2024 Battle Lab SCRP Application

For summer 2024, I have funding for 2 full-time research students. While some upper-level coursework and lab experience in chemistry and biology is a plus, I will consider interested students at any level of experience from freshman to juniors from any major background. In addition to the material available online, there's more information about our lab/news/profiles of current and past students available at http://chbattle.com.

For your application, you'll first need to read some background information outlining our research project, how current and past students have contributed to the work, and current open research questions contained in the "Battle Lab- Quadruplex Sensors (Sp2024)" PDF below. Note: you may need to copy this link, sometimes PDF's don't play nice!

https://drive.google.com/file/d/1NXLNcCU3NhEq1cDFjM-z-DQ_ML4RmQ3Q/view?usp=sharing

Once you've read through this overview, you'll need to complete the following process:

1. Once you've read the research overview linked above, schedule an appointment with me to talk about the projects, ask any questions you have, and learn a little more about our lab's setup and approach. The easiest way is to book a time with Calendly: https://calendly.com/chbattle/meeting

Then, put together an application that answers the following 5 questions to submit:

2. In one short paragraph, explain what most interests you about this project.

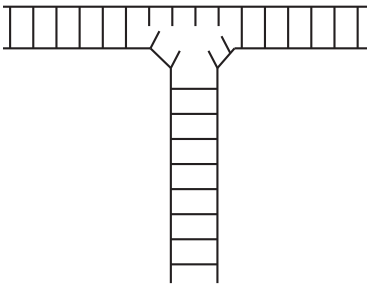
3. Briefly (one paragraph) describe your career interest or long-term goals post-Willamette.

4. In 1-2 paragraphs, describe how you see taking part in SCRP as benefiting your personal or academic development.

5. Much of the work we do in the lab involves creativity in determining sequences that will base-pair to yield specific structures. Suggest a series of DNA sequences that will assemble to make a structure that resembles a capital "H" with the constraints listed below. For sequence annotation, start with the 5'-terminus followed by a list of bases, for example: 5'-TCATGCT-3'. You should also include a sketch showing how you expect the strands to assemble- an example for a "T" is shown below, yours should include specific bases (A, T, G, C) at each position.

   Note: remember that DNA strands assemble in an anti-parallel fashion- that means that the 5' end of one strand pairs with the 3' end of its complement. **There is no single right answer for this! Show me how you think through it.**

   - Each side of the "H" should be no more than 20 base-pairs long, and the "bridge" of the "H" should be no more than 10 base-pairs long
   - Strands are between 15 and 40 bases long.
   - Each line should be formed by a base-paired duplex- single strands are not rigid enough.
   - So that strands assemble exactly, make sure that there aren't overlaps of more than 3 consecutive base-pairs between different strands.
   - Long runs of the same base can de-stabilize structures, so make sure there aren't any sections with of more than 4 of the same base in a row.



- For there to be an angle (turn) in a structure, leave at least 2 unpaired bases for flexibility as shown in the example above.

6. You have a 150.0 uL solution of DNA, and you want to determine the concentration using Beer's Law. You take 6.0 uL from the DNA solution and dilute it to 3.00 mL with DI water. You then take an absorbance spectrum of this sample, and determine that the absorbance at the maximum (260 nm) is 0.650. Given that the molar extinction coefficient of the DNA is 135,000 L/mol*cm, and knowing you used a 3 mL cuvette:

    a. Calculate the concentration (in μM) of the DNA sample in the cuvette using Beer's Law.

    b. Using the concentration in the cuvette and the dilution from the original stock solution, calculate the concentration of DNA in the original sample in units of mM.

    c. To make the sample easier to work with, you want to dilute it to a working stock solution that contains 1 mM of DNA. Starting from the 144 μL of your original solution remaining, calculate how much water you would need to add to dilute your sample, in μL.

    d. For long-term storage, you want to aliquot your stock solution into vials containing 25 nanomoles (nmol) of DNA each. First, calculate the total nmol of DNA you have to work with, then determine how many 25 nmol aliquots you would make, and how many nmol would be left over at the end.

You do not have to immediately know how to answer these questions to fill out this application! The intent is for you to take some time thinking through some of the practical things we do in lab and for me to see how you work through a problem. For the last two parts, you can scan/take pictures of handwritten work to submit.

I am more than happy to make time to meet with you and explain any concepts you need to answer these questions as well as help you work through the problems themselves.