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Title: Continental-scale nitrogen pollution is shifting forest mycorrhizal associations and soil carbon stocks

Running head: Nitrogen pollution and forest mycorrhizas

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9 **Abstract:** Most tree roots on Earth form a symbiosis with either ecto- or arbuscular mycorrhizal 10 fungi. Nitrogen fertilization is hypothesized to favor arbuscular mycorrhizal tree species at the 11 expense of ectomycorrhizal species due to differences in fungal nitrogen acquisition strategies, 12 and this may alter soil carbon balance, as differences in forest mycorrhizal associations are 13 linked to differences in soil carbon pools. Combining nitrogen deposition data with continental-14 scale U.S. forest data, we show that nitrogen pollution is spatially associated with a decline in ectomycorrhizal vs. arbuscular mycorrhizal trees. Furthermore, nitrogen deposition has 15 16 contrasting effects on arbuscular vs. ectomycorrhizal demographic processes, favoring 17 arbuscular mycorrhizal trees at the expense of ectomycorrhizal trees, and is spatially correlated

18 with reduced soil carbon stocks. This implies future changes in nitrogen deposition may alter the

capacity of forests to sequester carbon and offset climate change via interactions with the forestmicrobiome.

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21 Introduction: Forests represent 31% of global land surface area (Food and Agriculture 22 Organization, 2010) and currently offset ~2.4 Pg of CO₂ emissions every year by storing carbon (C) in live plant biomass and soil (Pan et al., 2011). A central component of this C storage 23 24 capacity may be the presence of different members of the forest microbiome. Two dominant 25 classes of mycorrhizal fungi, the arbuscular mycorrhizal fungi and ectomycorrhizal fungi (AM 26 and EM, respectively), form a symbiosis with the roots of most trees on Earth, enhancing access 27 to soil nutrients and water (Smith & Read, 2009; van der Heijden et al., 2015). AM fungi 28 primarily rely on inorganic forms of N (Hodge & Fitter, 2010; Phillips et al., 2013) and small 29 organic N compounds (Whiteside et al., 2012). In contrast, EM fungi are thought to rely more 30 heavily on organic N sources (Phillips et al., 2013), having a greater capacity to invest in N

31 degrading extracellular enzymes that access complex organic forms of N in soil, such as proteins 32 and chitin (Fernandez & Kennedy, 2016). EM fungi are associated with both slower 33 decomposition of soil organic matter by free-living microbial populations and increased soil C 34 storage (Gadgil & Gadgil, 1971; Averill et al., 2014; Averill & Hawkes, 2016; Fernandez & 35 Kennedy, 2016; Kyaschenko et al., 2017), potentially by competing with free-living soil 36 microbes for these organic N resources or differences in plant or fungal organic matter chemistry 37 (Averill & Hawkes, 2016; Fernandez & Kennedy, 2016). These distinctions between AM and 38 EM fungi lead to two important predictions: 1- that inorganic N inputs to ecosystems will favor 39 AM associated trees at the expense of EM associated trees, and 2- that inorganic N driven 40 declines in EM composition of forests will reduce the belowground C storage capacity of the 41 forest biome.

42 Continental scale inorganic N deposition provides an opportunity to test predictions of 43 how N, plant-microbial systems, and soil C interact at large spatial scales. N deposition in the 44 U.S. has increased 5-10 times over preindustrial levels, predominately due to fossil fuel burning 45 (Aber et al., 2003). Variability in N emission source locations, topography, wind and rainfall 46 patterns produce a heterogeneous geographic distribution of N deposition in the U.S., allowing N 47 deposition patterns to be leveraged as an unintentional inorganic N addition experiment. 48 Previous species-level analyses suggest that both AM and EM tree growth rates can respond 49 positively to N deposition (Thomas *et al.*, 2010); however, it is unclear whether or not these 50 species-level responses translate to changes in the relative balance of EM vs. AM associated 51 trees at the community-level, which regulates landscape-level soil biogeochemical cycling.

52 To determine if N deposition is changing the total composition of these symbiont types at 53 a scale that could impact the C storage capacity of the biosphere, we analyzed the relative 54 abundance of AM and EM trees in 2,760 U.S. forest plots, comprised of 65,769 trees, coupled 55 with direct site-level observations of soil C stocks collected from the U.S. Forest Service's Forest 56 Inventory and Analysis database (Forest Inventory and Analysis, 2014, Fig. 1). We analyzed 57 how anthropogenic N deposition is spatially correlated with the relative abundance of AM and 58 EM trees, as well as current forest growth, tree recruitment, mortality rates, and total soil C 59 stocks, using a Bayesian statistical framework. Doing so enabled us to ask if N-fertilization via 60 anthropogenic N deposition favors AM at the expense of EM associated trees and if these 61 changes in forest mycorrhizal composition may translate to differences in soil C balance.

