

# The Spatial Co-occurrence of Soil Microorganisms

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Soil biota play an important role in the quality of the soil and plant productivity. However, they are underrepresented in the research, and their behavioural patterns are still not well-known. Investigating relationships among the microorganisms is time consuming when done with sampling soil, but with the new approach of using a simulating model, this problem could be simplified. By analysing the population dynamics of the organisms, applying the spatial co-occurrence algorithm and observing spatial dispersal plots, we found that in both predator-prey and competitor relationships, Bacteria goes extinct first, and its population numbers influence their predators more than it influences its competitor.

Additional Key Words and Phrases: soil biota, co-occurrence network, trophic network, Pearson coefficient, soil simulator

## 1 INTRODUCTION

For a while now, ecologists have been interested in relationships between species, however those interests were mainly focused on above ground organisms. Lack of research on soil microorganisms could be explained by the difficulty to be easily seen, hence making them difficult to study, and the lack of appeal compared to some above ground species. The disparity in data between different species of microorganisms has also been noted, where, for example, Bacteria, Fungi and Formicoidea have a larger number of sampling sites and scattered distribution compared to Rotifera, Collembola, and Acari [5]. However, there has been a progressive increase in ecologists that are interested in researching soil biota and functionalities within their community, mainly due to the "awareness that not only do soil organisms regulate major ecosystem processes, such as organic matter turnover and nutrient cycling, but they also act as important drivers of vegetation change" [2].

Current methods of extracting information on microorganisms that reside in soil include the extraction, quantification, and identification of molecules from soil that are specific to certain microorganisms, or advanced fluorescence microscopic techniques. Some of the limitations of such methods are that not all signature molecules used to identify microorganisms are known, or phospholipid fatty acid, which is a notable molecule to analyse soil, is produced by many organisms and while it can be distinguishable among different groups, it does not always mean it is unique to only one group. Another useful method is nucleic acid technique, specifically favoring the usage of ribosomal RNA to ribosomal DNA. However, the efficiency of extraction can differ among the soils and microorganisms, which means that differences observed in the activity of particular organisms across soil samples may actually be artifacts of the extraction procedure itself. Another issue is that the detection of rRNA has mostly been used on prokaryotes, while eukaryote ribosomes have

not been studied well, so their representation in public databases is not as extensive which makes their identification problematic [7].

Due to above mentioned problems, a solution has been found on tracking the population numbers, and it was implemented in a form of a simulator that depicts 9 soil species that range from 1  $\mu\text{m}$  to 0.5  $\text{mm}$  in body size. Depicted species are as follows: Bacteria, Fungi, Root-feeding Nematodes, Bacterivorous Nematodes, Fungivorous Nematodes, Omnivorous Nematodes, Fungivorous Mites, Omnivorous Mites, and Collembolans. This simulator is a spatiotemporal soil model, capable of mimicking different sampling methods, by adjusting sampling patterns, and varying diameter and depth of soil samples. More importantly, the model depicts interactions between different organism groups, based on trophic and co-occurrence networks [12]. Trophic networks depict how species influence each other in the ecosystem, via processes such as mutualism, parasitism, competition and predatorism. Each species holds a trophic level, which is defined by the trophic level of its prey plus 1, and such levels are a useful measure of how far a species is from the sources of biomass in its ecosystem [9]. Co-occurrence networks as an analysis method can be constructed to showcase potential relationships, and lifestyle patterns amongst the co-occurring organisms [4]. The simulation model requires initial values for all variables that will control the way interactions between organisms evolve throughout one simulation occurrence. Such variables are reproduction rate, competition rate, dispersal rate and range, maximal biomass, etc. This simulator will be used to determine population numbers throughout virtual time passage, which are then mainly going to be used to determine co-occurrence between microorganisms.

The goal of this thesis is to inform the reader about the spatial co-occurrences between selected microorganisms (Bacteria, Bacterivorous Nematodes, Fungi and Omnivorous Nematodes) and explain the results using the known behaviour of these species. In Section 2, we will cover closely related works, while in Section 3 we will introduce the research questions. Section 4 will talk about the methodology of the research, after which we will touch upon the results of each research question separately in Section 5. Lastly, in Section 6 we will discuss the results, and consider the possibilities for future research.

## 2 RELATED WORKS

In this section, we will briefly touch upon related works in the field of network data science applied to microbial organisms.

Over the years, researches have been conducted on soil biota and interactions among them. In the 2018 study on microbial diversity and soil biological networks in the Southern Hemisphere [3], the researchers tested soil samples from 647 locations from Australia and Antarctica. These sites had information available on the diversity of Bacteria, Archaea and/or Eukaryotes. They focused on finding correlation networks of these organisms across latitudes and environmental conditions. Their findings were dependent on already acquired samples that were taken throughout a span of 3 years, and at different times of the year which urged them to use

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climatic parameters averaged at the annual level. Next to that, they focused on less than 12 species of microorganisms which overlooks more complicated relationships among them. In the end, their findings indicated that the diversities of soil Archaea, Bacteria and Microeukarya largely co-vary across multiple locations in the Southern Hemisphere. These results suggest that the diversity of particular soil taxa can predict the diversity of other soil organisms and that sites that are more diverse in Bacteria and Archaea also support a more diverse community of Micro-Eukaryotes.

