Draft 1

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\_\_BIG QUESTIONS–:

#What if, as a part of my thesis or even just as a lab... why don't we aim to standardize soil measurement strategies, definitions,, protocols.. we need to be doing these things on equal levels in order to be able to properly compare/contrast/understand.   
 #- could seek through SES and just discuss with individuals.  
  
 #- how can we ensure that we are measuring as universal as possible? \*steming from the SES discussion. We need to be making measurements and definitions \_\_common use\_\_\*.

# Introduction

*questions*: Why do we care about knowing soil fungal carbon functionality?

* fungal communities are primary decomposers
* fungal communities are some of the only decomposers that can break down lignin and cellulose.
* fungal communities are dominant in old growth forest systems
  + need support in old growth systems functionality.. are they are more productive or biodense?
* regardless of support or rejection of old growth forest logging we are drastically reduce a (more or less) finite resource. This resource contains *information*.

overall goal / message to display is that we do not know how these forest soil microbial communities differ in terms of functionality. (INSERT CARBON) This is a huge issue as we are making major decisions (such as logging old growth forests) without fully understanding the below-ground processes. We are running under this assumption that old growth forest soils are the same (or at least operate the same) as younger/managed soil systems.

I think the overall message or story I want to tell is that these systems are dynamic and that AGE MAY INFLUENCE FUNCTIONALITY. I retain an unbiased nature as to whether or not these older systems are more “functional” than younger systems but I can without a doubt say that we need to understand them more fully before we continue to decimate and eradicate them.

#### What points will support my thoughts on this?

* We know that forest communities change over time
* We *know* that microbial community influences functionality (NEED MORE RESEARCH ON THIS)
  + microbial communities influence soil chemistry, plant community, above-ground and below-ground biodiversity
  + these are all dynamic attributes… each are linked and as one changes resulting changes will follow…
* I need to have a better understanding of HOW current forest soils are being assessed… (NEED MORE RESEARCH ON THIS)
* Need more information on how microbial communities change over time.
* Need specific examples showing that we are only looking at WHO is there rather than WHAT the are doing\*.
  + eukaryotic transcriptomics.
* Need some information showing functionality of different forest succession stages.

#First Paragraph:

***intro sentence*** : (needs mad work, don;t event have to open this way, just an idea.)

Current unknowns and controversies in the literature among old growth forests demand a more comprehensive and collective understanding of the fate and function of these systems. Dissagreements and misconcepts regarding these systems are ever present in today’s world of science. A recent example is shown in the exchange (Luyssaert et al. (2008), Gundersen (2021), and Luyssaert (2021)) in the journal Nature debating the functionality of old growth systems in terms of their carbon sequestration capabilities. We believe that the misrepresentation of the below ground community is a significant contributor to such contrasting findings as well as the lack of clarity in soil science and ecosystem functionality.

***body*** :

This study aims to determine how soil fungal communities differ among forest sucessional stages (SS’s) in community structure and carbon **functionality**. Emerging research suggests that increase in forest SS may be associated with a number of below-ground processes. For example, it is evident that microbial community composition responds to forest succesional development. As forest age increases we see a shift from a r-strategic dominated community (variable environment dominated by bacteria) to a k-strategic dominated community (“stable” environment dominated by fungi) Zhou, Wang, and Luo (2017). Additionaly, this shift is accompanied by a general increase in microbial biomass carbon (FACT CHECK). Contrarily, we see drastic reductions in both microbial biomass and diversity when forests are “reverted” to *stand initiation* stages (CITATIONS). It is clear in the literature that both physical and chemical disturbance leads to substantial decreases in biomass and biodiversity of the microbial community (CITATIONS). Fungi have been chosen as our model organism to analyze soil microbial community and functionality as they become the primary decomposers as forests age. A number of studies have analyzed fungal community composition in search of “who is there,” but far less have looked into fungal soil functionality through fungal metatranscriptomics in search of “what are they doing” (subject to change). There is evidence suggesting a positive correlation between soil microbial diversity and soil ecosystem functionality (Delgado-Baquerizo et al. 2016). Understanding this link between microbial community composition and forest functionality may greatly change what we know about forest functionality and will certainly impact future forest management and preservation strategies. ***(needs work)***. It will be a part of this project to test the ability of different genomic community analysis methods to provide “accurate?” information regarding that community. We are aware that a experiment such as this could easily take up the entirety of a Ph.D. and that environmental sample are notoriously difficult to accurately measure in terms of genomics. We will analyze inoculated soils with known microbial communities and test the ability of certain methods (whole genome sequencing, metagenomics, and metatranscriptomics) to provide accurate representations of the community. The results from this experiment will dictate our future community analysis methods. We hope that this project will provide insight in whether or not old growth forests are functionally different from managed systems as that this understanding may shape future forest ecosystem analysis and the resulting management practices.

***if this is the goal that means i need to add a little emphasis on the deterioration of the old growth forests and problems with losing these systems (objectively)*** + could add this to the next paragraph regarding fungi and old growth forest deterioration.

