

Disease-spreading in monoculture and mixed-species forests

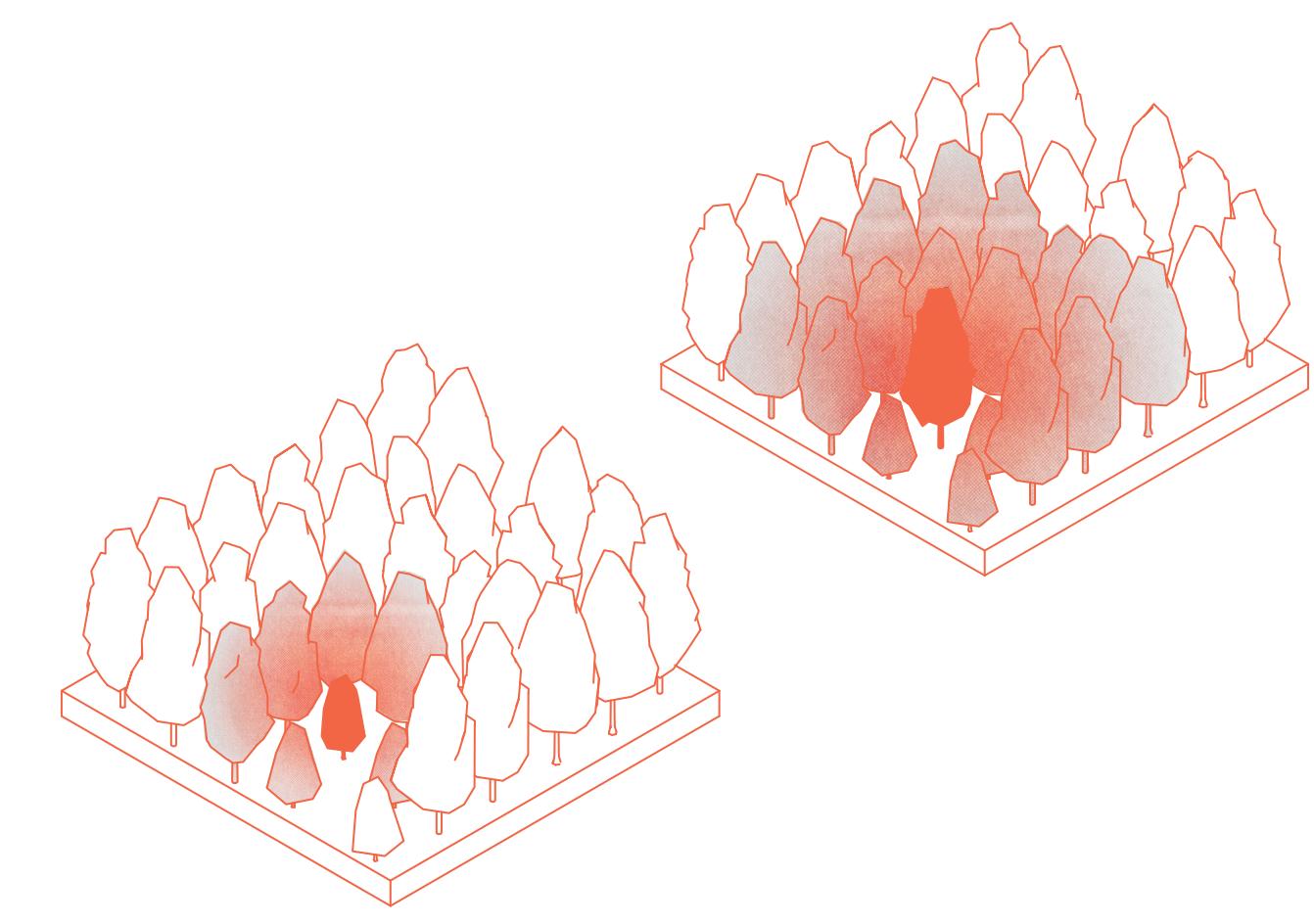
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Diversifying forests by introducing a secondary species is a proactive approach to disease control. While this method may reduce the yield of the primary timber species, it can ultimately lead to a healthier forest and improved long-term economic outcomes by reducing disease-related losses. Through simulations we aim to investigate how the diversification of an agricultural forest affects disease-spreading.

METHOD

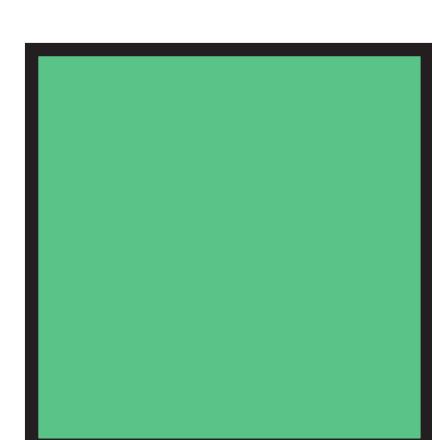
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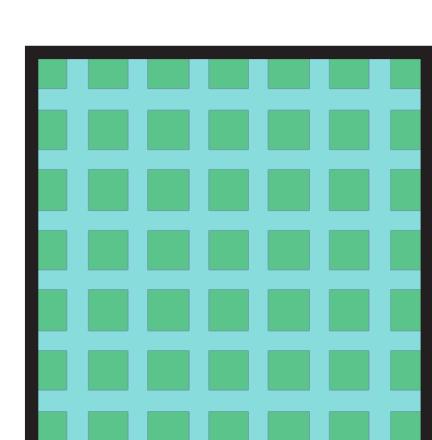
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SIMULATIONS



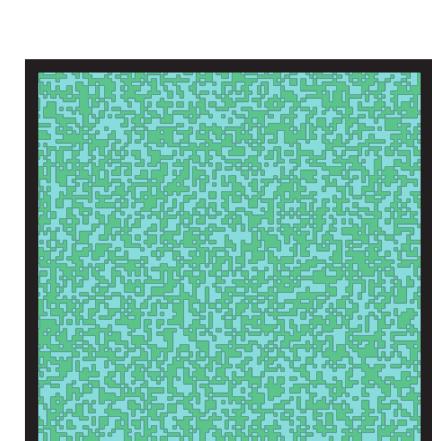
HOMOGENEOUS

Monoculture forest consisting solely of species A, the more susceptible tree.



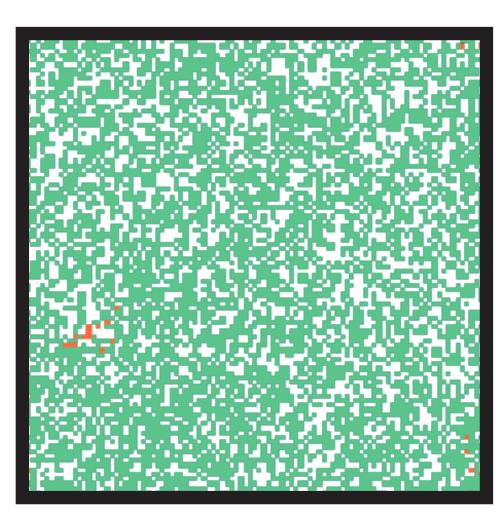
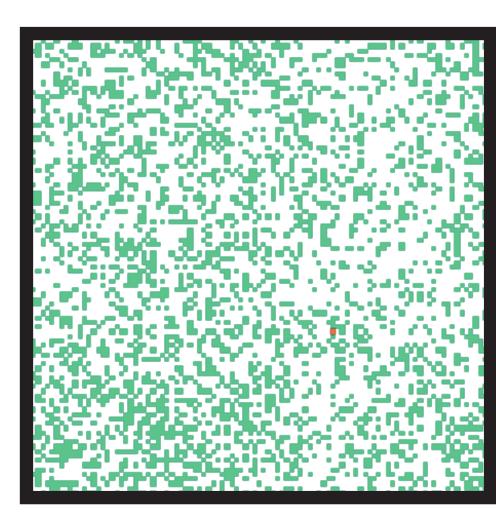
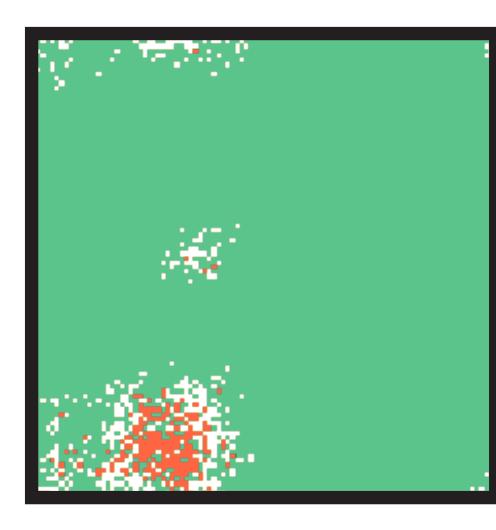
GRID-LIKE

Mixed species forest with rows of Species B, planted to form a barrier against the disease.

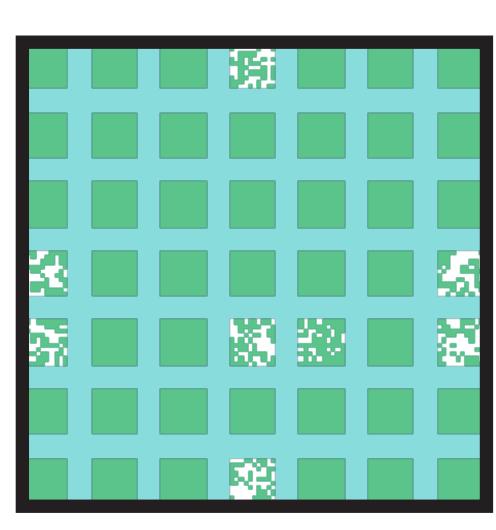
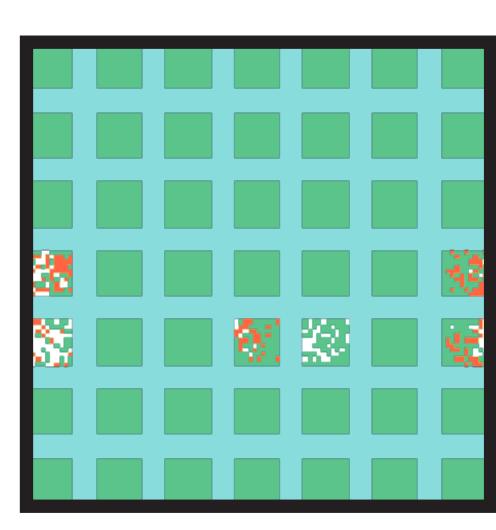
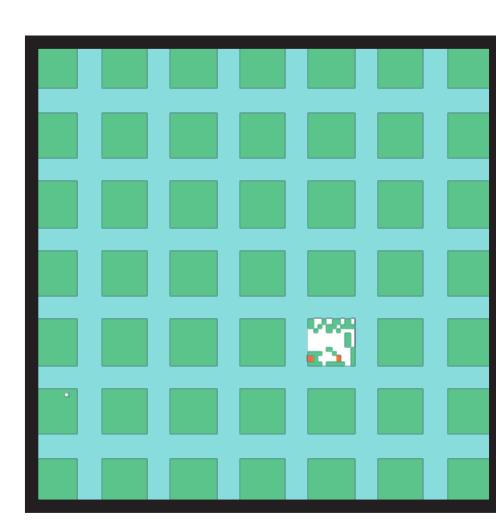


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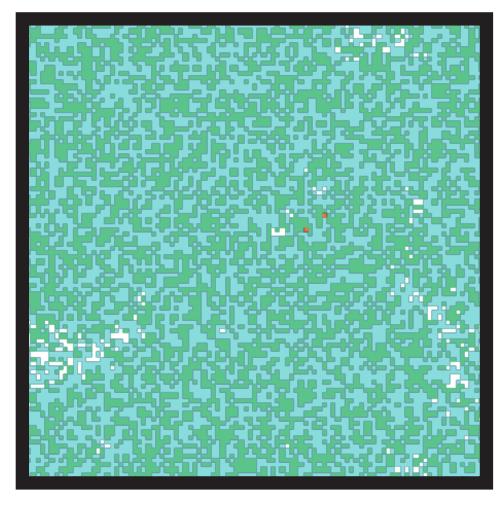
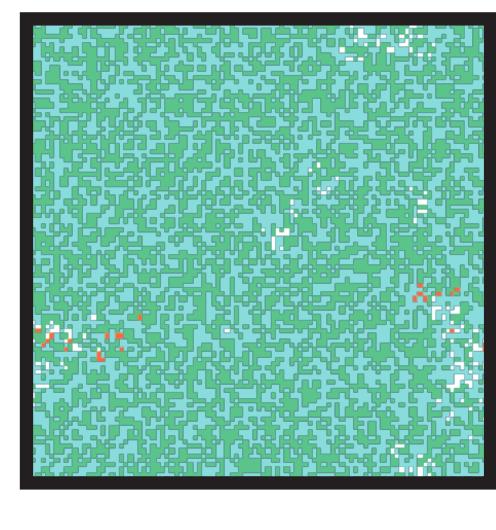
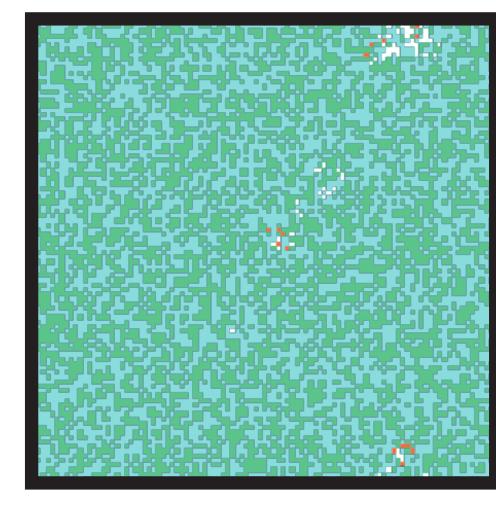
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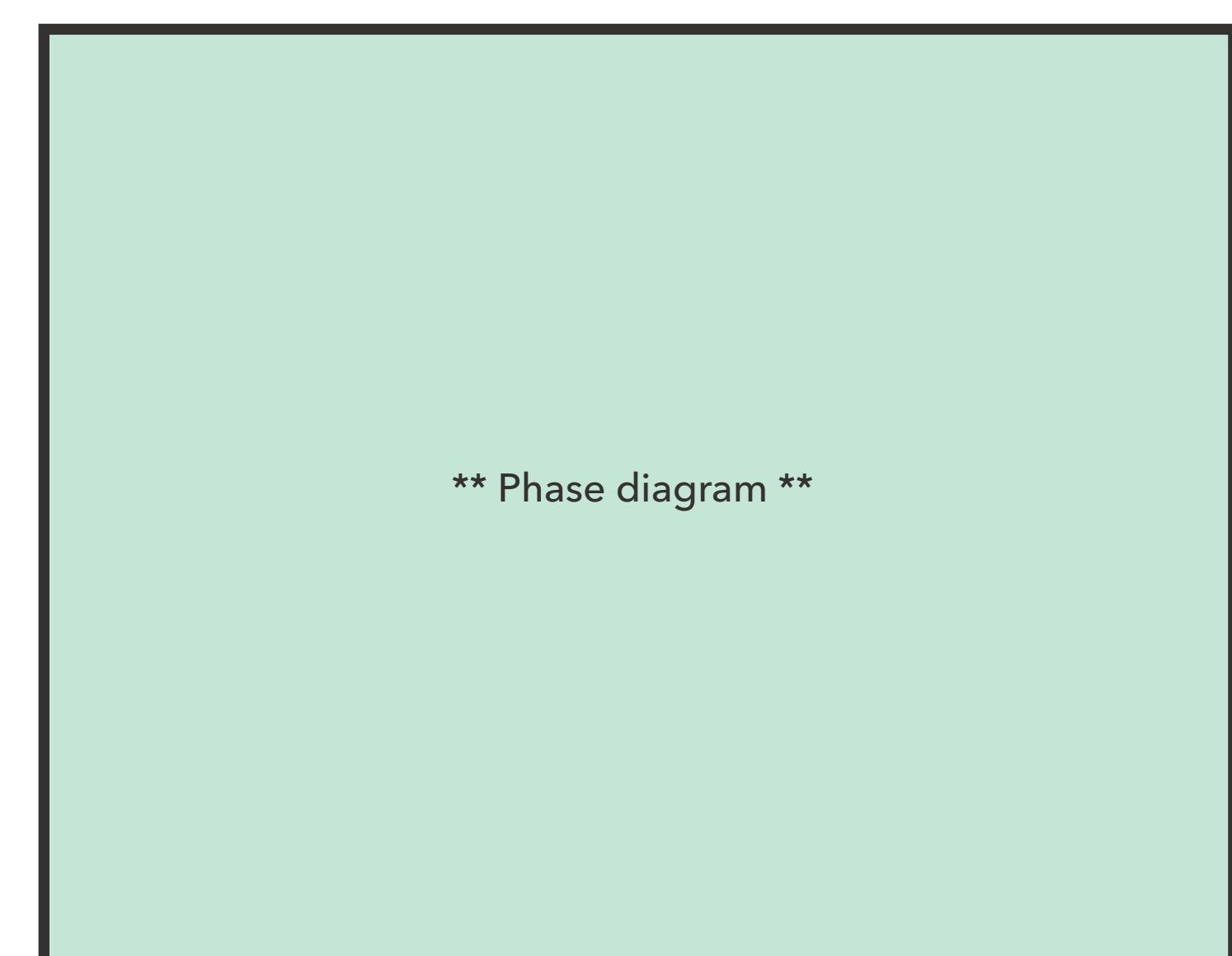
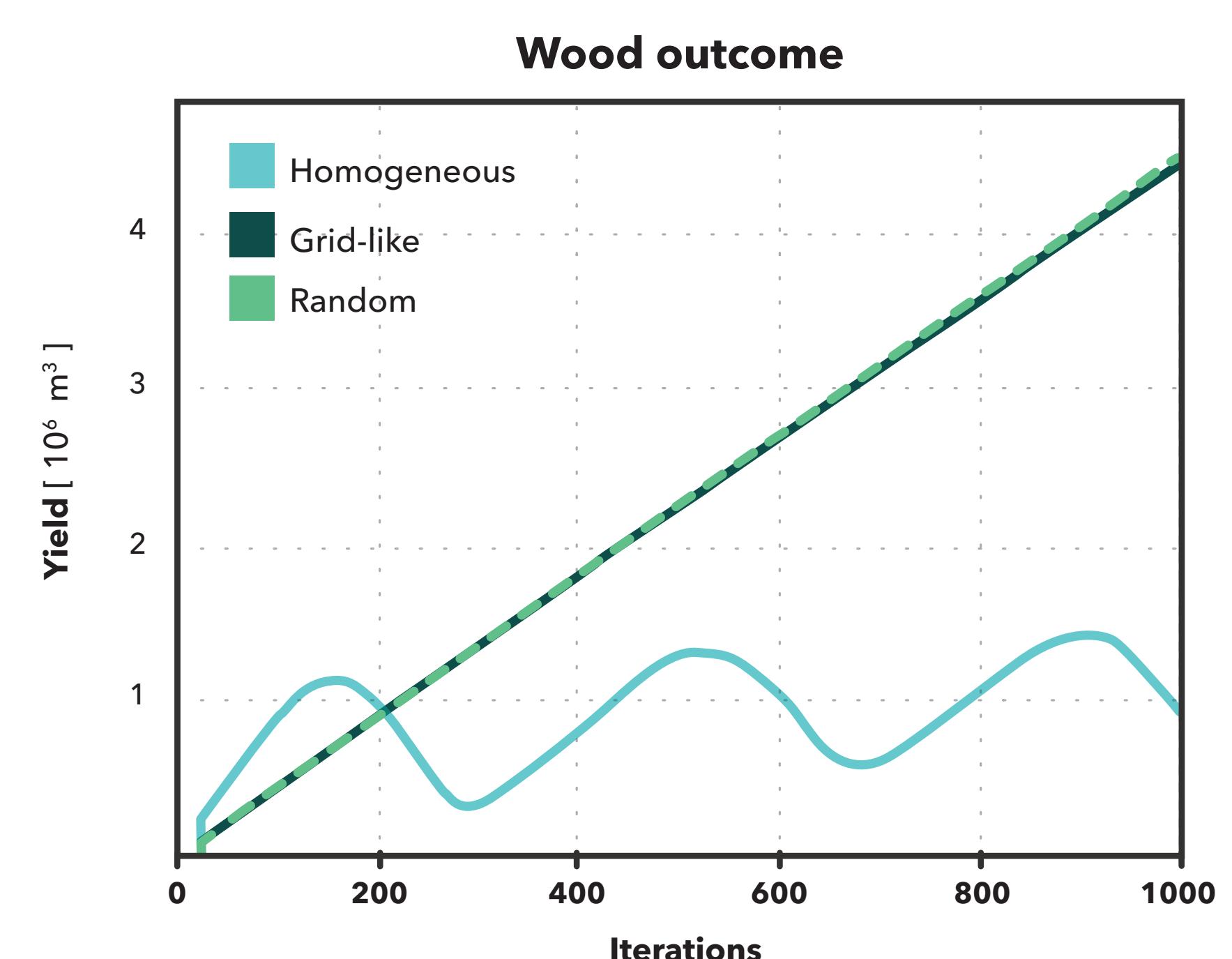
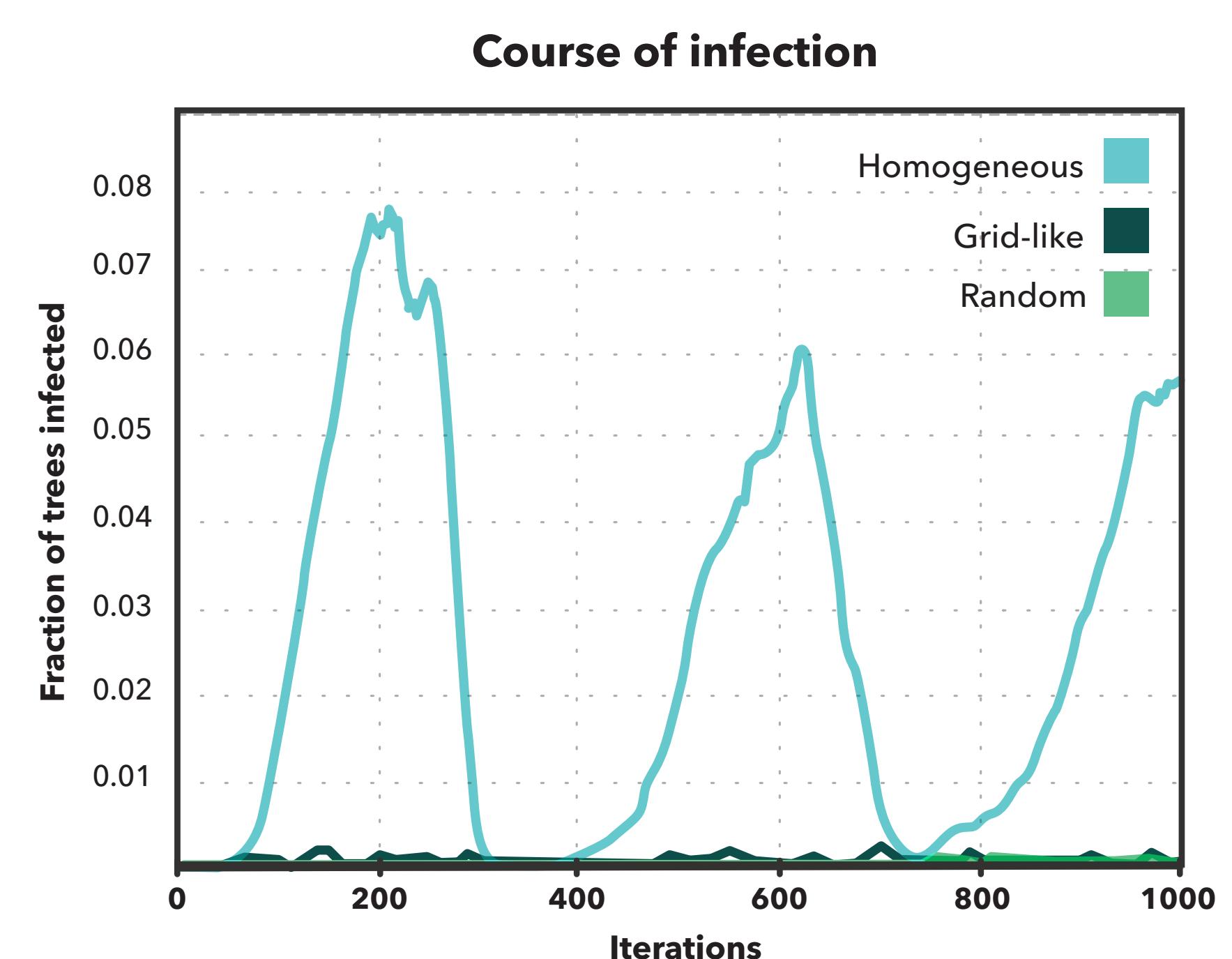
HOMOGENEOUS: Once a tree gets infected it doesn't take long before the whole forest is wiped out.