Similarly to this simulator, a 2021 research [1] developed a model of a community of three cryptic Nematode species, in order to explain the coexistence of these closely related species. This model also incorporated the reproduction, competition, dispersal, and resource use. They found that dispersal and competitive effects interact to drive the dynamics of the Nematode community. Dispersal offered them an escape from the competition when the densities of organisms became too high, thus it mediated the co-occurrence of closely related species. The model accounted only for interactions that were competitive between Nematodes as the experimental studies have shown that competition was by far the most important interaction among the cryptic species. They also found that the Dauer formation, which could be a significant aspect of Nematode life history, remains unexplored in the context of co-occurrence among cryptic species. This larval stage, triggered by crowding and reduced food availability, could lead to increased dispersal, but its role in mediating coexistence requires further research. In the end, they acknowledged that the generalization of the co-occurrence results should be taken with a grain of salt as several important factors, like environmental conditions, were not included in the model.

Another research from 2017 [11] focused on soil food web structure and carbon cycling in soils, and analyzed the network structure of almost all taxonomic groups of soil biota. To obtain the network structure, they applied the Spearman's rank correlation, and established that there has been increased correlations between Bacteria and Fungi. They observed that Bacteria and Fungi displayed a hump-shaped trend, while Mycorrhizal Fungi exhibited a consistent increase throughout succession. Similarly, the number of taxa for Fungivorous Cryptostigmatic Mites, Predaceous Mesostigmatic Mites, Root-feeding Nematodes, and Bacterivorous Nematodes generally rose over succession, while some other species groups showed no significant change. These findings will be essential for comparing to the information we will obtain from the simulator.

### 3 PROBLEM STATEMENT

This paper will focus on different types and intensities among the soil microorganisms, and the dependencies on variable values of the simulator. Hence, the following research questions were formulated.

#### 3.1 Research Questions

**RQ1A:** How do the simulated soil microorganisms spatially co-occur with each other, and how strong are those co-occurrences?

**RQ1B:** How dependent are these spatial co-occurrences on the conditions that were initially set in the simulator?

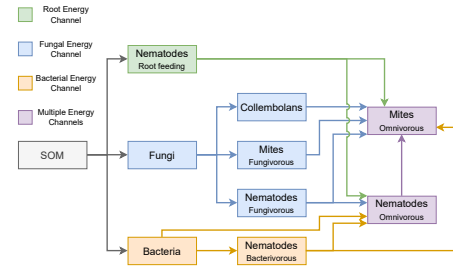


Fig. 1. Food web

**RQ2:** How does the trophic model compare to the newly found co-occurrence network, do the competitors, or predators and preys co-occur or do they avoid each other in space?

## 4 METHODS OF RESEARCH

In this section, we will be discussing the proposed methodology for each research question separately.

### 4.1 Method for Research Questions 1 A and B

As research questions 1A and 1B are closely related to each other, the methodology for answering them will be covered in this section.

The model of the soil is depicted as a cube of  $200 \times 200 \times 1$  or  $100 \times 100 \times 1$  dimensions, meaning that it is divided into 200 cells in width and length, and 1 cells into depth, each cell being  $0.5 \times 0.5 \times 0.5 \text{ mm}$ . It was decided to run the simulations using both proportions, in order to observe how the population density impacts population numbers and spatial co-occurrence coefficients among the microorganisms. Before running the simulations, we had to decide which species we will include in the experiments, for which we used the food web that depicts the nine species, and their relations between each others (see Figure 1). After careful consideration, we concluded that we will experiment with the following pairings: Bacteria and Bacterivorous Nematodes, Bacteria and Fungi, and Bacteria, Bacterivorous Nematodes and Omnivorous Nematodes. We wanted to observe a prey-predator pairing, for which we chose Bacteria and B. Nematodes, as their relationship is somewhat isolated, in a sense that Bacteria are the only prey in the food web for Bacterivorous Nematodes. Second pairing to observe was between competitors, and in this case those are Bacteria and Fungi, as they are both feeding on Soil Organic Matter. For the third group of organisms, we wanted to choose a more complicated relationship, therefore we decided on the triangle between Bacteria, Bacterivorous Nematodes, and Omnivorous Nematodes. All three organisms are connected to each other, since Bacteria is a common prey to B. Nematodes and O. Nematodes, but O. Nematodes also consume B. Nematodes.

After choosing the combinations of microorganisms, we started preparing the initial conditions for the simulation runs. For the research question 1A, we kept the weight of the edges between the organisms to 0.5. This weight influences the initial dispersal of microorganisms in space, and at 0.5 it is random. We ran multiple simulations for the same setting to observe the differences among them. For research question 1B, we decided to analyse how the

weight between edges and initial population numbers influence the population existence and spatial co-occurrence coefficients. For pairings between Bacteria and B. Nematodes, and Bacteria and Fungi, we ran simulations where the weight of the edge was first 0, and then 1. For the triangle between Bacteria, B. Nematodes and O. Nematodes, we first set the weight of the edge between Bacteria and B. Nematodes to 0.5, and weights of the edges between those two and O. Nematodes to 0.25. Later we changed the first weight to 1, and other edges to 0.5. The reason behind this is that unlike B. Nematodes, O. Nematodes can eat both Bacteria and B. Nematodes, hence the weights of those connecting edges were halved. Second initial condition that we wanted to observe was the initial population, which was applied to pairings Bacteria and B. Nematodes, and Bacteria and Fungi in the model of dimensions  $200 \times 200 \times 1$ . The initial population of Bacteria was kept the same, while the population numbers for B. Nematodes and Fungi were first halved, and afterwards halved again. Thus, if the initial population number for B. Nematodes was 750, for the first experiment we set it to  $750/2 = 375$ , and the second one to  $375/2 = 187.5$  which we rounded to 180.

