



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

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CTTTAAGTATATTAATTCGTGCTGAATTAAGTCACCCAGGGATATTTATTGGAAATGATCAAATTTATAACGTAATTGTTACAGCTCATGCATTTATT  
ATAATTTTTTTTATAGTAATACCAATTATAATTGGAGGATTTGGAAATTGATTAGTTCCTTTAATATTAGGAGCTCCTGATATAGCATTTCCTCGAATA  
AATAATATAAGTTTTTGAATATTACCTCCTTCTTAACTCTACTACTTTCTAGTTCAATAGTAGAAAATGGAGCAGGGACAGGATGAACAGTTTATCC  
TCCTCTTTCATCAGGAACAGCACATGCTGGAGCTTCTGTTGATTTAGCAATTTTCTCTCTTCATTTAGCAGGGATTTTCATCTATTTTAGGAGCAGTAAA  
TTTTATTACTACTGTTATTAATATACGATCATCTGGAATTACTTTAGATCGATTACCTTTATTTGTTTGATCTGTAGTAATTACTGCTATTTTACTTTT  
TATCTCTTCCTGTATTAGCTGGAGCTATTACTATATTATTAAGTATCGAAATTTAAATACTTCTTCTTTGACCCAATTGGAGGAGGAGA
```

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).