# Reviewer comments and author responses

I would like to thank the 2 anonymous reviewers for their very helpful advice. Particularly, I would like to thank them for the constructive way they framed their comments. This paper was led by an undergraduate research team and it was nice to not have to censor anything from them :)

## Reviewer 1:

The reviewed manuscript is focused in the recovery of soil fungal community in a long term under coniferous temperate forest in -Utah over a 20 year Chrono sequence.

In my opinion, the authors addressed an interesting topic. There is general knowledge in this field but I think that under the current scenario of climate change, the insight provided for this specific site could be interesting. The authors did a deep work to select adequate sites to be used in the study. With a total of 22 sites were they sampled unburned and burned plots which had burned between 1 and 20 years prior to the study. Despite there are some minor points that should be addressed, in my opinion, the results should be thoroughly revised and focused in different way to optimize the fieldwork carried out. Finally, the discussion section is clearly deficient.

Thank you for your helpful and productive comments. We have made our best effort to take your advice in order to improve our manuscript, especially in fully revising our discussion section. In-line responses to your specific comments are below in blue text.

Some specific comments:

It is not clear if the authors included every year prior to the study or some years included in that interval. This is bit confusing. (i.e. in the Figs 1 and 4 we can see 6 different times prior to the study (4, 7, 12, 13, 16 and 19 years). The sites are dominated by Pinus edulis, which is well adapted to very dry conditions. Maybe this could explain part of the results and a specific comment about it could be included in the conclusion to avoid extrapolate so specific results to other ecologically different forests. The hypothesis is concise and can be test with the experimental design proposed by the authors. The methodology is generally well described and gives the reader a good approach about the whole work.

Yes, the years shown in figs 1 and 2 are the only prior burn time points that we could find that were similar enough in plant community and other factors. We decided that reducing noise, especially in plant community structure, was more important for our hypothesis than examining other burn years along our chronosequence. We have added a note in the manuscript to address this :

“Effort was made to reduce site variability, especially in plant community structure, and this took precedence over chronosequence sampling density.”

In the Fig4-B is not very clear why some sites within the same year are associated to different annual mean temperature. It is supposed after the description that the burned and unburned plots are nearby and ecological conditions should be similar? Sorry if I misunderstood something here.

This is probably because there was some replication in “time since burn” between different sites. We did not have full factorial replication for these variables though. So, while paired burned/unburned plots did have the same (or very close) ecological conditions, there are a few instances where different ecological conditions (i.e., mean annual temp) are represented by more than one burn year.

The strong reduction of Basidiomycota in burn plots after 14, 17 and 20 years is really interesting. A reader could deduce that after a fire, Ascomycota and Basidiomycota are the predominant Phyla, and that after some years Basidiomycota are reduced. However if we observe the presence of Basidiomycota in the non-burn plots, we can think that maybe this could be due to a site effect since Basidiomycota also dominates in some of the non-burn sites. Also, it is known from many other previous studies that Basidiomycota are predominant in most studied ecosystems. Indeed, in those ecosystems not affected by fire…Maybe specific discussion could be added here.

This is a great observation. In contrast to some work that has been done from other biomes, the longer-term reduction in Basidomycota is unexpected.

We have added this to the discussion section as follows: “ The broad diversity patterns we observed generally reflect those seen in related research. For example, our forest soils were dominated by Ascomycota and Basidiomycota phyla, but this dominance was reduced over time since burn as other phyla such as Mucormycota, Rozellomycota, and Olpidiomycota became detectably more abundant roughly 14 years after fire. However, where other work in Boreal forests found that Basidiomycota was initially reduced after fire and recovered over time (Sun et al., 2015), our results from this montane biome show Ascomycota following that pattern instead. “

The result showed in the figure 3 is not clear to me. If you want to know if 20 years after fire the community diversity was recovered. Maybe you could include here, those plots including this information. Alternatively, if you want to address the most recent effects of fire you could include these other plots. However, mix all of them in the same analysis is something not clear.

We have added a year-by-year analysis you suggest as a supplemental figure. We tried to find a way to fit it into the main manuscript, but it didn’t fit well with the main story in our opinion. It is a useful set of plots though, so thank you for the suggestion.

