

Data integration to investigate Microbial Abundance in Terrestrial and Aquatic Ecosystems and its Causes

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Abstract

Microbial organisms provide an important role in recycling inorganic compounds for living plants and animals to consume in a more manageable way. For example, microbial communities in aquatic ecosystems provide oxygen in the biosphere through photosynthesis such as *Cyanobacteria*. In terrestrial ecosystems, *Rhizobium* is a bacteria that nitrogen fixation in soil for usable nitrogen to plants. The overall purpose of this study is to provide more insight on the correlation between microorganisms and the various changes that can occur such as temperature, soil composition, pH, and moisture using data presented from NEON Laboratories.

Computational analysis using R-script will be used to analyze and display results and patterns found in the results section. Through this study, it is shown that on a monthly scale, major controlling factors on microbial cell count in aquatic ecosystems are specific conductance and water temperature. This illustrates that as water temperatures increase, it can boost microbial metabolism, initiating biological processes like photosynthesis faster. In terrestrial ecosystems, soil temperature and soil moisture are major contributors to biomass on a monthly scale, which can boost decomposition of organic matter and methane. These findings illustrate that microorganisms act as both a driver and indicator of climate change with hypothesized contributing factors such as temperature, moisture, oxygen saturation, pH, carbon percentage, nitrogen percentage, lipid concentration, and specific conductance.

Keywords: terrestrial microbial biomass, aquatic microbial cell density, seasonality

Significance Statement:

Aquatic and terrestrial microbes are the drivers and indicators of climate change that can be quantified through environmental factors such as temperature, moisture, oxygen saturation, pH, carbon percentage, nitrogen percentage, lipid concentration, and specific conductance that can be illustrated through a biospheric model developed under a global database. Seasonality and localization of these microorganisms that inhabit in certain abundance represents the acceleration of certain biomechanical feedback loops which can be used in the advancements in green microbiology to sustain and mitigate climate change.

Introduction

Climate change has created a decline in soil microbial biomass across the globe from 1992 to 2013. There is little knowledge in the aspect of the biomechanical processing that incorporates the result of climate change. Microorganisms can live in various environments in different temperatures, pH, water activity, pressure, and radiation. Marine biomes cover almost 70% of the Earth's surface with phototrophic microorganisms using the energy of the sun within the top surface of water columns and deeper zones using organic and inorganic chemicals for energy production (Cavicchoili et al., 2019). This is one reason as to the ability for bacteria to live in various ecosystems as displayed in Figure 1.

Microorganisms include domains such as archaea, bacteria, and eukarya. Archaea are known to be extremophiles that can withstand harsh conditions like pH and extreme temperature fluctuations. Bacteria are prokaryotes that only live in suitable temperatures, appropriate pH,

viable nutrient environments, and ranges in the various levels of oxygen needed depending on the certain bacteria. Eukaryotic organisms are multicellular which comprises organisms like plants and animals. These domains drive important biological processes like recycling nutrients, decomposition, photosynthesis, ammonification, nitrogen fixation, and various others.

Microorganisms can be viewed as both drivers and indicators of climate change as they actively contribute to greenhouse gasses like in carbon dioxide, nitrogen oxide, and methane through examples like methanogenic archaea.

In aquatic ecosystems, the carbon cycled through these microorganisms eventually a majority of carbon ends up at the bottom of the ocean through cyanobacteria and phytoplankton which can create a nutrient imbalance while reducing the amount of carbon in the air. Microbes in aquatic ecosystems play a dominant role in “pumping” carbon into the ocean into the soil similar to a “conveyor belt” that transports and stores carbon in oceans within these high pressurized environments (Sanmukh et al., 2015). This phenomenon is similar to a double edged sword that indicates the actions of microorganisms to be both an indicator and a driving force of climate change fluctuations.

In terrestrial ecosystems, soil microbes play major roles in decomposition of organic matter to be released into carbon into the atmosphere or used in the soil by plants. The ability to process organic material allows transfer of matter and energy above and below ground which has lasting effects on nitrogen enrichment and climate change (Delgado-Baquerizo et al., 2016). Terrestrial ecosystems and aquatic ecosystems rely on both parties creating a complex feedback loop that cycles through fluctuations in temperature, moisture, oxygen saturation, pH, carbon percentage, nitrogen percentage, lipid concentration, and specific conductance. Understanding

these interactions in this feedback loop are critical for predicting impacts of climate change and developing strategies and technological advancements to mitigate and sustain these effects.

