Assignment 3: Drift
Computational Genomics

Objectives: Become familiar with using simulations to understand the effects of parameter selection.

Tasks:

1. Accept the assignment at https://classroom.github.com/a/DxV-bi7K
2. Update `src/af.py` to consider fitness values for each allele where zero is neutral fitness, less than zero is deleterious, and greater than zero is advantageous.
    a. The number of fitness values you take should match the number allele specified (HINT. use `nargs='+'` in `parser.add_argument` to take an array of values, then make sure the two match)
    b. Pass these fitness values to `one_generation()` where you then adjust the expected number of offspring based on an additive model (fancy way of saying, just take the sum of fitness values)
3. Expand the simulation from a plot of a single run to the collection that stats after many runs (HINT: at the end of each run take the last allele frequency as the representative value)
4. Design a new experiment to understand the different effects of drift and selection.
5. Update `README.md` and `doc/drift.tex` (or similar) to include your new experiment.
6. Push your final code to GitHub.
7. Submit your final PDF to Canvas.