The figure 5 shows data for 24 sites. In M&M described 22. Bit confusing. Also in this figure. What are the bars showing? seems to be strange to find differences with so broad SD or SE or ?? for the non-burn plots in the first two graphics and for the Burn plots in the graphics 3 and 4. If the comparison is for each couple of plots. The results could be presented in a more clear way. If the differences are including all the plots in each burn and non-burn treatment, also the results could be showed in a different way. Finally if in the data the authors are including all the plots in different times, this can be confusing since the evolution of the taxa after the disturbance can be masked by this effect. I would suggest to perform an analysis per time period and then the reader could be this evolution. It is strange to find differences for only four taxa. In addition, a time detailed analysis could let us to find much more variation, short-term effect, middle-term effect and

evolution. With the ecological implication in terms of ecosystem recovery after fire,…Maybe ordination analysis (NMDS in this case after Hellinger transformation of the community matrix different times could be a good option.

See previous response. We have included the suggested yearly analysis figure as a supplement. We have also decided, as suggested by reviewer 2, to move this figure to the supplement as well as it is rather confusing and detracts from the main story of the manuscript.

In my opinion, the discussion is absolutely deficient. It is almost no developed, too general, not based in scientific literature… In my opinion the good work carried out previously deserves a deeper discussion, scientifically supported.

Thank you for this feedback. We feel you were correct to take issue with the depth of our discussion. We have thoroughly revamped and added to the discussion section to take the opportunity to fit our results into context with previous work and do some speculation about why this phenomenon was seen in this ecosystem. Please see the tracked changes below for our full edits as there are too many to list here.

## Reviewer #2:

This manuscript provides insight about how the post-fire trajectory of soil fungal communities can be affected by mean annual temperature. The methods and analytical approaches seem technically sound and conclusions are well-supported by the data. I have a conceptual concern with this study, some broad suggestions for the discussion, and several minor considerations.

I would like to see a stronger conceptual explanation of what the authors are considering when they discuss "recovery". It seems that the authors assume that the unburned soil fungal community is a static and desirable state that the post-burn community is moving toward. This may not be a reasonable assumption in 2 ways: (1) It seems the unburned communities are as variable across sites as they are between burned and unburned treatments (Fig. 2). Perhaps there is so much variability in unburned communities that we can't expect burned communities to "recover" to the same community as the adjacent unburned site because of stochastic factors. (2) It is unclear how many of these fungi are tightly associated with plant communities. Even so, fungal communities (if not their distances) would be expected to relate to plant communities and the plant post-fire literature suggests that there is a successional trajectory and that sometimes different plant communities re-establish after

wildfire. For example, in some places, wildfire has resulted in long-term transition from forest to grassland or shrubland habitats. If that kind of change occurs we may expect that a "recovered" fungal community could look very different from that in the unburned pinyon-juniper forest - a "recovered" fungal community 100 years after the fire could mean a rich and functional group of soil fungi associated with grass or shrublands. There is also a circularity in the sense that soil fungal communities can impact the establishment of vascular plants (perhaps favoring grasses or non-native plants), and that the kinds of vascular plants may affect the kinds of fungi that can live in the soils (i.e. plant-soil feedback loops).

Thank you for this important note, and apologies for not being clear about this in the original manuscript. For the purposes of this project, we define “recovery” as resemblance to an adjacent unburned plot. It is assumed that no fungal community can be fully “recovered” given that communities are always changing. Unburned fungal communities are also under constant flux, but as burned communities begin to more closely resemble adjoining unburned sites, we treat that as “recovery” in the sense that fire effects are beginning to give way to other site-level forces such as edaphic properties and plant community influences.

We have added text to this effect in the introduction, paragraph 1.

Methods:

I am surprised to see a pinyon-juniper woodland/forest at 5500 ft described as "alpine". I might consider this montane, but I think of alpine habitats in Utah as generally being over about 8000-9000 ft and with mixed forest and meadow communities. I suggest reconsidering the use of the word alpine here.

Done.

Pinyon Pine and Juniper should both include their scientific names.

Done.

Results:

Fig 1 is helpful, but the scale for number of years since burn could be clearer by using a different color gradient that more clearly distinguishes older and newer fires.

We have updated fig 1 to a much more divergent color scale. Thank you for the feedback.

Fig. 4 and lines 15-30: As there was an interaction in the previous results, I'm curious about whether it was tested for here. It appears that one of the 13-year-old burn sites had particularly consistent fungal communities; it stands out from the other sites here and it might be helpful to include a consideration of how this site may be interesting or different in the discussion.

