 수는?		
11	11382	꼬마 정민
더 큰 수를 더하는 문제		
12	10171	고양이
\' 등의 문자에 주의하며 고양이를 출력하는 문제		
13	10172	개
\', \ 등의 문자에 주의하며 개를 출력하는 문제		

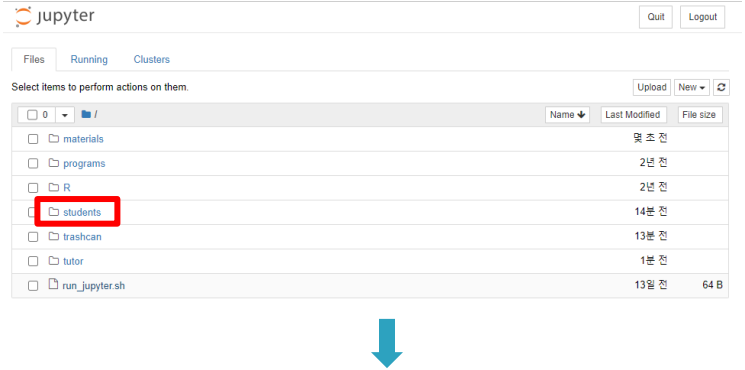
Python tutorial

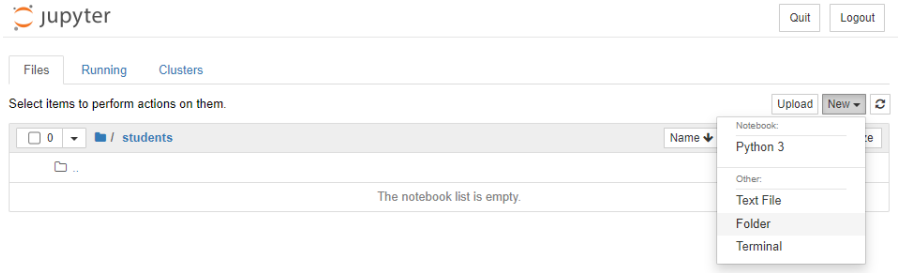




Jupyter notebook 접속

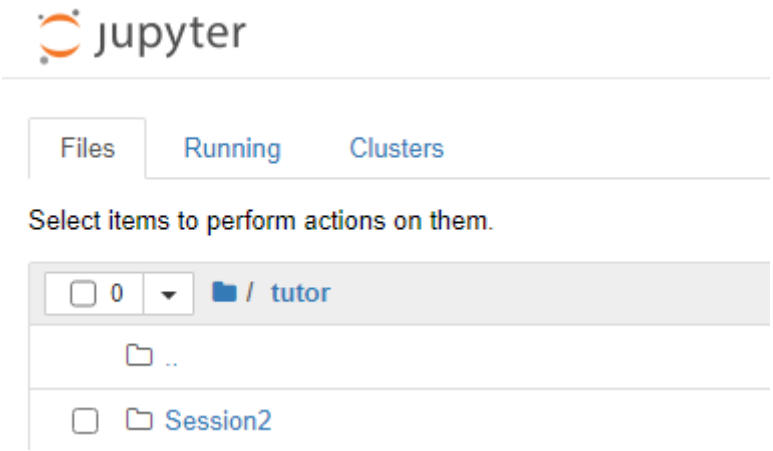
Jupyter notebook 접속





Make a new directory:
학번_영어이름
Ex) 2023123456_hyunwookim

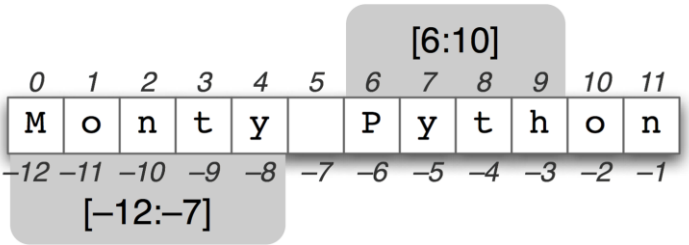
Make Session2 directory



Basic Python - string

python implements 0-based indexing

```
$ python_string.ipynb
```




```
>>> rna='AGCTT'                [OUTPUT]
>>> print(rna[2:4])            CT
>>> print(rna[0:1])            A
>>> print(rna[3:])             TT
>>> print(rna[:3])             AGC
>>> print(rna[:-2])            AGC
>>> print(rna[::-1])           TTCGA
```

http://www.nltk.org/book/ch03.html

Basic Python - string

```
>>> dna = 'GCAATGG'
>>> print(dna)                    "GCAATGG"
>>> rev = dna[::-1]
>>> print(rev)                    "GGTAACG"
```

Basic Python - string

Code continues from the previous one

```
>>> rev = dna[::-1]
>>> comp = rev.maketrans('ACGT','TGCA')
>>> rev_comp = rev.translate(comp)
>>> print(rev_comp)
    "CCATTGC"
```

