Reading Assignment
Using Python documentation or any other source familiarize yourself with NumPy.

Submission instructions
Follow the same submission instructions as before. Send completed assignments to Howard and cc Kirill. Submit this assignment as a Python notebook that shows the code and the final plots.

Problem 1
Let's simulate mutations during PCR. Assume your are amplifying a sequence of $L = 100$ base pairs starting from a single sequence. Each PCR cycle the number of molecules doubles, and the entire amplification consists of $n = 13$ cycles. At each duplication event, every base pair is copied correctly with probability $1 - \mu$ or replaced by a different nucleotide with probability μ; all three possible substitutions occur at equal probability $\mu/3$. In this problem, we will explore three values of μ: 10^{-4}, 10^{-3}, and 10^{-2}.

For each mutation rate do the following. Determine the expected number of distinct sequences at the end of the PCR. Visualize the distribution of relative abundances of these sequences. Compute the effective number of sequences using the definitions based on entropy and Simpson's index.