We think this might be a trick of replication that you are seeing. Since there were more than 1 13-year burn sites, and each had different temperatures, the interaction between time-since-burn and mean annual temperature was definitely tested. However, you are correct that one of those 13-year sites does stand out as having very consistent communities. We have redone analyses with this site removed to see if it was driving the patterns observed and have added a note in the discussion addressing this and the implications it might have on our results as follows:

“Additionally, one of the site pairs in this study, burned 13 years prior to observation, had highly similar fungal communities (Fig. 3). Removing this site did not affect the significance of mean annual temperature in our model, but did reduce the effect size. It seems clear that local stochastic processes in community assembly can reduce our ability to detect broader patterns.”

Lines 33-38: "When location-specific plant community data was added to linear mixed-effect models…" I suggest relating plant communities directly to fungal communities rather than to the distances between them. Alternatively, look at the distances between plant communities compared with distances between fungal communities. The way this analysis is set up doesn't optimize the ability to understand how fungal community change relates to those of vascular plants.

Thank you for this advice. We included a new mantel test to compare plant and fungal community distances as suggested and found no significance. We think that due to the strong similarity in plant community between each location, there was no real difference to detect. This might seem counter-intuitive, but we feel that this is a strength of our study; that plant community (known to be a strong covariate of fungal community) can be effectively ruled out as a covariate in our results. The following text was added:

“Additionally, a Mantel test between plant and fungal community distances showed no significant correlation. These results likely stem from the high similarity in plant communities at each location.”

Fig 5: This figure is difficult to interpret. Are the letters and numbers along the bottom names of sites? Consider simplifying the display by aggregating across sites, explaining further in the text, or relegating it to the appendix.

Moved to supplemental material. The site-level changes in specific fungal taxa are probably distracting to the main message of the paper.

Discussion:

The discussion is honest about the potential limitations of the study but comes short in terms of interpreting the main findings and relating them to the literature. I'm left with several questions that I wish the authors would speculate about or tie to other studies. In particular: Why might mean annual temperature affect fungal communities returning to unburned communities? What variables have been found to affect soil fungal communities in other studies? Is the diversity and composition found here comparable to those found in other studies? What kind of practical impacts do you think this finding may have in terms of plant communities or ecological functioning at these sites?

This is a very fair criticism. We have added additional text and citations to our discussion directly addressing the particular questions you mentioned, as well as some others. See tracked changes below for details.

# Tracked Changes

Long-term soil fungal community recovery after fire is impacted by climate change

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**Abstract**

Though much is known about fungal importance to forest health, there is very little information about factors that impact soil fungal community recovery time after a fire. Soil samples were taken from burn sites within one ecotype of temperate coniferous forest in Utah over a 20-year chronosequence. Sites were selected from available historic burns and were similar in plant community structure, elevation, slope, and aspect. Fungal DNA from these samples was compared to soil from paired unburned sites nearby to measure community similarity and estimate soil fungal recovery rates. Differences between paired burned and unburned sites remained fairly stable over a decadal time scale overall, but fungal community structure was found to recover more quickly in areas with a higher average annual temperatures. A significant positive correlation in community recovery was seen in areas with a difference of as little as two degrees Celsius per year. The only other environmental variable that significantly interacted with time since burn was annual mean precipitation. As global temperatures increase, alpine fires are increasing as well, but these results suggest that fungal community recovery time will be shortened under new climate scenarios.

**Introduction**

The effect of fires on belowground microbial communities has received increased attention in the past decade due to the importance of microbes to overall ecosystem recovery. Soil microbes interact with plants during disturbance recovery to shape resource availability, community assembly and successional trajectories (Knelman et al., 2015; Sikes et al., 2016; Weidner et al., 2015). Ecosystem recovery from fire disturbance is thus dependent on microbes that facilitate plant succession either directly via obligate symbioses (Dickie et al., 2017) or indirectly via processes such as resource liberation and soil stabilization (Bonner et al., 2019; Claridge et al., 2009; Fuentes-Ramirez et al., 2018). For the purposes of this project, we define “recovery” as resemblance to a nearby unburned plot. It is assumed that no fungal community can be fully “recovered” given that communities are always changing. Unburned fungal communities are also under constant flux, but as burned communities begin to more closely resemble adjoining unburned sites, we treat that as “recovery” in the sense that fire effects are beginning to give way to other site-level forces such as edaphic properties and plant community influences.

