



Bioinformatical problem solving with Python



Wednesdays 17:30-19:00, M801
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- Download the vcf file
'Apo_cl2_scaffold2_5Mb_stats.vcf' from Github.
- This vcf file contains a complete header (lines starting with '##').
- Each variant site has now an INFO field with different statistics.
- Expand your previous script to filter variant sites by the DP (>1000) and AC (>10) statistic. Calculate mean individual heterozygosities for the filtered sites only.

- A method of designing software systems where data of a specific identifiable type, as well as the code that operates on that data, are packaged together in a modular, reusable unit known as an object.
- Object: Entity that stores a specific state (variables) and behavior (methods). E.g., cars have state (e.g. current speed) and behavior (e.g. changing gear).
- Class: A class is a template/blueprint that is used to create objects.
- Instance: A unique copy of a class representing an object.

- `my_list = list()`
`type(my_list)`
→ `<class 'list'>`
- `my_list.extend([1, 2, 3, 4, 5])`
`print(my_list)`
→ `[1, 2, 3, 4, 5]`
- `dir(my_list)`
→ `[..., 'append', 'clear', 'copy', 'count', 'extend', 'index', 'insert', 'pop', 'remove', 'reverse', 'sort']`
- But we can also design our own custom classes!

- Write a class to represent a DNA sequence.
- Implement the `get_gc_content` function as a method working on the stored sequence string.

```
class Sequence:
```

```
    """Stores a DNA sequence as string."""
```

```
    def __init__(self):
```

```
        self.name = "Human gene 123"
```

```
        self.dna = "ACTTGCATCGT"
```

```
    def get_gc_content(self):
```

```
        g_count = self.dna.count('G')
```

```
        c_count = self.dna.count('C')
```

```
        return (g_count + c_count) / len(self.dna)
```

- `my_sequence = Sequence()`
→ Creates a new instance of the 'Sequence' class
- `dir(my_sequence)`
- `help(my_sequence)`
- `print(my_sequence.dna)`
→ `ACTTGCATCGT`
- `gc_content = my_sequence.get_gc_content()`
`print(round(gc_content, 2))`
→ `0.45`

- The 'Sequence' class stores a predefined DNA string.
- It would be much more useful if the DNA sequence can be defined when creating the object instance.
- We can modify the '.__init__' method (constructor) to take a string as argument.

class Sequence:

"""Stores a DNA sequence as string."""

def __init__(**self**, my_name, my_dna):

self.name = my_name

self.dna = my_dna

def get_gc_content(**self**):

g_count = **self**.dna.count('G')

c_count = **self**.dna.count('C')

return (g_count + c_count) / len(**self**.dna)

my_sequence = Sequence("Human gene 123",
"ATGCGGTCT")

- Extend the “Sequence” class with a method to extract a substring of the DNA sequence.
- Extend the “Sequence” class with a method that returns a dictionary with the counts of each base in the DNA sequence.
- Write a method that returns an instance of the sequence class containing the reverse complement of the DNA sequence.

- Classes can inherit attributes and methods from other classes (base class → derived class).
- Derived classes add functionality or overwrite existing functionality.
- For example:
Base class 'Bird': can eat, fly, walk, etc.
Derived class 'Duck': can also swim, quack, etc.

```
class Bird:
    """Base class representing a bird."""
    def __init__(self, my_name):
        self.name = my_name
    def fly(self, dest):
        print("I'm flying to destination ", dest, ".", sep="")

class Duck(Bird):
    """Derived class representing a duck."""
    def quack(self, times):
        print("I'm quacking ", times, " times.", sep="")
```

- `my_bird = Bird("Harald")`
`isinstance(my_bird, Bird) → True`
`my_bird.fly("Honolulu")`
- `my_duck = Duck("Donald")`
`isinstance(my_duck, Duck) → True`
`isinstance(my_duck, Bird) → True`
`isinstance(my_bird, Duck) → False`
`my_duck.quack(5)`
`my_bird.quack(5)`
- `issubclass(Duck, Bird) → True`
`issubclass(Bird, Duck) → False`