After all the simulation experiments were done, we collected the data frames that included the tick which presented a point in time, the id of the organism, and x, y and z coordinates of that organism unit. To calculate the *spatial co-occurrence coefficient* through time, we created an algorithm that would populate a list for each organism in a pair with the number of occurrences in  $2 \times 2 \times 1$  square. This square would slide through the entire model, without overlapping, and collect number of units for microorganism A and append it to the first list, and then do the same for microorganism B while appending it to the second list. Afterwards, to calculate the coefficient at a point in time, we created a loop that retrieves coefficients from every five ticks, starting at tick 0 and ending at the first tick where the coefficient is NaN, as that signifies that one of the microorganisms became extinct. To calculate the co-occurrence coefficient, we utilised the Pearson coefficient function from the Numpy library in Python [6], which requires two lists of numbers, in our case integers that represent numbers of microorganisms in the square.

To create population graphs, spatial co-occurrence coefficients graphs and spatial plots, we utilised the Matplotlib library in Python [8]. The population graphs depict how the population numbers of the species changed throughout the timeline of the simulation. The co-occurrence graphs show how the coefficients fluctuated through the simulation, and the spatial plots show the dispersal of microorganisms in space at a specific point in time. To choose those specific points in time, we observed population and co-occurrence graphs and searched for unusual spikes in co-occurrence, or sudden declines and increases in population numbers.

## 4.2 Method for Research Question 2

To compare the initial trophic and newly found co-occurrence network, we will apply visual analysis of both figures. What will be compared is the energy flow on the trophic network and co-occurrence coefficients between selected species. For example, on the food web as seen on *Figure 1*, energy flows from the Bacteria to Omnivorous Nematodes, in other words they are in a predator-prey relationship. Thus, on the correlation network, we will observe what is

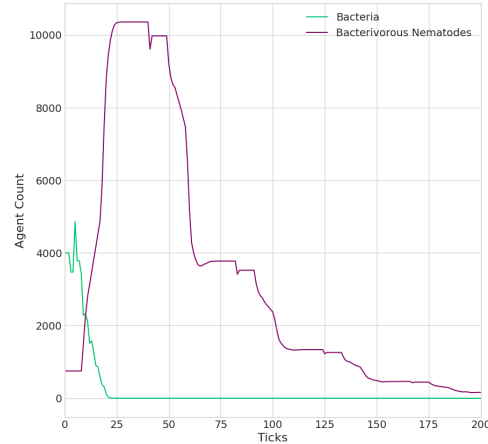


Fig. 2. Population between Bacteria and B. Nematodes

the strength of their coefficient and if they often spatially co-occur. Next to this, we will observe if new strong correlations appear in a co-occurrence network that were not yet depicted in the trophic network. These findings should be then explained using the research about soil microorganisms or by discussing them with the experts.

## 5 RESULTS

The simulation runs for each case did not differ from each other, so no averaging of spatial co-occurrence coefficients was applied.

### 5.1 Results for Research Question 1A

**5.1.1 Bacteria and Bacterivorous Nematodes.** *Figure 2* shows the change in the population numbers for Bacteria (B) and Bacterivorous Nematodes (BN) with starting populations of 4000 and 750 units respectively, for the model of dimensions  $200 \times 200 \times 1$ . The B population first spiked in numbers, before it rapidly declined and died out. Its predator, B. Nematodes, at first kept their population steady, until the population of their prey spiked, so their population rapidly started growing as well. The BN population also started to decline shortly after the B population went extinct, possibly due to having no more nutrients. *Figure 3* shows the change in spatial co-occurrence coefficients, which dropped as the B population declined, and rose once when both populations experienced an increase. Naturally, when there was no more Bacteria, the coefficient plunged to 0. Looking at the spatial plots, on *Figure 4*, the BN population is dispersed in space and in the vicinity of B, later even forming small clusters around the remaining Bacteria, after their population grew and B's declined. The spatial plots depict the state of population at depth  $z=0$ , as majority of microorganisms existed there.