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63 Materials and Methods:

64 General Analysis Approach: This analysis aimed to isolate the effect of N deposition on soil C 65 storage, the relative abundance of EM vs. AM trees, and EM vs. AM basal area growth, recruitment and mortality rates across the continental U.S., while controlling for the potential 66 effects of mean annual temperature, mean annual precipitation, soil pH, soil C:N or total N 67 68 stock, and soil clay content. This is done using a Bayesian multiple regression framework, 69 where the relationship between all environmental predictors and individual EM or AM tree dynamics are estimated simultaneously. In Bayesian analysis, a probability distribution is 70 71 estimated for each dependent variable (i.e. EM or AM relative abundance data, growth rates, 72 recruitment counts, mortality occurrences and soil C stocks) as it is regressed against the 73 independent variables in the multiple regression model (Dietze, 2017). A relationship between 74 a dependent and independent variable can be considered significant if the 95% credible interval 75 of the corresponding parameter estimate does not overlap zero. We implemented these models 76 in a Bayesian statistical framework because it allowed us to account for variable re-census 77 intervals in forest inventory data without transforming data, and in basal area growth, 78 recruitment and mortality models it allowed us to flexibly fit non-linear relationships and more 79 complex probability distributions. Furthermore, Bayesian models allow us to propagate 80 uncertainty by sampling from the distribution of each parameter estimate in our model when 81 estimating the predicted effect of N deposition on a dependent variable of interest (Dietze, 82 2017). For example, when we estimate the effect of N deposition on the relative abundance of 83 EM trees in a forest holding all other predictors constant at their means, the 95% credible 84 interval of the mean effect at a given level of N deposition reflects not only the uncertainty in 85 the N deposition effect, but also the uncertainty in temperature, precipitation, pH, C:N, clay and intercept parameter estimates. 86

Only predictors with parameter estimates where 95% credible intervals did not overlap zero are discussed as having a significant effect in the main text. When reporting or visualizing the effect of a single predictor variable (say N deposition) on a dependent variable, we varied the predictor over its entire range in the data set, holding all other predictors constant at their mean values. In this way, we evaluated the effect size of a predictor in isolation, while 92 accounting for the effects and uncertainties of all other predictors in the model. Complete93 description of data collection and analysis are detailed below.

94 Data Collection: This analysis used all plots within the U.S. forest inventory and analysis 95 (FIA) data set (Forest Inventory and Analysis, 2014) that have paired soil C observations. Soil 96 C profiles are aggregated down to 20 cm depth in the mineral soil (if soils are this deep), plus 97 any overlying organic horizon profiles. This approach causes the total soil profile depth to vary 98 across sites, because while most profiles contain 20cm of mineral soil, the depth of the forest 99 floor horizon will vary. Because our analysis is premised on the hypothesis that EM ecosystems may slow decomposition due to an ecological interaction, it may be that variation 100 101 in organic horizon thickness is an outcome of this process. In contrast, we do not expect 102 mycorrhizal associations to modify the depth of the mineral soil horizon. Therefore, we 103 standardized soil element aggregation to a fixed depth in the mineral soil plus any overlying 104 organic material. This generated soils data (soil C, N, soil pH), paired with forest composition 105 data for each site. A subset of sites had been re-measured in time, allowing calculation of forest 106 basal area growth, recruitment and mortality rates. These two data sets were used for five down 107 stream analyses. We refer to the complete data set as the "abundance data set" and the second 108 that includes temporal remeasurement of forest properties as the "remeasurement data set". We 109 only used FIA plots that are forested and have no recent evidence of active management or 110 human harvesting. We note that most forests in the United States have some history of human 111 disturbance, and our analysis cannot account for time since last time stand replacing 112 disturbance. Full details of data filtering, soil aggregation, and other site selection procedures 113 are presented in the Supporting Information 1.