The overall objective of this research is to visualize microbial communities in various ecosystems. Another objective is to illustrate factors that correlate with microbial communities densities over a period of time. The final objective is to determine various uses for this knowledge to contribute to the advancements in Green Microbiology. One hypothesis of this study is that bacteria provide the most abundance in various environments as illustrated in Figure 1 due to the major contributing factor of specific conductance, water temperature, soil temperature, and soil moisture which can be used to accelerate biological compounds of interest through their respective biological processes. The significance of analyzing microbial communities in various environments is to view the vast potential of microorganisms to learn more about climate change and to incorporate this knowledge for the use in Green Microbiology to find sustainable solutions to ocean acidification, melting glaciers, and air pollution.

Methodology and Materials

This study was carried out by a compilation of the comprehensive data set by NEON; Water Community and Abundance, and Cell Count for 2014-2023, Soil Periodic 2014 to 2023, Benthic Community Microbes and Group Abundance 2014-2023, Soil Microbial Community Count and Group Abundance 2014-2023, and Soil Biomass 2020-2023 as illustrated in Figure 2. The comprehensive data was isolated and simplified with factors of interests in the respective categories in monthly and seasonal variations.

Next, R-Script templates were made using nonmetric multidimensional scaling and principal component analysis. Some models and tools used in this study were “readxl” to read

Excel files, “ggplot2” to plot, “sf” for spatial data handling, “ggspatial” for better visuals, “scatterpie” for addition of pie charts, and “maps” to render world maps. The data used for the analysis in this study are displayed and archived at

https://docs.google.com/document/d/1dkufMJ5NSeyass2HviZ3ePuo_Flr25Jb_V59wfEOjsc/edit?usp=sharing

The figures created and illustrated within this study was a global map with abundance fluctuations in microbial communities across different parts of the United States at different ecosystems as displayed in Figure 1. Another model made was a methodological map to illustrate the work pathway of the production within this study and the thought process that occurred within the study as shown in Figure 2. The next chart made was a correlation matrix as described in Figure 3 to describe various factors that can affect each type of ecosystem. Finally, a correlation plot illustrated the hypothesized correlation between nucleic acid concentration and mean copy number within various ecosystems as illustrated in Figure 4. The figures were then analyzed and results and patterns were recorded as described in the results section.

