# Library Class Exercises

You have discovered a new species of fish on an expedition into a cave system in Mexico.

- What do you want to learn about this organism?

- How would you go about learning those things?

We are planning SBS, which means we need a primer. Why is this problematic? How might you go about solving this problem?

Your species of fish has a haploid genome of ~20,000 Mbp. If we want ~98% probability of seeing each base in the genome, how many 300 bp sequences do we need?
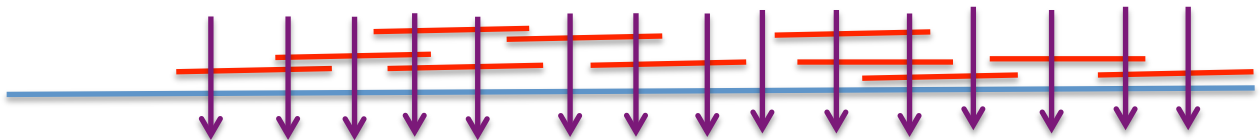
What is the coverage of the locations indicated by the arrows? What is the average coverage for this given set of locations? How can we calculate the expected coverage from the number of reads?

Determine the alignment value for the following sequences. Use the following values. What is the best alignment?

Match =+1, Mismatch =-2, Gap =-5

GACGT   ACGGT