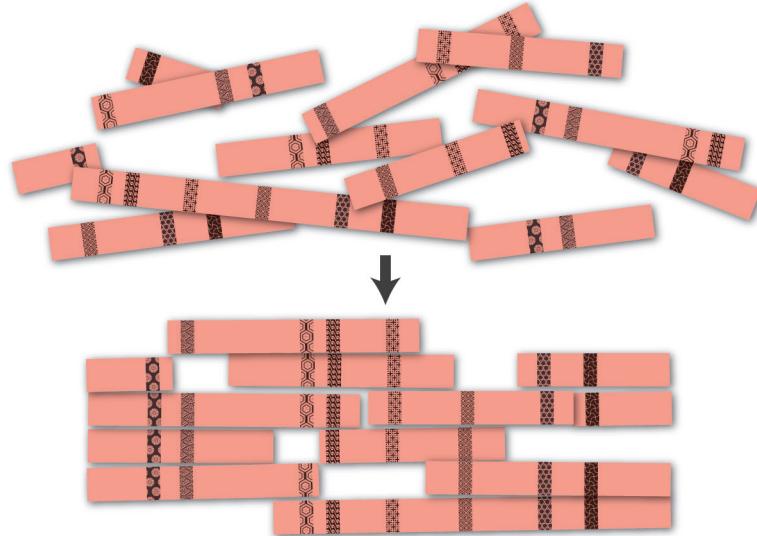


## “Connect-A-Contig” *A Hands-On Sequence Assembly Activity*

### Abstract

Students align different lengths of paper “DNA” based on the distance between “markers” to generate a DNA consensus sequence. This kinesthetic activity can be used as a classroom demonstration, solved in small groups of students, or done individually. The activity helps students conceptualize how different lengths of tagged DNA can be used to generate a physical map of a genome.



### Learning Objective:

Overlapping sequences or features on short segments of DNA can be used to assemble much longer contiguous DNA sequences, or “contigs.”

### Time required

- Prep time: minimal, for review and copying only
- Class time: About 20 minutes to introduce the activity, allow students to assemble a contig set, and then discuss the activity. Note that while contig sets 1 – 3 should each take a few minutes for students to assemble, contig set #4 is significantly more difficult and will take longer for students to solve.

### Materials

- Scissors
- Copies of contig sets, one set per individual or groups of 2-3 students. Consider copying each contig set on a different color of paper to eliminate crossover between the different sets.

### Features

Descriptive illustrations walk you through solutions to each paper simulation.

### Classroom Implementation

To describe the simulation prior to passing out the contig sets, review the Genome Mapping webpage with your students. Explain that it will be the job of the students to act like the computational software genomic researchers use to assemble genomes. They will need to match up the spacing of the genomic markers (the patterned bars) on the overlapping shorter lengths of DNA to infer the

spacing on the longer genomic sequence. Consider solving one set together as a class, and leaving the remaining three contig sets to be solved in small groups.

Distribute a contig set to each group of students. If students need scaffolding, suggest that they begin by orienting each strip of paper in the same direction. This helps make patterns apparent and matching easier.

Students should record their solution to a “consensus sequence” for each of their contig sets. Display the solution to each contig set and ask students to compare their answers.

Variations: For an easier activity, include the consensus sequence. For an extra challenge, leave it out.

## Discuss observations with your class:

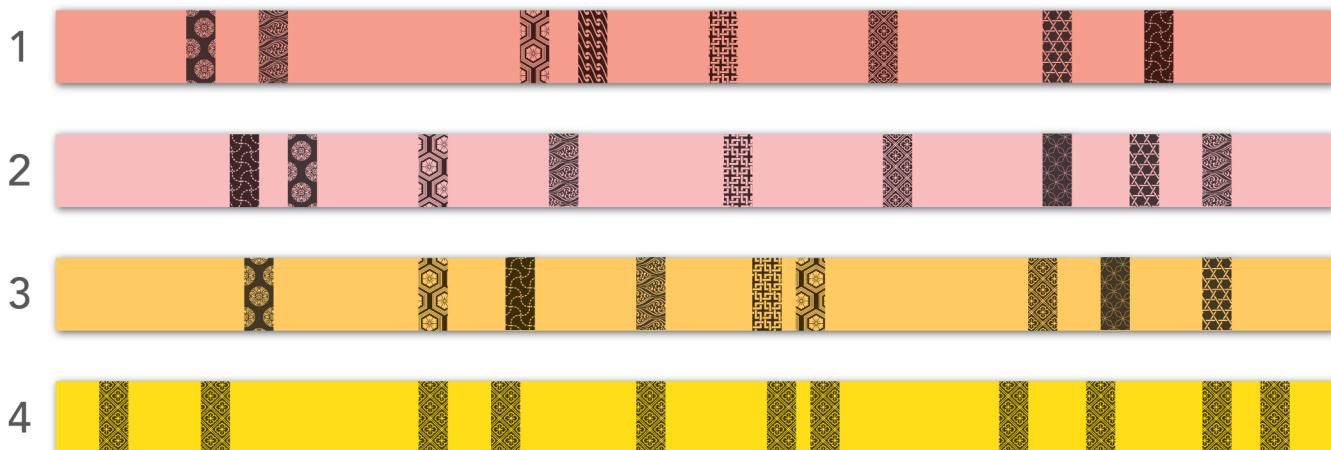
Which pieces of DNA/paper are the most informative? Why?

Explore the concept of “depth of coverage.” Which markers in each set provide the greatest depth of coverage?

What do the patterned tags on the paper strips represent? Restriction sites: where an enzyme will nick the DNA at a predictable sequence, and in this case, add a fluorescent tag. In the exercise we used restriction sites to generate a map of a sequence from a single genome.

If you have a reference sequence, it’s easier to align other tagged sequences to it than to build a reference sequence from scratch.

## Solutions to each of the Contig sets:



## Credits

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The Genetic Science Learning Center



## Funding

This material is based upon work supported by the National Science Foundation under Plant Genome Research Program Award #1339412. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.