Results

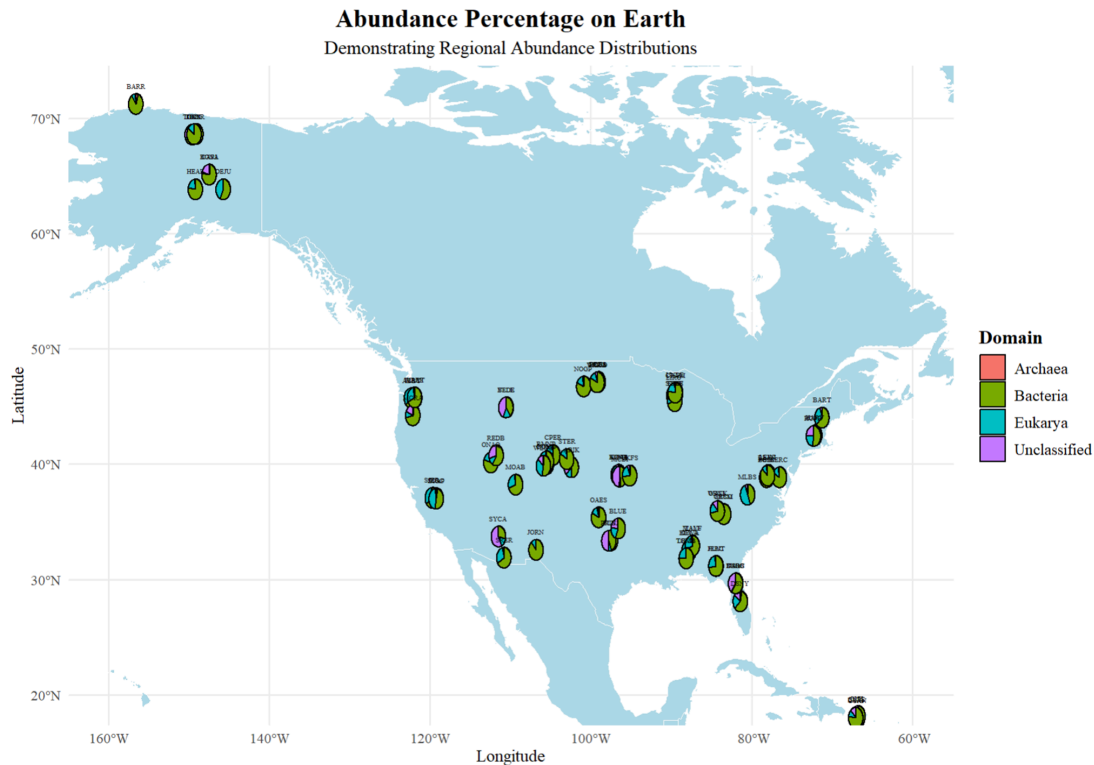


Figure 1. Abundance Percentage on Earth. The abundance of various microorganisms and the percentage in each allocated region.

In Figure 1, some findings that were interesting was that a majority of the microorganisms across aquatic and terrestrial environments largely are the bacteria. Some outliers were presented such as the west and east coast had spots with higher density in eukarya which can implement a correlation to more interaction with the ocean. In the middle region of America, it can be seen that there are high localization points of unclassified microorganisms which can represent various explanations with the likelihood of unculturable species.

