### What we will see here:

- 1. Some design patterns (Wrapper, Interfaces, Factory);
- 2. Testing without and with mocking;
- 3. Debugging sessions;
- 4. Unit tests vs integration tests;
- \* In a bioinformatics context:
- \* Using python;
- \* Somewhat inefficient code but easy to understand

... but I just realised on sunday evening, that this is too much, will probably need to do this in 2 meetings;

... this is an experiment, maybe next time get rid of the bioinformatics context and go directly to the point?

### Obs:

- That is a lot of things, but it is better to slow down and understand stuff than just rushing to present everything;
- Many of these things are fairly recent to me, feel free to correct me at any time;
- The choice of python is because it is the most used language in the group (I'd prefer to do in C++, but all of these things can also be done in C++);

### Contamination Finder tool

Pipeline:

1. Get reads

Reads (human)

### Contamination Finder tool

Pipeline:

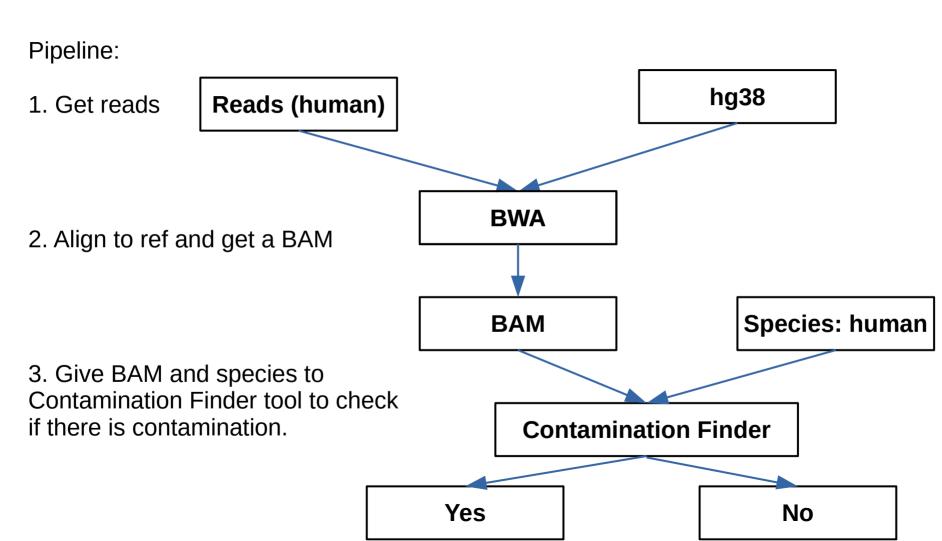
1. Get reads Reads (human)