114 Within each plot, each tree was assigned a mycorrhizal type based on the 115 supplementary data file in Phillips et al. (Phillips et al., 2013), which provides mycorrhizal 116 assignments for most tree species within the FIA database. This file was supplemented with 117 information on mycorrhizal status for western U.S. tree species (References provided in 118 Supporting Information 2). We calculated the relative abundance of EM trees as the basal area 119 of all live EM trees within a plot, divided by the total basal area of live trees within the plot. 120 We only analyzed sites where more than 90% of forest basal area consisted of AM or EM 121 mycorrhizal tree species (AM, EM, or a combination of the two types) at the time of soil 122 sampling (i.e. $(Basal_{AM} + Basal_{EM}) / Basal_{total} > 0.9$). Hence, a plot consisting of 50% EM and 123 50% AM trees by basal area would be retained in this analysis. We excluded plots with >10% 124 non-mycorrhizal, arbutoid, and eriocid mycorrhizal symbionts, as well as hosts that are known 125 to strongly associate with both AM and EM, but this only constituted 15% of the available 126 sites. The final abundance data set included 2,760 unique sites, encompassing 65,769 trees. 127 Past analyses along AM to EM gradients have demonstrated that the relative abundance of AM 128 vs. EM trees aboveground can be indicative of the abundance of these fungal community 129 members belowground (Nave *et al.*, 2013; Soudzilovskaia *et al.*, 2015; Cheeke *et al.*, 2016).

130 The second FIA database subset ("re-measurement dataset") represents the first re-131 measurement of all FIA forest plots after the initial soil sampling and was used for analyses of 132 basal area growth, recruitment and mortality. The majority of plots (1,912 of 2,760 plots) had 133 been re-measured since the time of the initial soil sampling. Initial visits were conducted 134 between 2000-2011. Re-measurement visits were conducted in 2004-2015. The average 135 duration of the re-measurement interval was 6.3 years. Because the soil properties used in this 136 analysis change slowly at this time scale, we are confident that the demographic patterns 137 observed in the re-measurement analysis are relatable to the initial soil conditions. We chose to 138 analyze the observation after the initial measurements, rather than the one prior, because many 139 of the soil sites included in the Phase 3 data are new to the FIA, and as a result, had no prior 140 observation of forest composition. Using the observations during and after the soil sampling 141 enabled more data to be included in the tree re-measurement analysis. The final data set used 142 for the analysis of tree mortality included 1,912 unique sites, encompassing 54,378 trees (Fig.

143

1).

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145 *Climate*, *N* deposition and soil clay data: Climate data for each plot were assigned using 146 PRISM 30-year 1981-2010 climate normal data products at 800-meter resolution for mean annual temperature (MAT) and mean annual precipitation (MAP) (PRISM Climate Group & 147 148 Oregon State University, 2017). Soil texture (% clay) data was extracted from the North 149 American Carbon Project Unified North American Soil Map at 0.25 degree resolution (Liu et 150 al., 2014). N deposition rates were determined using the National Atmospheric Deposition Program (NADP) 15-year mean wet and dry N deposition $(NH_4^+ + NO_3^-)$ from the 2000-2014 151 interval at 0.25° resolution (National Atmospheric Deposition Program, 2015). While 152 153 deposition data are for the most recent time interval available, comparison of wet N deposition 154 data from the 15-year 2000-2014 interval is strongly correlated with the 30-year 1985-2014 interval ($r^2 = 0.96$). Therefore, we are confident that 2000-2014 data are representative of 155 historical patterns of N deposition loads in the United States. It is important to note that the FIA 156 157 does not report_latitude and longitude data with exact precision; latitude and longitude 158 coordinates are limited in accuracy to ~800 meters. However, given the resolution of the data 159 products used here, and the fact that climate and N deposition variables are highly spatially 160 auto-correlated at the kilometer scale, the spatial accuracy of the climate and N deposition 161 products is on par with the spatial accuracy of the FIA site locations (Dietze & Moorcroft, 162 2011). In addition to not reporting exact spatial locations, the FIA randomly swaps 20% of 163 plots within a county. Because plots are swapped randomly, swapping should not bias our 164 parameter estimates, only increase uncertainty in our parameter estimates associated with 165 predictors derived from spatial products (MAT, MAP and N deposition). Furthermore, 166 variation in these predictors is much larger between counties than within, and therefore we can 167 still capture variation in forest and soil processes driven by these predictors, even if all sites 168 were randomly swapped within a county. Finally, the number and spatial scale of wet and dry 169 observation network sites is unlikely to capture small-scale point sources, which can generate 170 high levels of N deposition at very local scales. These effects will necessarily be missed by our 171 analysis. Despite this limitation, the >20x variation captured in the NADP N deposition data $(1.2-27.0 \text{ kg N ha}^{-1} \text{ yr}^{-1})$ may still inform the underlying drivers of variation in mycorrhizal 172 173 functional types.

