clickers exercise on lists
and tuples

list comprehensions

functions as objects

Write a function that takes a list of integers and a function as input and mutates the list replacing each element by the output of the function applied to each element.

A function that you may apply each time could be an addition, a multiplication, division or calculating the factorial of a number.

So you need to define two functions one called apply_to_all and a function of your choice, i.e. fact, add, etc.

map

# list comprehensions

$S = \{x^2 : x \text{ in } \{0 \ldots 9\}\}$

$V = (1, 2, 4, 8, \ldots, 2^{12})$

$M = \{x \mid x \text{ in } S \text{ and } x \text{ even}\}$

lambda

lambda<expression>

filter

reduce

# Dictionary

## name_list

| | |
|---|---|
| 0 | Pelagibacter |
| 1 | E. coli |
| 2 | V. cholera |
| 3 | Chlorobium |
| … | … |

## tax_list

| | |
|---|---|
| 0 | A-Proteobacteria |
| 1 | G-proteobacteria |
| 2 | G-proteobacteria |
| 3 | Chlorobia |
| … | … |

## genome_list

| | |
|---|---|
| 0 | ATCGTCGACC |
| 1 | TCTGGCATAA |
| 2 | GGACTAATTC |
| 3 | AATGGCCTT |
| … | … |

# List

| | |
|---|---|
| Pelagibac ter | Elem 1 |
| 1 | Elem 2 |
| 2 | Elem 3 |
| 3 | Elem 4 |
| ... | ... |

index     element

# Dictionary

| | |
|---|---|
| Key 1 | Val 1 |
| Key 2 | Val 2 |
| Key 3 | Val 3 |
| Key 4 | Val 4 |
| ... | ... |

custom index by label     element

store pairs of data
key
value

values
any type (mutable or immutable)
duplicates

keys
must be unique
immutable/hashable type

no order to keys and values

| lists | dict |
|---|---|
| ordered sequence of elements | matches 'keys' to 'values |
| look up elements using an integer index | look up one item using another item |
| | no order |
| indices have an order | |
| index is an integer | index can be any immutable/ hashable type |

Lets use a genome entry as input. For example you want to see how often does a amino acid appear in a proteome of a particular organism - you can get your own favourite or use the Pelagibacter.faa provided.

The idea is a given set of proteins for a genome you want to walk down the letters specific for a particular amino acid and for each amino acid-- you are going to count basically how many times it actually appears inside of that genome. In addition you want to know how many proteins that genome contains. In the first case you should create a dictionary providing each amino acids count and a list of proteins.

And once you have created that dictionary, then you can do things like find the amino acid that occurs the most often and how many times it does that. Or you extract the amino acids that occur at least some number of times.

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