Q2

2a) Certainly! Let's solve the given differential equation for the fish population growth to find the equilibrium population size and determine its stability.

a) To find the equilibrium population size, set the equation equal to zero:

\[ \frac{dN}{dt} = rN\left(1 - \left(\frac{N}{K}\right)^2\right) = 0 \]

From this equation, we can identify the equilibrium points when \(1 - \left(\frac{N}{K}\right)^2 = 0\). Solving for \(N\):

\[ \left(\frac{N}{K}\right)^2 = 1 \]

\[ \frac{N}{K} = \pm 1 \]

Therefore, the non-trivial equilibrium population sizes are \(N = K\) and \(N = -K\). However, since population sizes cannot be negative in this context, the equilibrium population size is \(N = K\).

b) To determine stability, let's evaluate the derivative of the population growth equation with respect to population size \(N\) and evaluate it at the equilibrium point \(N = K\):

\[ \frac{d}{dN}\left[rN\left(1 - \left(\frac{N}{K}\right)^2\right)\right] = r\left(1 - 3\frac{N^2}{K^2}\right) \]

When \(N = K\):

\[ \frac{d}{dN}\left[rN\left(1 - \left(\frac{N}{K}\right)^2\right)\right] \bigg|\_{N=K} = r\left(1 - 3\frac{K^2}{K^2}\right) = r(1 - 3) = -2r \]

The derivative at \(N = K\) is negative (\(-2r\)), indicating that the slope at this point is negative. This confirms that the equilibrium point \(N = K\) is stable.A screenshot of a math problem

Description automatically generated

dn/dt = rn(1-(n/K)2) -hn

A math problem with equations

Description automatically generated with medium confidence

3d. These commands likely generate a plot where:

The x-axis represents the population of juveniles.

The y-axis represents the population of adults.

The blue dashed line represents the J\_isocline, indicating where the adult population remains constant concerning changes in the juvenile population.

The red dashed line represents the A\_isocline, indicating where the juvenile population remains constant concerning changes in the adult population.

This plot helps visualize the equilibrium points and relationships between juvenile and adult populations in a given ecological or population dynamics model.

isocline\_exam.pdf

3f Exam\_3f\_Dynamics\_Hierarchical\_Age-Structured.pdf

marik\_answer\_exam3f.pdf

4a. <https://faculty.uca.edu/benw/biol4415/PopGNotes.pdf>

Derivation: w in general means “fitness”: a measurement of the relative ability ofindividuals with a certain genotype to reproduce successfully. wAA, for instance, means the relative ability of individuals with the AA genotype to reproduce successfully. w is always a number between 0 and 1. Adding ws to the Hardy-Weinberg equation allows you to predict the effect of selection on gene and allele frequencies in the next generation. Take the Hardy-Weinberg equation and multiply each term (the frequency of each genotype) by the fitness of that genotype. Add those up and you get the mean fitness, w (“w-bar”). Divide through by w, and you get the second equation. Here, each term of the equation is multiplied by the fitness of a genotype divided by the mean fitness. If a genotype is fitter than average, this quotient is greater than 1, and that genotype will increase in frequency in the next generation. If a genotype is less fit than average, the quotient is less than 1, and that genotype will decrease in frequency in the next generation.

<https://www.su.se/polopoly_fs/1.246482.1565013914!/menu/standard/file/HoessjerRyman_NeVFSTgenspatialmodel_JMB_2014.pdf>

<https://www.youtube.com/watch?v=9qj_Ny5ygiY>

<https://www.youtube.com/watch?v=H5VCNcChs3I>

Selection (4), overdominance and equilibria

<https://www.youtube.com/watch?v=uA390USKX8c>

Interference Effects of Deleterious and Beneficial Mutations in Large Asexual Populations

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6456326/>

To demonstrate that \(p^\* = 0\) or \(p^\* = 1\) (where \(p^\*\) denotes the equilibrium frequency of the gene), you'll want to find the points where the gene frequency (\(p\)) remains constant, implying it doesn't change across generations.  
  
In this context, when \(p^\* = 0\) or \(p^\* = 1\), it means either the gene has completely disappeared from the population (absent when \(p^\* = 0\)) or has taken over the entire population (fixed when \(p^\* = 1\)).  
  
For \(p^\* = 0\):  
- Set \(p\_t = 0\) in the equation \(p\_{t+1} = \frac{w}{\bar{w}}p\_t + \epsilon\_t\) and solve for \(p\_{t+1}\).  
- If \(p\_{t+1} = 0\) as well, it indicates the gene frequency stays at 0, which means extinction.  
  
For \(p^\* = 1\):  
- Set \(p\_t = 1\) in the same equation \(p\_{t+1} = \frac{w}{\bar{w}}p\_t + \epsilon\_t\) and solve for \(p\_{t+1}\).  
- If \(p\_{t+1} = 1\), it shows the gene frequency stays at 1, signifying fixation.  
  