174 Spurious relationships between N deposition and AM vs. EM relative abundance or 175 forest demographic processes are possible, if the geographic distribution of N deposition is 176 spatially confounded with other environmental factors known to influence forest dynamics. For 177 example, the highest levels of N deposition are found in the Midwest, where there is some 178 evidence of a shift from EM to AM species due to changes in fire regime (McEwan et al., 179 2011). To address this potential confounding among N deposition, forest mycorrhizal type, and 180 other environmental factors, we replicated our analyses, first excluding all states west of the 181 Mississippi River, and then excluding both Western states (comprised predominantly of EM 182 associated stands, and has, on average, the lowest levels of N deposition) and Midwestern 183 states.

184

Statistical Analysis

Modeling the relative abundance of EM trees: We modeled the relative abundance of EM trees at the plot level as a continuous beta distribution, which is designed to deal with proportional data on the interval (0,1), accounting for changes in variance as a function of the mean. Because our data set included many 0's and 1's, we transformed relative abundance values according to:

$$y = (y * (n - 1) + 0.5) / n$$

Where y is the relative abundance of EM basal area, bounded on the interval [0,1] and n is the sample size (Smithson & Verkuilen, 2006). This had the effect of transforming 0 and 1 values to 0.000210 and 0.99979. We also ran models with 0,1 transformation to 0.010,0.990 and 0.001,0.999. All models generated analogous results, with similar effect sizes. The parameters of the beta distribution, p_i and q_i were described as:

$$p_i = m_i * t$$
$$q_i = (1 - m_i) * t$$

We modeled m_i as the logit transform of the linear combination of MAT, MAP, soil C:N, soil pH, soil clay and N deposition. All parameters were assigned normally distributed, uninformative priors, save for *t*, which was assigned a gamma distributed, uninformative prior.

199 Modeling plot-scale basal area growth of surviving trees: Basal area growth was estimated at 200 the plot-level, on plots visited one measurement period after the initial soil measurement (i.e. 201 "re-measurement dataset"). Because this analysis is primarily concerned with which plant 202 mycorrhizal type is most abundant, we chose to analyze growth as basal area increment, rather 203 than C increment, as this better reflects which trees are largest and growing the fastest within a 204 plot. Basal area increment was modeled as a log-normal distribution, where the log of the 205 survival basal area increment was modeled as a linear function of previous basal area, climate, 206 soil and N deposition, and an interaction between N deposition and the relative abundance of 207 EM associated trees within a plot at the end of the measurement interval. Once models were fit, 208 visual inspection of the relationship between basal area growth and N deposition suggested an 209 intermediate 'hump' in the relationship between N deposition and stand basal area growth in the 210 full data set. To model this, we added a Gaussian relationship between N deposition and basal 211 area growth, in addition to the linear relationships, which took the form of:

$$g_1 * e^{\frac{(x-g_2)^2}{2g_3^2}}$$

Where g_1 , g_2 and g_3 are the parameters of the Gaussian distribution and x is N deposition. We placed a positive constraint on Gaussian parameter priors to aid in model convergence. Finally, models with Gaussian perturbations resulted in multiple alternative parameter combinations that were equally parsimonious, and therefore not all chains converged. To satisfy convergence criteria we subsetted model output to chains that converged on a similar area of parameter space, though we note there were several Gaussian parameter combinations that returned equivalent results.

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220 *Modeling tree-level mortality:* Mortality probability (M_i) was estimated based on the logistic 221 regression model for binary mortality data. Because the FIA census interval varies at the plot 222 level, we related annual mortality probability (p_i) of tree *i* to the observed binary mortality data 223 (M_i) using a Bernoulli likelihood (Dietze & Moorcroft, 2011),

$$M_i = Bern(1 - (1 - p_i)^{t_i})$$

224 Where t_i is the duration of the census interval for a given plot. p_i was modeled as the inverse 225 logit transform of z_i , where z_i is a linear combination of MAT, MAP, soil C:N, soil pH, soil 226 clay, mycorrhizal type, N deposition, and a linear interaction between N deposition and 227 mycorrhizal association. In calculating z_i , we accounted for the non-linear relationship between 228 tree diameter (D) and mortality probability by including two exponential terms. The first term 229 accounts for the initial decline in tree mortality probability as trees increase in size. The second 230 term accounts for the increasing mortality probability of large diameter, older trees. The 231 summation of these two relationships will generate the commonly observed "J" shaped 232 relationship between tree mortality probability and tree diameter (Dietze & Moorcroft, 2011). 233 The full expression of z_i was constructed as,

$$z_{i} = b_{1} * MAT + b_{2} * MAP + b_{3} * soil_{C:N} + b_{4} * soil_{pH} + b_{5} * soil_{clay} + b_{6}$$
$$* myc_type + b_{7} * N_{dep} + b_{8} * myc_type * N_{dep} + e^{-b_{9}*D} + e^{b_{10}*D}$$

Parameters $b_1 - b_8$ were assigned normally distributed, uninformative priors. Parameters b_9 and b₁₀ priors were assigned exponentially distributed priors, constrained to values greater than or equal to 0 to avoid fitting redundant model terms.