The B and BN populations in a model of  $100 \times 100 \times 1$  dimensions behaved similarly to the previous model, as the prey's population grew first, after which the predator followed. *Figure 3* depicts the co-occurrence coefficients through time, and it can be observed that B and BN occurred more strongly in a smaller environment rather than the larger one, which is explainable due to population density being higher. The co-occurrence coefficients followed the

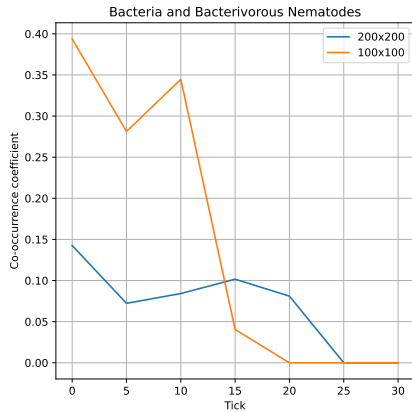


Fig. 3. Spatial co-occurrence for Bacteria and B. Nematodes

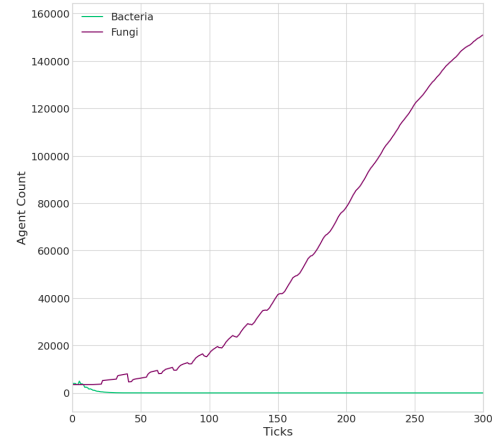


Fig. 5. Population between Bacteria and Fungi

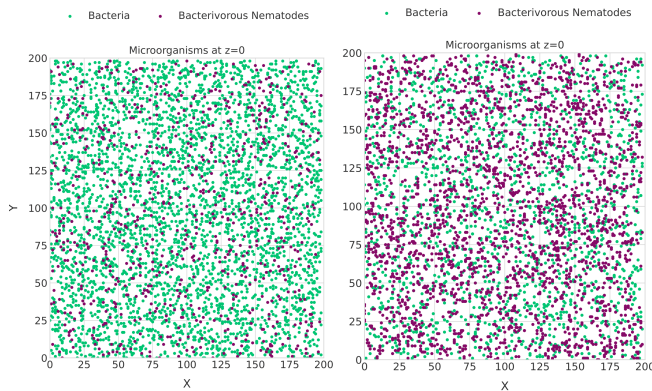


Fig. 4. Spatial Plot for Bacteria and B. Nematodes at ticks 7 (left) and 11 (right)

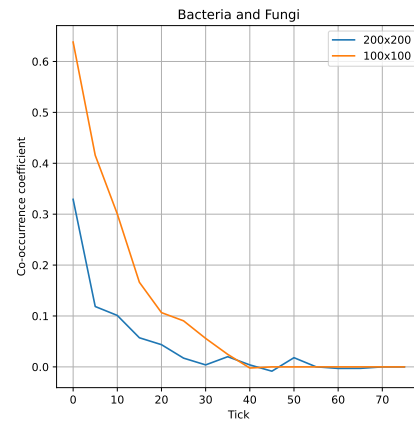


Fig. 6. Spatial Co-occurrence for Bacteria and Fungi

population numbers, where the larger the populations were and more similar in numbers, the co-occurrence would also grow.

**5.1.2 Bacteria and Fungi.** Figure 5 depicts the change of population numbers for Bacteria (B) and Fungi (F) in the model of dimensions 200x200x1, where the initial number of organisms for each species was 4000 and 3500 respectively. Both populations initially kept a steady number of units, and the B population was the first to die out, while the F population experienced a drastic increase in numbers. As B and F are competitors and both eat Soil Organic Matter, they were evenly dispersed in space and oftentimes occurred close to each other which can be noticed on Figure 7. The explanation of why B went extinct early in the simulation could be the way in which both species migrate. B rely on the presence of flagella that enable them to move through water films, or if such are absent, they rely on passive transport through soil via roots, fauna, or the general movement of water through soil. On the other hand, F produces filamentous hyphae that can penetrate and explore microhabitats of the soil. Due to these differences in mobility, F had more opportunities of looking for nutrients in soil, than B did, hence why their population grew and survived until the end of the simulation [2]. Figure 6, where the

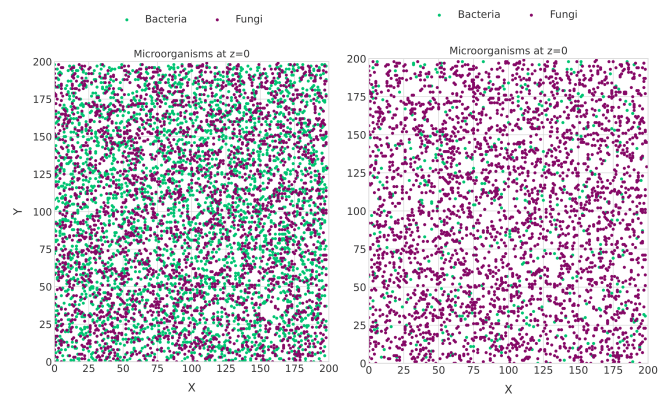


Fig. 7. Spatial plot for Bacteria and Fungi at tick 5 (left) and 20 (right)

spatial co-occurrence coefficients can be observed, shows that the coefficients dropped since the initialisation, most probably caused by the decline of B population.