DNA replication I (ssDNA)

replication.ipynb

```
import string

dna = 'GCAATGG'
rev = dna[::-1]
comp = rev.maketrans('ACGT','TGCA')
rev_comp = rev.translate(comp)
print( rev_comp )
```

```
CCATTGC
```

DNA replication I (dsDNA) – small practice

replication2.ipynb

print the dsDNA sequence representation including the 5’- and -3’ notation as below

```
5'-GCAATGG-3'
3'-CGTTACC-5'
```

```
import string
dna = 'GCAATGG'
comp = dna.maketrans('ACGT','TGCA')
rev_comp = dna.translate(comp)
print ( "5'-" + dna + "-3'" )
print ( "3'-" + rev_comp + "-5'" )
```

```
5'-GCAATGG-3'
3'-CGTTACC-5'
```

Inferring RNA products of transcription

transcription.ipynb

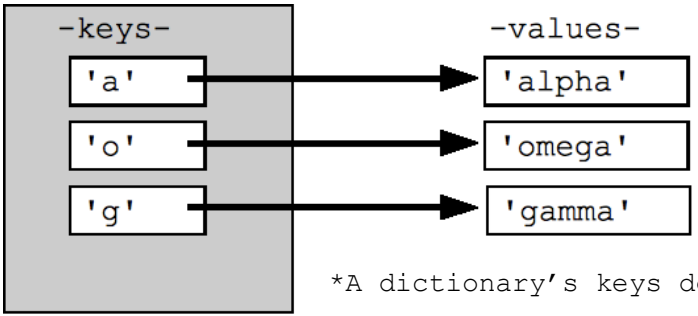
```
>>> dna = 'GCAATGG'
>>> print("The DNA sequence is " + dna )
>>> rna = dna.replace('T', 'U')
>>> print("and the RNA sequence is " + rna )
```

```
dna = 'GCAATGG'
print ( "The DNA sequence is " + dna )
rna = dna.replace('T', 'U')
print ( "and the RNA sequence is " + rna )
```

```
The DNA sequence is GCAATGG
and the RNA sequence is GCAAUGG
```

Basic Python - dictionary

dictionary.ipynb



*A dictionary's keys do not allow duplicates

```
code = {'UUU':'F', 'UUC':'F', 'UUA':'L'}
code
print ( code['UUU'], code['UUC'] )
```

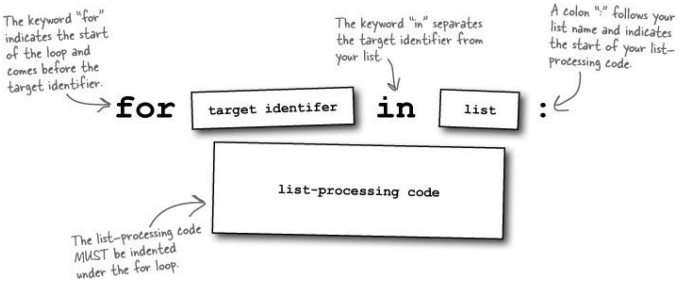
```
F F
```

```
code = {'UUU' : 'F', 'UUC' : 'F', 'UUU' : 'A', 'UUA' : 'L'}
print(code['UUU'])
```

```
A
```

https://cs.stanford.edu/people/nick/python-in-one-easy-lesson/

Basic Python - for loop




```
for i in range(0, 5, 1):
    print ( i )
print ( 'range(0,5,1)' )
print ( list(range(0, 5, 1)) )
print ( 'range(0,5,3)' )
print ( list(range(0, 5, 3)) )
```

```
0
1
2
3
4
range(0,5,1)
[0, 1, 2, 3, 4]
range(0,5,3)
[0, 3]
```

https://www.safaribooksonline.com/library/view/head-first-python/9781449397524/ch01.html

Code1.1 translation.py

translation.ipynb

```
code = {
    'UUU': 'F', 'UUC': 'F', 'UUA': 'L', 'UUG': 'L', 'CUU': 'L', 'CUC': 'L', 'CUA': 'L', 'CUG': 'L',
    'AUU': 'I', 'AUC': 'I', 'AUA': 'I', 'AUG': 'M', 'GUU': 'V', 'GUC': 'V', 'GUA': 'V', 'GUG': 'V',
    'UCU': 'S', 'UCC': 'S', 'UCA': 'S', 'UCG': 'S', 'CCU': 'P', 'CCC': 'P', 'CCA': 'P', 'CCG': 'P',
    'ACU': 'T', 'ACC': 'T', 'ACA': 'T', 'ACG': 'T', 'GCU': 'A', 'GCC': 'A', 'GCA': 'A', 'GCG': 'A',
    'UAU': 'Y', 'UAC': 'Y', 'UAA': '*', 'UAG': '*', 'CAU': 'H', 'CAC': 'H', 'CAA': 'Q', 'CAG': 'Q',
    'AAU': 'N', 'AAC': 'N', 'AAA': 'K', 'AAG': 'K', 'GAU': 'D', 'GAC': 'D', 'GAA': 'E', 'GAG': 'E',
    'UGU': 'C', 'UGC': 'C', 'UGA': '*', 'UGG': 'W', 'CGU': 'R', 'CGC': 'R', 'CGA': 'R', 'CGG': 'R',
    'AGU': 'S', 'AGC': 'S', 'AGA': 'R', 'AGG': 'R','GGU': 'G', 'GGC': 'G', 'GGA': 'G', 'GGG': 'G'
    }

dnaseq = 'GAACTGGGT'
print ( dnaseq )
rnaseq = dnaseq.replace('T', 'U')
print ( rnaseq )

for i in range(0, len(rnaseq), 3):
    codon = rnaseq[i:i + 3]
    amino_acid = code[codon]
    print ( '', amino_acid, end=' ')
```

```
GAACTGGGT
GAACUGGGU
 E  L  G
```

