Code Explanation: Phytoplankton Strain Dynamics

0.1 Why is 2*delta instead of delta inside the loop?

The 2δ inside the loop (for $j = 1$ to $M_s - 1$) and the δ at the boundaries ($j = 0$ and $j = M_s$) in the strain update equation are due to how we model the probabilistic shift of biomass between neighboring strains. Let's illustrate with an example:

Imagine we have 5 strains ($M_s = 4$), each represented by a circle:

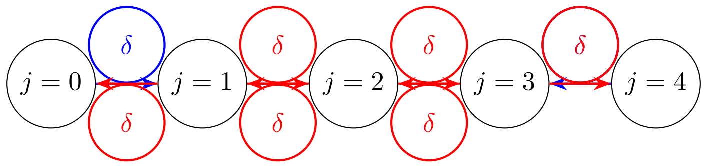

Figure 1: Biomass transfer between strains. Blue arrows (boundaries): transfer probability δ. Red arrows (inner strains): δ to each neighbor, totaling 2δ transfer from each inner node.

Let $\delta = 0.2$ represent the probability that biomass shifts from one strain to a neighboring strain.

* **Strain 0 ($j = 0$):** This strain is at the boundary. It can only lose biomass to strain 1. The fraction of biomass that remains in strain 0 is $(1 - \delta) = (1 - 0.2) = 0.8$.

* **Strain 1 ($j = 1$):** This strain is in the interior. It can lose biomass to *both* strain 0 and strain 2. It loses a fraction δ to strain 0 and a fraction δ to strain 2. The total fraction of biomass lost by strain 1 is $2\delta = 2 \times 0.2 = 0.4$. Therefore, the fraction of biomass that *remains* in strain 1 is $(1 - 2\delta) = (1 - 0.4) = 0.6$.

* **Strain 2 ($j = 2$):** Similar to strain 1, it loses δ to strain 1 and δ to strain 3, for a total loss of 2δ. The remaining fraction is $(1 - 2\delta)$.

* **Strain 4 ($j = 4$):** This strain is also at a boundary. It only loses biomass to strain 3. The remaining fraction is $(1 - \delta)$.

This explains why the update equation uses $(1 - \delta)$ for the boundary strains and $(1 - 2\delta)$ for the inner strains. The 2δ accounts for the biomass transferred to *both* neighboring strains.

0.2 Why only one delta at the ends and two deltas in the beginning? (Question and Answer)

Question: Why is the biomass transfer probability δ used for the boundary strains ($j = 0$ and $j = M_s$) while 2δ is used for the inner strains ($j = 1$ to $M_s - 1$) in the update equation? It seems like there are "more deltas in the beginning."

Answer: The difference between 2δ inside the loop and δ at the boundaries is not about "more deltas at the beginning" but about the *number of neighbors* each strain has.

- **Inner Strains ($j = 1$ to $M_s - 1$):** Each inner strain has *two* neighbors. When biomass shifts, each inner strain loses some biomass to *both* of these neighbors. If the probability of shifting to *one* neighbor is δ, then the total probability of shifting biomass *away* from an inner strain is 2δ. That's why the update equation for inner strains uses $(1 - 2\delta)$: it represents the fraction of biomass that *remains* in the strain after transfers to *both* neighbors.

- **Boundary Strains ($j = 0$ and $j = M_s$):** The strains at the boundaries only have *one* neighbor. Strain $j = 0$ only has a neighbor to its right (strain $j = 1$), and strain $j = M_s$ only has a neighbor to its left (strain $j = M_s - 1$). They can't transfer biomass "outside" the array. Therefore, they only lose biomass to *one* neighbor. The fraction of biomass lost is just δ. The update equation uses $(1 - \delta)$ because only one transfer is possible.

Analogy: Imagine a row of people. Each person represents a strain. They're throwing balls (representing biomass) to their neighbors.

- **People in the middle:** Each person in the middle throws balls to *both* the person on their left and the person on their right. They lose a total of 2 balls (if each throw has a probability of 1).
- **People at the ends:** The people at the ends only have *one* neighbor. They can only throw a ball to that one neighbor. They lose only 1 ball.

In summary: The difference between 2δ inside the loop and δ at the boundaries is not about "more deltas at the beginning" but about the *number of neighbors* each strain has. Inner strains have two neighbors, so they lose biomass to both, leading to a total loss probability of 2δ. Boundary strains have only one neighbor, so they lose biomass to only that one neighbor, leading to a loss probability of δ. This difference is essential for correctly modeling the biomass transfer at the edges of the system.