

COMP3212(2023/24): Computational Biology Lab Three - Part 1

Issue	26 February 2024
Deadline	08 March 2024

Part 1

- Implement the Fisher-Wright model for an infinite population and asexual reproduction, you will need to use an ODE integration library, e.g. `from scipy.integrate import odeint`
- Test it using the same parameters as in the slides (lecture 14 pg 19)
- Now implement the Fisher Wright model for a finite population using asexual reproduction.
- Run it a few times. what do you notice?
- Write a function to run the FW model multiple times and average the results
- Plot a graph after averaging over a number of runs.
- Does averaging over more runs for the finite model make it get closer to the infinite model?
- Now adjust your FW multiple runs model to return the take over time, i.e. when $x/N > 0.95$, and the proportion of mutants $p_x = x/N$, averaged over a given number of runs.
 - Plot graphs of how the take-over time depends on the selection strength s (assume $N = 10000$ and $n = m = 0.0001$)
 - Plot graphs of how the take-over time depends on the mutation rate n, m (assuming $N = 10000$ and $s = 0.01$)
 - Plot graphs of how the take-over time depends on the population size N (assuming $s = 0.01$ and $n = m = 0.0001$)
- Comment on what conditions are necessary for the mutant to take over the population.

Part 2

- Write a program to compute the transition matrix W for the Markov model
- Check that all the columns sum to 1
- Write a program to generate the Markov distribution for each time step.
- Calculate the average of this distribution for each time step
- Plot this for $N = 1000$, $s = 0.01$, $n = m = 0.001$ after $T = 1000$ steps
- Compare with the plot in the notes to check you have implemented this correctly.
- Use your previous code to generate a histogram of the number of mutants after the same number of time steps using the Fisher Wright model, and plot it with the Markov distribution after differing numbers of time steps (e.g. 100, 500, 1000), using the `density=True` option on `plt.hist` will help the scaling.

Part 3

- Implement a Fisher-Wright model for evolution using a genome of L binary values, either the original state or the mutant state.
 - initialise N individuals with a genome of $L = 10$ zeros each
 - Individuals with mutated genes have a selective advantage of $(1 + s)^f$ where f is the number of mutant genes in the genome.
 - Select individuals to reproduce with probability:

$$p_i = \frac{(1 + s)^{f_i}}{\sum_{j=1}^N (1 + s)^{f_j}}$$

- Mutate each child by flipping the gene at each site with probability m for flipping from $0 \rightarrow 1$ and n for flipping from $1 \rightarrow 0$, and $n = m$. `np.bitwise_xor` might help with this.
- Record for each time step the average number of mutations per site, on the genome, this will give the spread of the mutated gene
- Now make a similar model, but now including crossover:
 - select parents for the next generation with probability:

$$p_i = \frac{(1 + s)^{f_i}}{\sum_{j=1}^N (1 + s)^{f_j}}$$

- Generate one child per pair via *uniform* crossover

0	0	0	1	0	0
1	0	1	1	1	1

PARENT CHROMOSOMES

1	0	0	1	0	1
0	0	1	1	1	0

OFFSPRING CHROMOSOMES

- Plot a graph to compare the sexual model with the asexual model and the Markov model.
- Explore and describe what parameter values make the model deviate more from the Markov model

Report and marking

You can ask a demonstrator or myself to mark your work in the lab, or you can submit a pdf output from your work.