Currently, the reported effects of fire on belowground microbial communities have few consistencies other than a general agreement that full recovery to pre-fire conditions takes place on a decadal time scale (Holden et al., 2013; Köster et al., 2014; Treseder et al., 2004). Reported differences between studies include varied recovery times for bacteria and fungi (Bárcenas-Moreno et al., 2011; Bárcenas-Moreno & Bååth, 2009) and divergent effects of fire on microbial diversity and abundance in differing biomes (Allison et al., 2010; Dove & Hart, 2017; Hansen et al., 2019). The majority of studies have focused on time since fire as the main effect in their particular ecosystems, and the contrasting details about microbial recovery could be specific to the climatic and edaphic properties of the biomes in which they were observed.

Warmer and drier conditions in many ecosystems due to climate change are increasing the frequency and impact, and decreasing the predictability of, wild fires (Abatzoglou & Williams, 2016; Flannigan et al., 2009). Thus, it is important to continue building knowledge of how soil microbes respond to fires. Furthermore, it is important to understand not only how future climate scenarios alter fire regimes, but whether they will alter the recovery responses of microbial communities in those systems.

Here, we conducted an observational experiment along a 20-year fire chronosequence, comparing paired burned and unburned sites along an annual mean temperature gradient in a montane ecosystem dominated by pinyon pine (*Pinus edulis*) and juniper (Juniperus osteosperma*)* forests in Utah, USA. This ecosystem is expected to continue warming at a faster rate than most other biomes with a 20-year projected climate that includes an annual mean temperature of 2 deg C above baseline according to the IPCC AR5 regional synthesis report (Barros et al., 2014). The study design allowed us to test the hypothesis that a warmer climate could alter belowground microbial recovery rates after fires within a single biome.

**Methods**:

*Overview*

A range of historic fire events was used to select 11 forested regions of Utah that had burned between 1 and 20 years prior to our study. Each burned site was paired with an adjacent unburned site to serve as controls, giving us a total of 22 sites. Sites were selected to maximize similarity across a range of environmental variables. At each site, we collected burned and unburned soil from the organic horizon of 3 locations, measured canopy and ground cover vegetation, and collected vegetation samples for identification and herbarium curation. We used meta-amplicon sequencing to characterize fungal community structure from each soil sample.

*Site Selection*

The Utah Department of Natural Resources sourced Utah fire data for the previous 20 years. 300 GPS points 100 m inside of burn boundaries were used to compile national GIS layers including topography, land use and cover, human impacts, and climate data. Habitats were dominated by Pinyon Pine and Juniper, with common understory plant communities dominated by Asteraceae and Poaceae. Sites were spread across Utah from 38.5 to 41.6 deg latitude and ranged in elevation between 1483m and 2969m, with a median elevation of 1660m (Fig. 1). The annual mean temperature at sites ranged from -7.9C to -3.4C with a median of -5.0C. Soil types were predominantly a mixture Nielsen, Sterling, and Steed series.

Using these and other site characteristics (see S.I. Table 1), we built a pairwise distance matrix for every possible combination of variables, and selected a subset of the 300 sites that had minimal land variation, but still maintained substantial ranges in burn chronology and annual mean temperature (see S.I. Fig. 1). Effort was made to reduce site variability, especially in plant community structure, and this took precedence over chronosequence sampling density. All raw site data and full code for selecting study sites can be found in the Supporting Information.

*Field Collection*

Photography, site marking, and sample collection protocols were designed before field work began. Three soil samples were collected with sterile utensils from each site at a depth of 5 to 10 cm 0.5m from the site center in the North, East, and West cardinal directions. Soils were frozen at -80° within 6 hours of collection. Local plant cover was recorded and photographed and representative plant samples were collected for later identification. International Field Collection Forms were filed for each plant collection and all specimens are housed in the Utah Valley University Herbarium (UVSC).

*DNA Extraction and Library Preparation*

Genomic DNA from 0.25g of soil was extracted from each sample using DNeasy PowerSoil Kits (QIAGEN, Venlo, The Netherlands). Fungal DNA was amplified with the ITS1F (CTTGGTCATTTAGAGGAAGTAA; Gardes & Bruns 1993) and ITS2 (GCTGCGTTCTTCATCGATGC; White et al., 1990) primers, modified with the addition of Illumina adaptors (Caporaso et al., 2011) using the following protocol: 98 2 min; 22 cycles of: 98 15 s, 52 30 s, 72 30 s; 72 2 min). After 22 cycles, the PCR product was diluted 1:12 and 1 μL of this was used as a template for 8 more rounds of PCR with a 60 deg annealing temperature in which bi-directional barcodes bound to reverse complemented Illumina adaptors acted as primers. Resulting barcoded libraries were cleaned, normalized, and sequenced with the Illumina MiSeq platform (V3 chemistry, 2 × 300 bp).