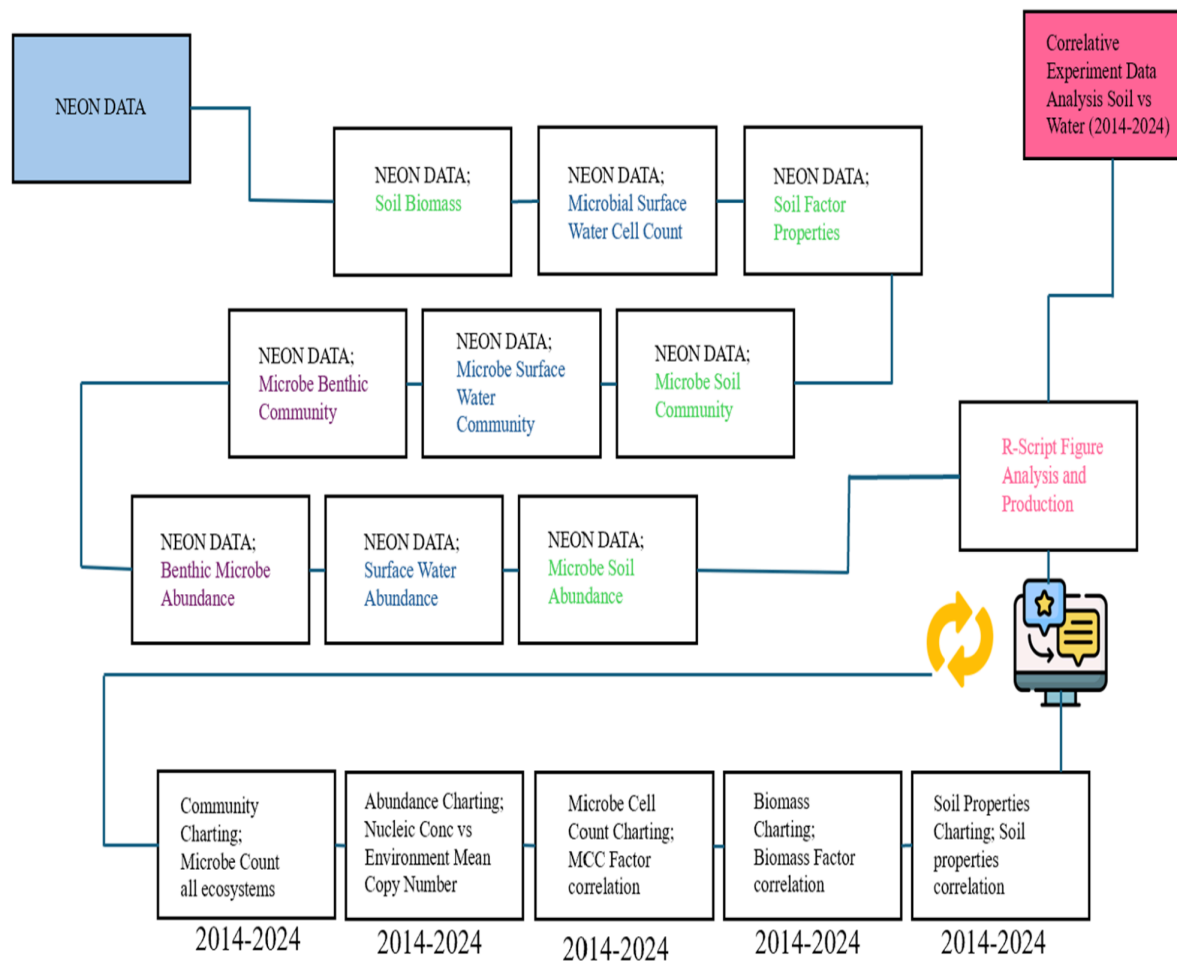


Figure 2. Methodology Map. Methodology to analyze categorized raw data samples distributed by NEON.

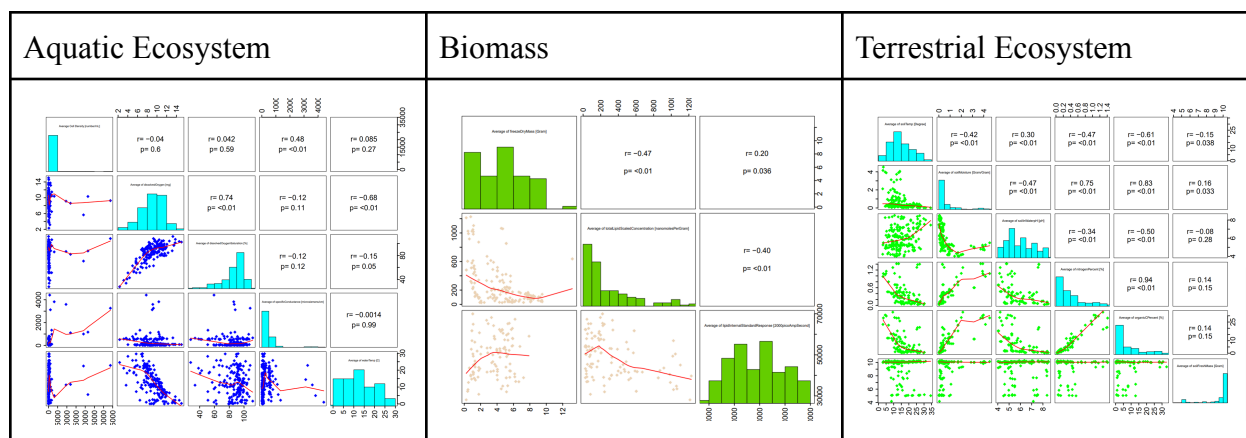


Figure 3. Correlation Matrix of Factors and Microbial Population. Relative variation in seasonal temporal scale in correlation to microbial cell density in aquatic systems and biomass in terrestrial systems.

In Figure 3, there is a clear correlation between specific conductance and water temperature that contribute to the microbial cell density in various sites within the USA in the aquatic ecosystem. Another result found was that there was a large variation in biomass that accepts the null hypothesis of all contributing factors like freeze-dry mass, lipid concentration, and lipid response providing insight that biomass has no significant correlation between any of the displayed factors. Finally, Figure 3 depicts a clear correlation between soil moisture and soil temperature that contribute to the biomass in various sites within the USA in the terrestrial ecosystem with major factors in both aquatic and terrestrial ecosystems being temperature as a significant contributor to their respective communities.