GRID-LIKE: The rows of immune trees appear to successfully contain the disease to smaller patches.



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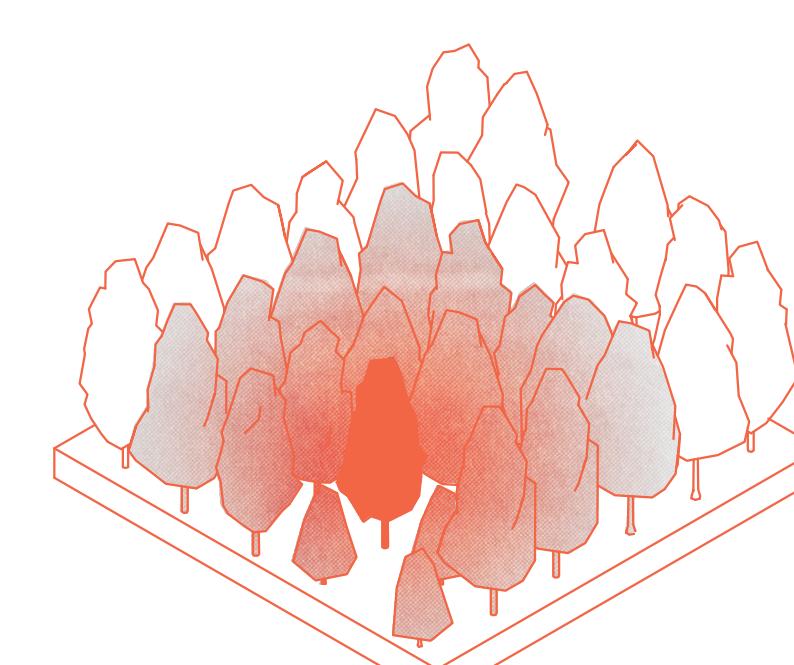
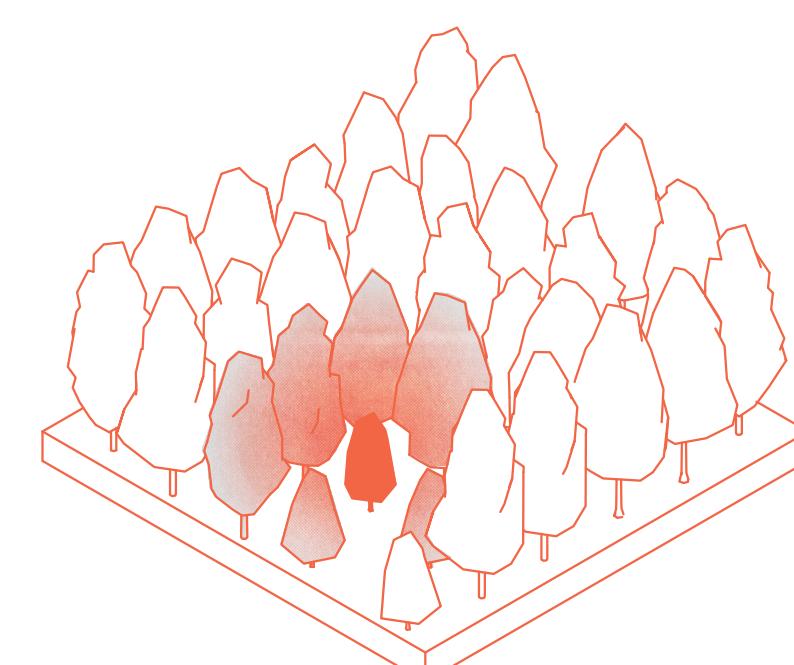


Here we describe the phase diagram and briefly discuss the conclusions that can be drawn from the simulation supported by the diagram.

Disease-spreading in monoculture and mixed-species forests

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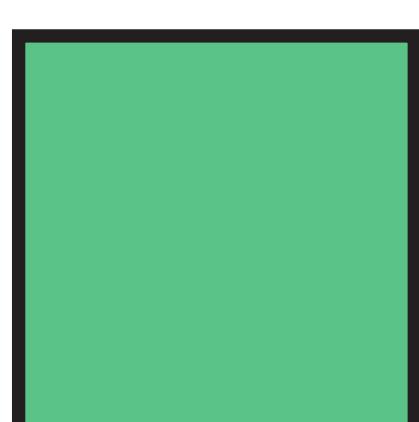
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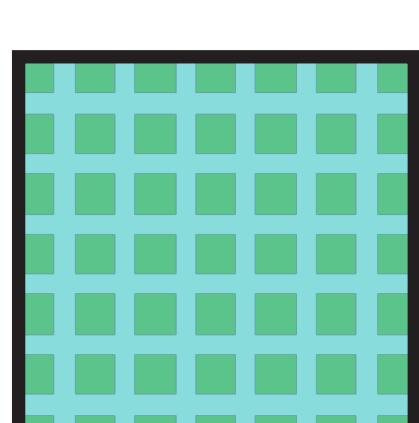
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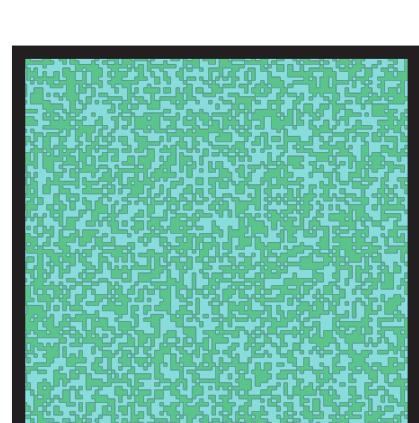
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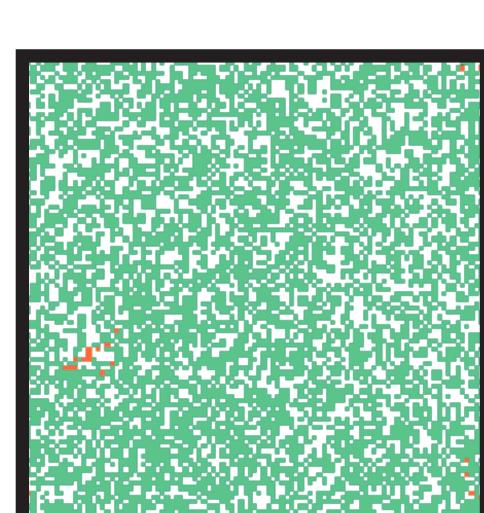
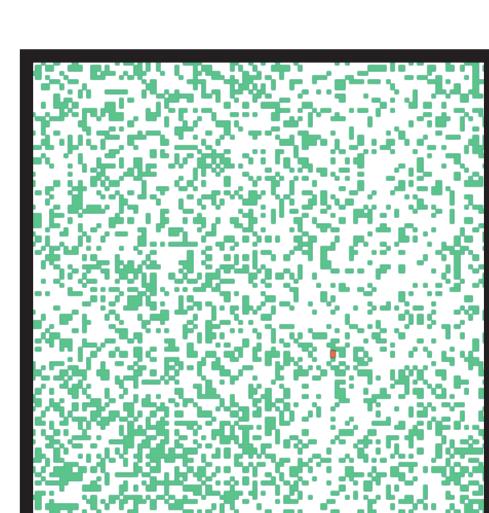
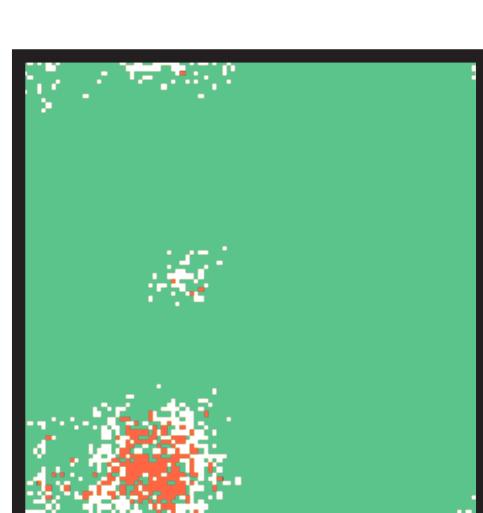
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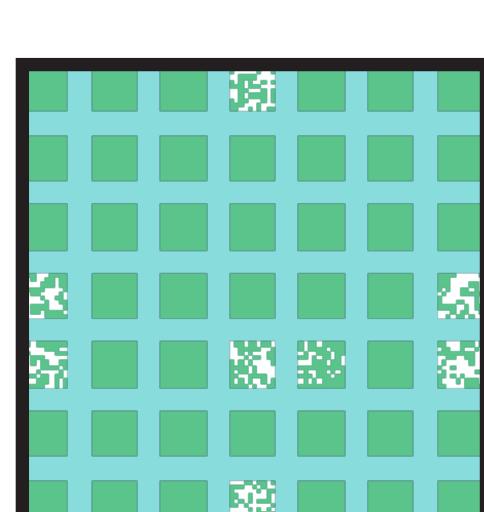
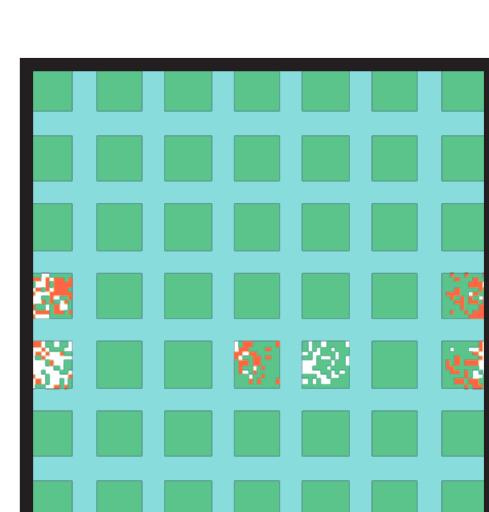
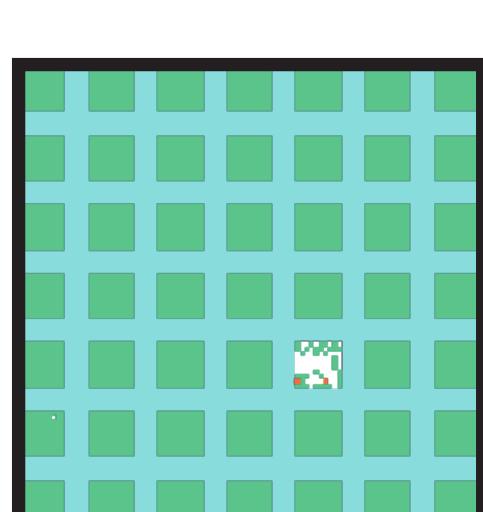


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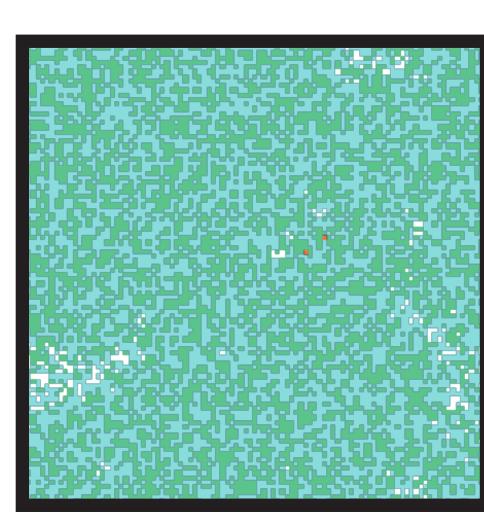
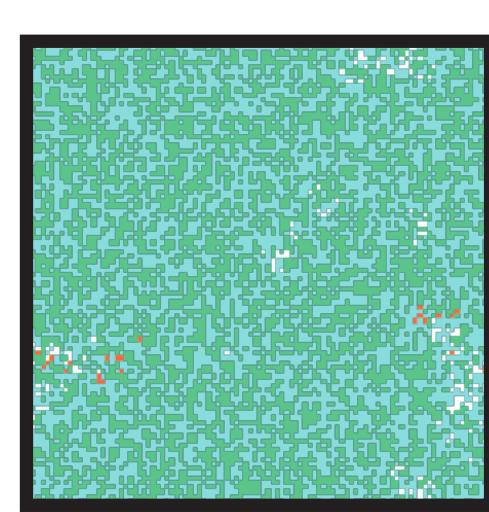
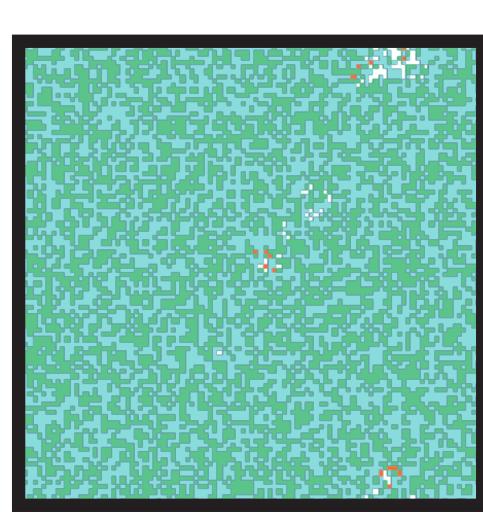
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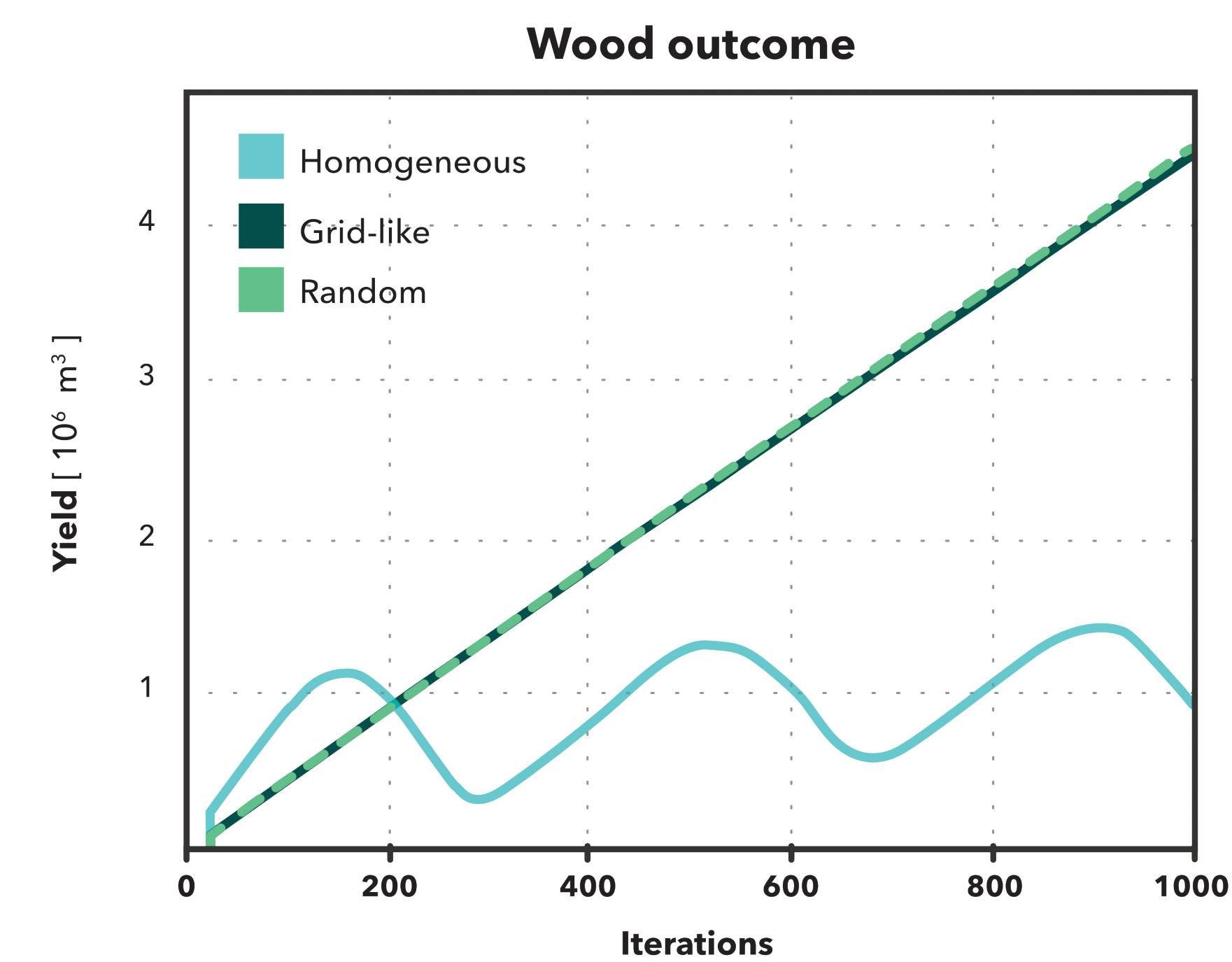
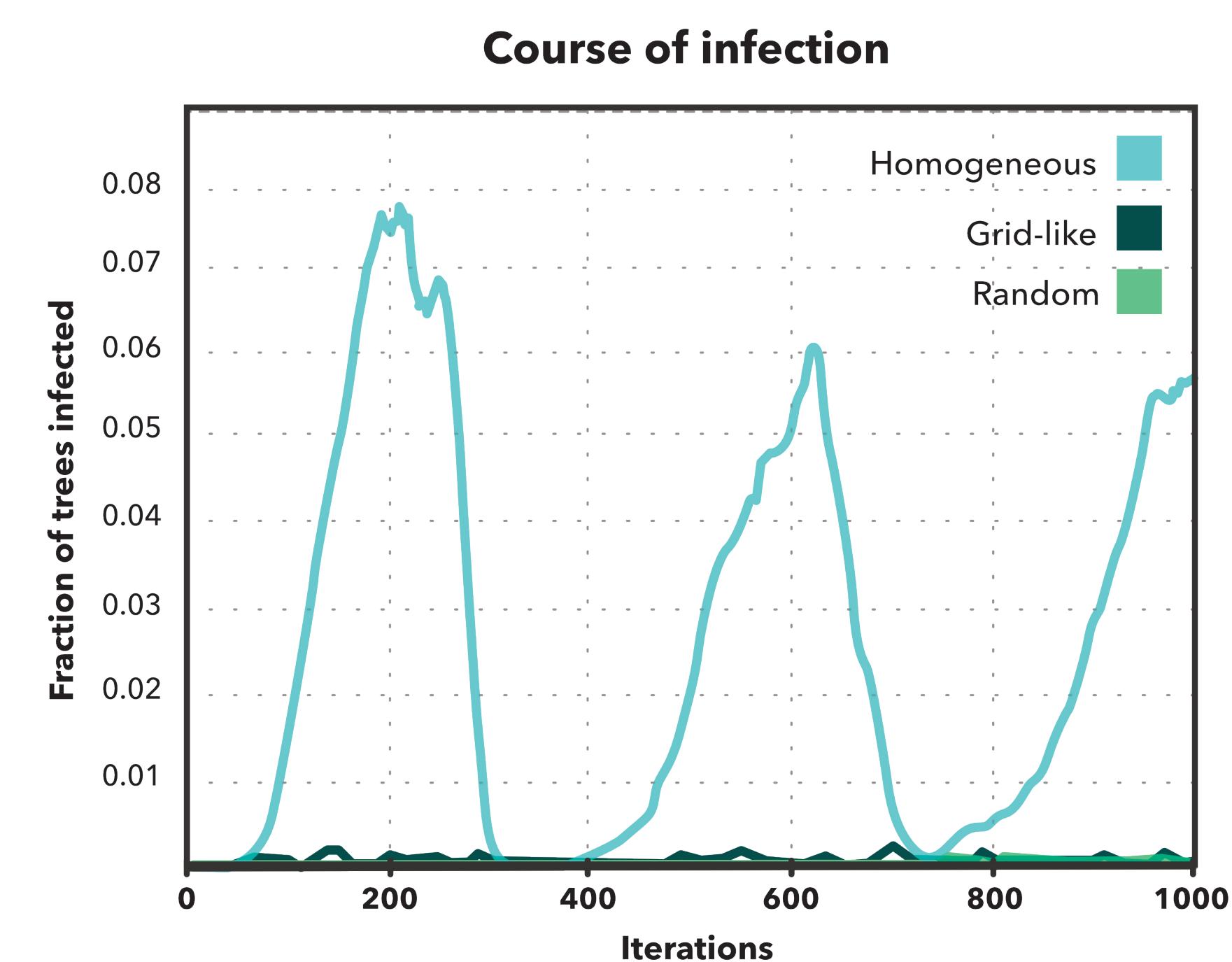
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INTRODUCTION