BWA

2. Align to ref and get a BAM

BAM

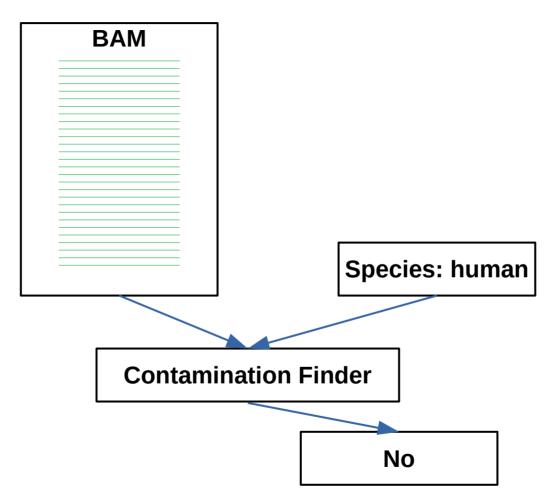
### **Contamination Finder tool**



### How to find contamination (not very realistic)

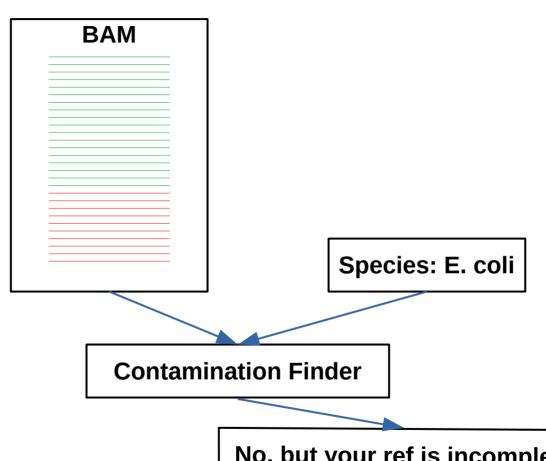
- 1. Get only the unmapped reads from the BAM;
- 2. Search them in a read index (e.g. http://www.bigsi.io/);
- 3. Get the most probable species for each dataset, and count the frequency of each species;
- 4. The most-frequent species is the putative contaminator;

Use case #1: All reads are mapped to the ref



Use case #2: Unmapped reads **BAM** map to E. coli mostly Species: human **Contamination Finder** Yes, E. coli

Use case #3: Unmapped reads map the same species the ref is



No, but your ref is incomplete

### **IMPLEMENTATION**

BAM module only

1. Provide a context-specific interface to more generic functionality: **pysam.AlignedSegment** interface (generic functionality) is huge: https://pysam.readthedocs.io/en/latest/api.html#pysam.AlignedSegment

Our context-specific interface:

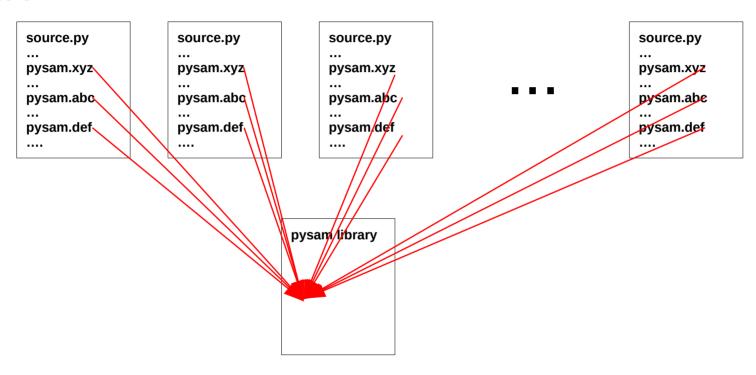
```
class BamRecord:
    def __init__(self, record: AlignedSegment)

def is_unmapped(self) -> bool

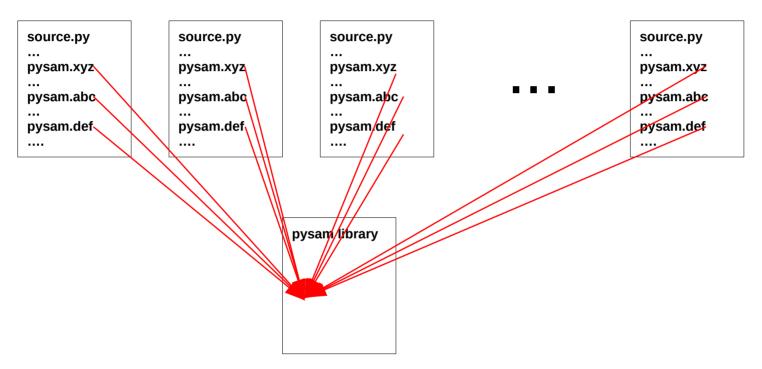
def get_sequence(self) -> str

def __eq__(self, other: "BamRecord")
```