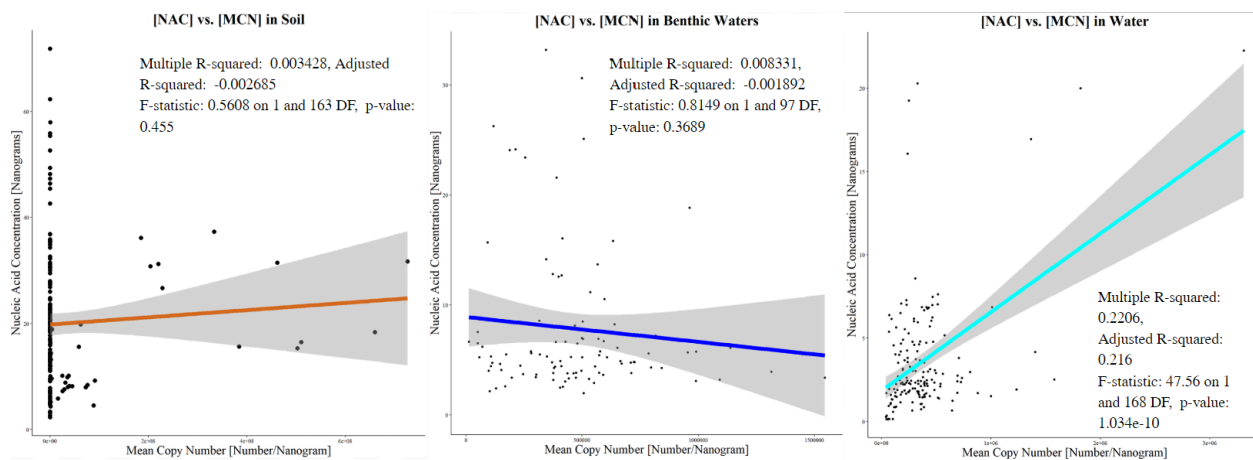


Figure 4. Nucleic Acid Concentration vs. Mean Copy Number within Various ecosystems.

Association plot for various ecosystems to Nucleic Acid Concentration [NAC] and the correlations.

In Figure 4, it can be seen that the orange line indicates a relatively weak positive correlation between Nucleic Acid Concentration and Mean copy number in soil. In the dark blue line, it can depict that there is a relatively negative correlation between Nucleic Acid Concentration and Mean copy number in benthic waters. Finally, in the last correlation chart, it can be seen that the cyan line illustrates the relatively negative correlation between Nucleic Acid Concentration and Mean copy number in aquatic systems. This illustrates that the relationship within the nucleic acid concentration is very similar in aquatic ecosystems, illustrating that the DNA is very similar in these ecosystems.

Discussion

In Figure 1, some findings that were interesting was the abundance of microorganisms across aquatic and terrestrial environments largely consisting of the domain of bacteria. This can be due to the optimal living conditions that mainly are in the realm of the bacteria compared to archaea as these microorganisms normally inhabit very harsh environments. Some outliers as stated before were presented in the west and east coast with higher density of eukaryotic microorganisms which can implement a correlation to more interaction with the ocean. These microorganisms can represent species like protozoa which are grazers that feed on organic matter for larger organisms to feed on like shrimp which can explain the large abundance of eukaryotic microorganisms. In the middle region of America, there are high density spots of unclassified microorganisms which can represent various explanations with the likelihood of unculturable species as a large number of microorganisms cannot be cultured due to the limited technology of our time.

In Figure 3, there is a clear correlation between specific conductance and water temperature in relation to microbial cell density in various sites within the USA in the aquatic ecosystem. Therefore, the major contributing factor for sustainability of these communities as well as key factors to drastically affect the carbon cycle. Specific conductance affects the carbon cycle by directly influencing the rate of photosynthesis while specific conductance usually is an indicator of dissolved materials that can be used for growth to enhance the uptake of carbon to directly be placed in the “conveyor belt” within aquatic ecosystems. Factors like freeze-dry mass, lipid concentration, and lipid response provide insight that biomass has no significant correlation between any of the displayed factors. This result may be due to the fact that lipid concentration is only crucial in the survival of these microorganisms for the sustainability of the cell membrane as an energy source and membrane fluidity which are usually found in eukaryotic microorganisms and most bacteria have cell walls. Finally, there is a clear correlation between soil moisture and soil temperature that contribute to the biomass in the terrestrial ecosystem which can result in similar analysis as factors in aquatic ecosystems where soil moisture and temperature can be an accelerant of biological processes like nitrification, ammonification, and denitrification which directly influences the sensitivity of materialization and decomposition of organic material (Gutiñas et al., 2012).