…

#Second Paragraph: (needs to build off a main point from the intro and needs to have a strong lead sentence)

Is it imoprtant to discuss how fungi are involved in ecosystem function? Even just a brief paragraph to support why we are looking at fungi as opposed to another group of microbes? could add in carbon maybe

#Third Paragraph:

***intro sentence*** :Understanding how shifts in microbial community impact ecosystem functionality with forest succession, and how the resulting soil characteristics respond, can greatly improve our ability to infer how ecosystems are influenced by environmental change (and how we can mitigate?). The findings of Delgado-Baquerizo et al. (2016) suggest ecosystem functionality is dependent on specific microbial diversity and that a shift in said diversity is likely to change the functionality and resulting ecosystem previsions/services. It is apparent that as forest systems transition into later successional stages, we see a major change in microbial ecosystem diversity (Yan (2020) and Zhou (2017)). These, among other studies (Sun (2021) and Zhou, Wang, and Luo (2017)), show that as forests age we see a shift from an r-dominated to a K-dominated microbial community. This is important as it not only shows that as forests age we shift into a fungal dominated soil ecosystem, but it also suggests that fungi are associated with forest ecosystem “stability” (see r/k-strategists for details). Furthermore, it has been shown (Jiang (2021)) that the relative abundance of certain fungal communities significantly increase with succession (more citations?). Conversely, it has been shown that bacterial groups decline or remain relatively unchanged along successional gradients (citations?). This suggests that fungi may become more involved in nutrient cycling as forest ages increase, or that bacteria are able to maintain functionality in different soil and environmental conditions. Understanding which organisms are present in soil systems is extremely important and there is a substantial amount of research present in the literature eluding to how microbial community composition changes among kingdoms (bacteria, fungi, etc) as forest age. Digging deeper, a majority of fungal community analysis revolves around genomic sequencing in search of the presence or absence within specific hierarchical classifications (i.e. phylum, class, genus, etc). However, this leaves us with massive oversight as to how these changes in community impact the corresponding ecosystem functionality.

could transition into genomics paragraph….

#Fourth Paragraph: (need more literature review)

***intro sentence*** : Understanding how functionality and microbial community change over time is crucial however, natural undisturbed succession is becoming increasingly rare by the day. Ecosystem disturbance is happening more frequently via both natural (extreame weather) and anthropogenic (logging/management) means….info on how disturbance influences microbial community…….. It is also important to understand that the type of disturbance may impact how the microbial community changes. Needs work, maybe add stuff how we need to maintain old growth systems and stuff…

#Fith Paragraph:

***intro sentence*** ….. maybe talk about parameters that have been shown to change as successional stages increase???

#Last Paragraph before conclusion:

***intro sentence*** The last paragraph could touch on the lack of clarity in old growth analysis and how current decisions, controversies, etc do not even consider that forest functionality may change with age/lack of disturbance.

Jiang (2021): Bacterial and *Fungal* community composition and functional changes with forest succession:

# - The results showed that forest succession significantly changed the community composition of bacteria and fungi, among which the fungal community was more sensitive to the changes with successional stage.

# - \*\*\* In this study, the soil total carbon and total nitrogen were the dominating factors affecting the soil microbial community and the structure of fungal functional groups..

Yan (2020): Fungi and beacteria functional genes ~ chronosequence - Soil microbial biomass (C, N and P) increased significantly in topsoil (0-20 cm) with vegitation succession. - Fungal abundances annd the Fungal:Bacterial was detected along a successional gradient (???)

- C and N cycle-related (potential) functional genes increased significantly and then stabbilized (\*)  
 - recalcitrant C degredation, N reduction, and denitrification-related genes increased and labile versions decreased  
 - \_\_fungal communitie were most correlated with ammonium N contents and root biomass\_\_

It is our belief that a significant portion of controversy/uncertainty in old growth forests (see Luyssaert (2021) for example) can be contributed to the lack of understanding in below-ground processes (CITATION?).

Above-ground forest processes have been studied for over a century (CITATION) and with this knowledge many regulations have been set in place. It has been noted (CITATION ~ somewhere in ogf book?) that many of these regulations have been set in place based almost soley on above-ground processes. Additionally, if in fact below-ground processes are considered, we are using “blanket understandings” of these systems as if they are all the same.

While controversy is ever present and results are variable potential trends may be emerging with the increased study of old forest chronosequences (CITATIONS?) stretching into the ***standardized old growth forest ranges***. A number of soil characteristics are appearing correlated with forest successional stage.

# Expiremental Design:

\_\_\*\*We are going to be analyzing soil fungal communities (meta - genomics,transcriptomics) of forest successional stages\*\_\_:

What parameters would also be interesting to know wth forest age (successional stage)? -**Q**: how are we defining forest “age” or successional stage. What range of area does this account for? What area do we sample over? How many areas will we measure to consider that forest covered? this leads back into how are we classifying forest stage (stand age only? how was stand age measured (check ogf book on that one)) -**Q**: are we accounting for type of disturbance? Because im pretty sure I have seen that type of disturbance may result in different forest response (Natural vs. athropogenic)

Parameters: - climate: temp, humidity, etc. - topsoil (%, depth, ratio, whatever) - lat,long, and elevation (analysis within systems?) - soil moisture - Field pH? - - % fungal biomass - % rna expression

Samples: how are we sampling? Is it possible to gps every sample? In theory gps samples could allow us to account for auto correlation between sample and are we breaking sampling methods down likey Tony or different? We need to make sure that we we are doing can remain constant across forests/sampling locations. - I feel like I tossed a grid idea around… what if you took

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