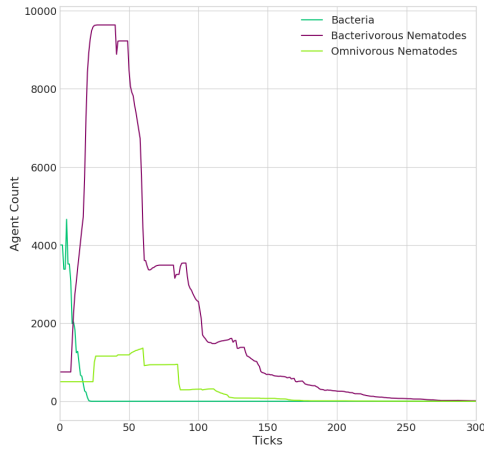


Fig. 8. Population graph for Bacteria, B. Nematodes and O. Nematodes

Even at the higher density of populations in soil, the behaviours of these two species remained the same. Co-occurrence coefficient was double in size at the start, due to the space being smaller, but it still followed the same trajectory as seen on Figure 6. The spatial co-occurrence in both cases was high in the beginning as there was still no population decline, and both B and F were situated close to the Soil Organic Matter. It was observed that in the competitors' case, the competitor with better mobility possibilities did not go extinct and managed to spread through the better part of the soil.

**5.1.3 Bacteria, Bacterivorous Nematodes and Omnivorous Nematodes.** At the start of the simulation with experimental settings, the population numbers for Bacteria (B), Bacterivorous Nematodes (BN) and Omnivorous Nematodes (ON), were 4000, 750 and 500 respectively. Figure 8 depicts the difference in population numbers throughout the timeline of the simulation, and it was noticed that the population change in B and BN organisms did not differ much from the first experiment when they were alone. Species B began declining pretty early in the simulation, and as their population declined, the BN experienced a rapid and great increase. The ON, as a predator that can consume both B and BN, was mostly impacted by the growth in BN population. A short time after BN experienced a rise, the ON population also grew due to having more prey to feed on. Their population, though, did not increase greatly, and as the BN population declined for the first time, they also started declining and eventually disappearing. The BN organisms no longer had their prey so their food source became scarce, and their population was not controlled by the predator, thus they also soon disappeared. The co-occurrence coefficients, as seen on Figure 9, followed the population numbers, when the B population was at its highest, so were the coefficients with other two species. The same phenomena was noticed between BN and ON, their coefficients were higher, when their populations experienced growth. By observing Figure 10, it was noticed that the B was evenly dispersed in space and BN and ON were always in its vicinity. After the B population disappeared, BN started distancing from ON.

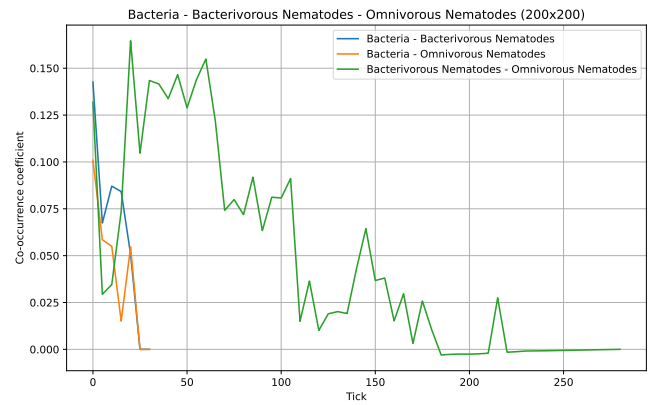


Fig. 9. Spatial Co-occurrence for Bacteria, B. Nematodes and O. Nematodes

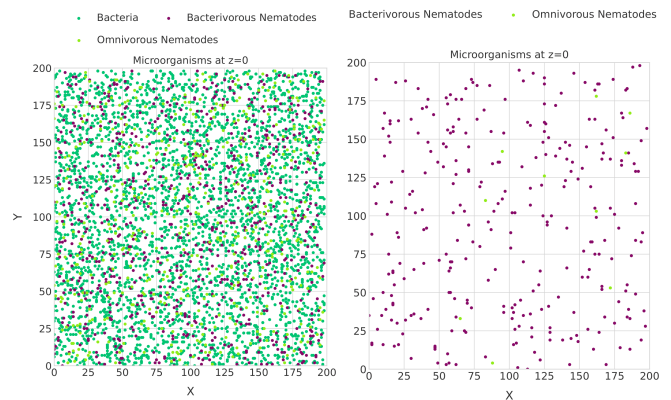


Fig. 10. Spatial plot for Bacteria, B. Nematodes and O. Nematodes at tick 5 (left) and 190 (right)

Even in the simulation with the higher population density the numbers followed the same path, the prey population grew first, after which their predator followed, and then the prey declined in their population so the predator was left without the food source. While the common prey, Bacteria, was still alive, both BN and ON spatially co-occurred, and this continued until their own populations started to deteriorate, after which they were less likely to be found in the same area as seen on Figure 11.

**5.2 Results for Research Question 1B**

When changing the initial weight of the edges between the species in the simulation and the starting population numbers, we focused on the model of dimensions of 200x200x1.