2. Our code is now less tightly-coupled to an external dependency, making it more maintainable:

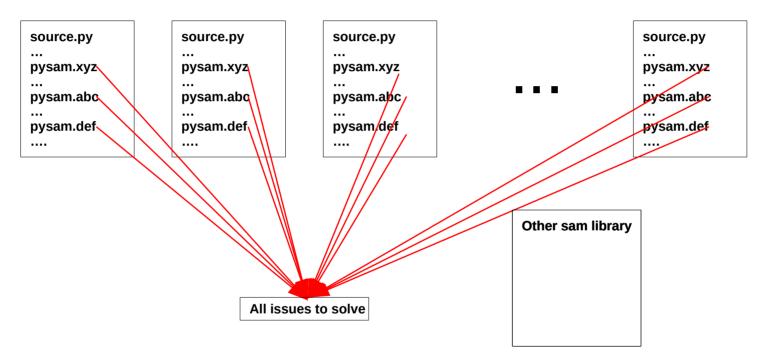


2. Our code is now less tightly-coupled to an external dependency, making it more maintainable:



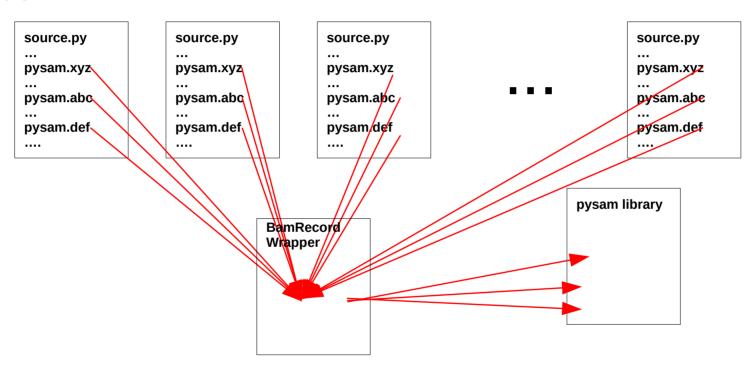
Let's change the SAM parsing library, because pysam has a bug or is too slow, etc...

2. Our code is now less tightly-coupled to an external dependency, making it more maintainable:

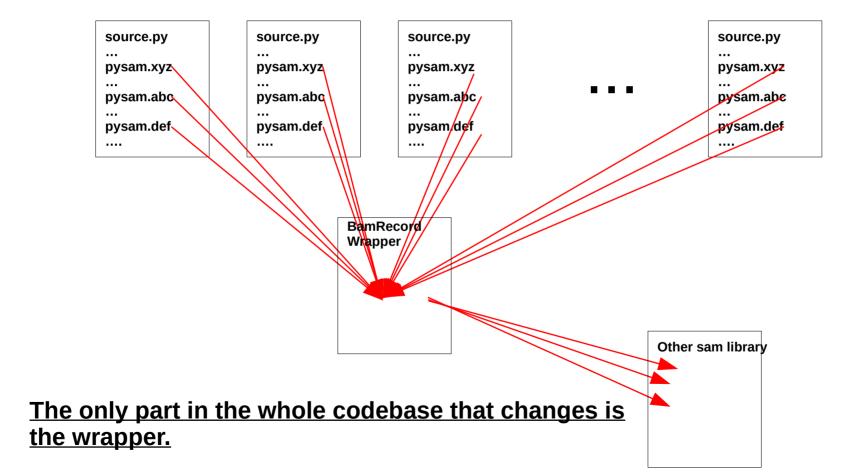


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### **TESTING OF BAM CLASS**

#### Function1

```
Instruction_1;
Instruction_2;
Instruction_3;
call_function_2();
Instruction_4;
Instruction_5;
call_function_3();
...
```

Unit test: should test this single unit:

#### Function1

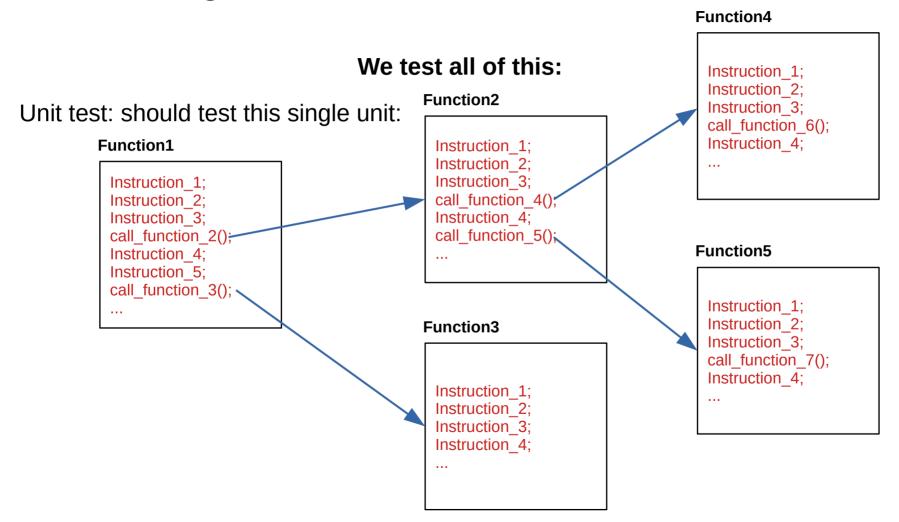
```
Instruction_1;
Instruction_2;
Instruction_3;
call_function_2();
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call_function_3();
...
```

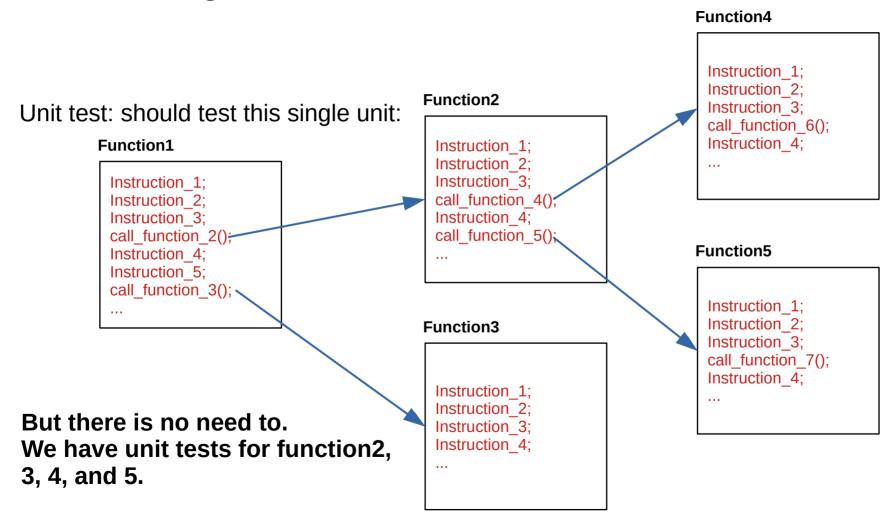
Unit test: should test this single unit:

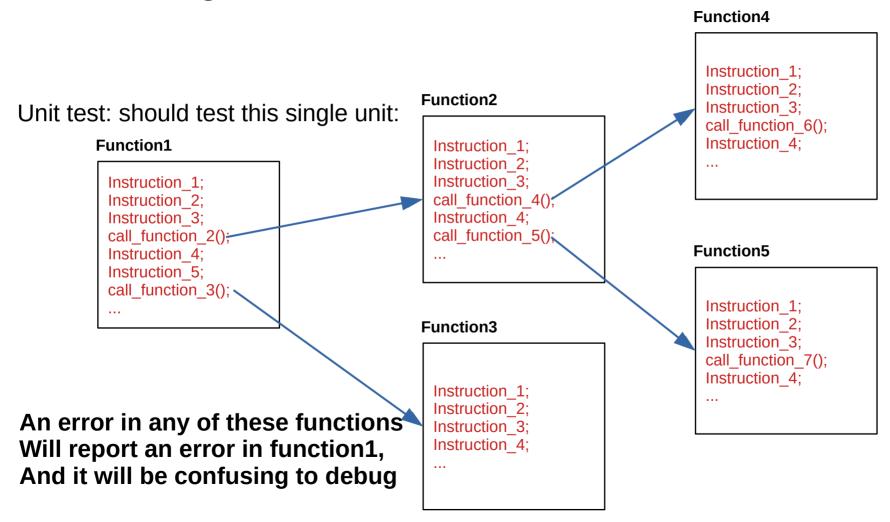
#### Function1

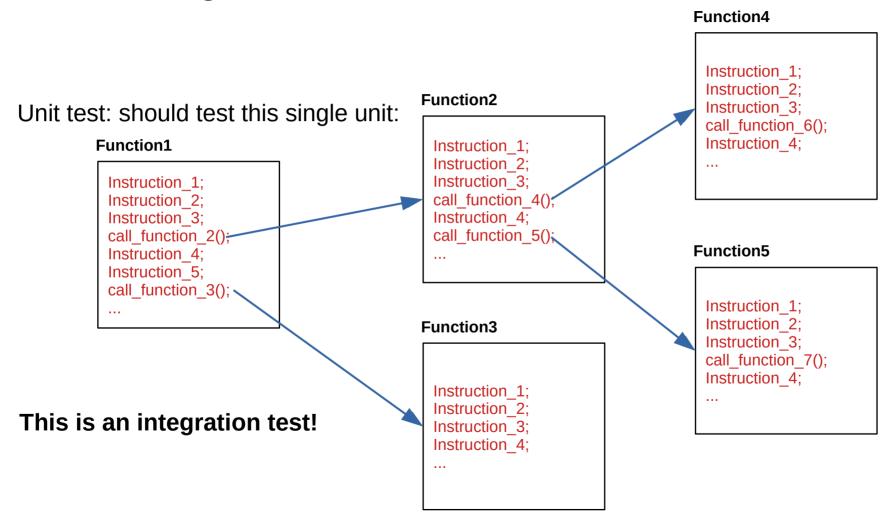
```
Instruction_1;
Instruction_2;
Instruction_3;
call_function_2();
Instruction_4;
Instruction_5;
call_function_3();
...
```

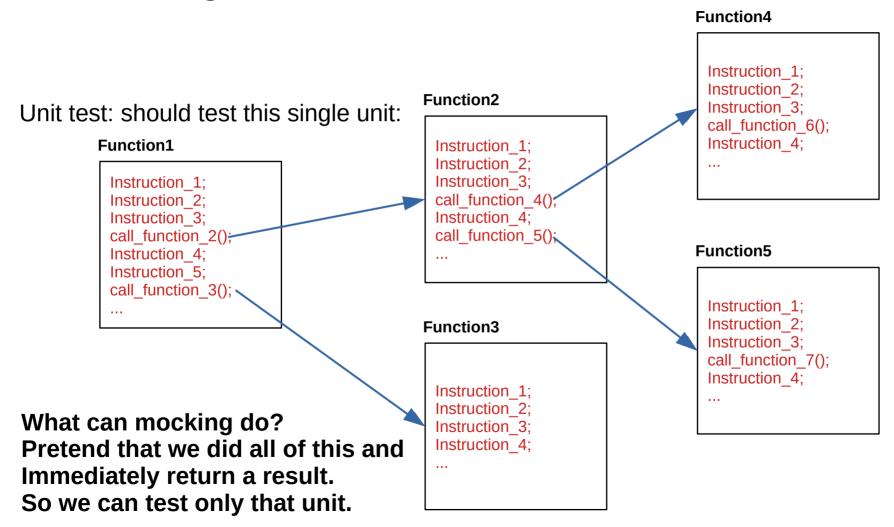
What happens if we use real objects, and not mocking (as we did)?