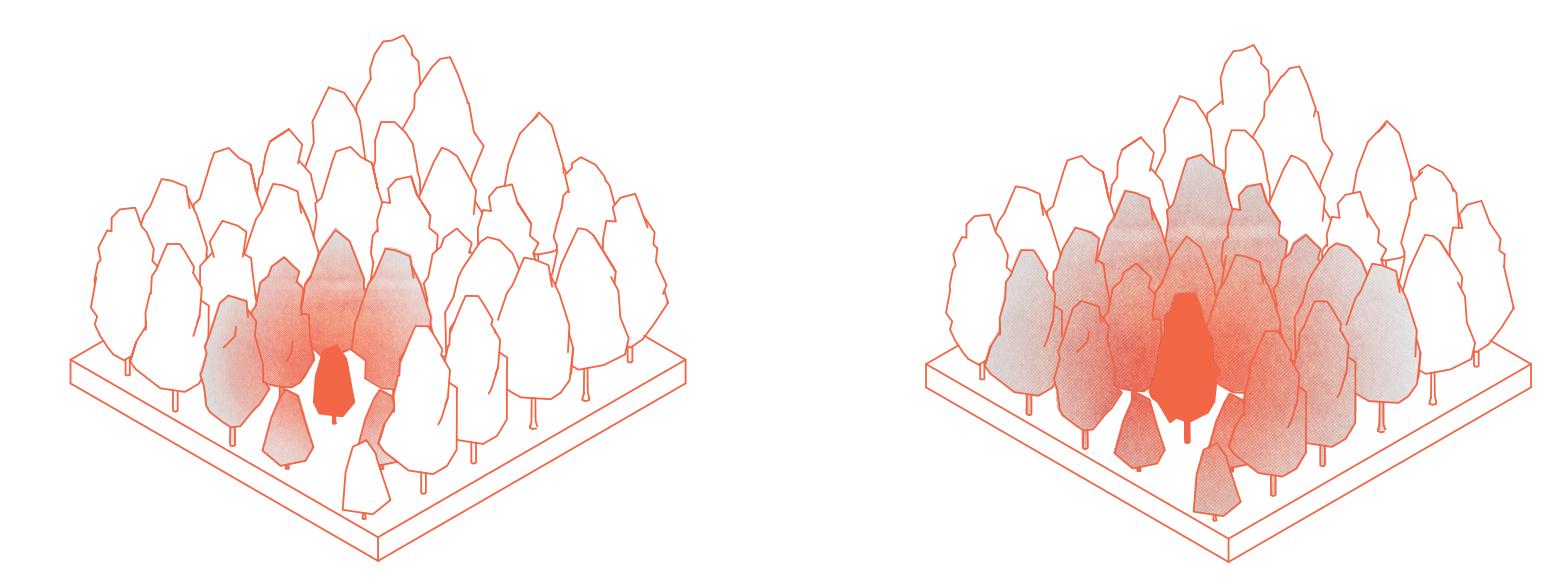
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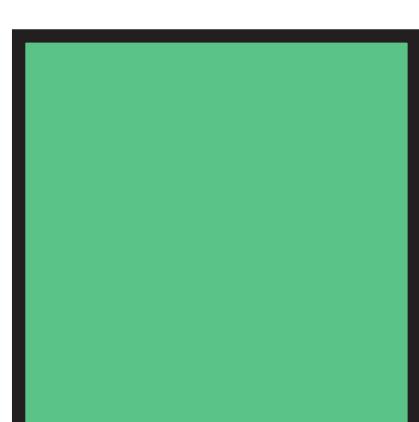
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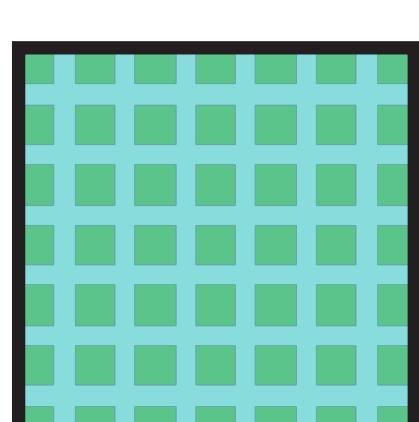
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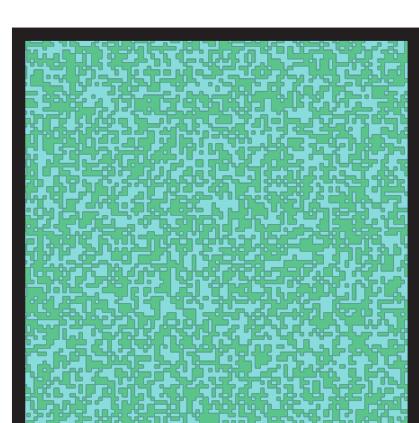
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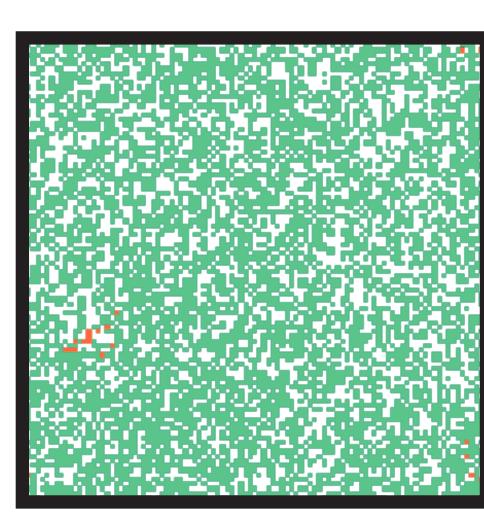
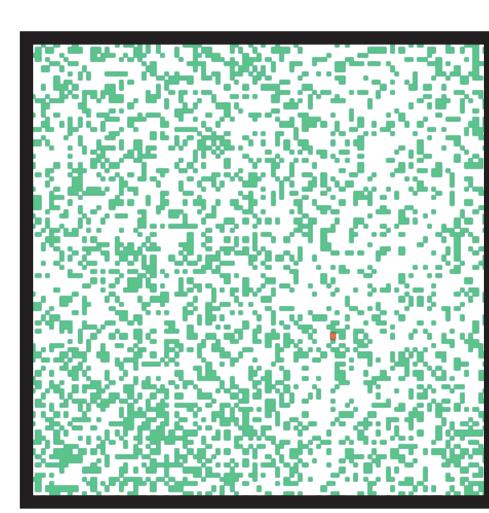
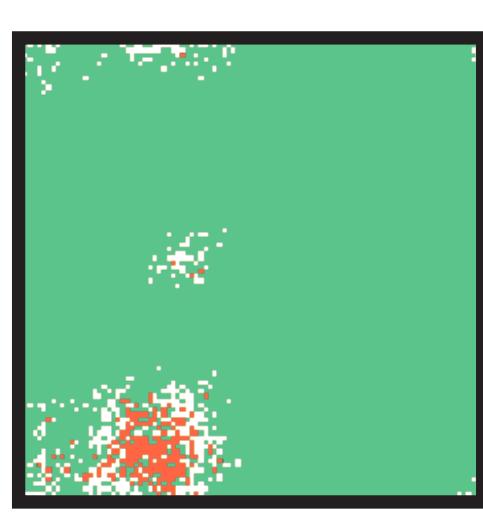
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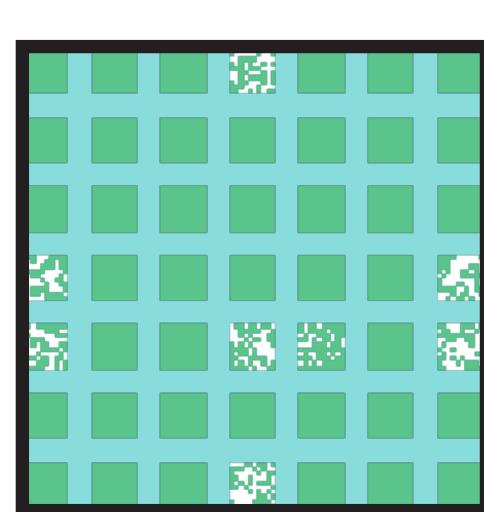
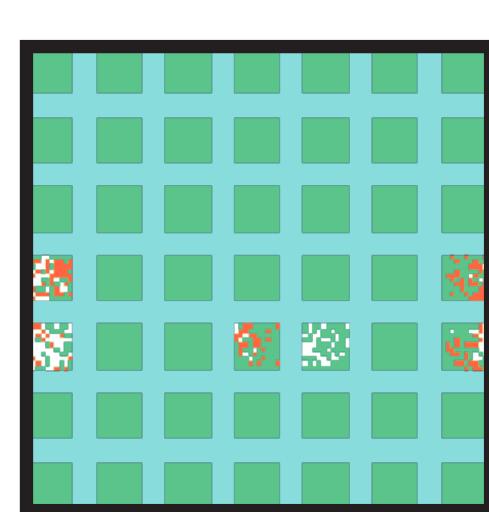
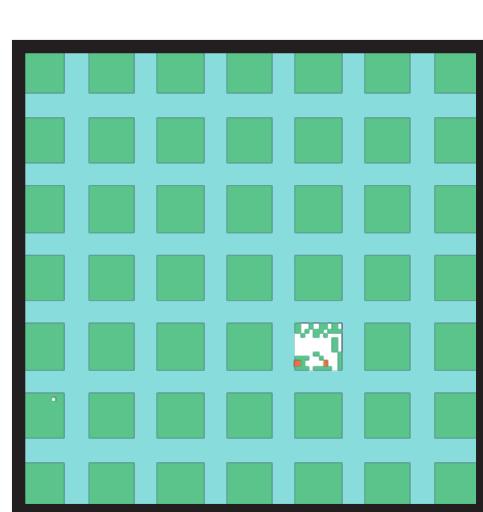


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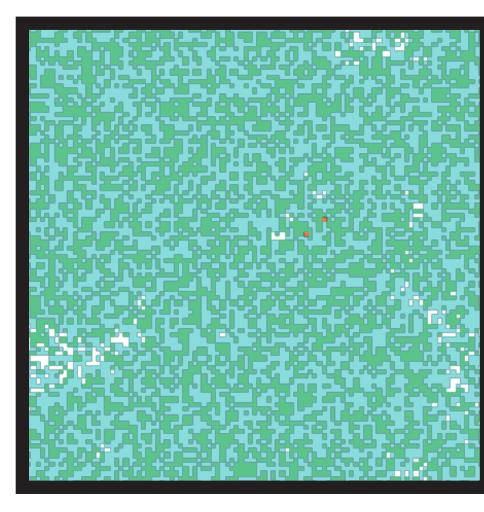
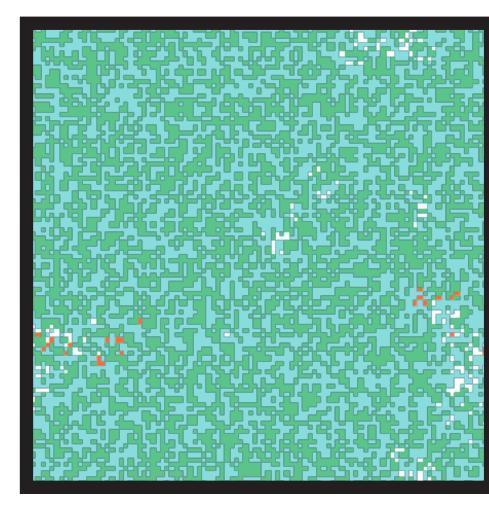
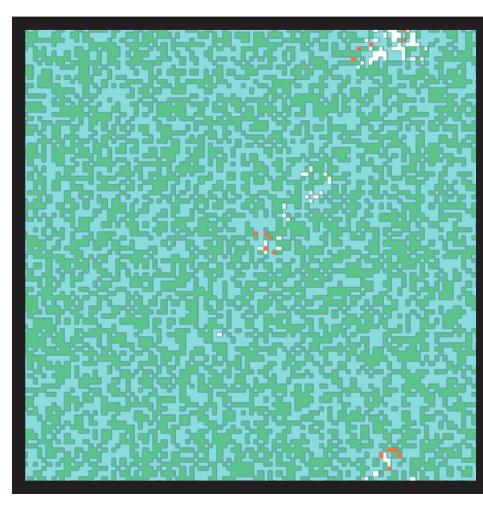
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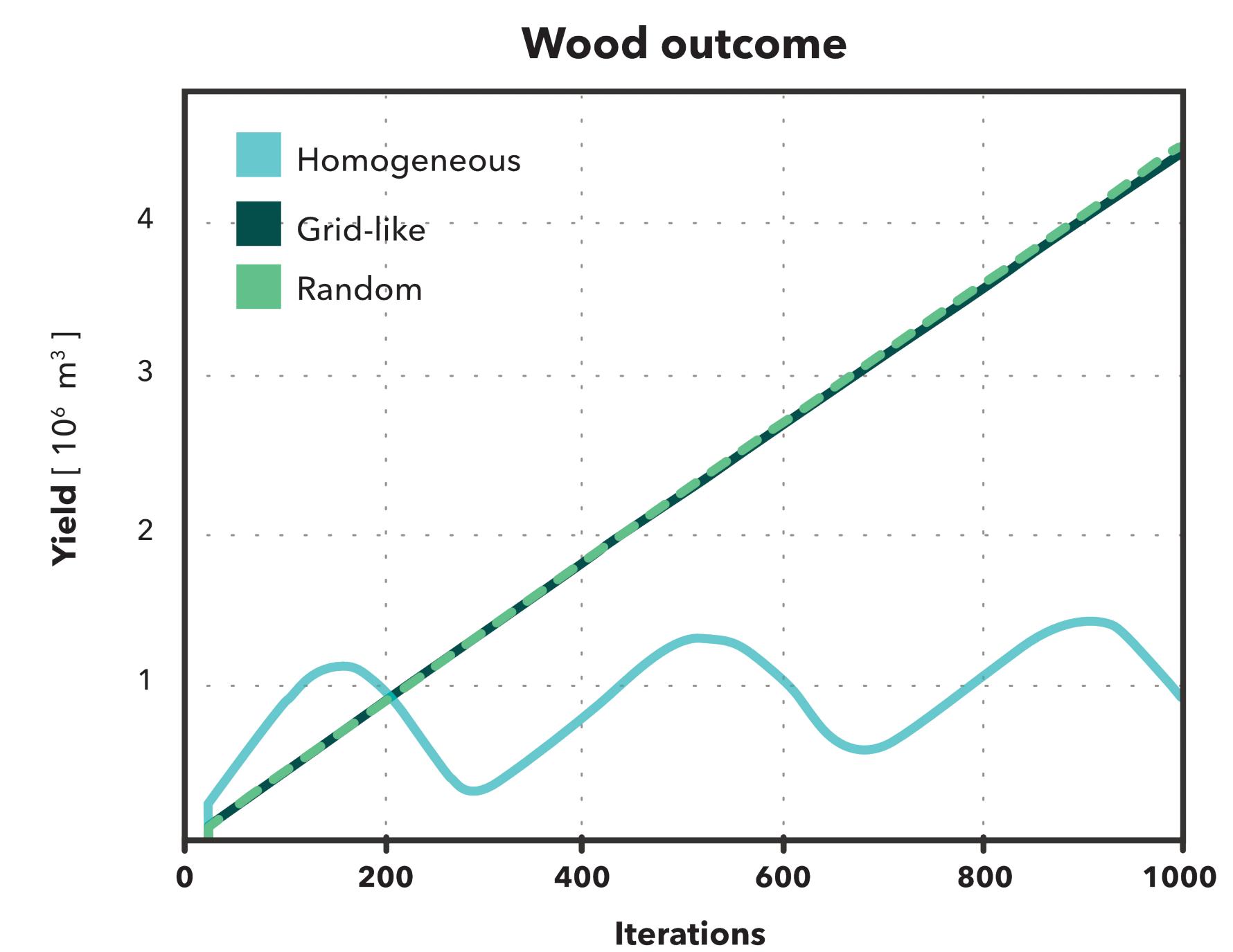
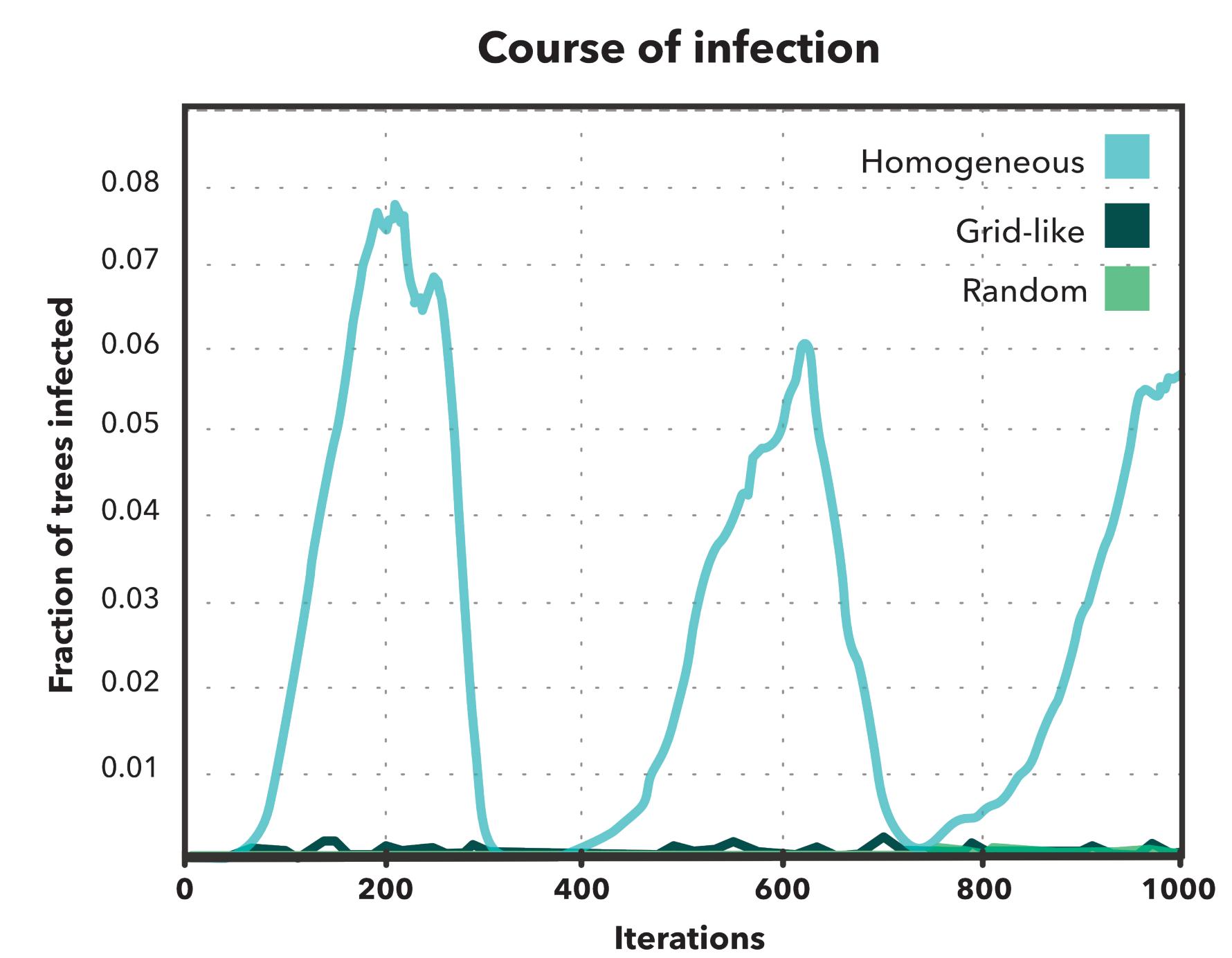


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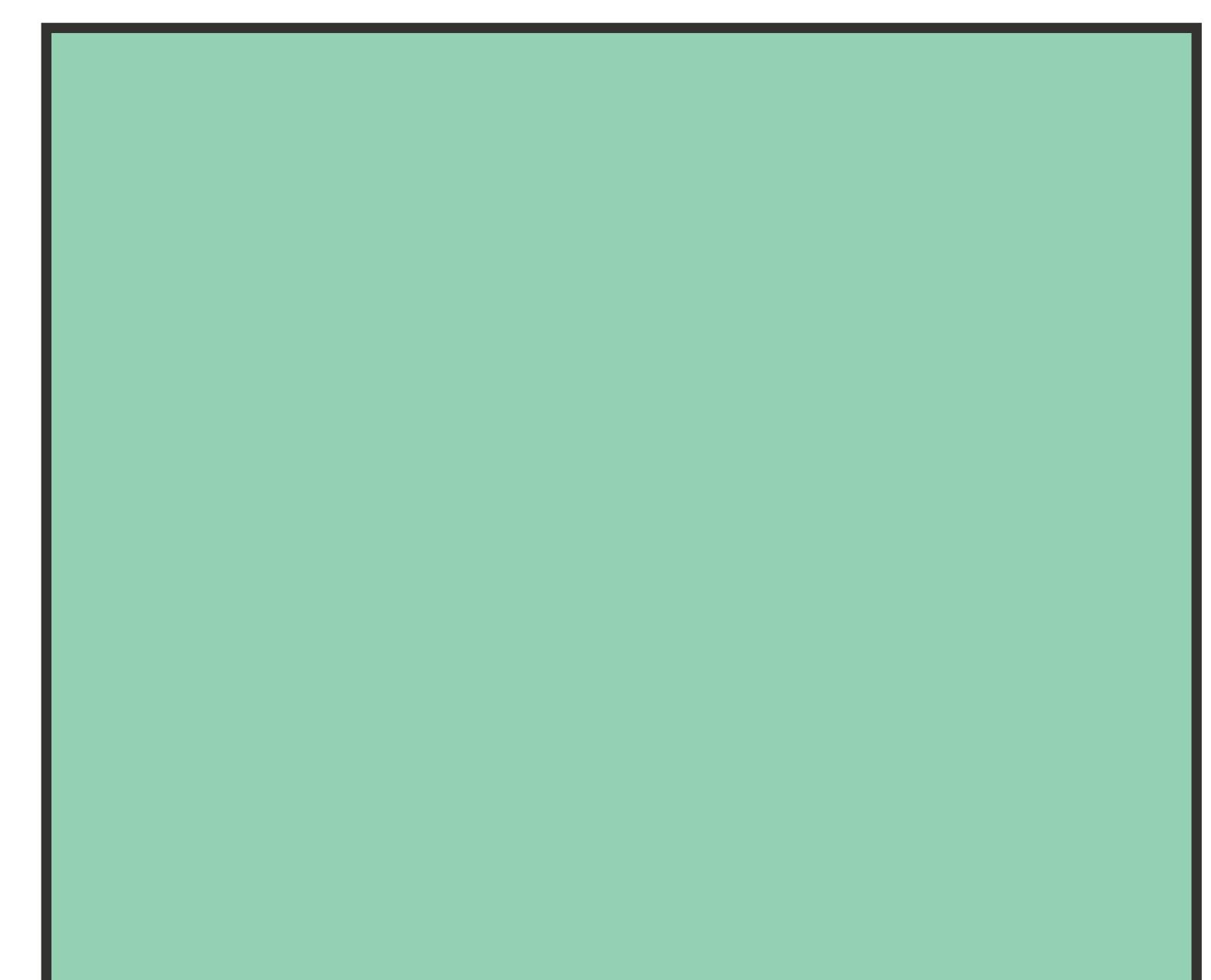
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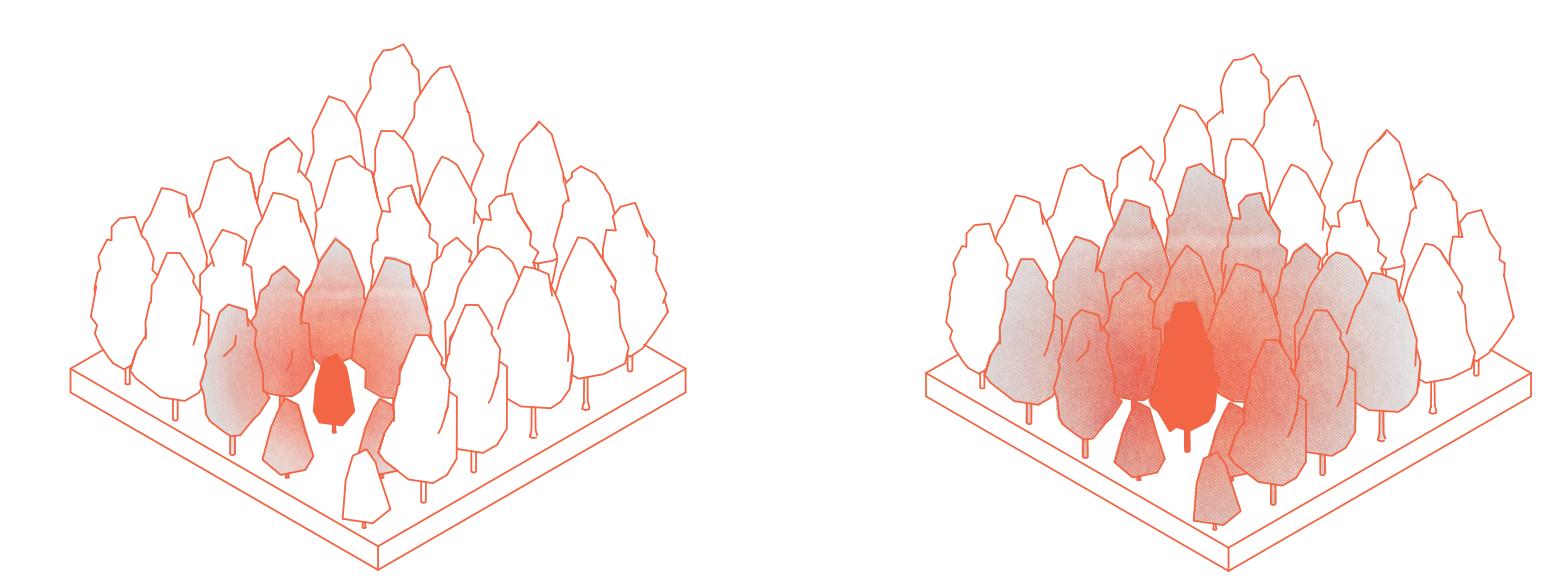
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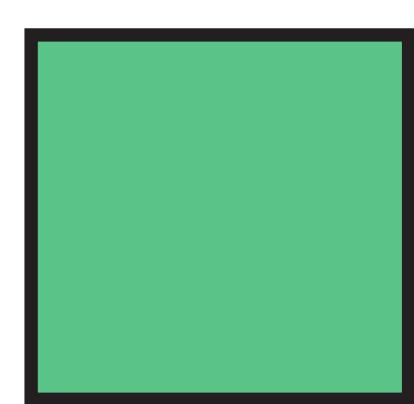
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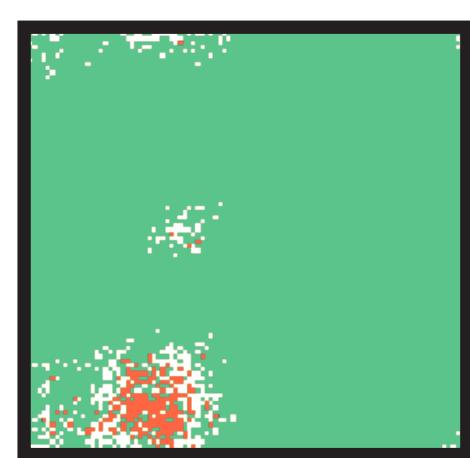
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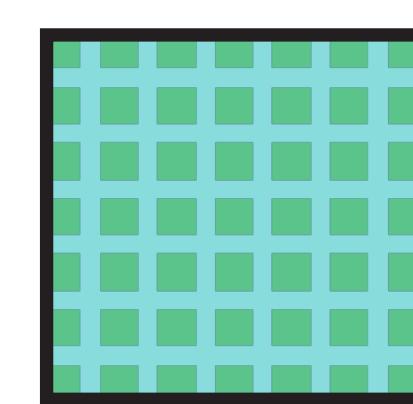