**5.2.1 Initial Weight Change.** Between the Bacteria (B) and Bacterivorous Nematodes (BN), there was no significant change in population numbers from the Figure 2, therefore the initial dispersal of microorganisms in space and their closeness to each other did not affect the way their numbers grew or declined. The impact of the weight change was noticeable on the spatial co-occurrence coefficients as seen on Figure 12, with the starting coefficient for weight

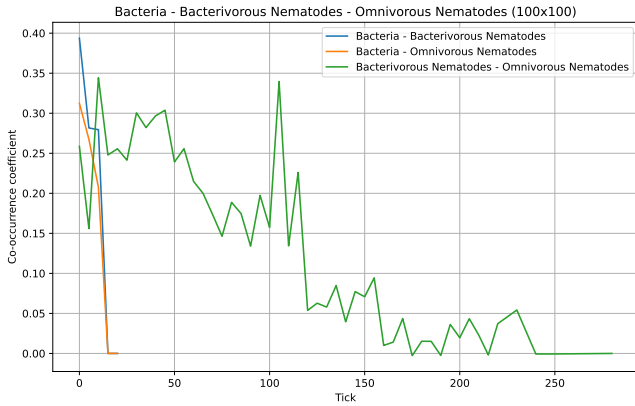


Fig. 11. Spatial Co-occurrence for Bacteria, B. Nematodes and O. Nematodes (100x100x1)

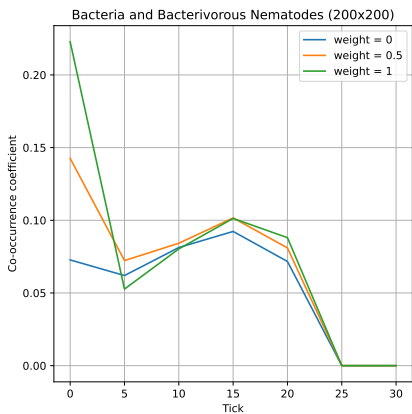


Fig. 12. Spatial co-occurrence coefficients for Bacteria and B. Nematodes

0 being twice as small than for weight 0.5, and the coefficient for weight 1 being almost double the size of weight 0.5. However, as population numbers did not change, and B and BN kept the same behaviour as before, with the prey growing and then declining in numbers first, the coefficients evened out and followed the same trajectory. On the spatial plots on *Figure 13* it was noticed that when the simulation setting was on weight 1, on depth  $z=0$ , all BN organisms were situated on B organisms. There was a bigger distance between B and BN organisms with weight 0. Surprisingly, the BN population for weight 1 has split itself between depths 0 and 1, while all BN population was on depth  $z = 0$  together with B for weight 0, and still the initial spatial co-occurrence coefficient was higher.

Similar occurrence was noticed in the case with Bacteria (B) and Fungi (F). Their population followed the same trajectory as *Figure 5*, where the B population went extinct quickly and F population remained and grew in numbers. As the population numbers stayed similar, the difference in coefficients was only noticeable in the beginning, when the coefficient for weight 1 was higher than for the other two as seen on *Figure 14*. The coefficients for weight 1 plummeted, possibly because unlike for weight 0, the F was dispersed to

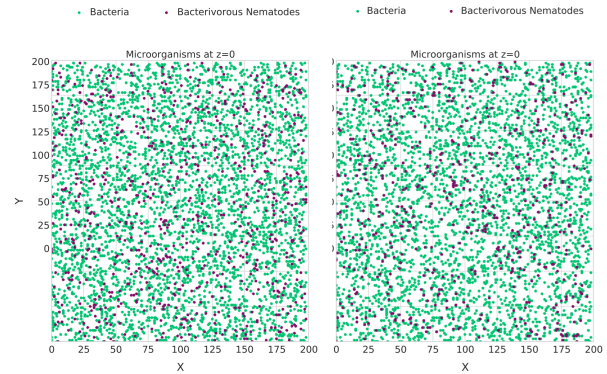


Fig. 13. Spatial plots at tick 0 for weights 0 (left) and 1 (right)

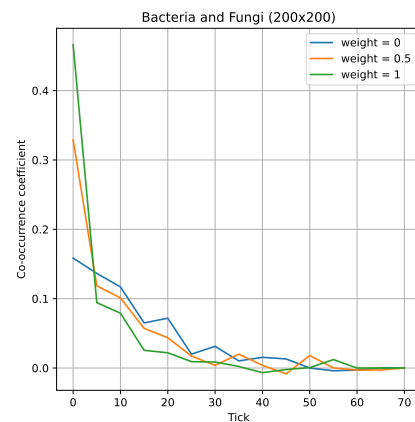


Fig. 14. Spatial co-occurrence coefficients for Bacteria and Fungi

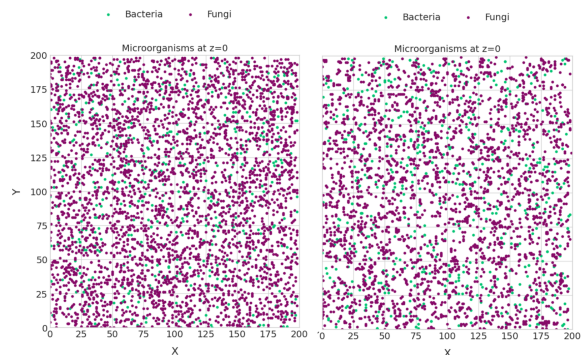


Fig. 15. Spatial plots at tick 20 for weights 0 (left) and 1 (right)

both depth  $z = 0$  and  $z = 1$ , but also because B and F populations started to separate. This could have been caused by their competitiveness and search for new food sources around them. By the end of the simulation it was less likely to find them coexisting in the same neighbourhood which can be seen on *Figure 15*.