What we learned today

python keywords, variables, strings, numerics, loops, dictionary

```
code = {
    'UUU': 'F', 'UUC': 'F', 'UUA': 'L', 'UUG': 'L', 'CUU': 'L', 'CUC': 'L', 'CUA': 'L', 'CUG': 'L',
    'AUU': 'I', 'AUC': 'I', 'AUA': 'I', 'AUG': 'M', 'GUU': 'V', 'GUC': 'V', 'GUA': 'V', 'GUG': 'V',
    'UCU': 'S', 'UCC': 'S', 'UCA': 'S', 'UCG': 'S', 'CCU': 'P', 'CCC': 'P', 'CCA': 'P', 'CCG': 'P',
    'ACU': 'T', 'ACC': 'T', 'ACA': 'T', 'ACG': 'T', 'GCU': 'A', 'GCC': 'A', 'GCA': 'A', 'GCG': 'A',
    'UAU': 'Y', 'UAC': 'Y', 'UAA': '*', 'UAG': '*', 'CAU': 'H', 'CAC': 'H', 'CAA': 'Q', 'CAG': 'Q',
    'AAU': 'N', 'AAC': 'N', 'AAA': 'K', 'AAG': 'K', 'GAU': 'D', 'GAC': 'D', 'GAA': 'E', 'GAG': 'E',
    'UGU': 'C', 'UGC': 'C', 'UGA': '*', 'UGG': 'W', 'CGU': 'R', 'CGC': 'R', 'CGA': 'R', 'CGG': 'R',
    'AGU': 'S', 'AGC': 'S', 'AGA': 'R', 'AGG': 'R','GGU': 'G', 'GGC': 'G', 'GGA': 'G', 'GGG': 'G'
    }

dnaseq = 'GAACTGGGT'
print ( dnaseq )
rnaseq = dnaseq.replace('T', 'U')
print ( rnaseq )

for i in range(0, len(rnaseq), 3):
    codon = rnaseq[i:i + 3]
    amino_acid = code[codon]
    print ( '', amino_acid, end=' ')
```

```
GAACTGGGT
GAACUGGGU
 E  L  G
```

```
import string

dna = 'GCAATGG'
rev = dna[::-1]
comp = rev.maketrans('ACGT','TGCA')
rev_comp = rev.translate(comp)
print( rev_comp )
```

```
CCATTGC
```

```
>>> rna='AGCTT'
>>> print(rna[2:4])
>>> print(rna[0:1])
>>> print(rna[3:])
>>> print(rna[:3])
>>> print(rna[:-2])
>>> print(rna[::-1])
```

Exercise

- Modify code 1.1(translation.ipynb) so the reverse complementary strand of the original strand sequence (`GAACTGGGT`) is translated. As with the original strand, we only consider the first reading frame of the nucleotide sequence, i.e. the first codon of the complementary strand is `ACC`

Exercise script and result

```
dnaseq = 'GAACTGGGT'
rev = dnaseq[::-1]
comp = rev.maketrans('ATGC', 'UACG')
rnaseq = rev.translate(comp)
print(rnaseq)

for i in range(0, len(rnaseq), 3):
    codon = rnaseq[i:i+3]
    amino_acid = code[codon]
    print('', amino_acid, end = ' ')
```

```
ACCCAGUUC
 T  Q  F
```

Assignment

- Using the code translation.ipynb and *dna_seq* below, generate and print **1) RNA (*rna_seq*) sequence** which is reverse complementary to the underlined DNA sequence segment, and **2) its translated amino acid sequence** (*aminoacid_seq*). The variable "dna_seq" must be present in your python script.

```
dna_seq = "ATGCTTGCAAATACGTCACGACAGTGAAAAA"
```

*hint 해당 sequence 부분을 indexing (ex, dna_seq[x:x]) 을 사용해 추출 ->Reverse complementary

```
rna_seq = "UGUCGUAUUUGCAAG"
aminoacid_seq = ??
```

Translation

- 과제 제출 : 09/17 Sunday 23:59
- 해당 코드 캡처를 한 뒤 워드에 첨부. 기입 하고 코드에 대한 설명 간략히 작성
  워드 파일명은 n주차_학번_이름 형식으로 제출(e.g. 2주차_2023123456_김현우)