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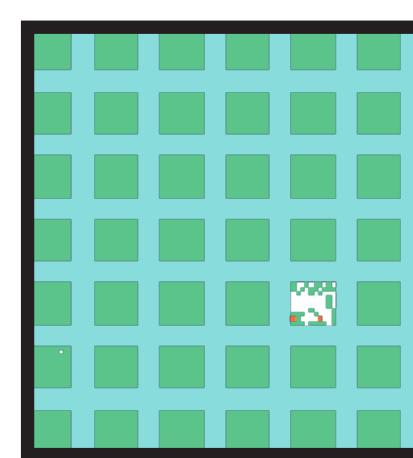


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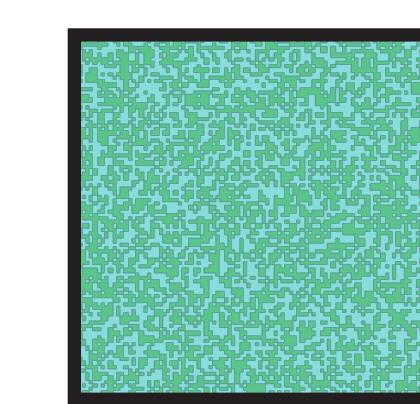


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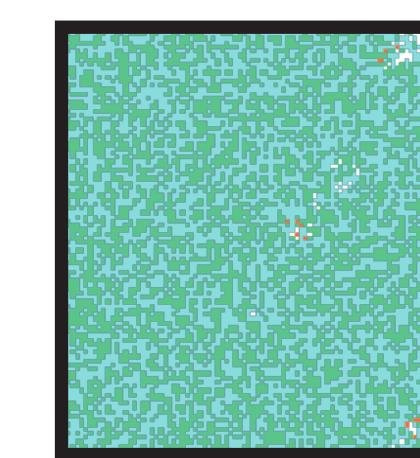


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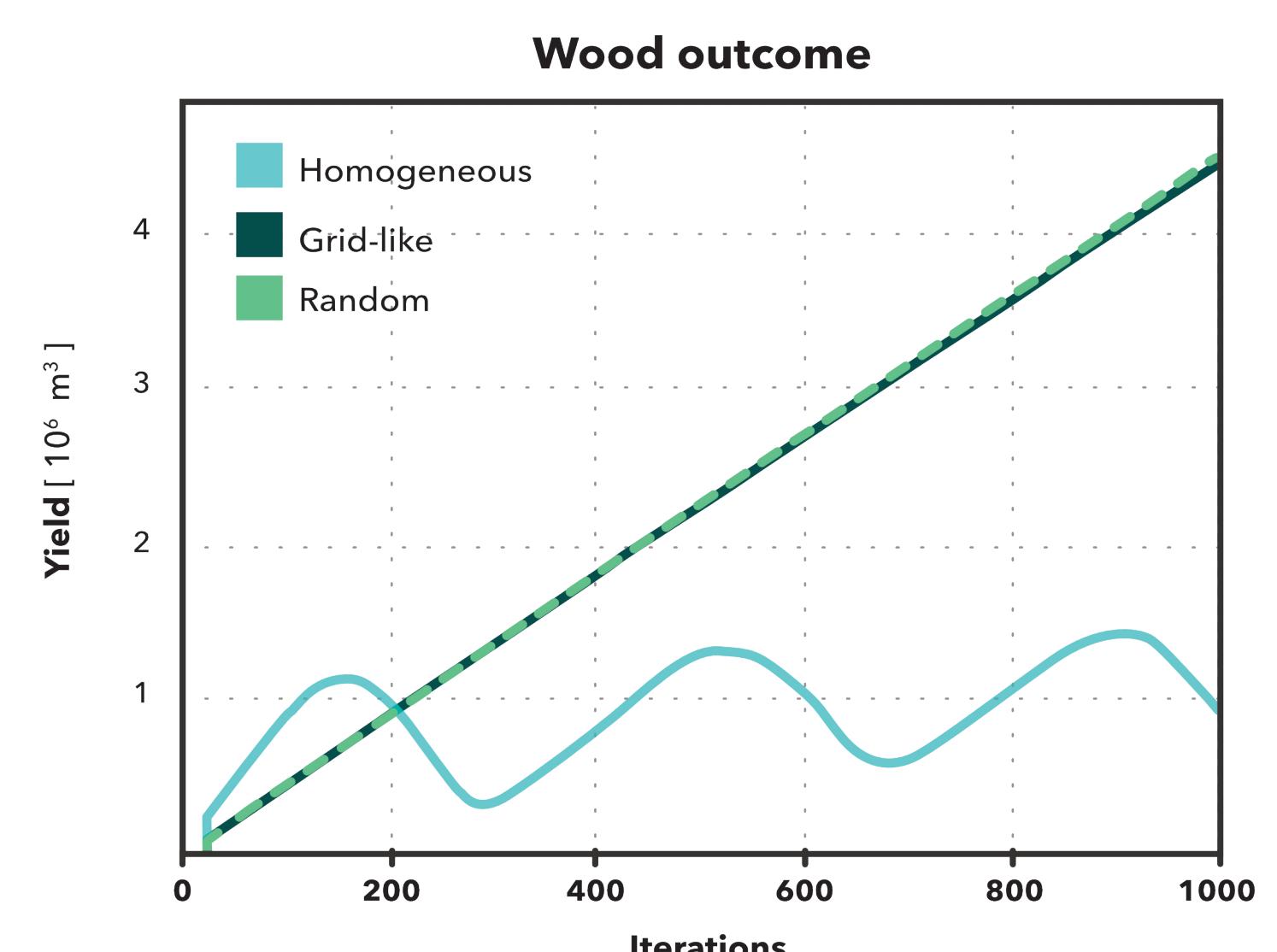
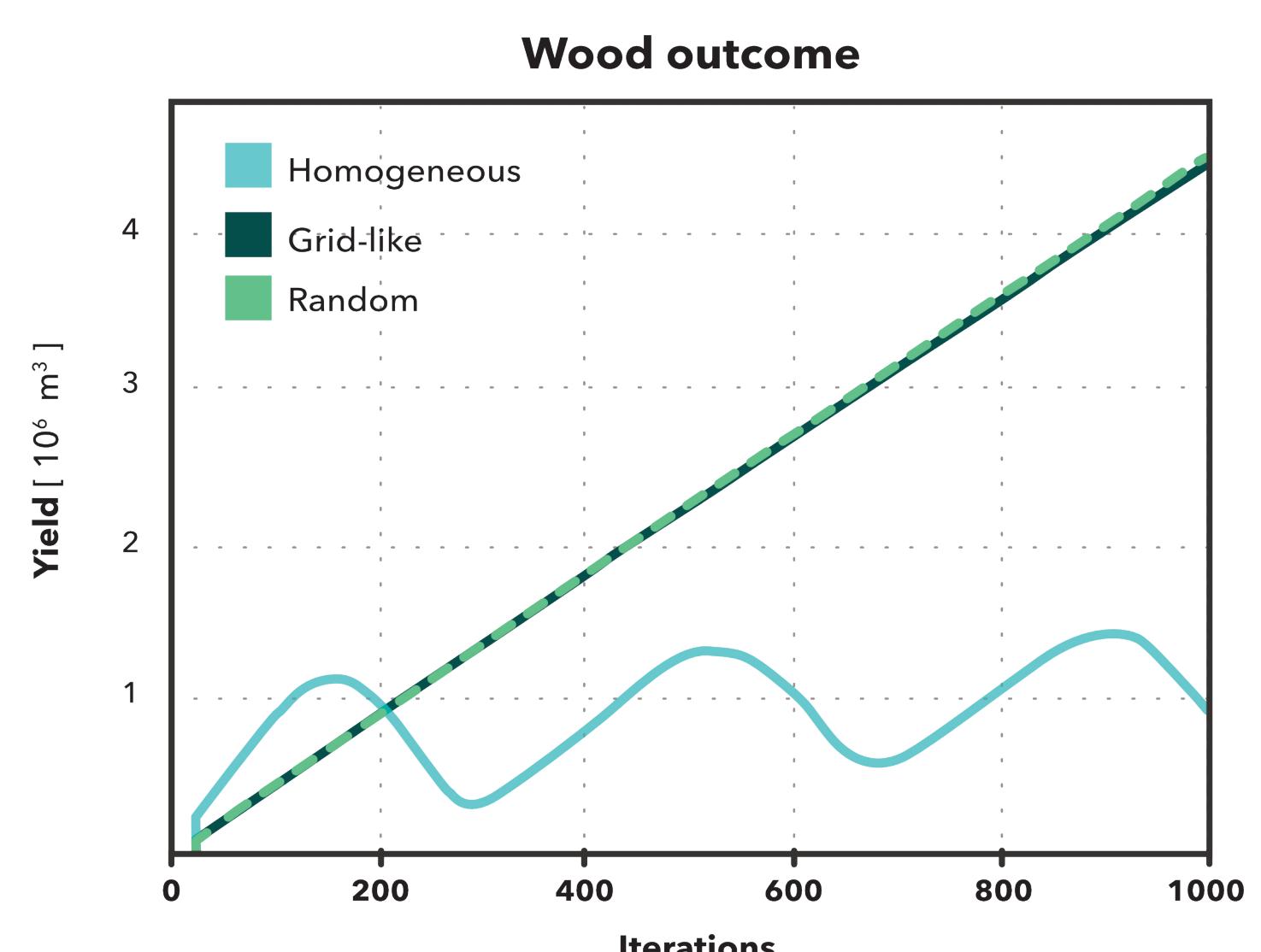
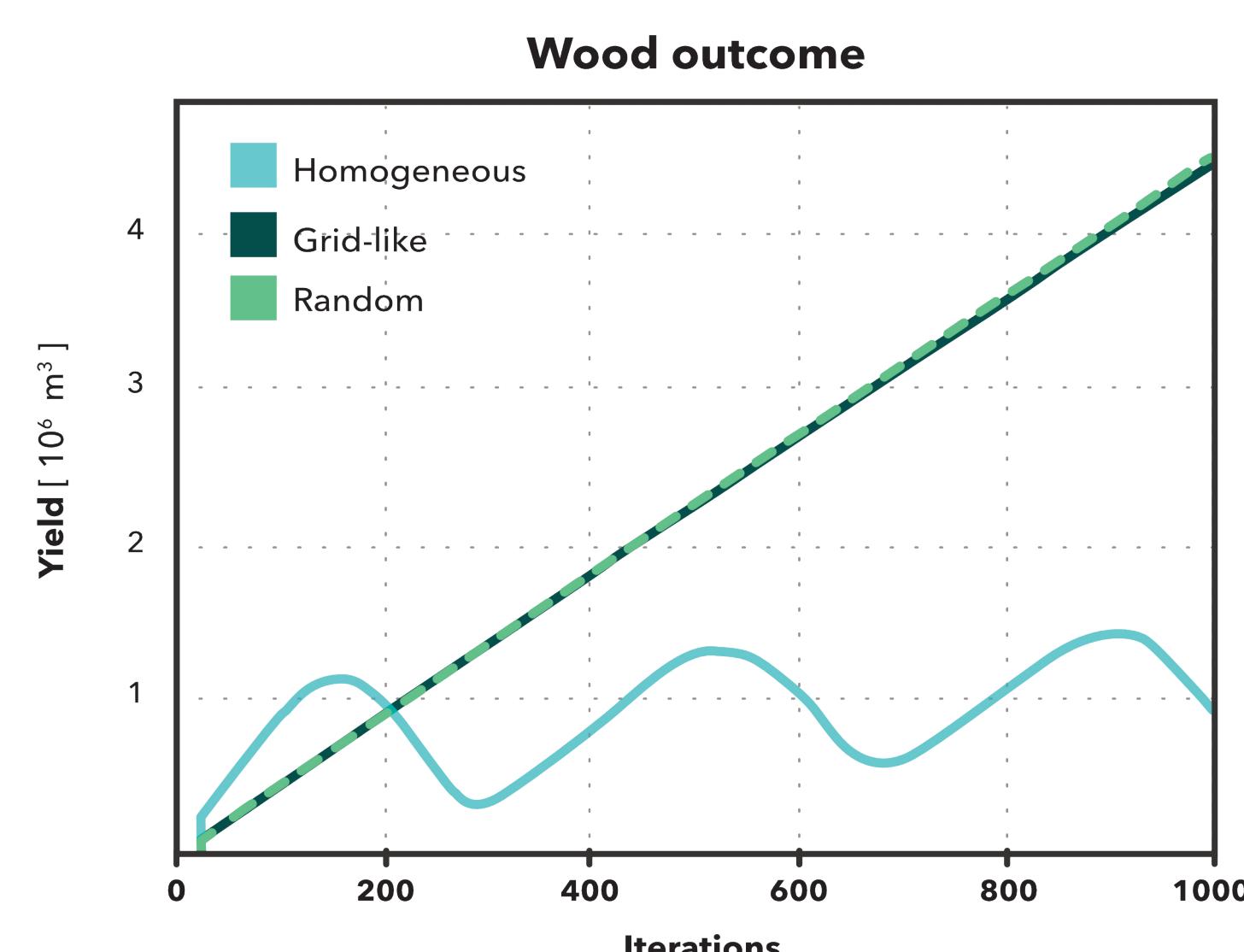
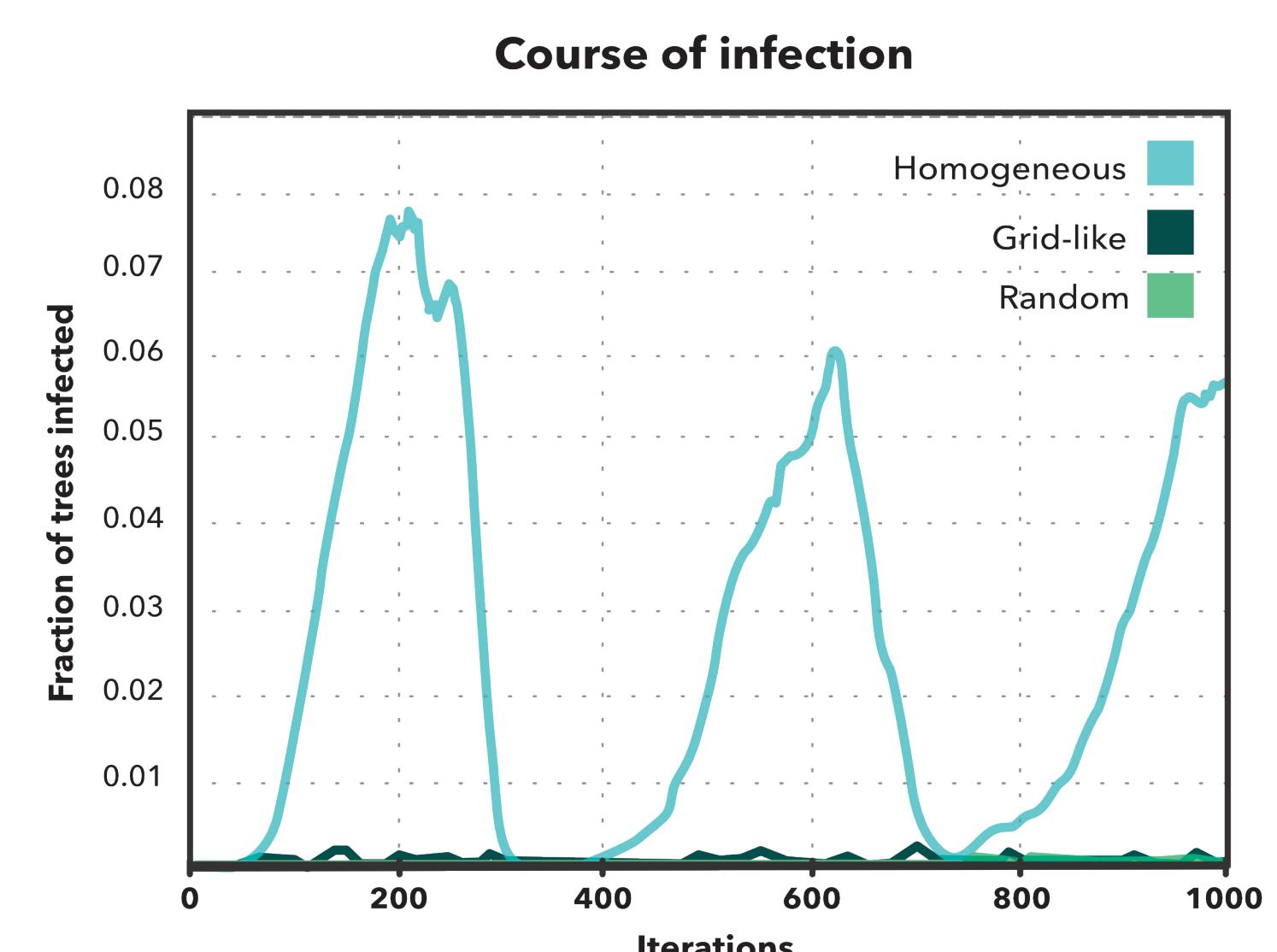
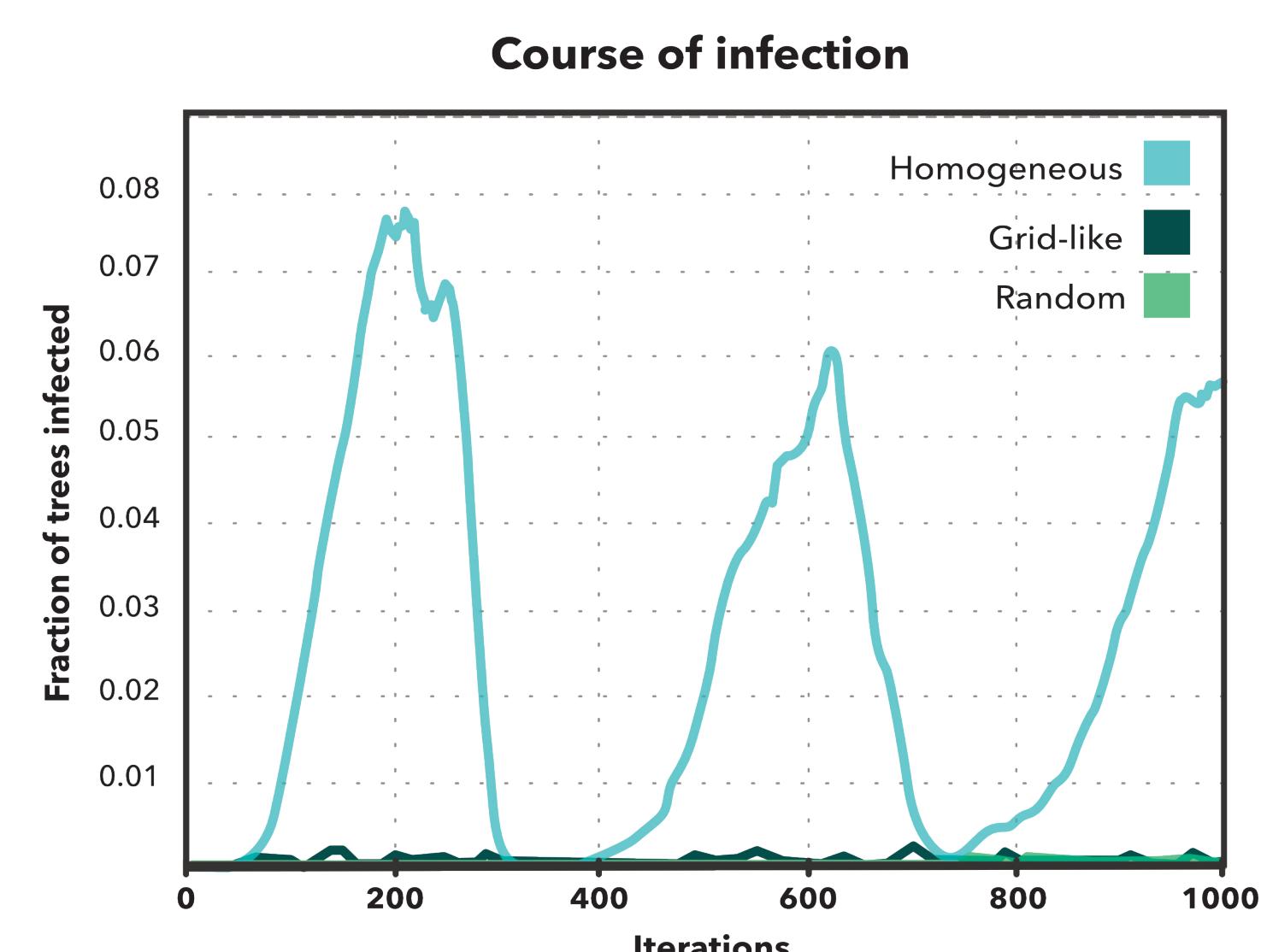
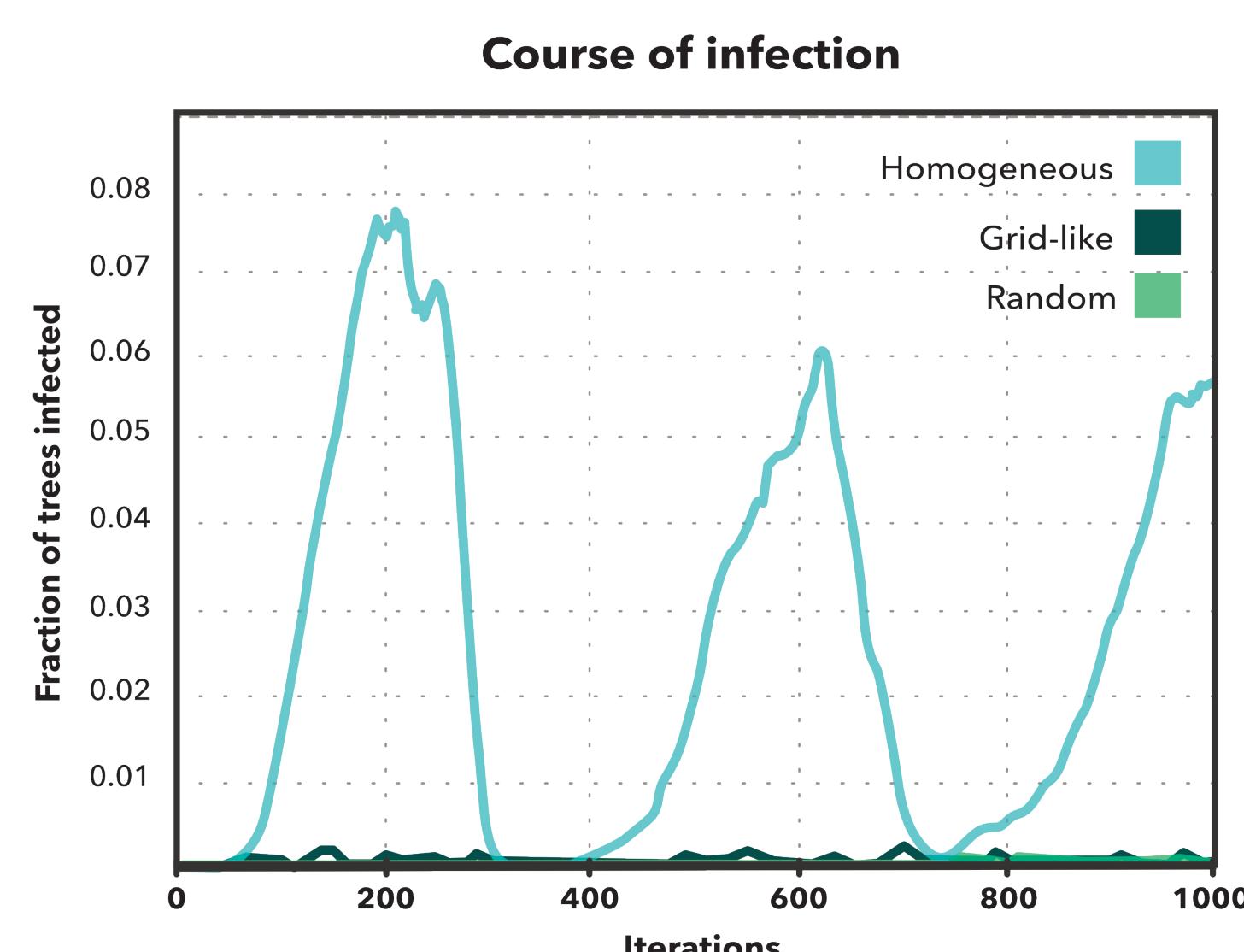


