

Finding a Gene in DNA

Translating into Code

Translating into Code

- Start with a simple approach rather than an all encompassing, always correct approach
 - What if stop codon TAG not 3N away? repeat?
 - What about looking for all three stop codons?
- Specify the method to write before translating into code
 - Return first substring that could be a protein, return "" if not found
 - First start codon ATG, first following TAG

Translating into Code

- Test with many cases, find problems
 - Arithmetic with integers in Java

```
public class TagFinder
{
    public String findProtein(String dna){
        int start = dna.indexOf("atg");
        int stop = dna.indexOf("tag", start+3);
        if ((stop - start) % 3 == 0){
            return dna.substring(start, stop+3);
        }
        else {
            return "";
        }
    }
}
```

Translating into Code

- Test with many cases, find problems
 - Arithmetic with integers in Java

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Arithmetic with Java

- Two numeric types we will use
 - `int` represents integers ... -2, -1, 0, 1, 2, ...
 - `double` represents real numbers, in programming "floating point" 1.2, 3.457, ...
- Arithmetic with integers
 - `+, -, *, /, %`
 - `5/2 == 2`

50

π

Arithmetic with Java

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 - `int` represents integers ... -2, -1, 0, 1, 2, ...
 - `double` represents real numbers, in programming "floating point" 1.2, 3.457, ...
- Arithmetic with integers
 - `+, -, *, /, %`
 - $5/2 == 2$
 - $6 \% 2 == 0$
 - $7 \% 3 == 1$

50



Testing and Debugging

5

Translate To
Code

6

Run Test
Cases

7

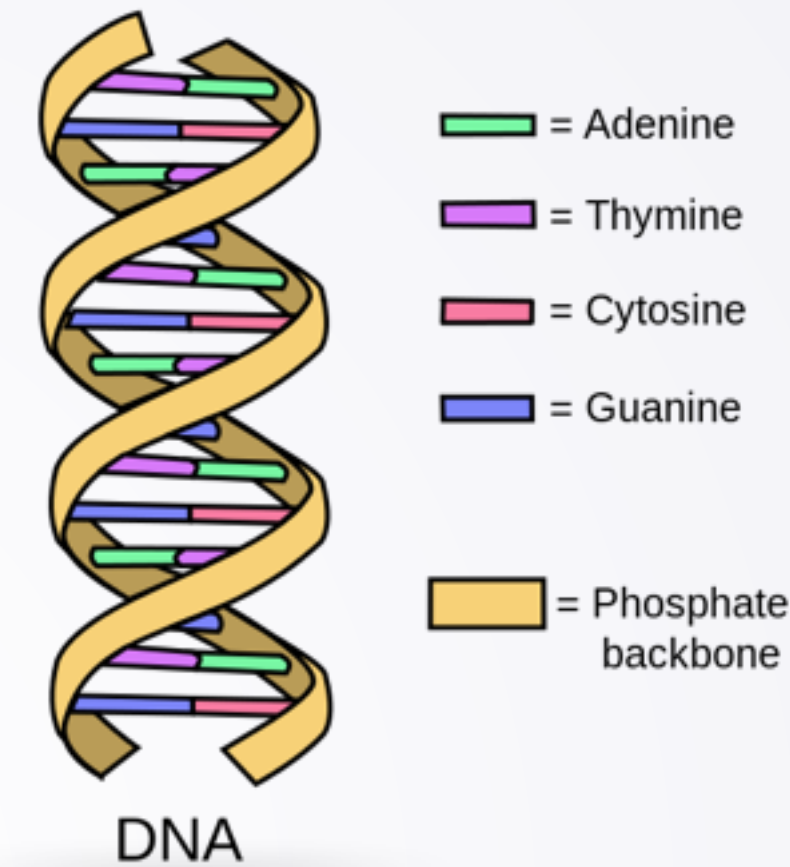
Debug Failed
Test Cases

- We have a working program; what's next?
 - Develop test cases: problem and code help
 - Edge cases or what could cause errors
- Common Java errors
 - Parameter concerns, e.g.,
`String.substring(x, y)`
 - Arithmetic, division by zero

Finishing Up

- If no start codon found ...
 - Return appropriate value

```
public class TagFinder
{
    public String findProtein(String dna){
        int start = dna.indexOf("atg");
        if (start == -1){
            return ""; // no start codon found
        }
        int stop = dna.indexOf("tag",start+3);
        if ((stop - start) % 3 == 0){
            return dna.substring(start,stop+3);
        }
        else {
            return "";
        }
    }
}
```



Finishing Up

- If no start codon found ...
 - Return appropriate value



— = Adenine
— = Thymine
— = Cytosine
— = Guanine

— = Phosphate backbone

DNA

```
public class TagFinder  
{  
    int start = dna.indexOf("atg");  
    if (start == -1){  
        return ""; // no start codon found  
    }  
    if ((stop - start) % 3 == 0){  
        return dna.substring(start, stop+3);  
    }  
    else {  
        return "";  
    }  
}
```