*Bioinformatics*

Reads were demultiplexed and barcode sequences were removed by the sequencing center. Quality filtration and bioinformatics were performed in R. Briefly, we extracted the ITS1 region, filtered forward reads based on quality, utilized a clustering-free Divisive Amplicon Denoising Algorithm (DADA) to infer Amplicon Sequence Variants (ASVs) (Callahan et al., 2016), removed chimeras and potential contaminants and assigned taxonomy against a custom ITS1 database.

The ITS1 region of the rDNA was extracted from all raw reads using ITSxpress (Rivers et al., 2018). Quality control on ITSxpress output consisted of removing reads with ambiguous base calls and those with a maxEE of >2, and truncating each read when quality scores dropped below 20. Due to lower quality, and to reduce false-positive detection, reverse reads were not used (Pauvert et al., 2019). Filtered forward reads were subjected to de novo chimera detection and removal in DADA2 and potential contaminants were inferred from extraction negatives and removed from all samples using the prevalence method in the decontam package (Davis et al., 2018). Cleaned and filtered ASVs were assigned taxonomy with the RDP Classifier algorithm against a custom database consisting of the UNITE database (v. 1.12.2017) and a custom set of outgroups including ITS1 sequences from metazoans and viridiplantae taken from NCBI. The outgroups added to UNITE can be found in the Supporting Material. Any sequences matching non-fungal taxa were removed. The remaining ASVs that were unambiguously assigned to fungi were used in all downstream analyses within the phyloseq R package (McMurdie & Holmes, 2013). All sequences have been deposited in the NCBI Sequence Read Archive under the accession PRJNA550446.

*Statistical Analyses*

   All analyses were performed in R (Version 3.4.4). A PermANOVA model of community composition as an interactive function of Burn Year, Fire Treatment, and Location was fit using the adonis function of the vegan package (Okansen et al., 2016). A community distance matrix was generated with the vegdist function of the vegan package. The community distance between paired burned and unburned sites at the same location was regressed against time since burn and decadal annual mean temperature in a linear mixed-effect model using the lme4 package (Bates et al., 2015) with paired community distance as a response and annual mean temperature and years since burn as predictors. P-values were obtained using the lmerTest package (Kuznetsova et al., 2017). Differential abundance of taxa between burn treatments was analyzed using a beta-binomial model with the corncob R package (Martin et al., 2020).

**Results**

No fungal community of any burned site we observed had fully rebounded to the alpha diversity or community structure of its unburned counterpart within the 20 year timeframe that was studied. All samples were dominated by Ascomycota and Basidiomycota, regardless of whether they were burned or not, but the relative dominance of these two main phyla decreased in older sites. In burned sites 14 years or older, Ascomycota and Basidiomycota still dominated in terms of relative abundance, but other phyla such as Mucormycota and Olpidiomycota were also more common (Fig. 2). Relative abundance of taxonomic groups did not correlate significantly with annual mean temperature, elevation, latitude, or soil type.

Alpha diversity was not significantly different overall between aggregated burned and unburned sites (Fig. 3), and there was no consistent pattern between burn status and Shannon diversity in between-site pairs.Beta diversity was significantly affected by burn status (P = 0.035), time since burn (P=0.001), and annual mean temperature (P=0.001) in an interactive PermANOVA model (S.I. Table 2). Further, there was a significant interaction term between time since burn and annual mean temperature (P=0.002).

Mean community distance between paired burned and unburned sites showed a small but significant decrease over time since burn, congruent with previous research showing the decadal scale of recovery for fungi after fires. However, in this study, we also found that annual mean temperature was an important predictor of the rate of recovery (Fig. 4; LMER; P < 0.0005), and each temperature increase of 1 deg C accounted for an additional 5% community similarity along our full chrono-series (S.I. Table 3).

When location-specific plant community data was added to linear mixed-effect models, no significant correlation between plant cover or plant community and paired fungal community distance was found. Additionally, a Mantel test between plant and fungal community distances showed no significant correlation. These results likely stem from the high similarity in plant communities at each location.