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238 Modeling plot level recruitment: Recruitment of trees was modeled using a zero-inflated 239 Poisson model, to account for the fact that the abundance of zeros in tree recruitment data is 240 often poorly fit by traditional Poisson models (Fortin & DeBlois, 2007). A multi-model 241 average was fit, modeling the occurrence of recruitment as a Bernoulli process, and then the 242 number of recruits as a Poisson process. The Poisson model was then weighted by the 243 probability of recruitment occurring estimated by the Bernoulli model in order to account for 244 zero inflation. Because the FIA census interval varies at the plot level, we related the annual 245 number of recruits (r_i) of plot *i* to the observed number of recruits over a given census interval 246 (R_i) using a Poisson likelihood,

$$R_i = Pois(r_i * t_i)$$

Where t_i is the duration of the census interval for a given plot. We fit separate models for AM and EM recruitment. MAT, MAP, soil C:N, soil pH, soil clay and N deposition were used as predictors for both Poisson and Bernoulli components of the model. Finally, the number of AM or EM recruits within a plot will strongly depend on the relative abundance of AM or EM trees already present within a plot (i.e. the apple does not fall far from the tree). To account for this, we included the relative abundance of AM or EM trees as covariates within models of AM or EM recruitment.

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255 *Modeling soil C storage:* Soil carbon was modeled as a linear function of MAT, MAP, soil pH, 256 soil clay, soil N stock, the relative abundance of EM tree basal area, and an interaction between 257 the relative abundance of EM tree basal area and soil N stocks. Models relating soil C and N at 258 large spatial scales generally violate the assumption of normality of residuals (Averill et al., 259 2014), as there are multiplicative errors associated with the measurement of soil C on an area 260 basis. Therefore, we modeled soil C with a lognormal distributed probability density, and log 261 transformed the soil N predictor. All parameters were assigned normally distributed, 262 uninformative priors. We considered accounting for residual spatial autocorrelation in this 263 model, yet initial semivariograms of soil C fit to an intercept only model exhibited little 264 residual spatial autocorrelation. Because of this, we proceeded to analyze all soil C 265 observations under the assumption they are spatially independent.

266

267 Bayesian model diagnostics and convergence: Forest basal area growth, mortality, recruitment 268 and soil C storage analyses were all analyzed in a Bayesian framework. Bayesian models were 269 fit using the runjags package for R statistical software (Denwood, in review; R Core Team, 270 2017). JAGS models were initialized with three chains, checked for convergence, and had 271 initial burn-in iterations removed before estimation of final parameter values. Parameter values 272 were estimated based on a minimum of 10,000 samples of 3 independent chains, after 2,000 273 adaptive iterations and 4,000 burn-in iterations. Parameter estimates were deemed converged 274 based on visual inspection of chain parameter estimates for the last 10,000 iterations, and 275 checking that Gelman diagnostic values for each parameter were below 1.1 (Gelman, 2014). 276 Additional samples were taken as necessary to achieve convergence.

277

Reporting of Results: We discuss results for predictors where the 95% credible interval did not overlap zero, which is our criteria for statistical significance, and refer to predictors that do not meet this condition as having no effect on the modeled dependent variable (Gelman, 2014). Recruitment mean and 95% confidence interval is reported as the mean number of recruits based on the fit of the Poisson model prior to discretization via the Poisson distribution, weighted by the probability of recruitment occurring based on the binomial model.

We plotted binned means of dependent variables in response to N deposition, controlling for the effects of other covariates in the model. To do this, we subtract the product of each parameter-covariate combination of each observation from the dependent variable, and add back in the mean value of the parameter-covariate combination from the data set. For example, if forest basal area growth was modeled by the function,

basal area growth_i = 0.5 * temperature_i + 0.1 * precipitation_i

To isolate the effect of precipitation on basal area growth and remove the effect of temperature, we would transform our observations of basal area growth to remove the variance associated with temperature using the following transformation:

basal area $growth_{T_i} = growth_i - 0.5 * temperature_i + 0.5 * temperature_{mean}$ Where basal area $growth_{T_i}$ is the transformed value of an individual basal area growth observation, controlling for the effect of temperature. Error bars represent the standard error of the mean within a bin, except for mortality bins where error bars represent 95% confidence intervals, calculated using the Pearson-Klopper method, implemented in the binom package forR statistical software (Sundar, 2014).