In Figure 4, it can be seen that there is a relatively weak positive correlation between Nucleic Acid Concentration and Mean copy number in soil. This shows that the abundance in soil shows higher nucleic acid concentration which is useful in this study as a way to show unbiased values as these samples are randomly selected and it shows that these microorganisms carry more gene copies in their genome which corresponds to their phylogenetic evolution and their overall function in climate change within the biosphere. In the dark blue line figure, a

relatively negative correlation exists between Nucleic Acid Concentration and Mean copy number in benthic waters. This can illustrate a diluted effect within the gene copies of individual microorganisms as not similar within deeper waters. This is accurate as these microorganisms can now inhabit archaic microorganisms that are in thermal vents or extremely cold and pressurized parts of the ocean and not just bacteria even though archaic microorganisms are low in abundance as depicted in Figure 1. Finally, the last correlation chart with the cyan line illustrates the relatively negative correlation between Nucleic Acid Concentration and Mean copy number in aquatic systems. This shows that within aquatic ecosystems, the DNA is very similar within these microorganisms in these ecosystems which can help evaluate the function of these microorganisms to generally be in tandem to work together or work within the same realm of a biomechanical process.

Previous research explored the specificities of either terrestrial or aquatic ecosystems and the effects to sustainability as each environment has their own specific carbon fingerprint and in terrestrial ecosystems, microbial abundance affects necromass, enzymatic activity, and carbon metabolism (Verrone et al., 2024). In aquatic ecosystems, it was found in another study that relative abundances of phyla varied across habitat types (Fig. S8) but on average, the meta-community across all ecosystems was composed of Proteobacteria (38.4%), Verrucomicrobiota (9.6%), Patescibacteria (7.9%), Acidobacteriota (5.3%), Myxococcota (5.2%), Actinobacteriota (5.2%), Bacteroidota (4.5%), Bdellovibrionota (3.8%), Planctomycetota (3.2%) and Cyanobacteria (2.7%) (Stadler & del Giorgio, 2021). But, further research is needed to investigate the pattern variations and changes of the abundance across space and over time in horizontal and vertical abundance of Biomass and Microbial Cell Density to further elaborate.

Conclusion

In conclusion, the overall purpose of this study is to provide more insight on the correlation between microorganisms and changes that can occur within factors such as temperature, soil composition, pH, and moisture using data presented from NEON Laboratories to understand key players to help sustain climate change through the perspective of Green Microbiology. Microorganisms play an important role in the vast biomechanical processes that result and effect climate change and the decrease in microbial population and diversity is alarming in both aquatic and terrestrial ecosystems.

The major contributing factors within aquatic ecosystems that help sustain microbial communities are water temperature and specific conductance useful as an accelerant for the hydro pump within the carbon cycle. But, it can also be used as a deterrent to slow down the carbon cycle if these factors are insufficient. In terrestrial ecosystems, factors like soil moisture and soil temperature play dominant roles in being drivers and indicators within the nitrogen cycle which can also be an accelerant or a deterrent to slow down these processes as it directly affects the microorganisms that inhabit this ecosystem.

Future research may be required for further advancements to this study such as the observation of changes through seasonal periods of time with correlation to the abundance of microorganisms that can provide insight on the temperature changes that occur from passage of time and when microorganisms are at their peak or their worse to evaluate biological process rates. As stated before, there is still so much information that is unknown about microorganisms and the roles they play within the grand scheme of climate change, but a goal that this study strived for was to get more insight and inspire more research to be done through microorganisms to find technological solutions to sustainability through Green Microbiology.

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