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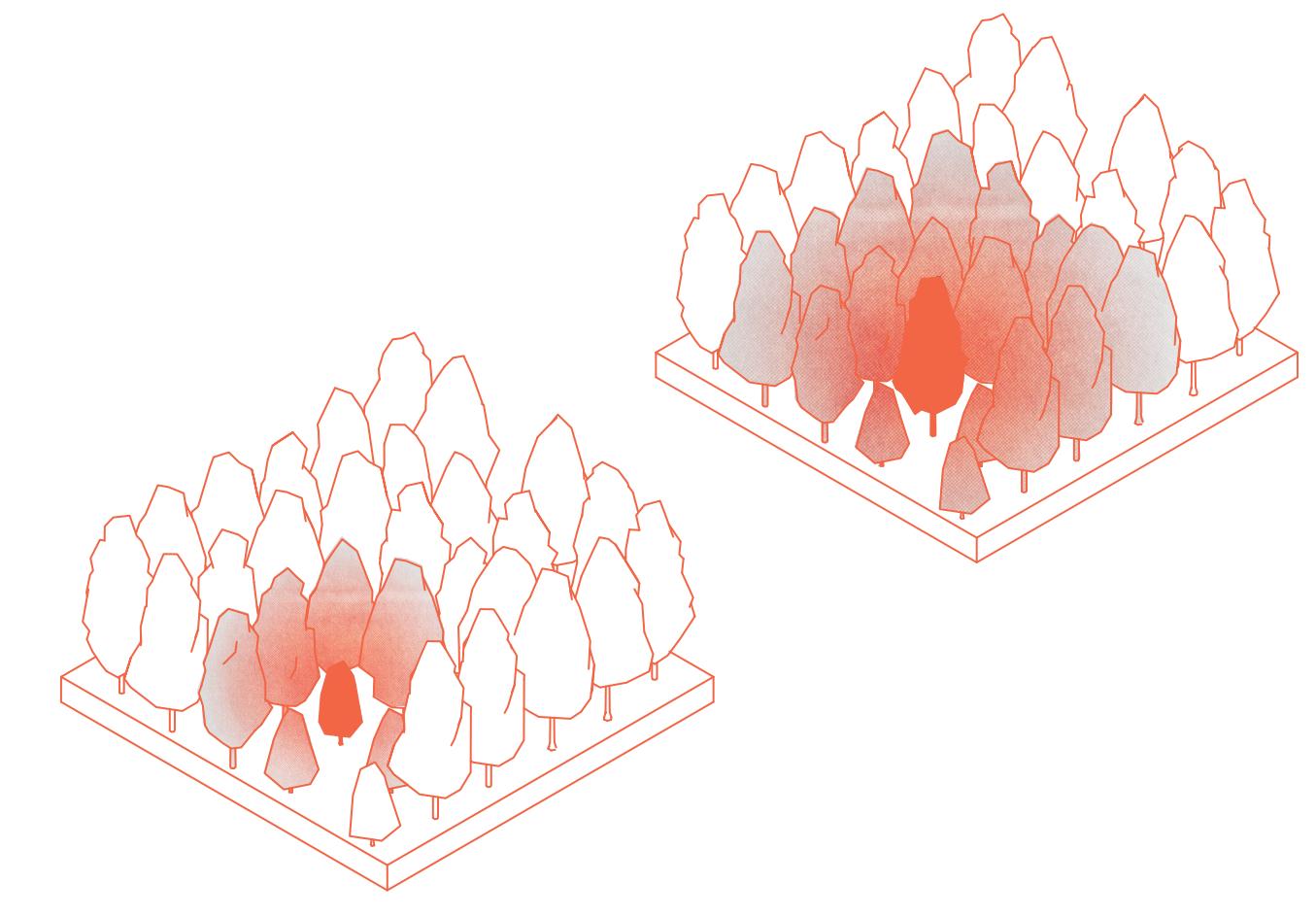
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Diversifying forests by introducing a secondary species is a proactive approach to disease control. While this method may reduce the yield of the primary timber species, it can ultimately lead to a healthier forest and improved long-term economic outcomes by reducing disease-related losses. Through simulations we aim to investigate how the diversification of an agricultural forest affects disease-spreading.

METHOD

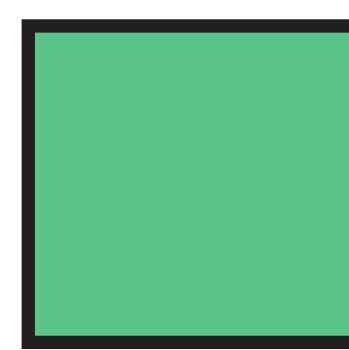
The forest is modeled as a lattice with periodic boundary conditions, simulating a smaller patch within a large agricultural forest. Initially, the forest is planted in a chosen configuration, with some trees infected from the start. An infected tree remains alive for a certain number of iterations, during which it can spread the disease, and is then removed, leaving an empty spot where a new tree can grow. The species of the new tree is determined probabilistically, based on the likelihood of planting species A versus species B.

At each iteration, the value of the forest is calculated as the average age of the healthy trees, adjusted by a factor representing the differing growth rates and timber yields of the two species. The simulation continues until a target forest value is reached, with the total number of iterations recorded.



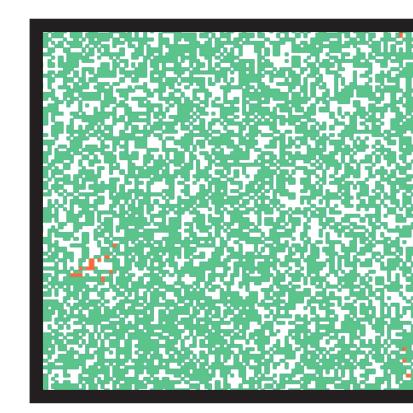
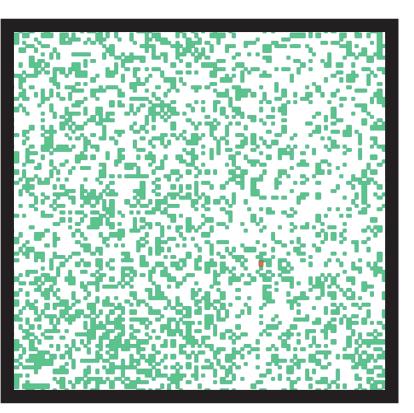
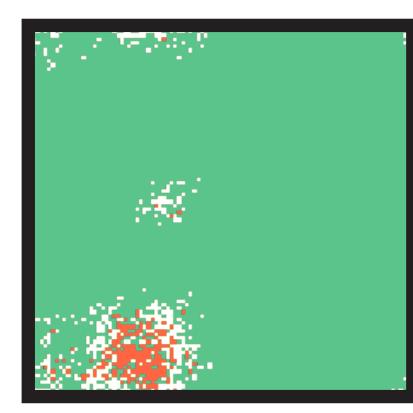
Disease spread is modeled using two mechanisms: infection radius and sporadic events. The infection radius simulates the root system, allowing diseases to spread not only to adjacent trees but also to those farther away, with the probability of infection decreasing with distance. Sporadic infection events mimic air-borne diseases, such as fungal spores, which can spread across the forest under favorable conditions like strong winds, leading to random infections even in trees with no infected neighbors.

SIMULATIONS

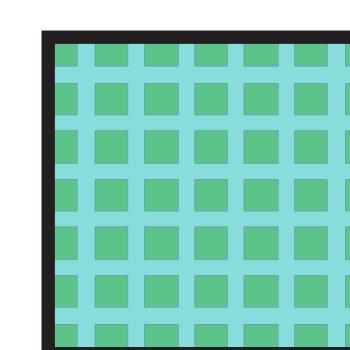


HOMOGENEOUS

Monoculture forest consisting solely of species A, the more susceptible tree.

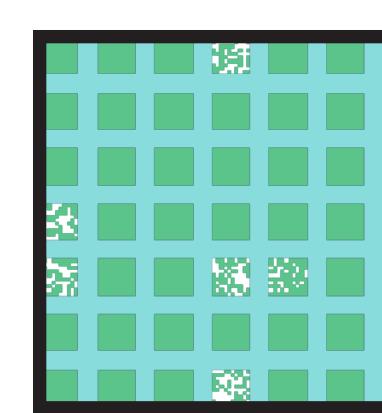
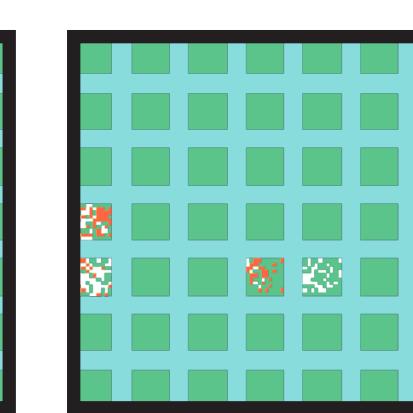
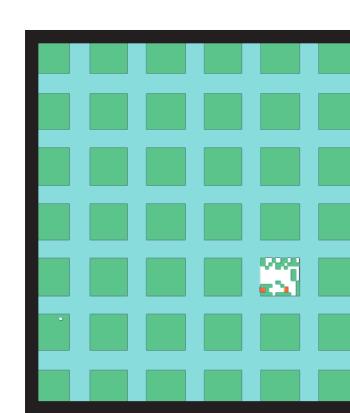


HOMOGENEOUS: Once a tree gets infected it doesn't take long before the whole forest is wiped out.

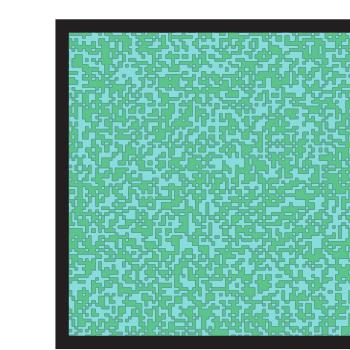


GRID-LIKE

Mixed species forest with rows of Species B, planted to form a barrier against the disease.

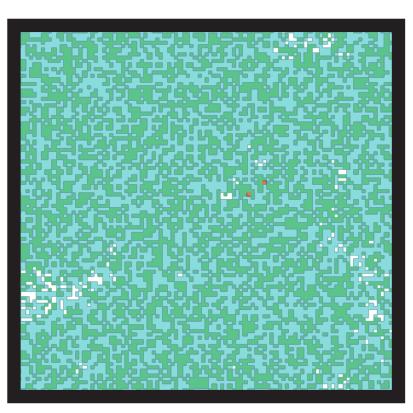
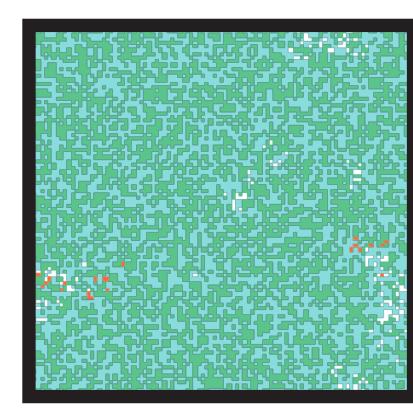
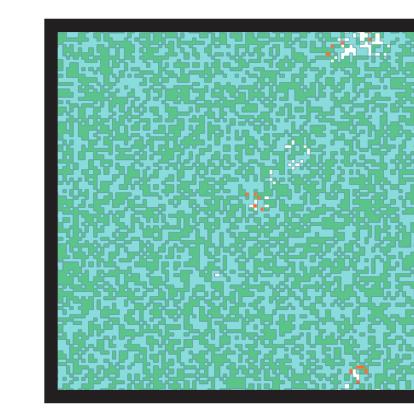


GRID-LIKE: The rows of immune trees appear to successfully contain the disease to smaller patches.

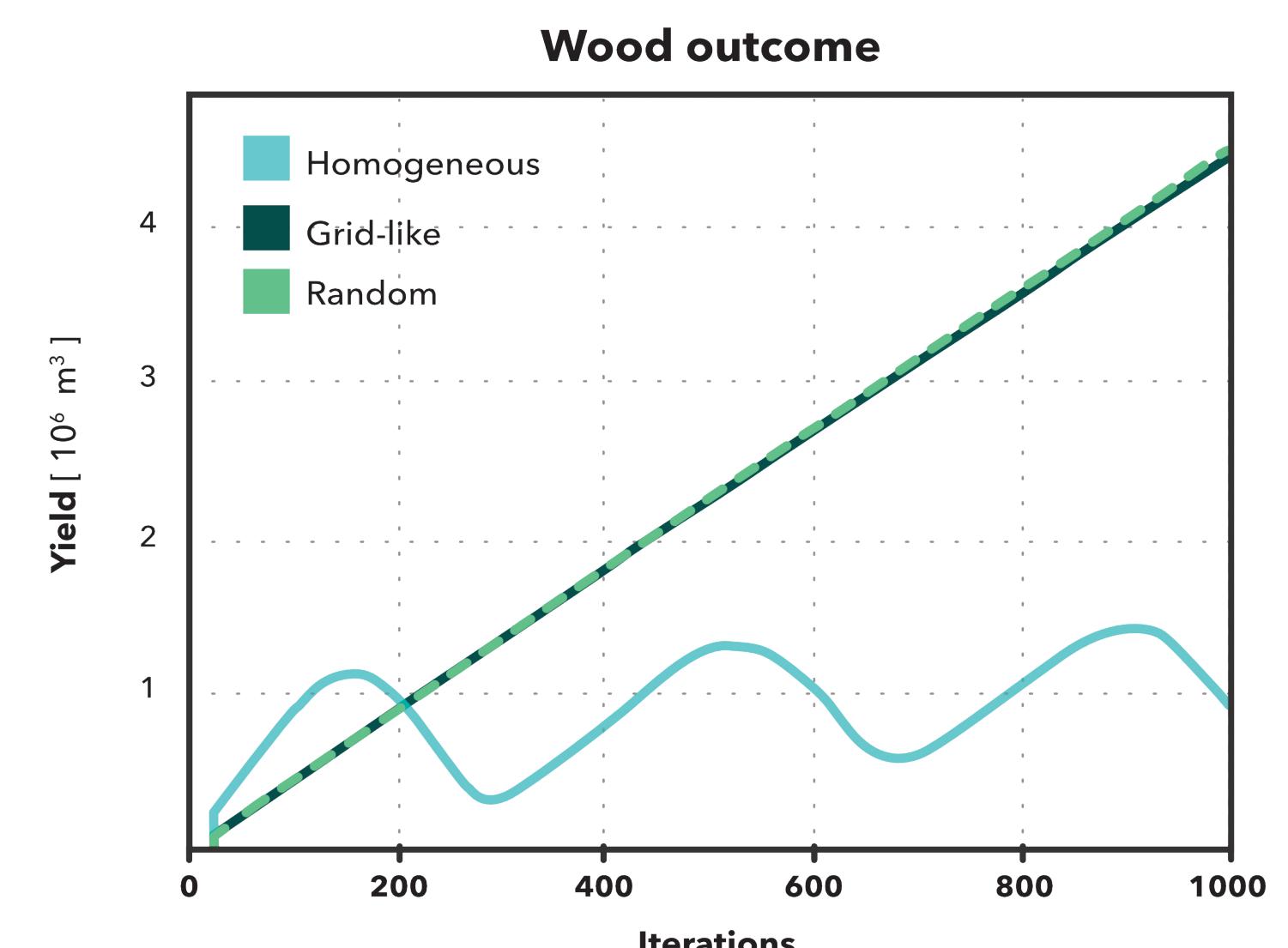
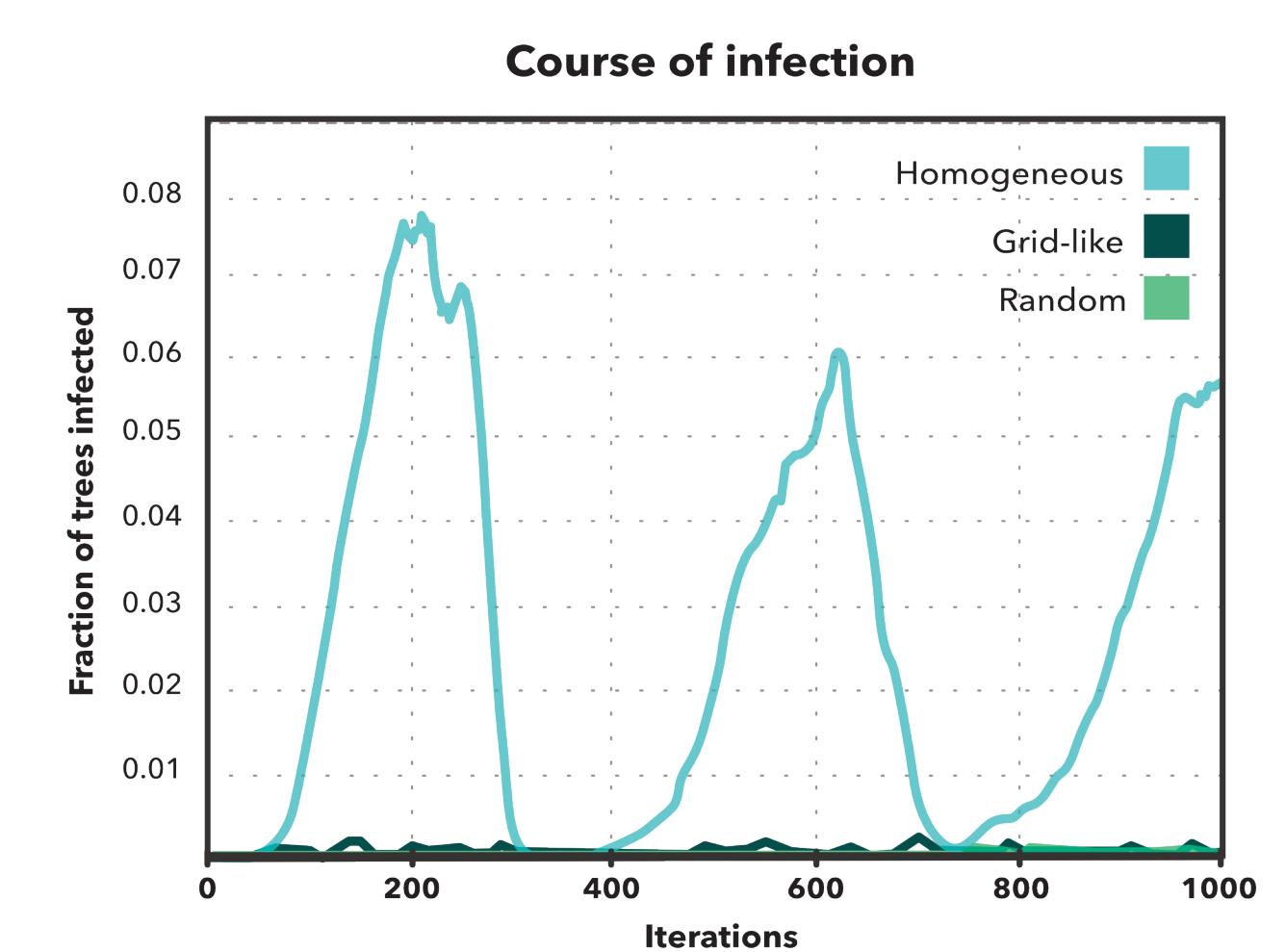
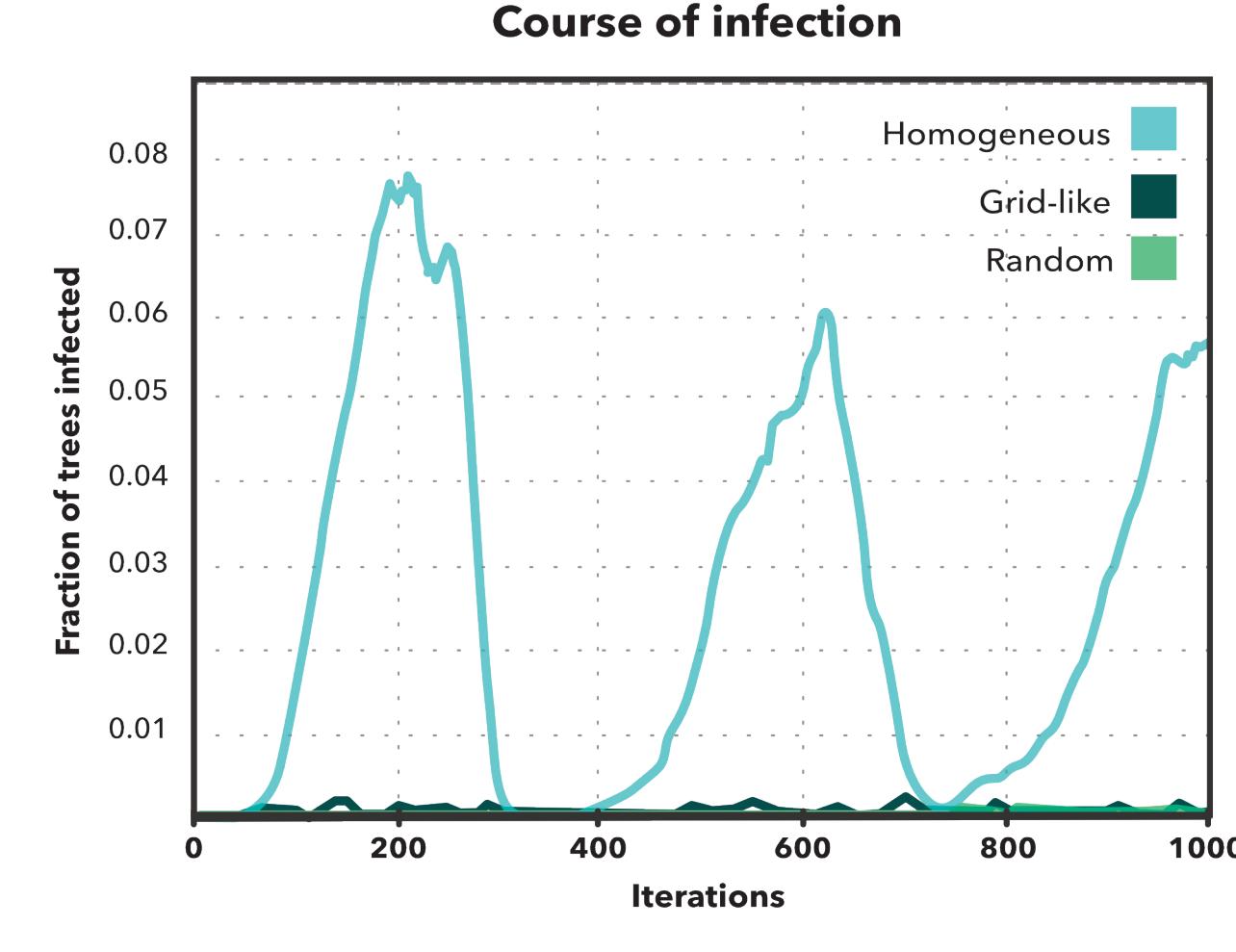
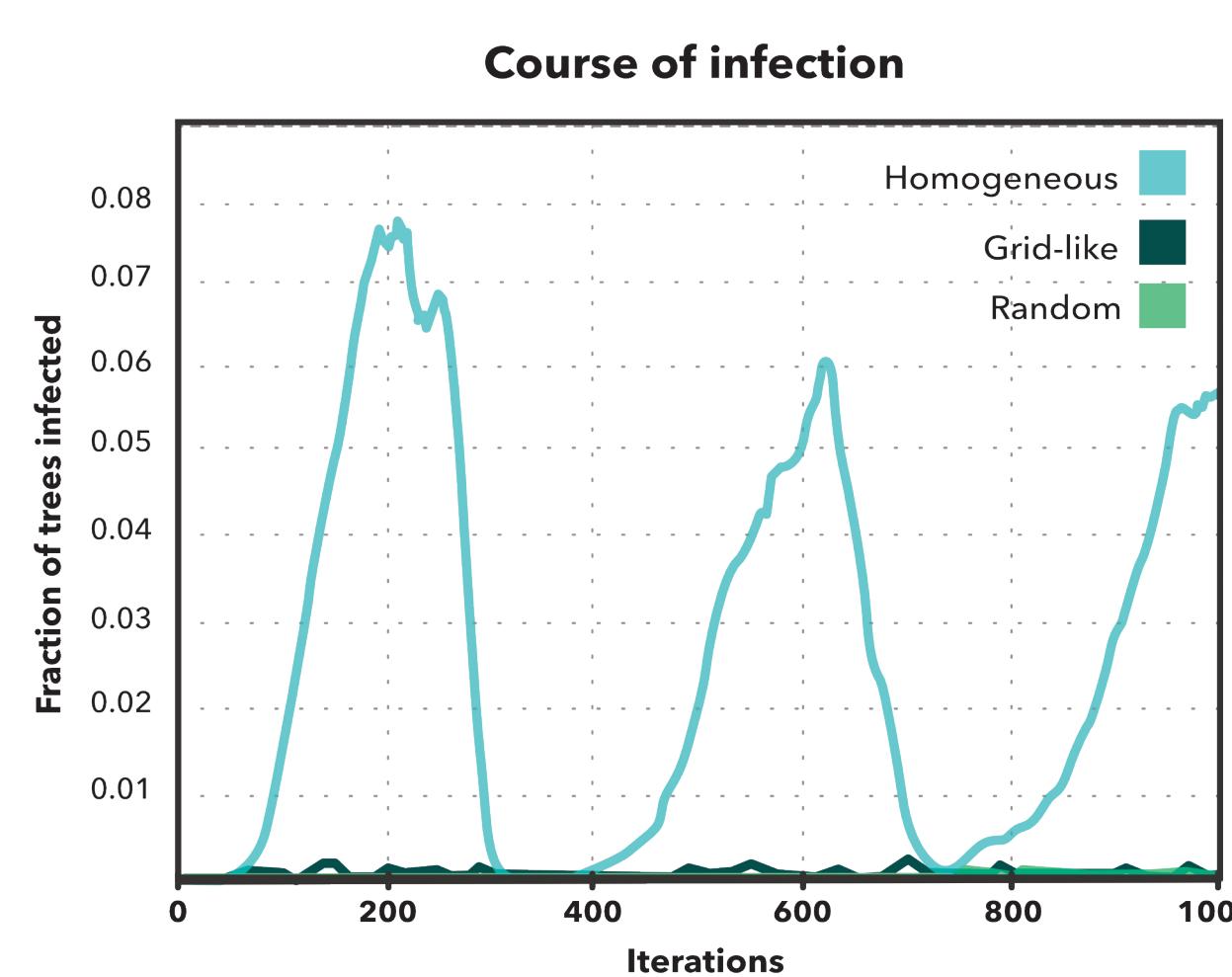


RANDOM

Mixed species forest, Species A and B are placed randomly with the same ratio as in GRID-LIKE, mimicking a natural forest.



