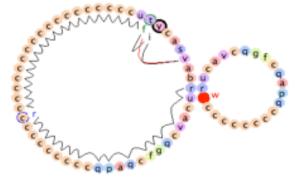# Understanding the Introduction of Genetic Variations by Random Mutation

An Avidian creating a copy of itself

Background

The basic components of the Darwinian evolutionary mechanism are variation (V), inheritance (I), natural selection (S) and time (T). This exercise focuses on variation and one basic way it can arise.

Natural selection acts upon phenotypic variations in a population of organisms. Variations can arise in a population in several different ways. Here we will look only at variations that may be introduced by genetic *mutations*—random changes in an organism's genome—and not at other processes such as recombination, horizontal transfer, etc. Genetic mutations may be substitutions (changes from one instruction to a different one), insertions (additions of an instruction into the genome), or deletions (deletions of an instruction from a genome).

As in nature, a population of Avidians—the model organisms in Avida-ED—can vary both phenotypically and genotypically. Like plasmids, Avidians have a circular genome composed of simple genetic instructions. Different genetic sequences can produce different phenotypic functions. Each instruction in the sequence is represented by a colored dot. During genome replication, point mutations may occur at random in the sequence. [Note: For simplicity, this version of Avida-ED allows only substitutions, not insertions or deletions.]

Your goal in this exercise is not to look at what exactly makes a sequence of instructions functional, but just to understand *how* mutations produce varieties of genetic sequences. Specifically, you will explore what it means to say that mutations occur at random at a particular rate.

Assignment Tasks

Pilot Study: Use the Organism Viewer to see how substitution mutations change the genomes of organisms.

   (i) In the Organism viewer, go to settings. Set the per site mutation rate to 10%. Keep repeatability mode set to Experimental. Flip back to the viewer.

  (ii) Drag in the @ancestor from the freezer and click Run to watch it replicate.

 (iii) Record the position and total # of any changes in the offspring's genome after replication. (Do this in clockwise order starting from the 3 o'clock position on the circular genome, which is the origin of replication).

  - Run #1: Mark differences from ancestral genome below.
    `Wzcagcccccccccccccccccccccccccccccccccczvfcaxgab`   Total#

Predict: What do you expect to see if you repeat your Pilot Study several times using the same ancestor with the same mutation rate?

       (1) Will the *specific* mutations always be the same?   Yes / No

       (2) Why, or why not?

       (3) Will the *number* of mutations always be the same?   Yes / No

       (4) Why, or why not?

Test: Repeat steps (ii) and (iii) from the Pilot Study at least three times (but not until AFTER you have written down your predictions above).

  - Run #2: Mark differences from ancestral genome below.
    `Wzcagcccccccccccccccccccccccccccccccccczvfcaxgab`   Total#

  - Run #3: Mark differences from ancestral genome below.
    `Wzcagcccccccccccccccccccccccccccccccccczvfcaxgab`   Total#

  - Run #4: Mark differences from ancestral genome below.
    `Wzcagcccccccccccccccccccccccccccccccccczvfcaxgab`   Total#

Results: Were your predictions confirmed or disconfirmed?

Discussion: Explain your results. What do your tests above reveal about how random mutations introduce genotypic variations in a population? (Use back of sheet.)

Future research: What patterns, if any, in the sequences and total number of mutations would you expect to see if you increased the number of runs (replicates)? How would you graph your data to better see whether your predictions are correct?