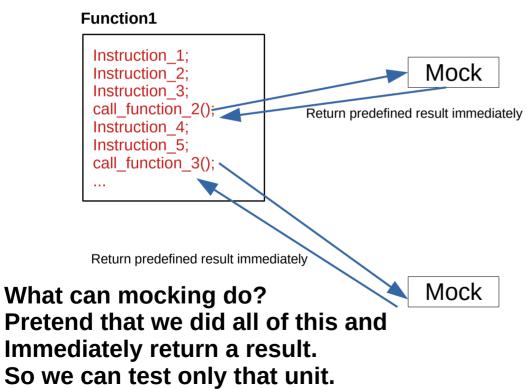


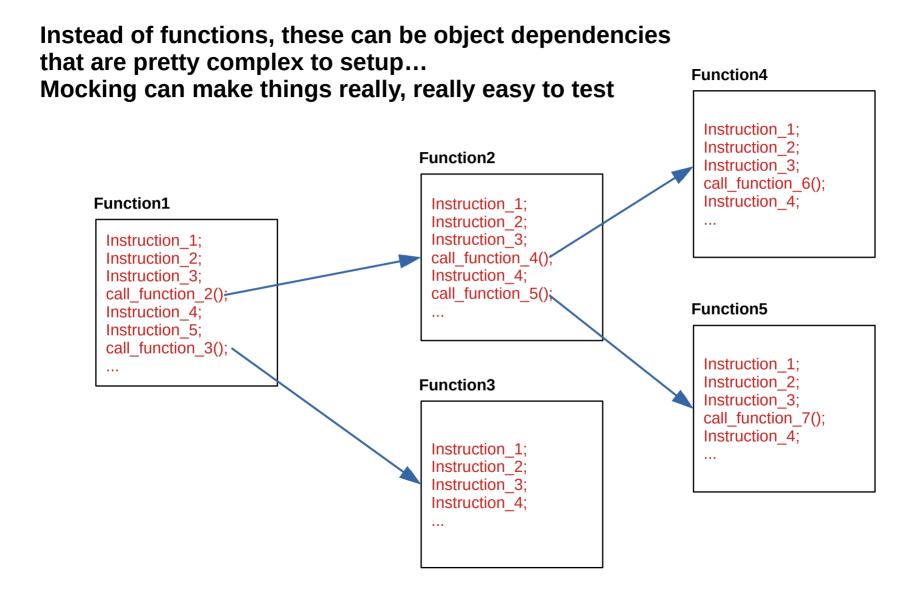






Unit test: should test this single unit:



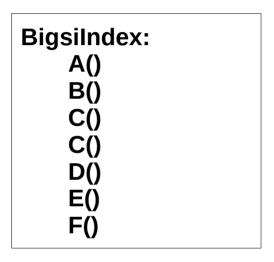


**BUT THE COOL PART IS THE SECOND PART!** 

**END OF FIRST PART...** 

1. Make the code rely on abstract concepts, not on real implementation

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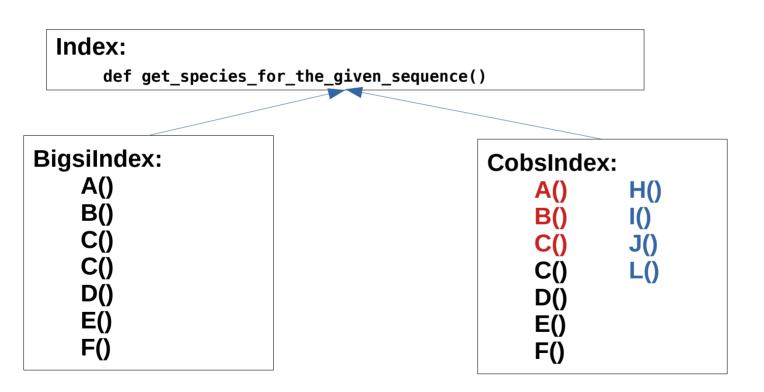
If you code based on the concrete implementation of the BigsiIndex, your code will be biased towards this implementation;

1. Make the code rely on abstract concepts, not on real implementation

CobsIndex	/ = \ =	
A()	H()	
B()	<b>I()</b>	
C()	J()	
C()	L()	
D()		
E()		
F()		

If you change index, you might need to recode a lot of stuff because the indexes might have different functionalities

1. Make the code rely on abstract concepts, not on real implementation



Interfaces/Abstract classes make your code rely on an abstract concept instead of concrete; And forces any Index to implement these concepts

### It makes even easier this presentation:

- With the Index interface, we don't really need to look at the implementation of the BigsiIndex, CobsIndex or ReindeerIndex;
- We know they respect our Index interface, and that is all that matters that is how we communicate
  with an Index in our codebase;

# Index: def get\_species\_for\_the\_given\_sequence()

# Don't care layer