RANDOM: The random configuration appears to be at least as successful at containing the disease as GRID-LIKE, despite there being more paths for the disease to take.



Disease-spreading in monoculture and mixed-species forests

Diseases can have devastating effects on forests, spreading rapidly and causing significant ecological and economic damage. Common prevention methods include removing infected trees, vaccinating trees, and diversifying forests. However, some diseases, like root rot caused by basidiomycota, remain undetected until severe symptoms or tree death occur—by which time the disease may have spread extensively.

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METHOD

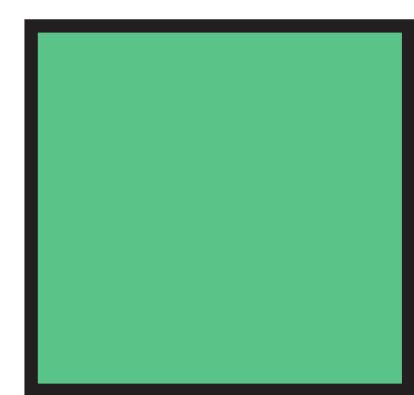
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At each iteration, which corresponds to a time step of one year, the value of the forest is calculated as the sum of the age of trees that are healthy and have reached a minimum harvest age. The sum is adjusted

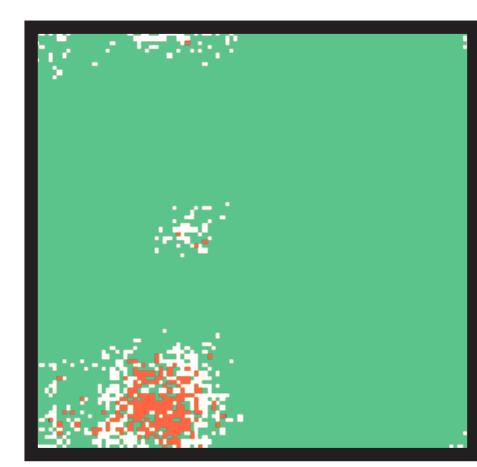
by a factor representing the differing growth rates and timber yields of the two species. The simulation continues for the maximum lifetime of the tree species that are about 200 to 500 years.

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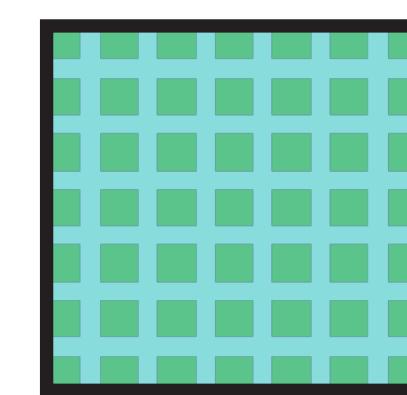
SIMULATIONS



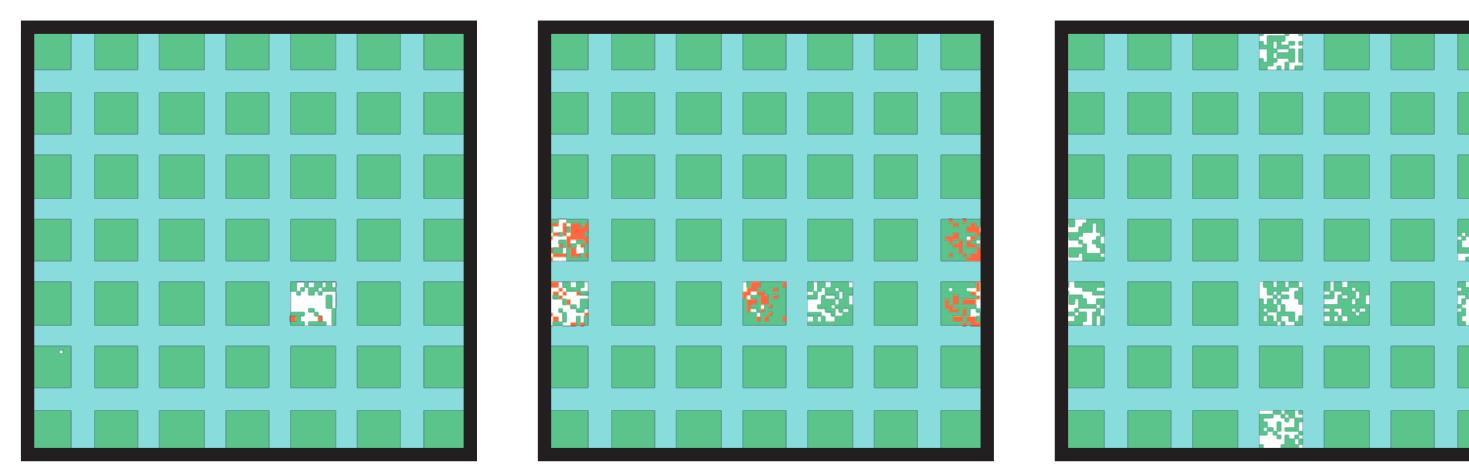
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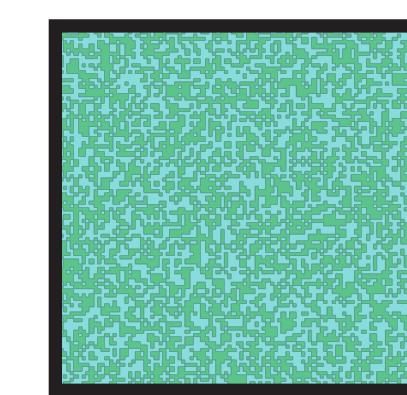
HOMOGENEOUS: Once a tree gets infected it doesn't take long before the whole forest is wiped out.



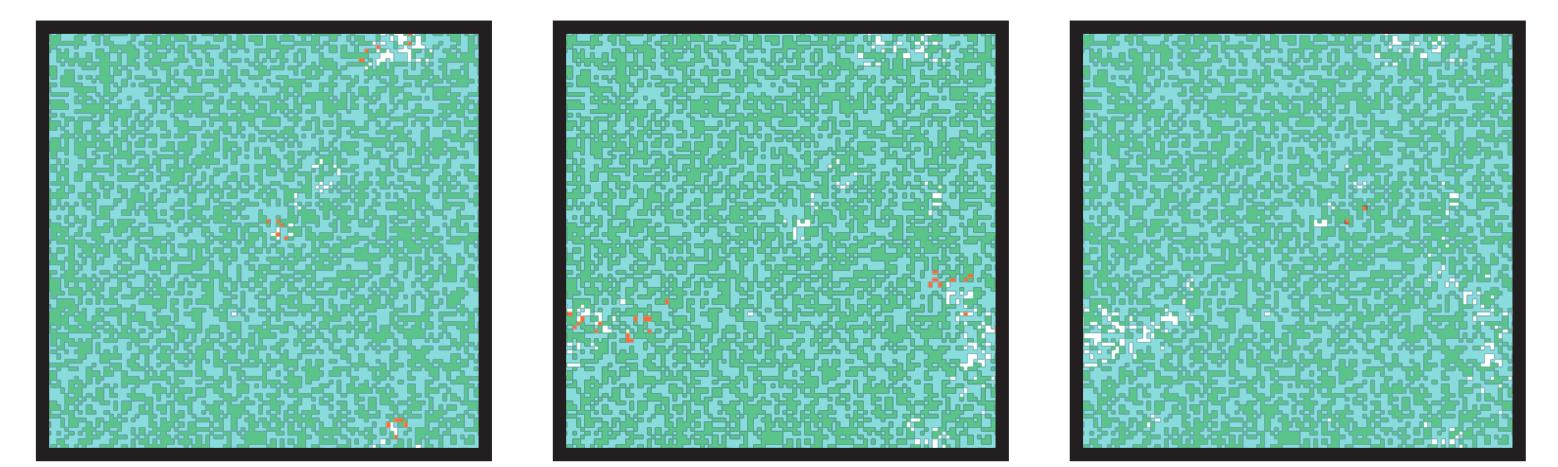
GRID-LIKE
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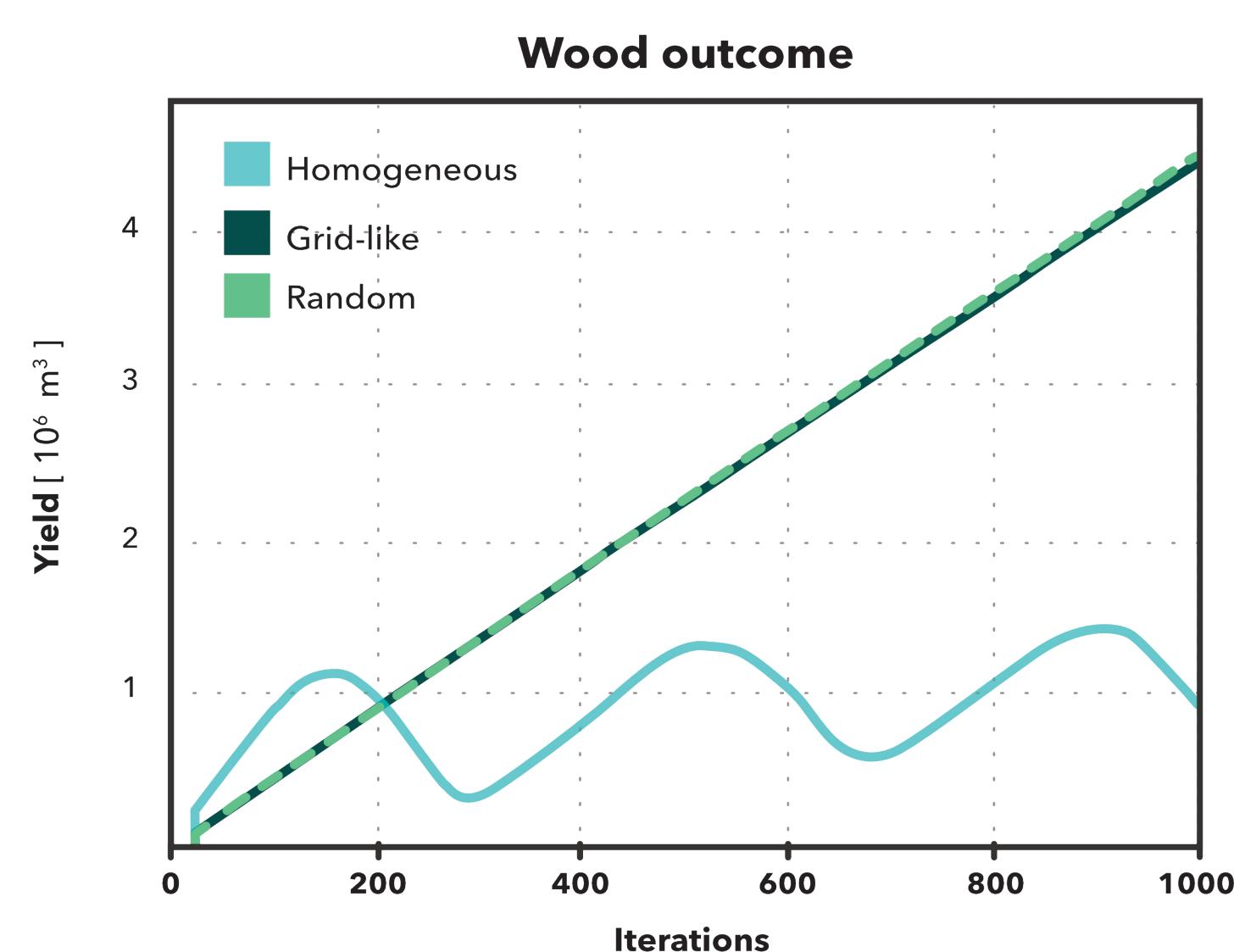
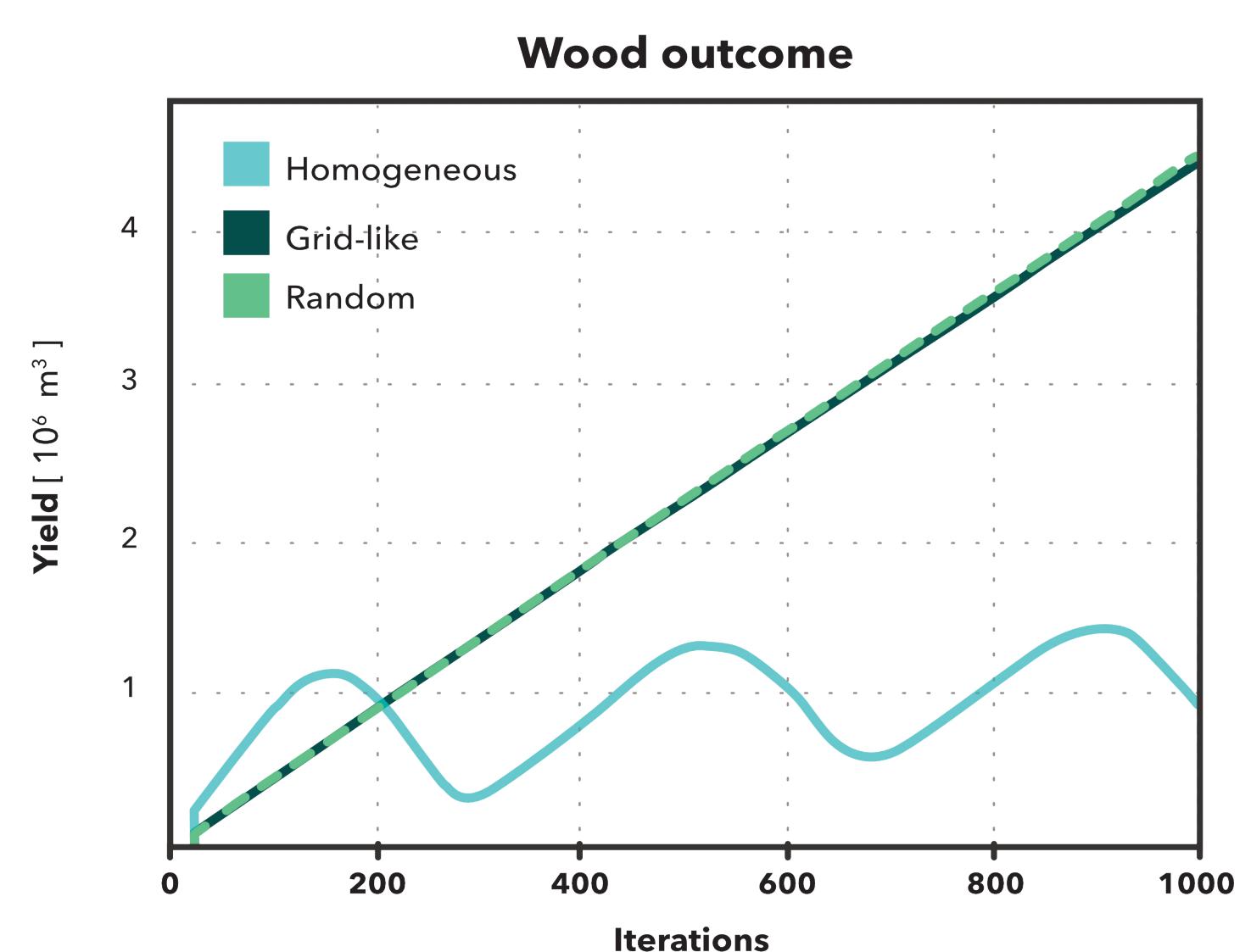
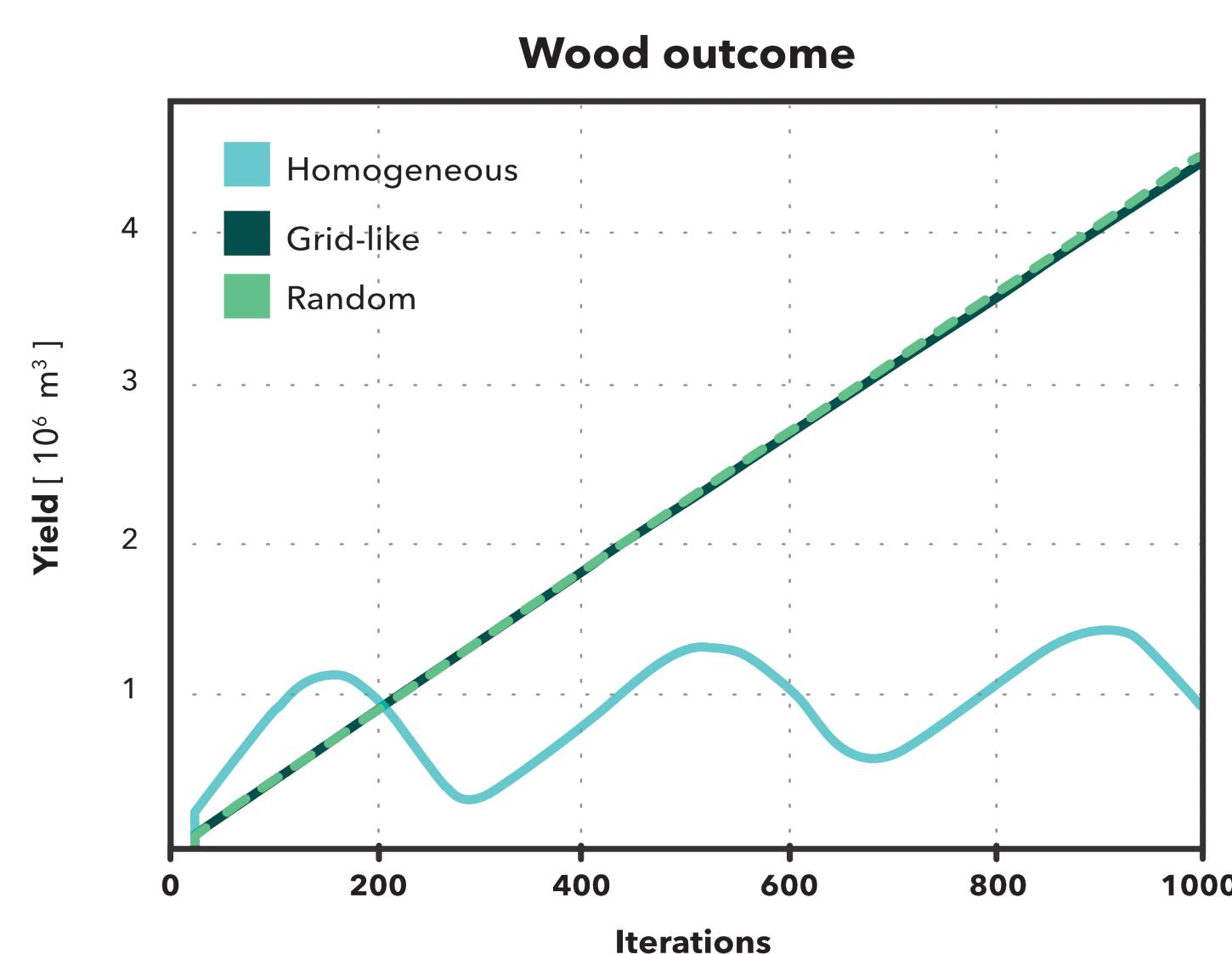
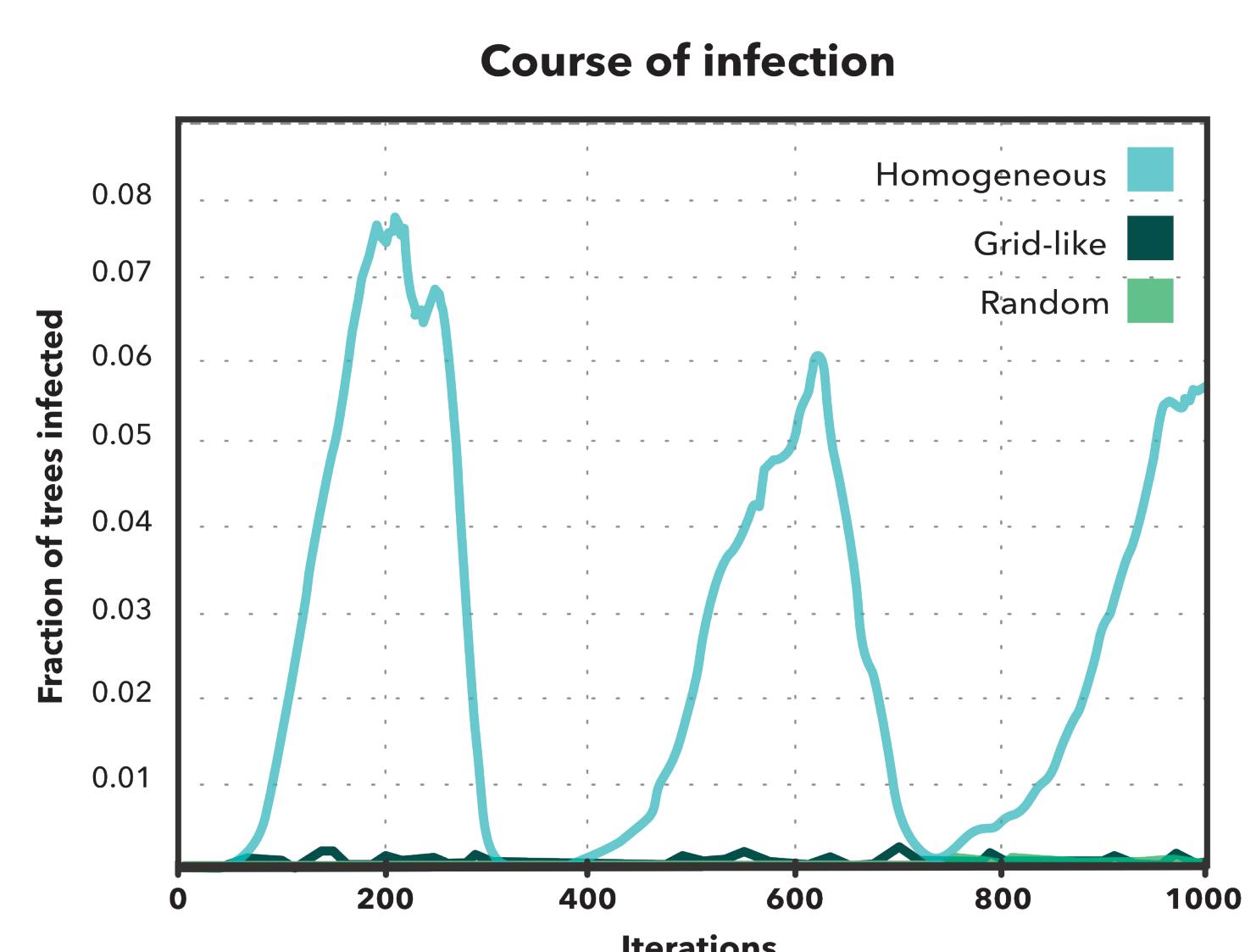
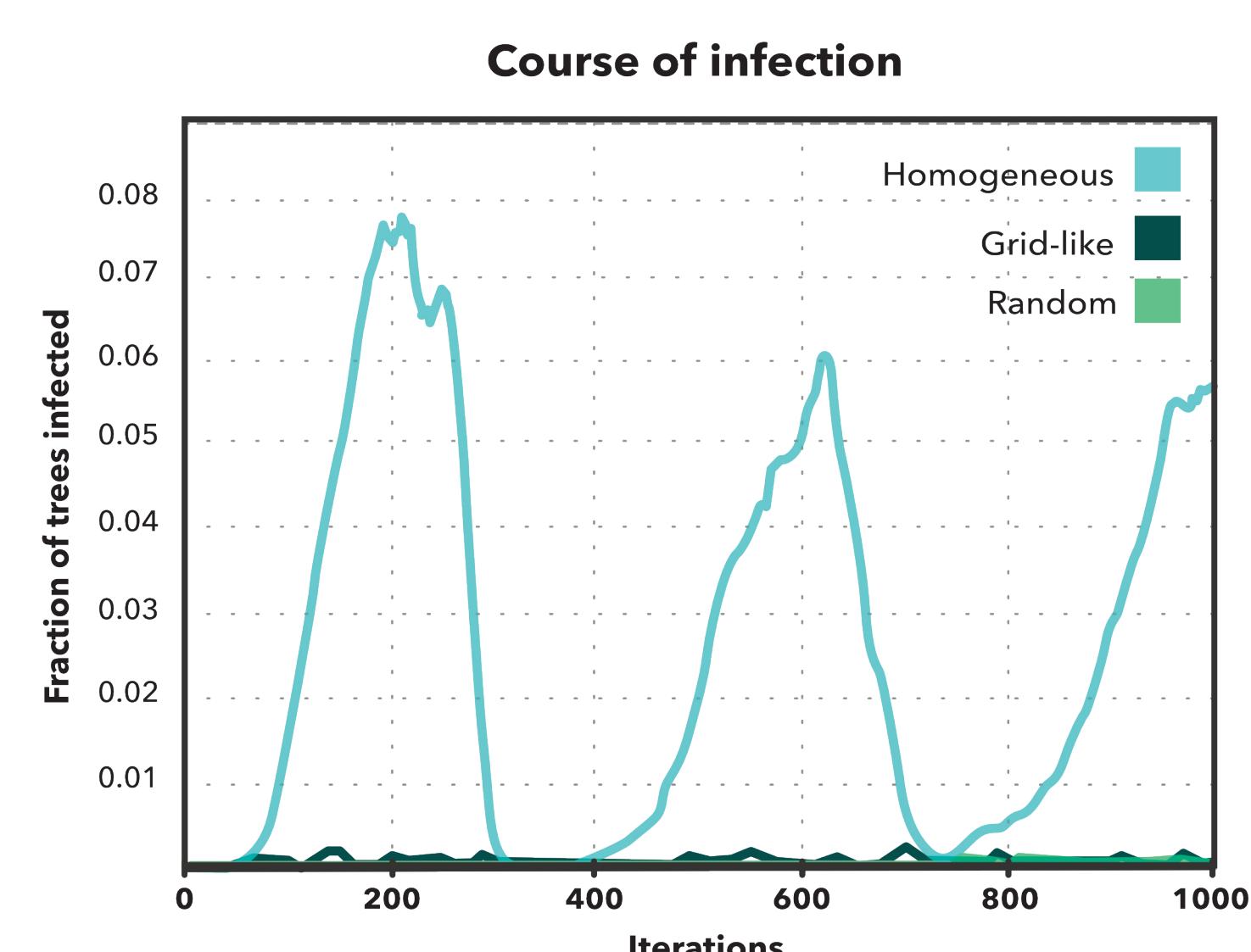
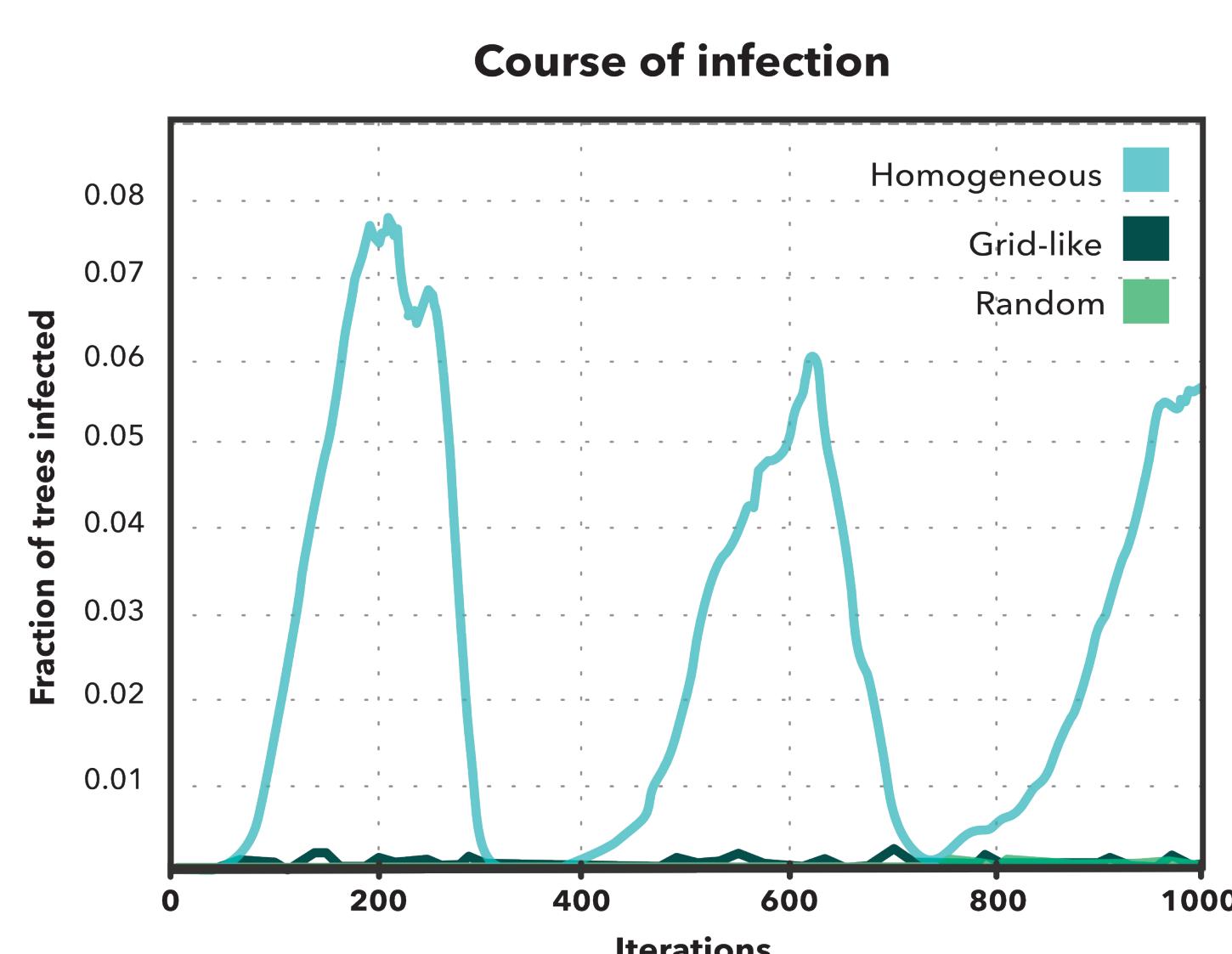
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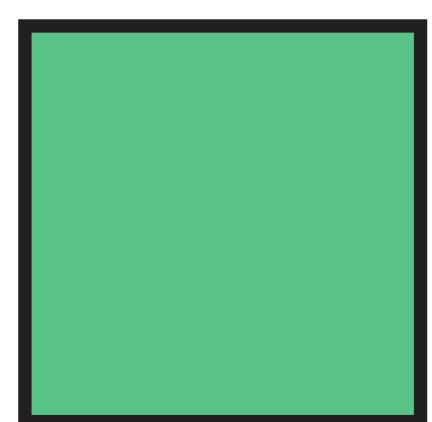
The forest is modeled as a lattice with periodic boundary conditions, representing a smaller patch of an agricultural forest. Initially, trees are planted in a chosen configuration—homogeneous, grid-like, or random. Disease is introduced randomly over time and space. Infected trees remain alive for a set number of iterations, spreading disease before being removed, leaving empty spots for new growth. New trees, of species A or B, grow probabilistically in empty spots, reflecting species planting likelihoods.

