Pre-Lab

Audience

This lab is appropriate for High School (grades 10 and above); AP Biology (completed or currently enrolled) is a suggested pre-requisite.

Important terms

Here are some important terms you may already be familiar with or could look up and links to some resources to review before watching the presentation.

- Reverse compliment

- Algorithm

- Positive control

- Negative control

- Experimental design

- BLAST

Bioinformatics Lab Computer Setup

To follow along with this laboratory you will need:

1. Access to an up-to-date web browser such as Chrome or Firefox.

2. (Optional) We suggest getting a DNA Subway account through CyVerse. To get an account, go to https://user.cyverse.org/

Resources

Sanger DNA Sequencing

   DNA Sequencing animation: https://dnalc.cshl.edu/resources/animations/cycseq.html

DNA Barcoding

   DNA Barcoding animation: https://dnalc.cshl.edu/resources/animations/dna-barcoding.html

BLAST Search Exercise (from online video)

>mosquito-1F
CTTTAAGTATATTAATTCGTGCTGAATTAAGTCACCCAGGGATATTTATTGGAAATGATCAAATTTATAACGTAATTGTTACAGCTCATGCATTTATT
ATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTTCCTCGAATA
AATAATATAAGTTTTTGAATATTACCTCCTTCTTTAACTCTACTACTTTCTAGTTCAATAGTAGAAAATGGAGCAGGGACAGGATGAACAGTTTATCC
TCCTCTTTCATCAGGAACAGCACATGCTGGAGCTTCTGTTGATTTAGCAATTTTCTCTCTTCATTTAGCAGGGATTTCATCTATTTTAGGAGCAGTAAA
TTTTATTACTACTGTTATTAATATACGATCATCTGGAATTACTTTAGATCGATTACCTTTATTTGTTTGATCTGTAGTAATTACTGCTATTTTATTACTTT
TATCTCTTCCTGTATTAGCTGGAGCTATTACTATATTATTAACTGATCGAAATTTAAATACTTCCTTCTTTGACCCAATTGGAGGAGGAGA

Blast website: **https://blast.ncbi.nlm.nih.gov/Blast.cgi**

Laboratory Questions

These questions can be completed using the **Companion packet: Using DNA Subway to Analyze DNA Barcoding Sequences (Pages 9-14)** and by watching the video.

1. Why is it important to remove excess Ns from the end of the sequences?

2. Will a sequence and its reverse complement sequence completely overlap?

3. Examining our BLAST results, do you notice hits that have the same statistics (e.g. alignment length, bit score, e-value, mismatches) but originate from different species? What does this tell you about the DNA Barcoding technique? (hint: read the 'More about BLAST' box in the main packet).