Biol 365 - Scientific computing - Final Project Write-up, due Monday 5/11 at 11:55 pm

Write a 6-8 page paper that summarizes your genetic drift project. The paper should be in an Introduction, Methods, Results, Discussion format of a scientific journal article, and should address the following:

- Introduction - Genetic drift background
    - What are allelic diversity and heterozygosity, and why are they important to maintain?
    - What is meant by "genetic drift"? What does it mean for an allele to be "fixed", and how does genetic drift cause fixation?
    - What was the cause of genetic drift in our simulation?

- Methods - Simulation approach
    - Describe how the program worked. What were the initial conditions? How did we simulate random mating? How did we simulate offspring growing up and replacing their parents?
    - How many generations did each simulation run use?
    - How many times was the simulation repeated? What was recorded for the initial single run, and what was recorded when the simulation was repeated?
    - Why did we use a "For...next" loop to control repeated runs of the model, but a "Do...while" loop to control the number of generations each run used?
    - How did you simulate an increase in population size? How did you simulate immigration?
    - What kind of organism did the model most closely resemble?

- Results
    - First version - 50M/50F, run once for 500 generations.
        - Did a single allele become fixed? If so, which one?
        - Did they change in a predictable way, or was the change over time unpredictable?
        - How did heterozygosity change?
        - How did allelic diversity change?
        - Include graphs to illustrate the changes.
    - Second version - repeat the first version 100 times.
        - How often did an allele go to fixation (that is, how many of the 100 runs had an allele go to fixation)?
        - Did all of the alleles go to fixation about an equal number of times?
        - What was the average amount of time to fixation across the 100 repetitions?
    - Third version - 100 M/100 F.
        - Did the time to fixation change in a consistent way?
        - Did larger population size prevent loss of diversity entirely, or did it just reduce the rate of loss?
    - Fourth version - 50 males and 50 females, one male immigrant per generation.
        - Was one immigrant per generation enough to prevent loss of alleles?
        - How did the number of runs with fixed alleles change?
        - How did time to fixation change?
        - If an allele was lost it could be replaced by an immigrant entering the gene pool - how does this compare to the other models?

- Discussion
    - Discuss the results - according to our simulation, how does population size and immigration affect time to fixation, heterozygosity, and allelic diversity? Were the results as expected, or did we see different patterns in our simulation models than population genetics theory tells us to expect?
    - The primary advantage of studying models rather than real organisms is that we can do experiments in a model that would be very difficult, if not impossible, to do in the real world. The primary disadvantage of studying models instead of real organisms is that the models are not real, and if we failed to capture important features of real organisms in our models, we may be misled by our findings. Address these strengths and weaknesses as they pertain to our genetic drift models. Discuss how the choices we made in building the models might affect the results we saw. Specifically, name any ways you can think of that the simulations were not realistic representations of real-world populations. What insight can we gain about real populations from these simulation models, in spite of the issues you raised?