297

298 **Results:** Across the continental U.S., N deposition was associated with a greater abundance of 299 AM compared to EM dominated forests (Fig. 2a). Furthermore, we observed contrasting 300 relationships between AM vs. EM basal area growth and recruitment rates with increasing N 301 deposition. AM trees grew faster with increasing levels of atmospheric N deposition compared to 302 EM trees (Fig. 2c,d,e). In addition, N deposition increased AM tree recruitment rates, while EM 303 recruitment rates declined (Fig. 2f, 2g,h). N deposition also increased the probability of tree 304 mortality, however we detected no difference between the mortality rates of AM vs. EM 305 associated trees (Fig. 2b). These relationships were robust to subsetting the data set to exclude 306 the western U.S. or both the western and midwestern U.S. states (Supporting Information Fig. 1-307 2).

308 In an effort to quantify this potential influence of forest disturbance, we analyzed the 309 relationship between N deposition and stand age in the FIA data set. We found younger forest 310 sites tended to have higher levels of N deposition, yet this relationship was lost once western 311 U.S. states were excluded. To determine if correlation between forest age and N deposition may 312 be biasing our results we re-ran models of EM relative abundance including forest age as an 313 additional covariate. We found a negative relationship between forest age and EM relative 314 abundance, inconsistent with a positive correlation between N deposition and forest age driving 315 our findings. Furthermore, inclusion of the stand age covariate did not change the parameter 316 estimate of N deposition in our model of EM relative abundance.

Aboveground forest responses to N deposition were also associated with changes in the C content of U.S. forest soils. At low levels of N deposition, EM forests stored more C in soils than AM forests (Fig. 3a). However, N deposition interacted with mycorrhizal type; at the highest levels of N deposition C-storage decreased and the difference in C-storage between AM and EM forests disappeared (Fig. 3b). Subsetted analyses showed EM sites were still associated with elevated soil C content, though the interactive effect of mycorrhizal type and N deposition on soil C was lost (Fig. S3, S4).

We report full model output (parameter estimates, standard deviations, and significance values) in Supporting Information 1 Tables 1-6. We also provide beta factors (the change in dependent variable associated with 1 standard deviation variation in each independent variable)in Supporting Information 1 Tables 7-12.

328

329 **Discussion:** AM and EM fungi are the dominant groups of forest mycorrhizal fungal symbionts 330 worldwide (Read & Perez-Moreno, 2003; Phillips et al., 2013). These fungi have long been 331 thought to represent adaptations to differences in ecosystem N availability (Read, 1991), but 332 ecosystem-scale validation of this hypothesis has been challenging, as it takes decades to observe 333 changes in forest composition. Our analysis demonstrates that N deposition from anthropogenic 334 sources is spatially correlated with lower EM abundance and greater AM abundance in U.S. 335 forests, supporting this hypothesis (Figure 2a). Our analysis of demographic process rates also 336 shows higher levels of N deposition drive a suite of changes in basal area growth, recruitment 337 and mortality rates favoring AM trees at the expense of EM trees (Figure 2b-2h). This result 338 implies that N deposition is currently changing the balance of AM and EM associated trees in 339 U.S. forests. In addition, the interaction between mycorrhizal strategies, N deposition, and soil C 340 storage indicates that ongoing changes in forest composition – particularly of the soil 341 microbiome – with N inputs may have downstream consequences for belowground C 342 sequestration and global climate change, to the extent that a loss of EM forest community 343 members with increasing levels of N deposition translates to a loss of soil C from forest floor and 344 upper mineral soil layers.

345 Our analyses of forest composition and demographic process rates control for soil C:N 346 ratio and soil pH (key indicators of soil fertility), and we excluded sites with evidence of recent 347 human management. However, we cannot rule out the potential influence of correlations between 348 historical forest disturbance regimes and forest mycorrhizal composition, which may be 349 confounded with N deposition. In an effort to quantify this potential influence of forest 350 disturbance, we analyzed the relationship between N deposition and stand age in the FIA data 351 set. We did find that younger forest sites tended to have higher levels of N deposition, yet this 352 relationship was lost once western U.S. states were excluded. Furthermore, incorporating stand 353 age into our analysis showed a *negative* relationship between stand age and relative abundance of 354 EM trees- i.e. older stands had more AM trees, and did not change N deposition parameter 355 estimates. Based on these findings we believe it is unlikely that correlations between N 356 deposition and historical forest disturbance regimes are driving our results.

