EEB313 Project
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For our culminating group project, our objective is to investigate the genetic underpinnings of resistance and susceptibility to Powdery Mildew infection in Sugar Maple (Acer *saccharum*) and Norwegian Maple (Acer *platanoides*) trees. We are dedicated to exploring the alleles responsible for these traits and simulating their evolution over time. Additionally, we aim to analyze the dynamics of Powdery Mildew spread within Sugar Maple populations after reaching a threshold susceptibility level. To further enrich our analysis, we will investigate the population size and mortality rates of Sugar Maples during our study.

Hypotheses:
Our null hypothesis posits that there will be no discernible genetic shift in susceptibility between Norwegian Maples and Sugar Maples, even when threshold allele frequencies are achieved. In contrast, our alternative hypothesis predicts that a critical threshold of significant allele frequencies (resistance alleles in Acer *platanoides* and susceptibility alleles in Acer *saccharum*) will lead to the transfer of the Powdery Mildew pathogen from Norway Maples to Sugar Maples. This shift in susceptibility within the two species will serve as evidence of a potential host-jumping event in the context of Powdery Mildew fungal infection.

To execute this study, we will gather critical variables from existing literature, including the threshold allele frequency of resistance in Norwegian Maples, susceptibility in Sugar Maple, initial population sizes of both maple species from real patches in a specific region of Ontario, mutation rates, and other pertinent factors such as:

1. **Powdery Mildew Spread Model:** We will develop a comprehensive model for the spread of Powdery Mildew within Sugar Maple populations once the threshold susceptibility allele frequency is attained. This model will consider factors like environmental conditions, transmission rates, and infection dynamics.

2. **Population Dynamics:** We will monitor the population size of Sugar Maples throughout the study, taking into account birth and death rates. This data will be used to understand how disease susceptibility affects the tree population over time.

3. **Powdery Mildew Mutation Rate:** Investigating the mutation rate of the Powdery Mildew pathogen itself is crucial, as it may influence its ability to infect both tree species. This will be an essential variable in our analysis.

4. **Environmental Factors:** We will explore the impact of environmental factors, such as temperature, humidity, and soil conditions, on disease transmission rates and their potential role in the genetic shift between the two maple species.

5. **Generation Time:** We will run the simulation multiple times using a varied number of generations for each one: eg., after 50 years, 100 years, 1000 years, etc.

5. **Genetic Analysis:** We will conduct genetic analysis, including DNA sequencing, to identify specific alleles associated with resistance and susceptibility in both maple species. This will allow us to correlate genetic changes with disease dynamics.

In the simulation phase, we will leverage the R programming language to estimate the timing of allele transitions and model Powdery Mildew spread within Sugar Maple populations over many generations, considering the variables outlined above.

In the data analysis stage, we will employ a range of statistical tests and data visualization techniques to draw meaningful conclusions. These tests may include:

- **Chi-squared tests:** To assess the significance of genetic changes in allele frequencies over time.
- **Survival analysis:** To analyze the impact of Powdery Mildew on the survival of individual trees in Sugar Maple populations.
- **Correlation analysis:** To explore relationships between environmental variables, genetic changes, and disease dynamics.
- **Bayesian modeling:** To estimate the probabilities of disease transfer events between tree species.

Data visualization using tools such as ggplot2 and Leaflet will help communicate our findings effectively.

This comprehensive study promises to provide profound insights into the intricate interplay of genetics, disease dynamics, and population ecology within Sugar and Norwegian Maple trees, ultimately contributing to our understanding of host-pathogen interactions and the potential for host jumps in fungal infections.

Citations

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Slippers B, Stenlid J, Wingfield MJ. 2005. Emerging pathogens: fungal host jumps following anthropogenic introduction. Trends in Ecology and Evolution. 20(8), 420–421. doi:https://doi.org/10.1016/j.tree.2005.05.002.