Understanding whether the gene frequency remains at 0 or 1 across generations, regardless of the starting frequency, confirms the equilibrium status of the gene.

Certainly! The concept you're referring to is related to the equilibrium points in population genetics.

In this context, the equilibrium points \(p^\* = 0\) and \(p^\* = 1\) represent scenarios where the gene frequency remains constant over time, indicating the absence of the gene in the population or the gene's fixation, respectively.

The theory behind these equilibrium points involves understanding the dynamics of gene frequencies in populations undergoing selection.

- \(p^\* = 0\) implies the gene has been eliminated from the population. To confirm this theoretically, if you start with \(p\_t = 0\), applying the selection equation \(p\_{t+1} = \frac{w}{\bar{w}}p\_t + \epsilon\_t\) where \(p\_{t+1}\) represents the next generation's gene frequency, and if \(p\_{t+1} = 0\) as well, it demonstrates that the gene frequency remains at 0 over subsequent generations, confirming its elimination.

- \(p^\* = 1\) signifies fixation, meaning the gene has completely taken over the population. To illustrate this theoretically, if you start with \(p\_t = 1\), applying the selection equation \(p\_{t+1} = \frac{w}{\bar{w}}p\_t + \epsilon\_t\) and if \(p\_{t+1} = 1\), it demonstrates that the gene frequency remains at 1 over successive generations, signifying fixation.

These equilibrium points are essential in understanding the outcomes of selection pressures on gene frequencies within populations and serve as theoretical milestones in population genetics models.

This problem involves analyzing the dynamics of gene spread in a population, considering both deterministic and stochastic processes. Here's an approach to solving each part:

a) To ignore stochasticity (setting 𝜖𝜖𝑡𝑡=0), we consider the equation without the random term:

\[p\_{t+1} = \frac{w}{\bar{w}} p\_t(1-p\_t)\]

Equilibria occur where \(p\_{t+1} = p\_t = p^\*\). Setting \(p^\* = 0\) or \(p^\* = 1\):

At \(p^\* = 0\):

\[p^\* = \frac{w}{\bar{w}} p^\*(1-p^\*) = \frac{w}{\bar{w}} \cdot 0 \cdot (1-0) = 0\]

At \(p^\* = 1\):

\[p^\* = \frac{w}{\bar{w}} p^\*(1-p^\*) = \frac{w}{\bar{w}} \cdot 1 \cdot (1-1) = 0\]

Thus, \(p^\* = 0\) and \(p^\* = 1\) are equilibria of the system.

b) The stability criterion for \(p^\* = 0\) can be determined by analyzing the slope of the function \(p\_{t+1} = \frac{w}{\bar{w}} p\_t(1-p\_t)\) around \(p^\* = 0\). For stability, the slope at \(p^\* = 0\) should be less than 1 in absolute value. The derivative at \(p^\* = 0\) is:

\[\frac{dp\_{t+1}}{dp\_t} = \frac{w}{\bar{w}}(1 - 2p^\*) = \frac{w}{\bar{w}}\]

For stability, \(\left|\frac{w}{\bar{w}}\right| < 1\). So, the stability criterion for \(p^\* = 0\) is \(-1 < \frac{w}{\bar{w}} < 1\).

c) Here's an example of an R script that simulates the gene spread for 1000 generations:

```R

simulate\_gene\_spread <- function(N, w) {

p <- 1 / (2 \* N)

pt <- numeric(1000)

for (i in 1:1000) {

pt[i] <- p

fitness\_mean <- w \* p + (1 - p)

deviation <- rnorm(1, mean = 0, sd = sqrt(1 / (fitness\_mean \* (1 - p))))

p <- w \* p \* (1 - p) + deviation

if (p <= 0 || p >= 1) {

pt <- pt[1:i]

break

}

}

return(pt)

}

set.seed(123) # Setting seed for reproducibility

pt <- simulate\_gene\_spread(100, 1.05) # Change N and w values as needed

plot(pt, type = "l", xlab = "Generation", ylab = "p\_t", main = "Gene Spread Simulation")

```

This script initializes \(p\) with a value of \(1/(2N)\), runs the simulation for 1000 generations, and breaks the simulation if \(p\) reaches 0 or 1.

d) Here's an R function to calculate the probability of fixation:

```R

calculate\_fixation\_probability <- function(N, w, num\_simulations = 1000) {

fixation\_count <- 0

for (i in 1:num\_simulations) {

pt <- simulate\_gene\_spread(N, w)

if (tail(pt, 1) == 1) {

fixation\_count <- fixation\_count + 1

}

}

return(fixation\_count / num\_simulations)

}