Each iteration (one year) calculates forest value as the sum of healthy trees' ages that meet harvest criteria, adjusted for species-specific

growth rates and timber yields. Simulations run for the maximum species lifespan (200–500 years).

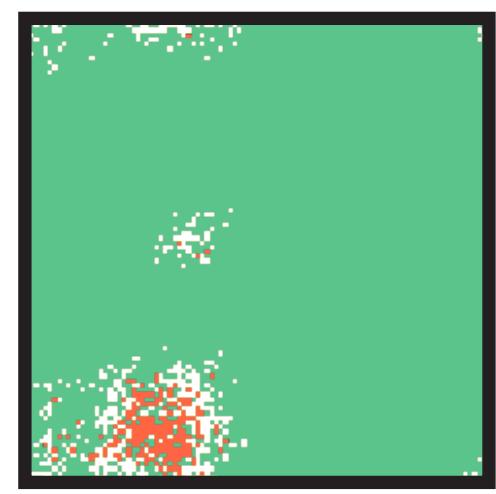
Disease spreads via two mechanisms: infection radius and sporadic events. Infection radius simulates root systems, allowing spread to nearby and distant trees, with decreasing probability over distance. Sporadic events mimic airborne infections (e.g., fungal spores), introducing randomness even without infected neighbors. Simulations explored mono- and two-species forests under varying initial conditions and disease dynamics.

SIMULATIONS

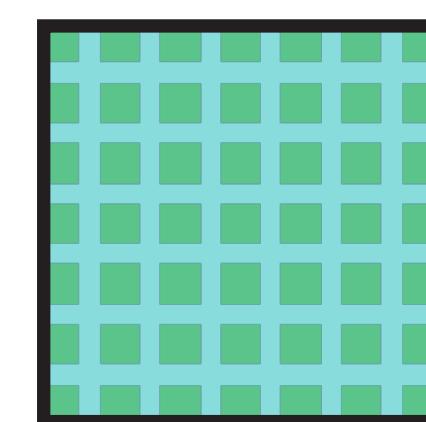


HOMOGENEOUS

Monoculture forest consisting solely of species A, the more susceptible tree.

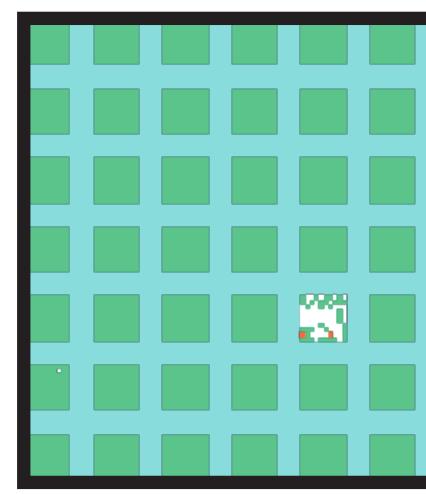


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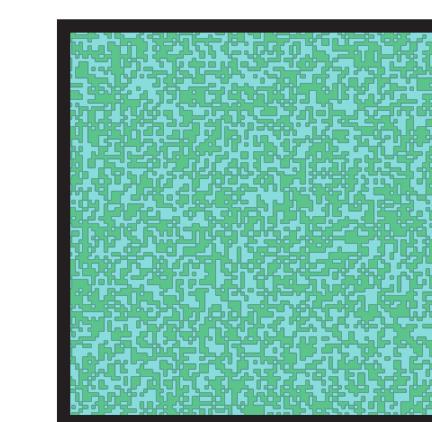


GRID-LIKE

Mixed species forest with rows of Species B, planted to form a barrier against the disease.

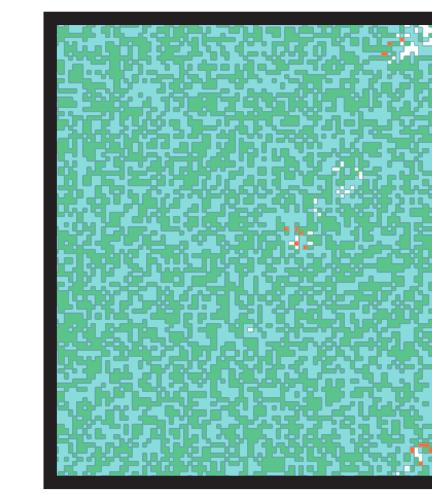


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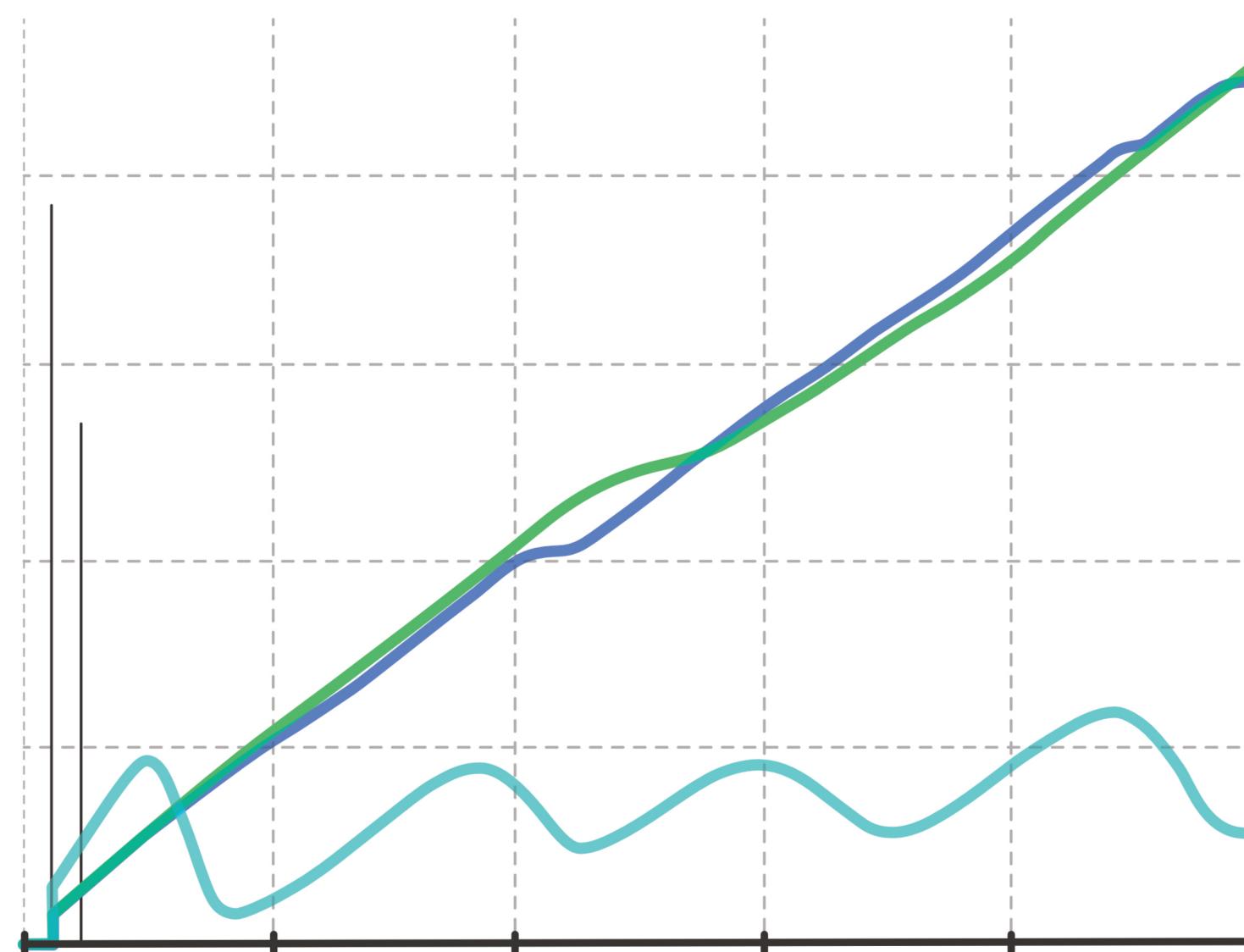
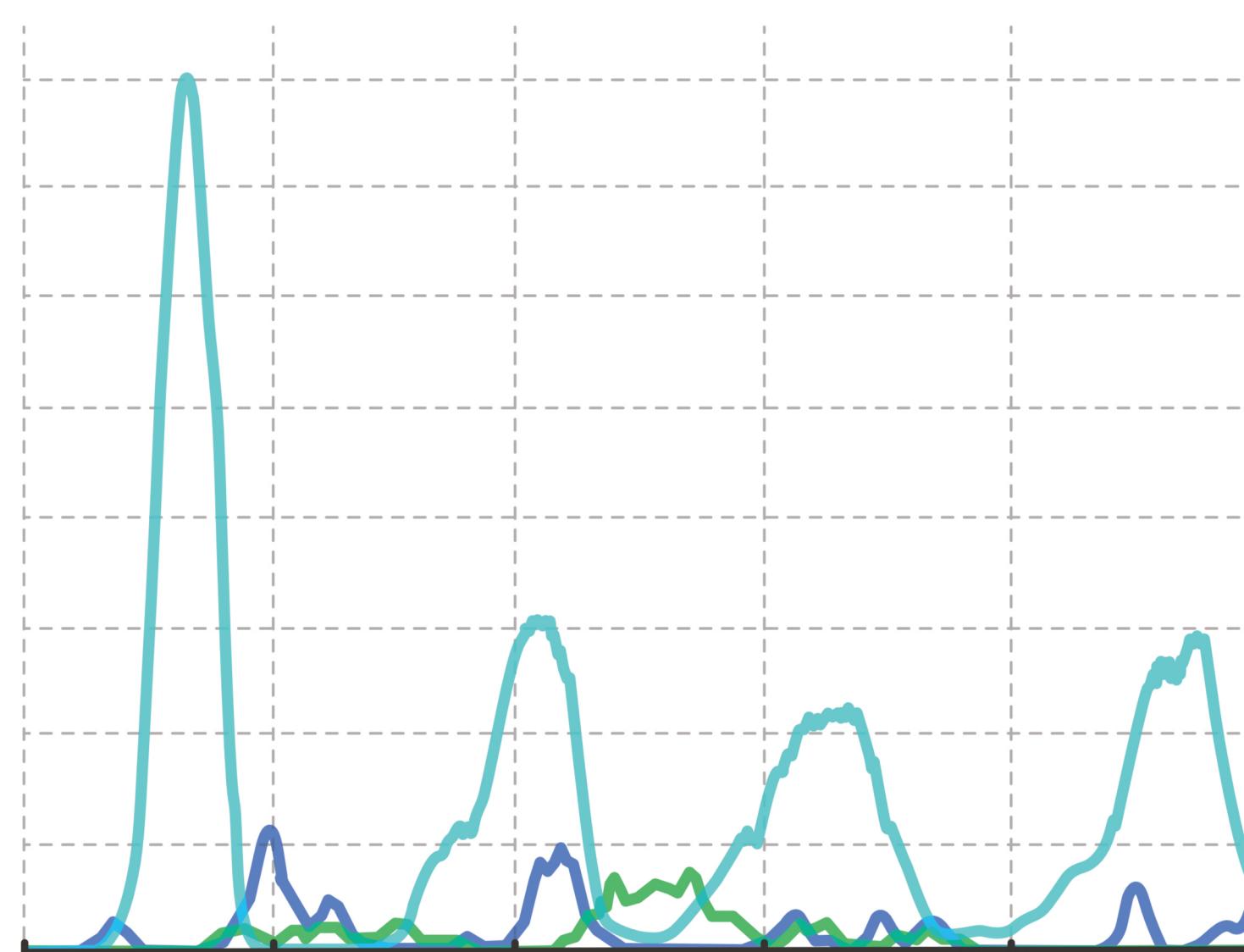