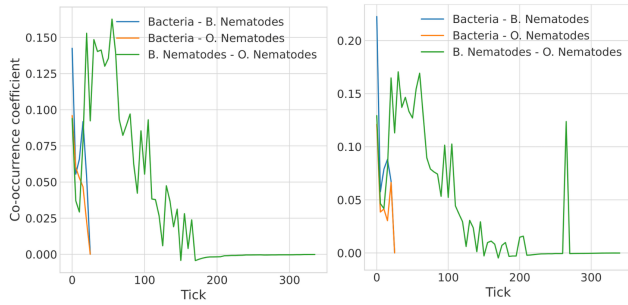


Fig. 16. Spatial co-occurrence coefficients for Bacteria, B. Nematodes, and O. Nematodes, weight between B and BN being 0.5 (left) and 1 (right)

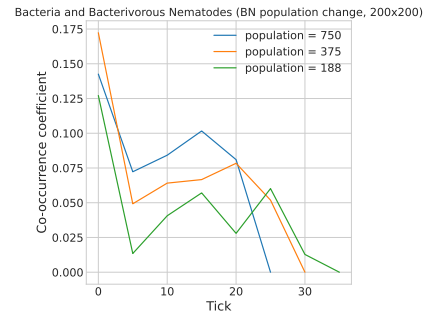


Fig. 18. Spatial co-occurrence coefficients for Bacteria and B. Nematodes

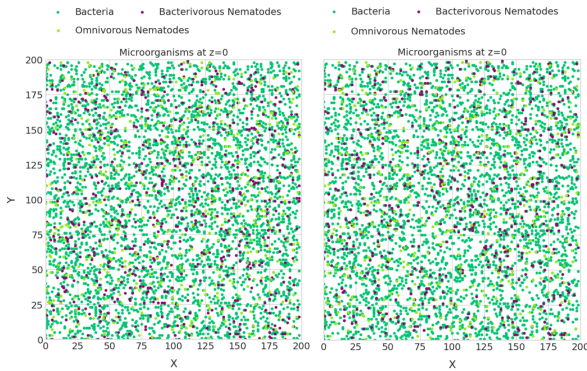


Fig. 17. Spatial plots at tick 0 for weight between B and BN being 0.5 (left) and 1 (right)

A slightly different approach was done for the simulation between Bacteria (B), Bacterivorous Nematodes (BN) and Omnivorous Nematodes (ON), yet the behaviour regarding the population numbers remained the same. The predator is always following their prey's growth in the population and eventually their decline. As before, the simulation where the weight was higher, also had a higher spatial co-occurrence coefficient in the beginning which can be compared in Figure 16. Afterwards, these coefficients started fluctuating, especially between BN and ON, after B went extinct. The difference in the spatial dispersion of the microorganisms is not as obvious as for the before mentioned cases, in the beginning they are somewhat evenly dispersed in space, with B and BN co-occurring more often, and ON being in their vicinity as seen on Figure 17.

For all experiments, it was noticed that the simulation with the higher weight between the edges, also had a higher spatial co-occurrence coefficient at the beginning. This did not result in all coefficients afterwards being higher than the ones from a simulation with the starting weight 0, as those sometimes grew higher. The weights did not impact the behaviour of the species, as their population numbers also did not change a lot from the original simulation.

**5.2.2 Initial Population Change.** For the experiments between Bacteria (B) and Bacterivorous Nematodes (BN), the initial population of BN was lowered from 750 to 375, and then 188, yet the population

numbers graphs depicted the same trajectory and roughly the same population numbers as for the original experiment. Interestingly, when observing the Figure 18, it was noticed that the extinction of population B is postponed when initial BN population is 188, compared to the other two, which seemed natural as less predators posed a smaller threat to the B population. Though the population numbers remained the same during the simulation, the coefficients were quite different, but they did increase and decrease around the same ticks. Even if BN recovered its population, it still did not manage to get in the neighbourhood of B. The reason for this could be that a majority of BN organisms was not placed near B, and even though they grew in the population, they still could not migrate towards them fast enough. So they stayed in their positions and reproduced, while B was not in their vicinity.

Similarly to the previous experiments, the initial population for Fungi (F) was lowered from 3500 to 1750, and afterwards to 875, while the Bacteria (B) population remained the same. As in the earlier case, the population numbers and trajectory stayed similar to the original experiment, even though the initial population was lowered. On Figure 19 it was noticed that the the spatial co-occurrence at the beginning of each experiment was high and then plummeted afterwards. It was early for both population numbers to change, so the explanation for this decrease in coefficients could be credited to competition between B and F, and need to move away from each other in order to access more Soil Organic Matter.

### 5.3 Results for Research Question 2

From the results, it was gathered that unlike food web which depicted static relations among the microorganisms, the spatial co-occurrence network was temporally dynamic and depended on the population status of the microorganisms.

As seen in Figure 20, the spatial co-occurrence between Bacteria and Bacterivorous Nematodes remained positive in the simulation with the experimental conditions. Considering that they are in a predator-prey relationship where Bacteria is the only prey to B. Nematodes, it would be expected that they co-occur more often. However, this was not the case and the coefficients were not as high, and throughout the simulation they declined.

