

## 5E Lesson Plan

<b>Teacher: Taylor Neel and Yusra Nahri</b>
<b>Date: 6/27/17</b>
<b>Subject / grade level: Biology 9th/10th grade</b>
<b>Materials: computers with Python software, paper slips with program instruction, coding reference sheets, sheet with the correct program, exit slips</b>
<b>Essential Standards and Clarifying Objectives:</b> <b>BIO.B.2.3.1:</b> Describe how genetic mutations alter the DNA sequence and may or may not affect phenotype (e.g., silent, nonsense, frame-shift).  <b>BIO.B.2.4.1:</b> Explain how genetic engineering has impacted the fields of medicine, forensics, and agriculture (e.g., selective breeding, gene splicing, cloning, genetically modified organisms, gene therapy).
<b>Lesson objective(s):</b> <ul style="list-style-type: none"><li>• Students will be given an introduction to coding and bioinformatics.</li><li>• Students will understand the concept of the tumor suppressor gene p53.</li><li>• Students will successfully run a program in Python which identifies the mutations in a gene sequence.</li></ul>
<b>Differentiation strategies to meet diverse learner needs:</b> <ul style="list-style-type: none"><li>• Students working in small groups.</li><li>• Providing students with paper slips to help them put together the program and easily manipulate the order of operations that run the program until they discover the most effective program.</li></ul>
<b>ENGAGEMENT</b> <ul style="list-style-type: none"><li>• Ask probing questionings about mutations ie. "What is a mutation?", "How are mutations studied?", "What can be the result of mutations on an individual?", "What could be an efficient way to locate mutations in DNA?"</li><li>• Lead into what bioinformatics is and why it is important.</li></ul>
<b>EXPLORATION</b> <ul style="list-style-type: none"><li>• In groups of 2-3 have students create an algorithm that would allow them to identify the difference (mutation) between a normal DNA sequence and mutated DNA sequence.<ul style="list-style-type: none"><li><input type="checkbox"/> Ex for a line in the algorithm: "First we need to identify the normal gene sequence, then we need to identify the cancer gene sequence."</li><li><input type="checkbox"/> Ex for what would be written on a paper slip: seqLen(control) ⇒ means it calculates the length of the control sequence.</li><li><input type="checkbox"/> Ex for what would be written on the reference sheet:</li></ul></li></ul>

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Comparators include: < if less than, > if greater than, == if equal to, != if not equal to

- In their groups the students will use paper slips that the teacher previously created which contain each line of code for the program that will be able to find the difference between two DNA sequences. A reference sheet will also be provided to the students to help them learn Python's syntax.
- Students will work in their groups and tape the strips of paper with each line of code in the correct order onto a full sheet of paper and hand it into the teacher.
  - Each pair of students should be given the paper labelled "code paper slips." Instruct the students to cut this table into slips. Each slip should be numbered with a line of code and the meaning of that line. The students will need to put the lines of code in an order that will yield a workable program. They can tape or glue the slips of paper in order on a plain piece of paper. Once the teacher checks the completion of this activity, he/she will provide the students with the correct code. They will then check their code for accuracy and discuss what they should have done differently or what worked well.

### END DAY 1

### START DAY 2

#### EXPLANATION

- Hand back students' papers with their taped strips of code and also give students a typed handout of the correct program.
- In their groups allow them to compare the effectiveness of how they organized their code and the correct order the code should be for the program, giving time for them to reflect and share on problems they came across.
- In their groups students plug in the correct program into Python and run it, finding the mutations between the normal and mutant gene sequence.

#### ELABORATION

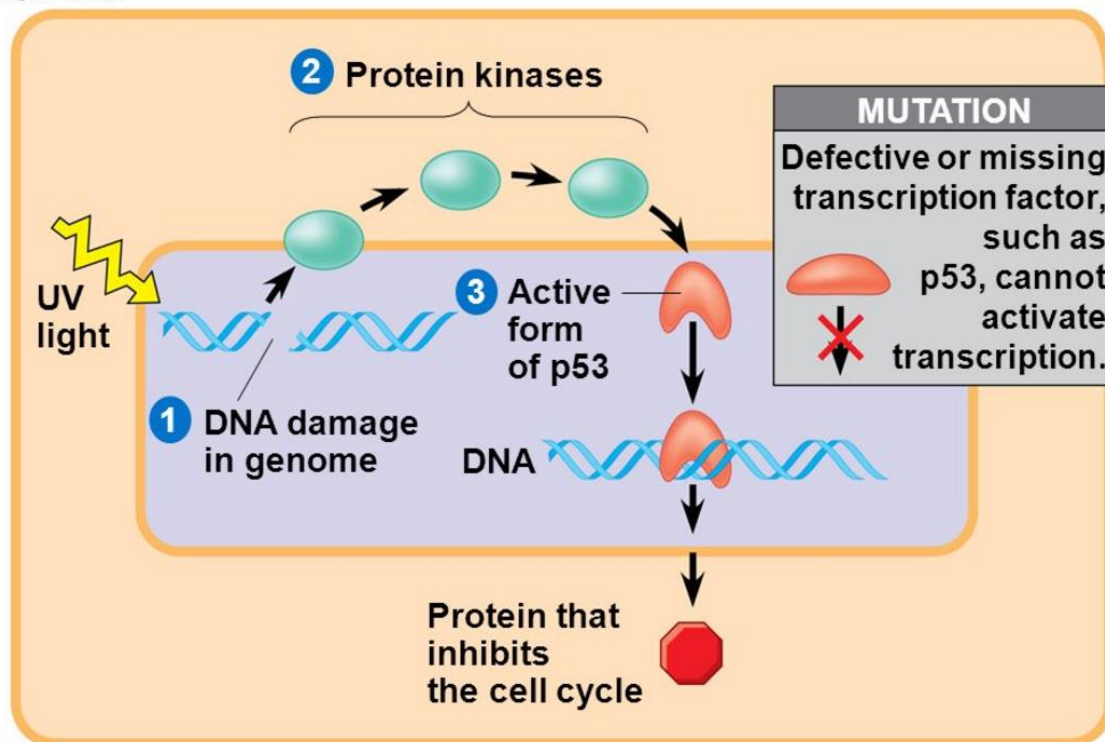
- Have a discussion of why we did this activity and why it would be useful in the real world.
- Use genome browser BLAST to show students that the sequence we used is real gene from the genome.
  - Look up p53 gene in GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>).
  - Under "Analyze this sequence", click "Run BLAST". Alternatively, copy the ascension number of the gene and vision the BLAST website (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>)
  - Check the box for your gene (the first option). Check the box for an unrelated organisms (scroll down to an organism with a non-human scientific name).
  - Click Download→ FASTA(Aligned Sequence).
  - Go to <http://www.ebi.ac.uk/Tools/msa/muscle/>
  - Copy the contents of the file that you generated in BLAST into the box.
  - Change the output format to Pearson/FASTA.
  - Hit "Submit".
  - Hit "Download Alignment File"
  - Right Click → Save As → "gene\_name.fasta". For example, WNT3A would be wnt3a.fasta
    - Save the file to the desktop
- Discuss the function of the p53 gene including a picture of the pathway.

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### EVALUATION

- Screenshot of the program
- Exit slip with the question: "What happens when p53 has a mutation?"

Figure 18.24b



(b) Cell cycle–inhibiting pathway

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