357 Our analysis supports the conclusion that N deposition is currently shaping the relative 358 abundance of AM and EM trees in U.S. forests and will continue to do so in the future. This is 359 because N deposition favors AM basal area growth and recruitment at the expense of EM basal 360 area growth and recruitment (Fig. 2c,h), but does not have a differential effect on mortality 361 through time. Furthermore, basal area growth and recruitment curves cross. This combination of 362 crossing temporal demographic responses to N deposition means that, given sufficient time, a 363 pressure of high N deposition rates will transition an EM forest to an AM forest, or the 364 suspension of high N deposition rates may revert an AM forest to an EM state.

We observed strong spatial relationships between N deposition, mycorrhizal type, and 365 366 soil C stocks after accounting for major environmental factors known to influence mycorrhizal 367 basal area growth in forests across space (climate, total N stock, and other soil properties), 368 suggesting that these patterns are foundational for predicting changes in soil C stocks with N 369 pollution. Our observations are also consistent with theoretical work showing that EM associated 370 trees can stabilize soil C by inducing N limitation of microbial decomposer communities (Read 371 & Perez-Moreno, 2003; Orwin et al., 2011; Phillips et al., 2013) and with experimental data 372 validating predictions from this theory (Averill & Hawkes, 2016). Elevated C storage in EM 373 ecosystems may also be driven by additional mechanisms, such as differences in input litter 374 chemistry between AM and EM trees or fungi (Cornelissen et al., 2001; Fernandez & Koide, 375 2012; Phillips et al., 2013). Regardless of the particular mechanism, our analysis suggests that 376 global change impacts on plant-microbial interactions in forest ecosystems may have large 377 consequences for C sequestration at continental scales.

378 The negative correlation we observed between N deposition and soil C stocks contrasts 379 other empirical work showing that N inputs broadly suppress the activity of microbial 380 decomposers in forest ecosystems (Janssens et al., 2010). One reason for this underlying 381 discrepancy may be fundamental differences in how N is added via N deposition compared to N 382 fertilization experiments. While both additions may result in the same annual rate of N input, N 383 fertilizer intended to simulate anthropogenic N deposition is frequently added as several doses at 384 far higher concentration than is experienced in continuous low-concentration N deposition in 385 North American temperate forests (Vadeboncoeur, 2010). High concentration additions of 386 mineral N to soil may transiently overwhelm microbial N demand, driving elevated nitrification 387 and acidity (Gundersen & Rasmussen, 1990; Tian & Niu, 2015; Chen et al., 2016) compared to

388 what would occur under more realistic anthropogenic N loading regimes. N fertilization 389 experiments frequently observe changes in pH (Ramirez et al., 2010; Riggs et al., 2015) and soil 390 water potential (Braddock et al., 1997), suggesting that there may also be a direct effect of 391 elevated salinity and osmotic stress on microbial growth and activity when adding N fertilizers 392 (Averill and Waring 2018). Our analysis explicitly controls for soil pH, and this may explain the 393 discrepancy in results. In addition, we found that N deposition effects on soil C depend on the 394 relative abundance of EM community members (Fig. 3a). Such a phenomenon may result if N 395 deposition relieves N limitation of saprotrophic microbial populations in soils due to competition with EM fungi for N resources, or if there are differences in organic matter chemistry between 396 397 AM and EM ecosystems. Either mechanism would result in N deposition increasing 398 decomposition activity and driving further losses of soil C.

399 The FIA soil sampling only extends to 20cm depth in the mineral soil. It is possible AM 400 and EM forests have differential effects at greater soil depths, and these patterns will be missed 401 by this analysis of shallower soil profiles. Furthermore, there is increasing recognition that 402 particulate vs. mineral associated organic matter may respond differentially and in contrasting 403 directions to changes in soil microbial activity (Schmidt et al., 2011; Cotrufo et al., 2013; Averill 404 & Waring, 2018). This analysis only considers bulk soil C, and cannot speak to differential 405 effects of mycorrhizal association on these finer scale soil C pools. Additional measurements of 406 soil mineral sorptive capacity, beyond what can be captured by basic soil texture measurements, 407 will likely improve statistical models designed to capture spatial variation in soil C storage.

408 Our analysis of the relative abundance of EM basal area in forests support the long-409 standing paradigm of what controls the abundance of EM vs. AM trees within a forest (Read, 410 1991; Smith & Read, 2009). In temperate forests of the U.S., EM trees are most abundant in cool 411 and wet habitats, while AM trees are more abundant in warmer and drier habitats (Fig. S6). We 412 found that soil C:N and soil pH were also strong predictors of the relative abundance of EM vs. 413 AM trees. Given that EM trees often generate acidic litter inputs to ecosystems (Phillips et al., 414 2013), it is difficult to say whether the soil pH is a cause or effect of the presence of EM trees. 415 Nevertheless, our finding that AM associations are more beneficial to trees under high soil N 416 availability compared to EM associations supports long-standing theories of differences among 417 mycorrhizal types (Read & Perez-Moreno, 2003; Phillips et al., 2013). Overall, our analysis

418 provides critical empirical support for long hypothesized environmental controls over the relative419 abundance of AM vs. EM trees within the temperate forest biome.