Differential abundance analyses yielded 4 fungal families that were significantly enriched in either burned or unburned locations across all sites (S.I. Fig. 2). The basidiomycetes Serendipitaceae and Thelophoraceae had greater abundance and variability in unburned sites, and the ascomycetes Microascaceae and an unclassified family-level taxon in Dothidiales had greater abundance and variability in burned sites.

The broad diversity patterns we observed generally reflect those seen in related research. For example, our forest soils were dominated by Ascomycota and Basidiomycota phyla, but this dominance was reduced over time since burn as other phyla such as Mucormycota, Rozellomycota, and Olpidiomycota became detectably more abundant roughly 14 years after fire. However, where other work in Boreal forests found that Basidiomycota was initially reduced after fire and recovered over time (Sun et al., 2015), our results from this montane biome show Ascomycota following that pattern instead.

**Discussion**

Though most studies on fungal recovery after fires have taken place in a single biome and focused on chronology as the main predictor, Dove and Hart (2017) showed via meta-analysis that the magnitude of at least the initial fungal community responses to fire can vary based on fire frequency and biome type. These are important observations because they suggest hypotheses to help explain observed discrepancies in fungal recovery trajectories between studies.

Here, we tested whether large-scale climatic factors could also help explain variance within a single biome. Comparing nearby pairs of burned and unburned sites along a forest fire chronosequence showed that climatic conditions can have a role in soil fungal community recovery trajectories. In particular, our observation that annual mean temperature of a site has a small but significant effect on recovery speed is a possible example of how local environmental variation can help explain discrepancies in fungal recovery times after fires.

Temperature directly affects microbial activity, but can also influence microbial community composition, competition, and secondary metabolite production (Bárcenas-Moreno & Bååth, 2009; Yogabaanu et al., 2017). Warming temperatures also affect plant succession trajectories (Prach et al., 2007) and plant succession is an important covariate for understanding fungal succession (Davey et al., 2015; Rudgers et al., 2007; Zhang et al., 2018). Taken together, the linkages between plant and fungal succession dynamics and temperature are difficult to uncouple. By limiting our study to a single biome and to sites with very similar plant communities, we were able to isolate, to some degree, the effect of temperature on fungal recovery from fire. Other factors besides plant community have been directly linked to fungal community dynamics, however. For instance, it has been shown that soil pH and nutrient content are strong drivers of fungal community structure (Glassman et al., 2017). Since fire can have a strong impact on soil properties such as pH, C:N ratio, and SOC content (Boerner et al., 2009), it is possible that these edaphic characters varied between burned and unburned paired sites, though these variables were not measured in this study. Additionally, one of the site pairs in this study, burned 13 years prior to observation, had highly similar fungal communities (Fig. 3). Removing this site did not affect the significance of mean annual temperature in our model, but did reduce the effect size. It seems clear that local stochastic processes in community assembly can reduce our ability to detect broader patterns.

In this montane biome, with mean annual temperatures below freezing, liquid water can be a limiting resource for plant and fungal growth (Monson et al., 2002, 2006). An increase in mean annual temperature at these sites likely means more days when fungi can be metabolically active. Our results support this assumption, in that warmer temperatures led to quicker recovery times.

Due to ongoing recent climate change, any chronosequence studies must inevitably deal with the potential covariance of time since burn and mean annual temperature. There was some correlation between these two variables in the present study, with older sites tending toward lower mean annual temperatures, which could be an effect of climate change (S.I. Fig. 2). We were unable, however, to acquire site-specific environmental variables from 20 years prior, to test this due to lower resolution of these observations from that time period.

Additionally, climate warming is inextricably linked to other variables that have been shown to affect fire severity and fire frequency such as reduced soil moisture and increased fuel load (Harvey, 2016). These factors could also be important drivers of fungal recovery trajectories. These legacy factors were not considered in the present study since none of our selected sites had burned in the previous 75 years and were from very similar biomes, but they may be important to consider in work of this nature.

Our results indicate that even within a single biome, slight alterations to climatic variables like mean annual temperature can affect the rate of fungal recovery from fires. This has implications for broader disturbance modeling efforts. For example, the reduction and rebounding of soil fungal communities is important for dynamic vegetation models, but many disturbance models use predictors that are simulated in isolation, neglecting any potential interaction effects (Seidl et al., 2017). As climate warms and fires in these biomes increase in intensity and frequency, the loss of fungal diversity and ecosystem services could be, to some small degree, mitigated by increased recovery rates due to warming in these often frozen montane soils.

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