```

e) To plot the probability of fixation for a range of \(w\) values:

```R

N\_values <- c(20, 200)

w\_values <- seq(0.9, 1.1, by = 0.01)

prob\_fixation <- matrix(NA, nrow = length(w\_values), ncol = length(N\_values))

for (i in 1:length(N\_values)) {

for (j in 1:length(w\_values)) {

prob\_fixation[j, i] <- calculate\_fixation\_probability(N\_values[i], w\_values[j])

}

}

plot(w\_values, prob\_fixation[, 1], type = "l", xlab = "w-values", ylab = "Probability of Fixation", col = "blue", ylim = c(0, 1))

lines(w\_values, prob\_fixation[, 2], col = "red")

legend("topright", legend = c("N = 20", "N = 200"), col = c("blue", "red"), lty = 1)

```

This script generates a plot showing the probability of fixation for \(N = 20\) and \(N = 200\) over a range of \(w\) values from 0.9 to 1.1. It illustrates that smaller populations are more likely to accumulate deleterious mutations. Adjust parameters as needed for your specific analysis.

Q4c Certainly! This code simulates changes in the frequency of a gene (allele A) over generations in a population using a Wright-Fisher model with selection. Let's break it down step by step:

- `n <- 1000`: This line initializes a variable `n` to denote the number of generations for which the simulation will run.

- `N <- 1000`: Here, `N` represents the population size. In this case, it's set to 1000 individuals.

- `pt <- numeric(n)`: An empty numeric vector `pt` of length `n` is created to store the frequency of allele A over time (across generations).

- `w <- 1.1`: This variable `w` represents the fitness of allele A. It's set to 1.1, indicating that allele A has a selective advantage.

- `pt[1] <- 1 / (2 \* N)`: The initial frequency `pt[1]` of allele A at generation 1 is set. In this case, it's initialized to \( \frac{1}{2 \times N} \), assuming an initial equal frequency of A in a population of size `N`.

The simulation loop begins:

- `for (i in 1:n) { ... }`: This loop iterates through each generation from 1 to `n`.

Within the loop:

- `w\_hat <- w \* pt[i] + 1 - pt[i]`: `w\_hat` calculates the mean fitness of allele A within the population at generation `i`.

- `sd\_t <- (1 / w\_hat) \* sqrt(w / (2 \* N) \* pt[i] \* (1 - pt[i]))`: This calculates the standard deviation of fitness for allele A in generation `i` based on the allele frequency and fitness parameters.

- `pt[i+1] <- (w / w\_hat) \* pt[i] + rnorm(1, 0, sd = sd\_t)`: This updates the frequency of allele A for the next generation (`i+1`) based on the Wright-Fisher model incorporating selection. It considers the current frequency, mean fitness, and introduces a random element drawn from a normal distribution (`rnorm`) with mean 0 and standard deviation `sd\_t`.

- The `if (pt[i+1] <= 0 || pt[i+1] >= 1) { ... }` condition checks if the updated frequency `pt[i+1]` falls outside the valid range (less than or equal to 0 or greater than or equal to 1), indicating fixation or loss of allele A. If this condition is met:

- `pt[i+1] <- pt[i]`: It sets the frequency of the next generation (`i+1`) to be the same as the current generation, effectively stopping the simulation as the allele has reached fixation or loss.

- `pt <- pt[1:i]`: It trims the `pt` vector to retain only the valid frequencies up to the current generation, discarding any future generations beyond this point.

- `break`: This breaks out of the loop since the simulation is terminated due to fixation or loss of the allele.

This simulation loop models the change in allele frequency over generations considering selection, and it stops if the allele is fixed or lost within the specified number of generations.

what is fixation in population genetics

In population genetics, fixation refers to a state where a particular allele (a variant of a gene) becomes the only variant present in a population. At this point, every individual in the population carries that specific allele. Fixation occurs due to evolutionary forces like natural selection, genetic drift, or migration.

There are a few scenarios that can lead to fixation:

1. \*\*Natural Selection\*\*: If an allele provides a significant advantage in terms of survival or reproduction, it's more likely to increase in frequency and eventually fixate in the population. Conversely, if an allele is disadvantageous, it might be eliminated from the population.

2. \*\*Genetic Drift\*\*: In smaller populations, random chance plays a larger role in allele frequency changes. Due to random sampling during reproduction, certain alleles might, by chance, increase in frequency and ultimately become fixed or lost.

3. \*\*Founder Effect\*\*: When a small group of individuals establishes a new population, the allele frequencies in the new population might differ significantly from the original population due to chance. This can lead to fixation of certain alleles in the new population.

Fixation is an important concept in understanding how genetic diversity changes within populations over time. The process of fixation and the dynamics of allele frequencies are fundamental to understanding evolutionary changes in populations.