More interesting case was the one between Bacteria and Fungi, who are competitors in the food web (see Figure 21) and therefore do not have any energy flow between themselves. Due to their high

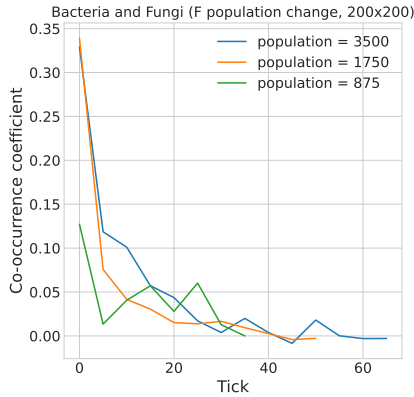


Fig. 19. Spatial co-occurrence coefficients for Bacteria and Fungi

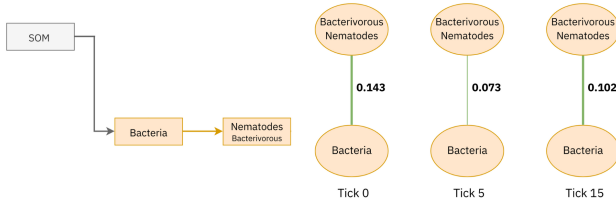


Fig. 20. Food web for Bacteria and B. Nematodes (left) and co-occurrence network (right)

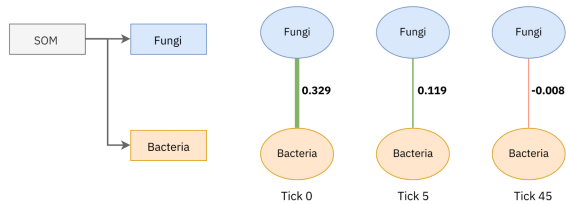


Fig. 21. Food web for Bacteria and Fungi (left) and co-occurrence network (right)

population numbers in the beginning, their co-occurrence coefficient was quite high, but as the time progressed, it declined. As we mentioned before, the reason for this could be their different migration capabilities with Fungi having the advantage. The coefficient declined and became negative, probably because both species looked for more Soil Organic Matter and dispersed in space.

For the third case, we had a more complicated network with three species that are in a predator - prey relationships: Bacteria, B. Nematodes and Omnivorous Nematodes (see Figure 22). All of the edges were approximately of the same weight, and corresponded to the energy flow in the food web. This, however, changed as Bacteria went extinct, and the edges in the co-occurrence network disappeared as well. Compared to the original food web, the relations between prey and predators remained with their spatial co-occurrence being positive, though it did change as the population of microorganisms changed. The competitors co-occurred in space at the beginning, but

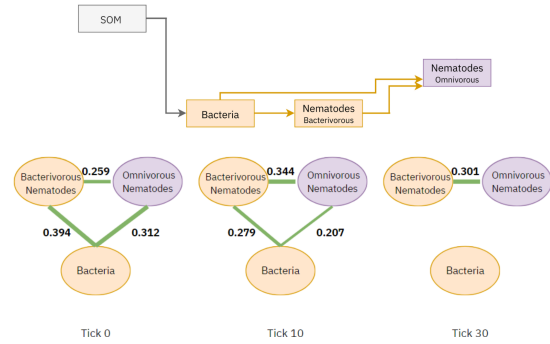


Fig. 22. Food web for Bacteria, B. and O. Nematodes (up) and co-occurrence network (down)

shortly after they dispersed from each other, making their relation weaker.

## 6 DISCUSSION AND CONCLUSIONS

The goal of this research was to calculate spatial co-occurrence coefficients among a set of chosen organisms and observe how the initial variables in the simulator influence the same.

It was noticed by Delgado-Baquerizo [3], while researching the effect of latitude on soil biodiversity, that there was a positive correlation between Eukaryotes and Bacteria, as well that larger diversity in Bacteria positively influences the diversity in Eukaryotes. Similarly to their research, it was observed that the population growth of Bacteria, was followed by growth in populations of Bacterivorous and Omnivorous Nematodes, both classified as Eukaryotes. In another study, conducted by Morriën [11], the Fungi and Bacteria populations were the highest ones, and the co-occurrence between them was very strong, which does not correspond to our results where the coefficients through time decline and are quite low. The predator-prey relationships that were analysed in our research follow a similar trajectory as the Nicholson-Bailey model, which depicts the over exploitation by the predator thus leading to the extinction of both prey and predators [10].

This research has potential limitations. Firstly, the space considered in the research is two dimensional, without examination of what the co-occurrence would be like if the depth dimension was included as well. Secondly, the initial dispersal of the microorganisms in space that is influenced by the weight variable, should be reassessed and possibly implemented in a different manner, so that the co-occurrence coefficient calculated at the beginning of the simulation better corresponds to the initial weight. Thirdly, when rerunning the simulation with the same initial settings, the "random.seed" variable should be changed in order to get different results that could lower the noise that was noticed in spatial co-occurrence coefficients graphs.

Finally, if this research were to be continued, the complete co-occurrence network, that includes all species in the simulator, would be composed and we would analyse the co-occurrence between all species that belong in an energy flow group.



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During the preparation of this work the author(s) used ChatGPT in order to adjust the code for visualisations, namely spatial co-occurrence coefficients graphs and spatial plots. After using this tool/service, the author(s) reviewed and edited the content as needed and take(s) full responsibility for the content of the work.

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