# DNA Detectives: Data Cleaning!

Week 2

# TGGGAATAAAACTGTCGCTAGCGCGGCTTTTTT GAAAATAGCGGC-----

AATACCAACTCCRRTMYCTGCCCTTANTCCATGCTGCGACTATGG AACAAGCCCCGTTGGCTTTGATGATAGTGACCATTATAGGGTCTT TAAAAAAGTGATCGCTTACTCGACTTGTAGTCAGTTGGGGTATA ACTTAATGAACCATGCTTTTTTTAAGGCTTTATTATTCTTAAGCG AAATGGGGGGTTAATAAAGTCCATTCCCCTTACTTACACCATGG GTTTCTATTCTAAAGATTTAATTTTAGAGTTGGCCTATGATCAAT TAACAGCCTTTTATTCAATCCGATTGGTTTATTTAACTTTTATAA GTTCTTGGAATTTAACCCTACCCTTGATATTATTAGCCTTGGGGA

# ATGACGTTGCAGTAGCCTACAGTTAG

What's wrong with this picture? (Assume that this is a full-length sequence.)

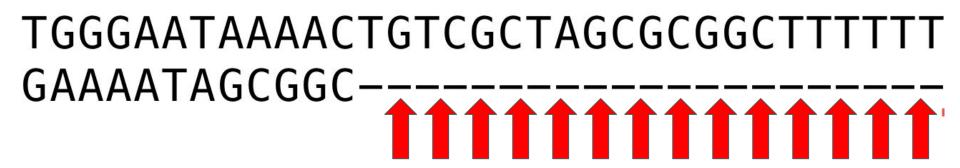
# ATAGTCATGCATCGTATGGCATATCGAT

Hint: recall the error that Biopython gave some of you when you tried to translate your sequence objects last week!

### ATAGATAAAATAAAATTTTTAATTACCG

the reveal...

# TGGGAATAAAACTGTCGCTAGCGCGGCTTTTTT GAAAATAGCGGC-----



AATACCAACTCCRRTMYCTGCCCTTANTCCATGCTGCGACTATGG AACAAGCCCCGTTGGCTTTGATGATAGTGACCATTATAGGGTCTT TAAAAAAGTGATCGCTTACTCGACTTGTAGTCAGTTGGGGTATA ACTTAATGAACCATGCTTTTTTTAAGGCTTTATTATTCTTAAGCG AAATGGGGGGTTAATAAAGTCCATTCCCCTTACTTACACCATGG GTTTCTATTCTAAAGATTTAATTTTAGAGTTGGCCTATGATCAAT TAACAGCCTTTTATTCAATCCGATTGGTTTATTTAACTTTTATAA GTTCTTGGAATTTAACCCTACCCTTGATATTATTAGCCTTGGGGA

AATACCAACTCCRRTMYCTGCCCTTANTCCATGCTGCGACTATGG AACAAGCCCCGTTGGCTTTGATGATAGTGACCATTATAGGGTCTT TAAAAAAAGTGATCGCTTACTCGACTTGTAGTCAGTTGGGGTATA ACTTAATGAACCATGCTTTTTTTAAGGCTTTATTATTCTTAAGCG AAATGGGGGGTTAATAAAGTCCATTCCCCTTACTTACACCATGG GTTTCTATTCTAAAGATTTAATTTTAGAGTTGGCCTATGATCAAT TAACAGCCTTTTATTCAATCCGATTGGTTTATTTAACTTTTATAA GTTCTTGGAATTTAACCCTACCCTTGATATTATTAGCCTTGGGGA

# ATGACGTTGCAGTAGCCTACAGTTAG

# ATGACGTTGCAG TAG CCTACAGTTAG

What's wrong with this picture? (Assume that this is a full-length sequence.)

# ATAGTCATGCATCGTATGGCATATCGAT

Hint: recall the error that Biopython gave some of you when you tried to translate your sequence objects last week!

What's wrong with this picture? (Assume that this is a full-length sequence.)



Hint: recall the error that Biopython gave some of you when you tried to translate your sequence objects last week!

# **ATAGA** TAAAATAAATAAAATTTTAA TTATACCG

#### Our findings:

- Missing nucleotide bases
- Bizarre IUPAC codes
- Stop codon in middle of sequence
- Sequence length not a multiple of 3
- Low complexity region

#### Our solution:

- As Biopython experts, we'll be designing fixes to these problems.
- And so begins the **data cleaning** phase of our research!