Assignment 8:

* The initialization of the first row/column for a 6x6 matrix is always 0 to 5, right? Or does it change with the gap cost such that a gap cost of 2 would create an initialized array of [0,2,4,6,8,10]?
* I got points taken off for not saying the alignment change for 1b (‘AATCG’ and ‘AACGG’), including when the gap\_cost equals 2, even though I’m pretty sure I did. Any clarification would be much appreciated.

Assignment 10:

* I’m still not entirely sure why we can’t directly translate the nucleotide sequences from the CDS feature. Since introns are noncoding sequences, wouldn’t they be excluded from the CDS feature? Do we get an incorrectly translated sequence?

Assignment 10.1:

* I realize the project had nothing to do with cell size. I believe I got the ‘cell size’ code by implementing the example code from the lecture and using it to make sure if the dataset created was independent by genotype. I remember I kept getting the same numbers for all three genotypes, so I implemented the graph to help backtrace the problem. By easily seeing if the graphs were the same, I could tell the genotype local variable was not being changed. With this, I eventually identified the problem was incorrectly labeling my variables ‘zeros’ and ‘ones.’ In retrospect, I should have removed this helper code before submitting to make things clearer.
* Did I get the correct phenotype by allele charts, heritability values, and hypothesis?

Assignment 12.2:

* What should the state transition graph be for the asynchronous model?