AMGEN® Biotech Experience

Scientific Discovery for the Classroom

Ireland

Activity booklet for ABE IrelandLab 6 Introduction to genomics and bioinformatics

Activity 1 Read this sequence and write its complementary sequence

Activity 2 Label the diagram to describe the components of the genome

3 [ ]

4 [ ]

2 [ ]

1 [ ]

5 [ ]

6 [ ]
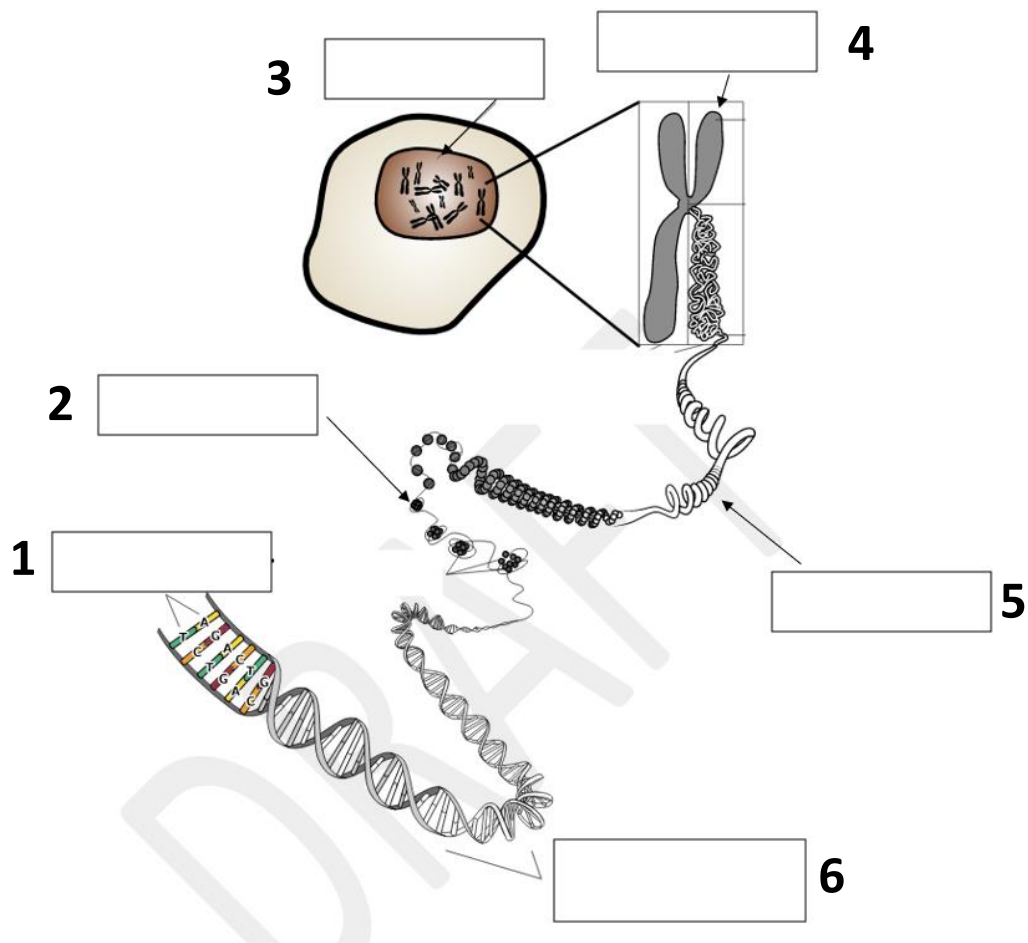
Activity 3 Answer these questions

1 What is one way that scientists deal with the problem of how small the genome is?

Can you name this process? (ABE Lab 5)

2 When scientists sequence the genome, why doesn't it matter which strand of the double stranded DNA is sequenced?

3 Why might it be important that scientists learn the sequence of letters that make up an individual's genome?

4 Discussion question - would you sequence your own genome? Why/why not?

**Activity 4 Identifying DNA sequences using BLAST**

Instructions:

I. Retrieve the sequences decoded from the sausage DNA samples.
  1. Open a Web browser and type the following address into the address bar:
     https://4273pi.org

1. Click on the 'SCHOOLS' tab and you will find a link to the sausage extract DNA sequences titled "Food Detective Sequences".. (When the DNA sequences are written out in a string of capital letters as they are here, we call this FASTA format.) Keep this tab open so you can copy and pastes the sequences when required.

II.   Time to BLAST

1. Open a new tab in your Web browser and do a Web search for 'NCBI BLAST'.
2. Check the first result has a name similar to 'BLAST: Basic Local Alignment Search Tool'. Click it.

1. On the page that then opens click 'Nucleotide BLAST'.
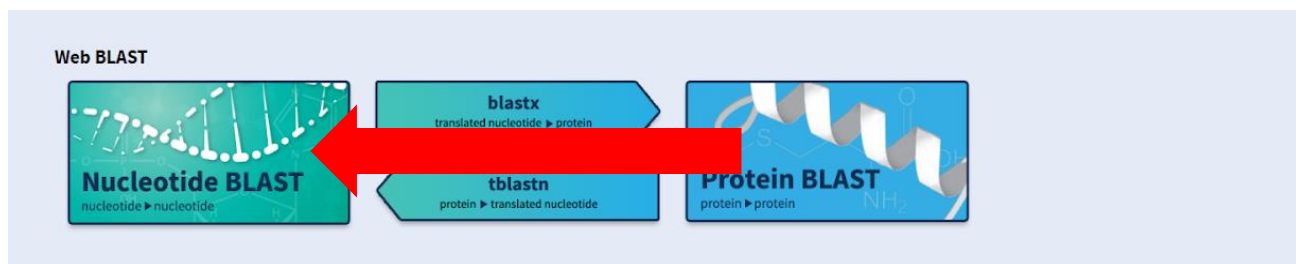
1. Paste 'Sequence_A' in FASTA format (as it is) into the box at the top of the page labelled 'Enter Query sequence'.

1. Under Choose Search Set, select the Nucleotide collection (nr/nt) database from the drop-down menu (see green arrow below). This searches the entire collection of DNA sequences in the database.

2.   Under 'Optimize for', select 'somewhat similar sequences' (see red arrow below).

1.   Click 'BLAST'.

BLAST may take a few minutes to run, do not refresh the page – be patient.
In a few moments, the results will appear on one long page titled 'BLAST Results'.

1.   Scroll down to the table of results. The first result in the table is the best match to Sequence_A in the database.

1.   In Table 1 below, record the latin species name (in the 'description' column), the common name (see Table 2), the accession number and the E-value.

1.   Repeat individual BLAST searches for Sequences B to H and complete Table 1 (You may work in groups and search 1 or 2 sequences each).

Activity 4 Complete table using BLAST results

Sequence	Species – scientific name	Species – common name	Accession number	E-value
A	*Sus scrofa*	PIG		
B				
C				
D				
E				
F				
G				
H				

Consider the following questions:

What do your results in Table 1 tell us about the sausage? What is a possible explanation?

What are the pros and cons of carrying out experiments in dry lab (using technology alone) environments compared to wet lab (working with chemicals & biomaterials) environments.