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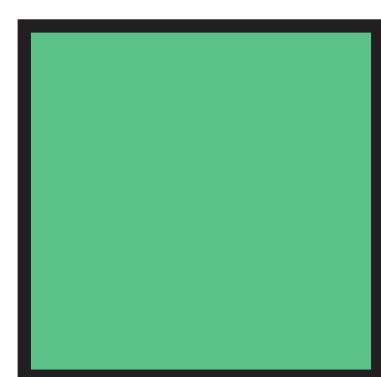
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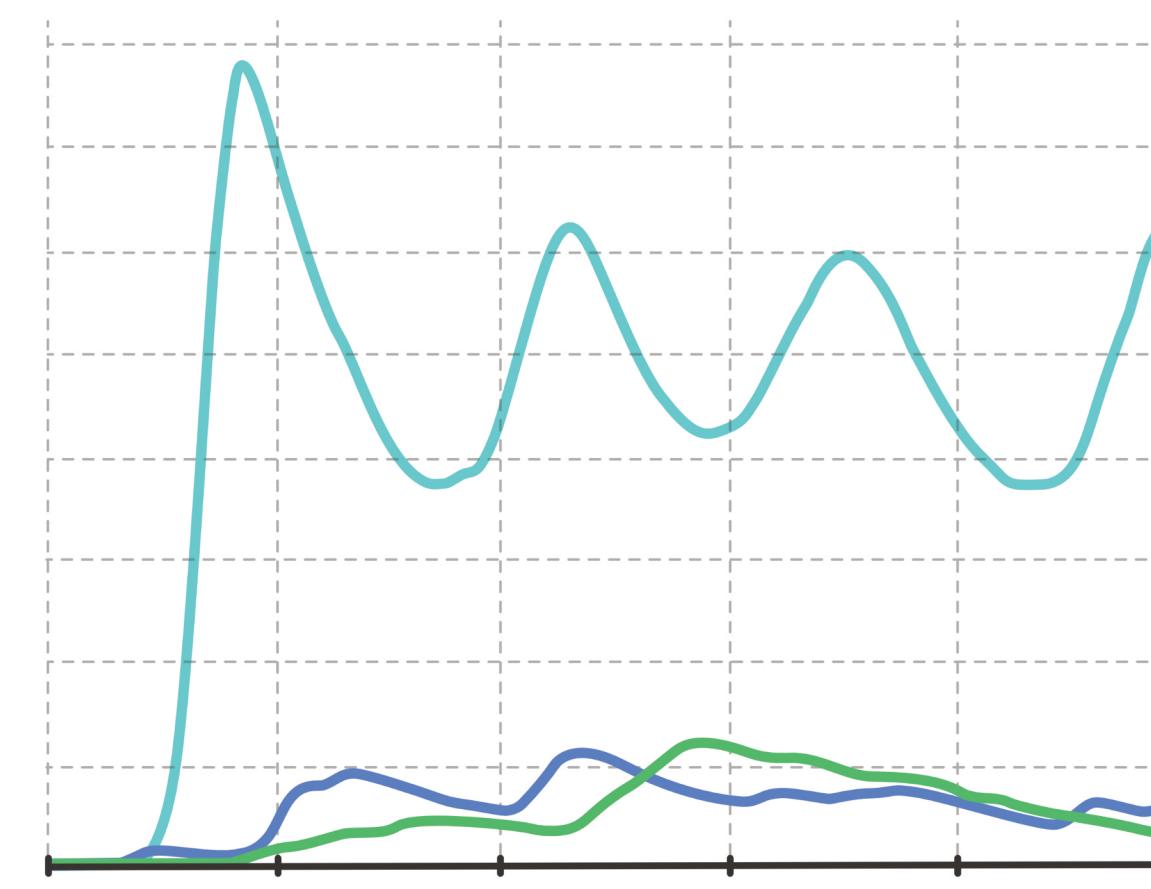
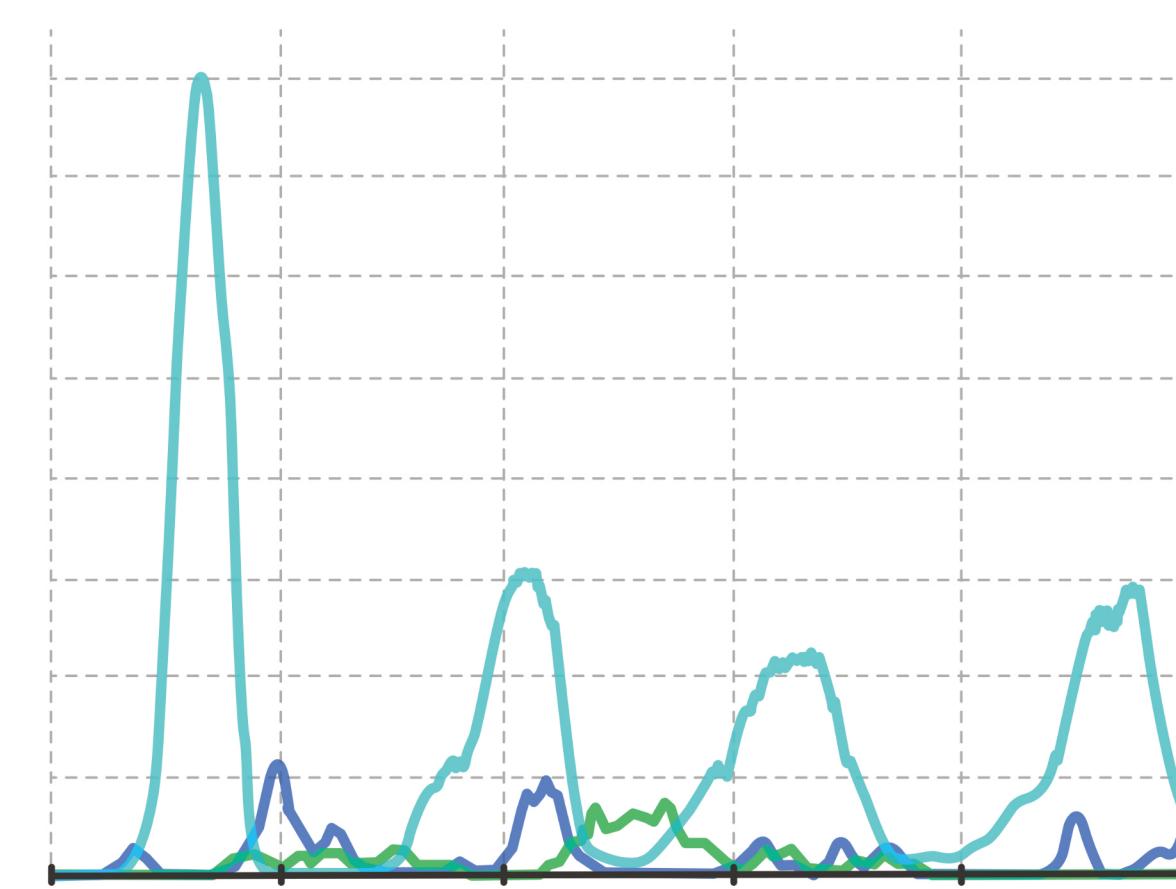
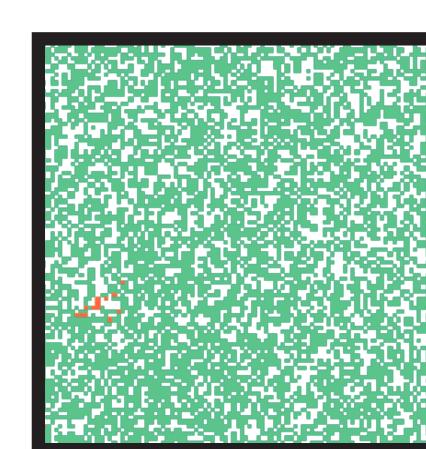
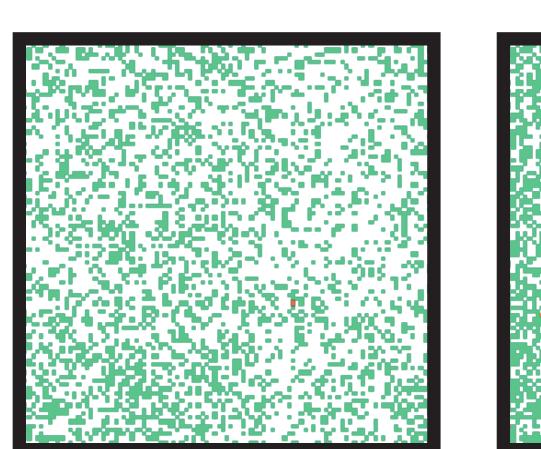
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SIMULATIONS

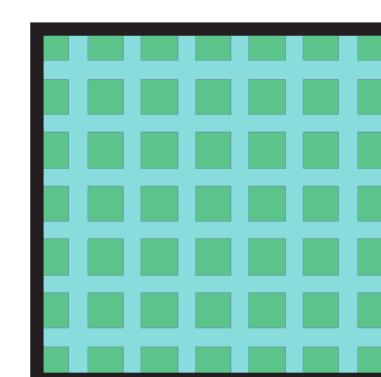


HOMOGENEOUS

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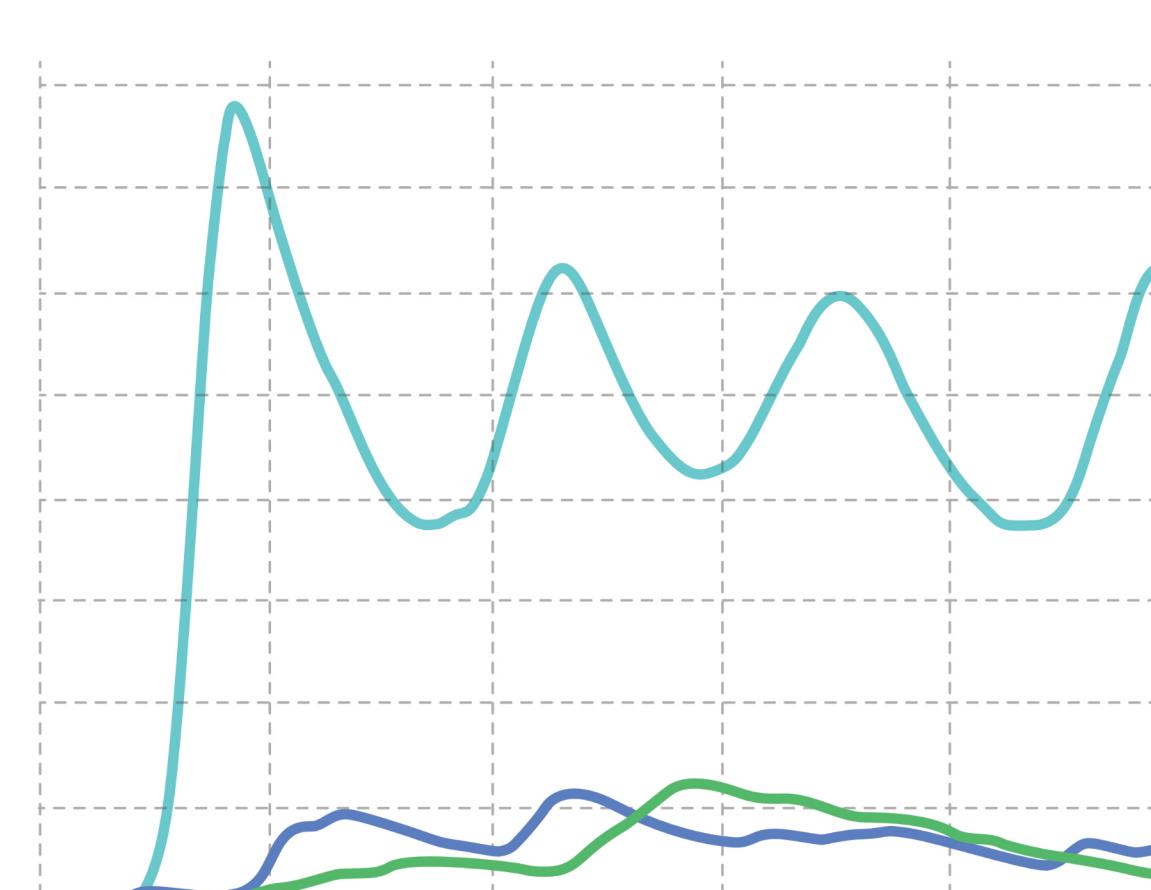
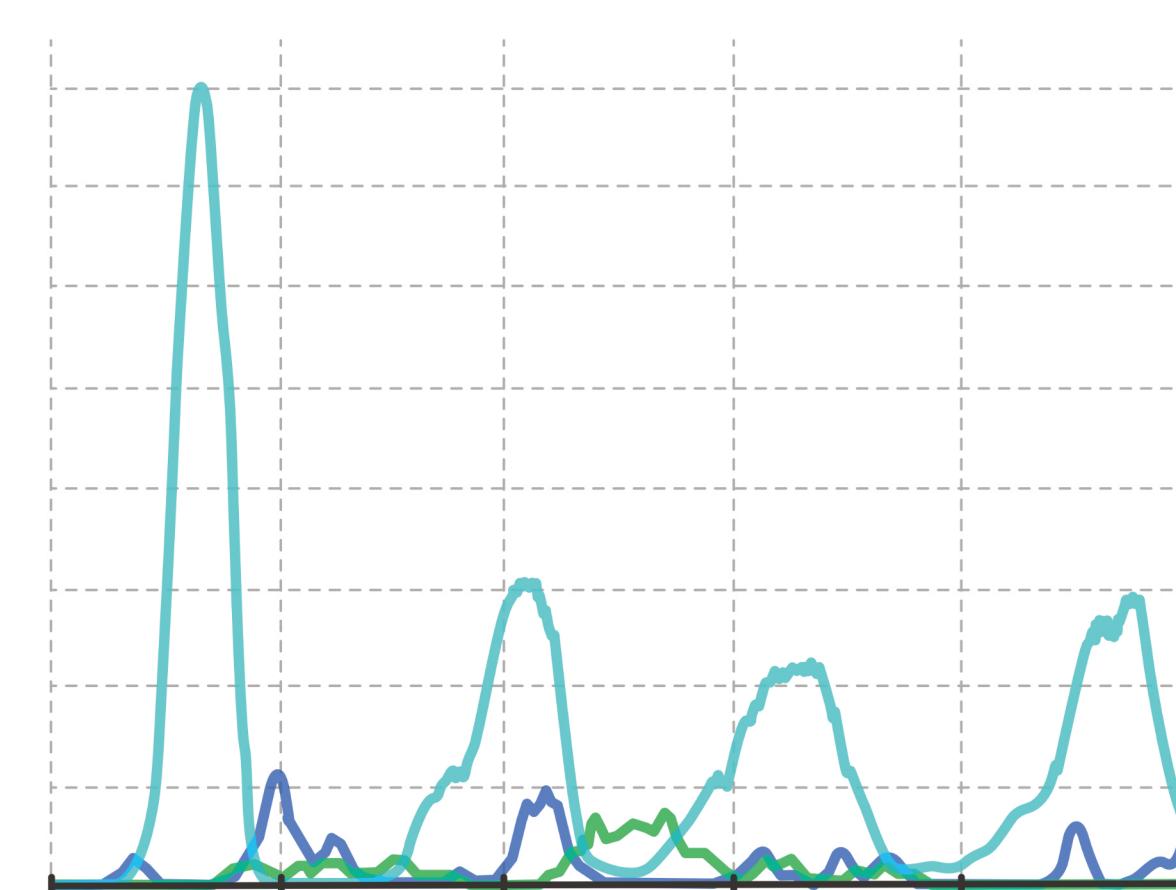
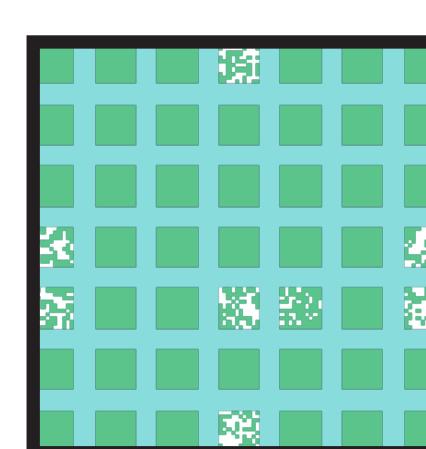
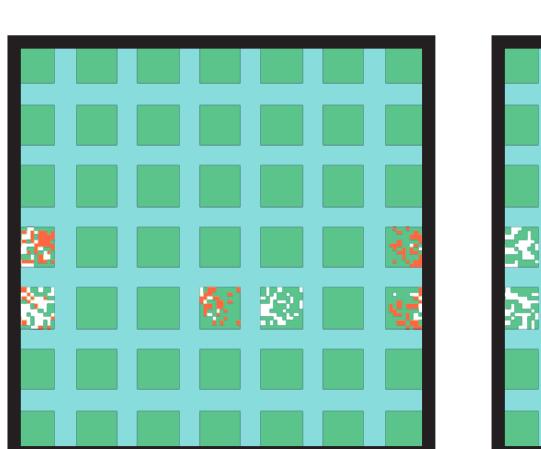
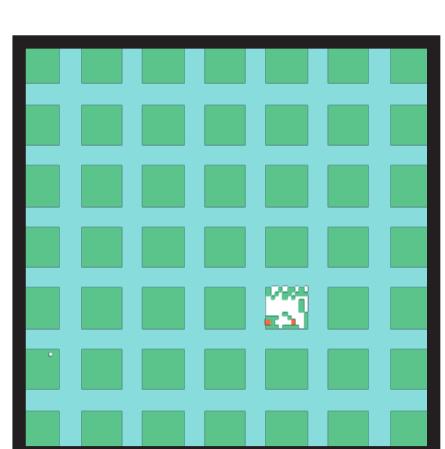


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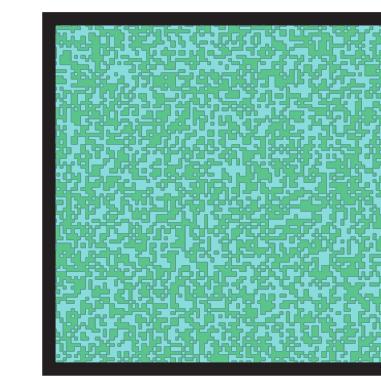


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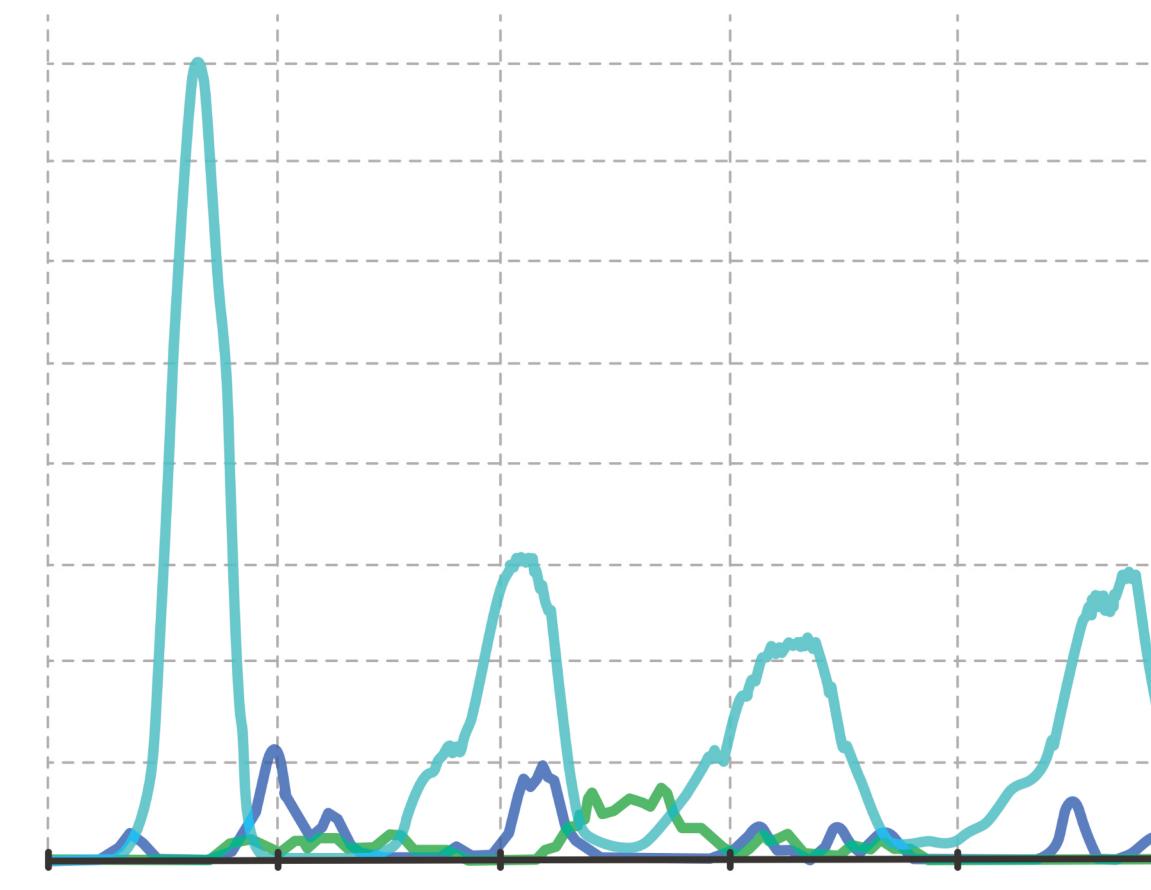
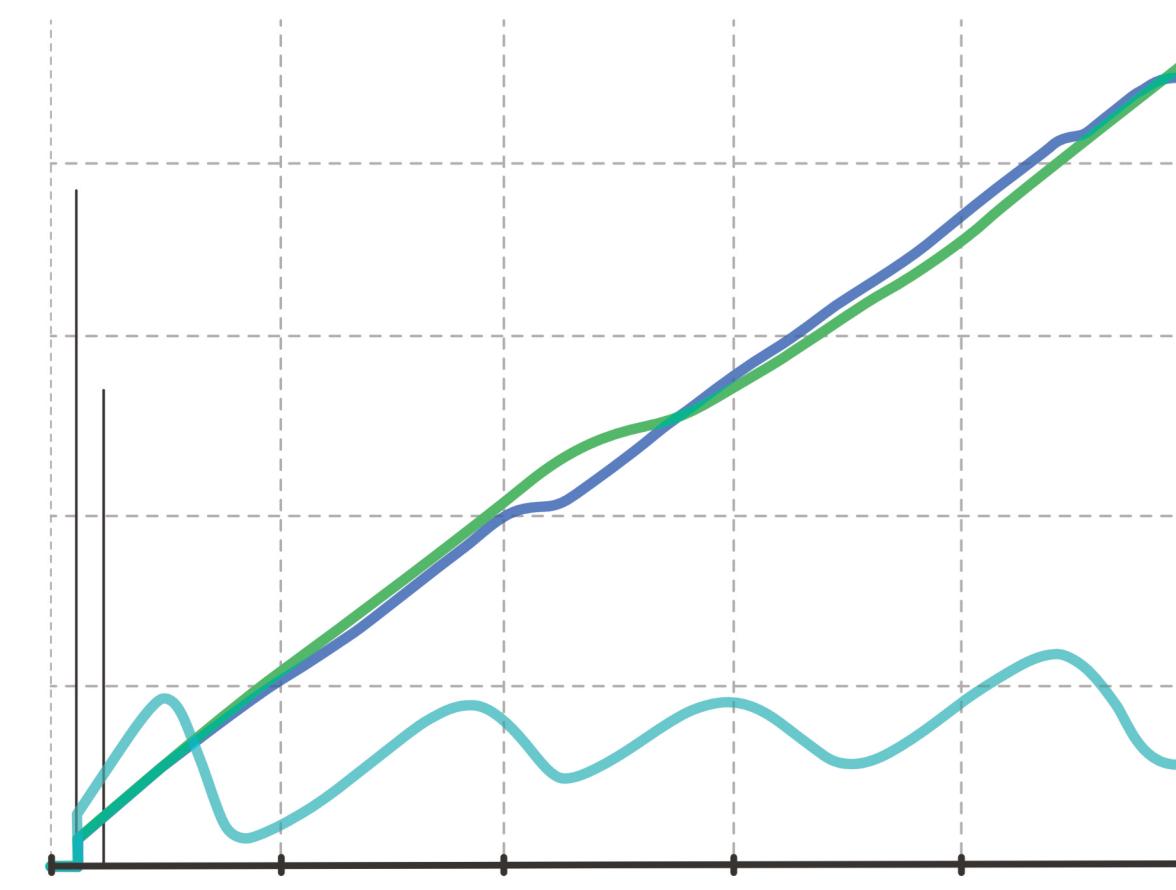
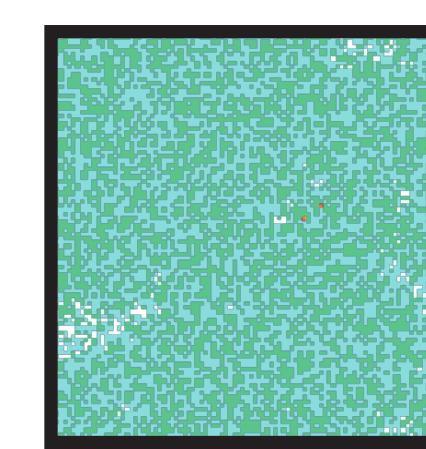
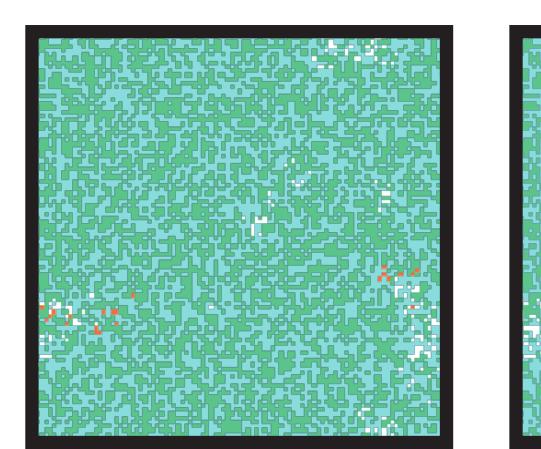
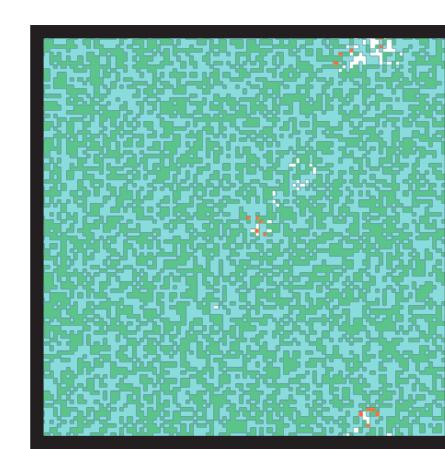


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