420 It is important to note that while this analysis assumes all EM trees behave the same, 421 there is substantial variability in ECM fungal communities even in forests dominated by a single 422 tree species (Clemmensen et al., 2013; Averill & Hawkes, 2016). This variation in composition 423 likely drives changes in the functioning of these mycorrhizal communities, as different EM fungi 424 are known to be differentially sensitive to N deposition (Lilleskov et al., 2002), and these 425 different N response sensitivities have been linked to different mycorrhizal exploration types and 426 resource preferences (Hobbie & Agerer, 2010; Hobbie et al., 2014). Differences in EM fungal 427 communities within forest types that affect tree demographic processes and soil C stocks will be 428 missed by this analysis, and likely contribute to uncertainty in model fits. We see simultaneous 429 modeling of both plant and soil microbial communities through time, as well as their interaction, 430 as an urgent next step in predicting future states of temperate forest ecosystems.

431 This study suggests a potential for losses of belowground C in response to N deposition, 432 which may substantially mitigate previously reported N deposition induced increases in 433 aboveground C storage (Thomas et al., 2010). Validating the relative contributions of N 434 deposition to C storage vs. loss will require repeated measurements of forest soil C profiles 435 across N deposition gradients in time. Our study provides a framework for how large-scale forest 436 inventory datasets could be used to predict the balance of ecosystem C stocks, specifically by 437 injecting critical aspects of soil microbial community composition into ecosystem models of the 438 terrestrial C cycle. AM and EM mycorrhizal associations have been linked to the ability of 439 ecosystems to sustain plant productivity in response to elevated CO₂ (Terrer et al., 2016) and 440 soil C storage capacity (Averill et al., 2014; Averill & Hawkes, 2016) via interactions with soil 441 N availability. The spatial extent of forest inventory data, coupled with the developing capacity 442 to remote sense forest mycorrhizal associations (Fisher et al., 2016), provides information to 443 develop and calibrate new simulation models that explicitly represent these divergent categories 444 of forest microbial symbiont types (Brzostek et al., 2014). This coupled approach promises to 445 advance a new class of ecosystem models that can address the role of the forest microbiome in 446 the C cycle at a scale necessary to understand ecosystem responses to global environmental 447 change.

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Figure Captions

Fig. 1. Distribution of sites used in all analyses, as well as the relative abundance of EM trees by basal area in each plot. All points were used in the analyses of the relative abundance of EM basal area and soils. Circles represent plots that were used in both the demographic analyses and the relative abundance analysis, while X's represent plots used in the relative abundance analysis only. N deposition data are based on the 2000-2014 mean wet + dry N deposition rates reported by the National Atmospheric Deposition Program. N deposition data are log transformed for visualization purposes only.

Fig. 2. Relationships between forest mycorrhizal abundance and mycorrhizal-specific demographic processes and N deposition. The relative abundance of EM trees is negatively correlated with N deposition (a.) N deposition had a positive effect on individual tree mortality rates, but there was no significant difference between AM and EM trees (b.) N deposition has a significantly more positive effect on arbuscular mycorrhizal (AM) basal area growth than EM basal area growth at the plot level (c., d.) such that these curves cross (e.) Nitrogen deposition had a positive effect on AM tree recruitment at the plot level but a negative effect on EM recruitment (f., g.) such that these curves cross (h.) Regression lines are based on the full

multiple regression output, holding all other predictors constant at their mean values. Shaded regions represent the 95% credible interval of the mean response. Points plotted are binned mean values and associated standard errors of soil C observations that have been detrended to remove variance associated with other predictors in the model. For additional detail see "Reporting of Results" in the Methods Section.

Fig. 3. Soil C storage as a function of EM relative abundance at low and high levels of N deposition. There is a positive relationship between soil C storage and the relative abundance of EM trees within a plot. However, there is an interaction between the relative abundance of EM trees and N deposition such that the effect is strong at low levels of N deposition (a.) but is completely absent at the highest levels of N deposition observed in the data set (b.) Regression lines are based on the full multiple regression output, holding all other predictors constant at their mean values. Shaded regions represent the 95% credible interval of the mean response. Points plotted are binned mean values and associated standard errors of soil C observations that have been detrended to remove variance associated with other predictors in the model. For additional detail see "Reporting of Results" in the Methods section.

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