

UC Irvine

UC Irvine Previously Published Works

Title

Global soil carbon projections are improved by modelling microbial processes

Permalink

<https://escholarship.org/uc/item/3hd31556>

Journal

Nature Climate Change, 3(10)

ISSN

1758-678X

Authors

Wieder, William R
Bonan, Gordon B
Allison, Steven D

Publication Date

2013-10-01

DOI

10.1038/nclimate1951

Peer reviewed

Global soil carbon projections are improved by modeling microbial processes

William R. Wieder¹

Gordon B. Bonan¹

Steven D. Allison²

¹National Center for Atmospheric Research, Boulder, CO 80307, USA

²Department of Ecology and Evolutionary Biology & Department of Earth System Science,
University of California, Irvine, CA 92697, USA

Corresponding Author:

William R. Wieder

Phone: 303.497.1352

Fax: 303.497.1348

email: wwieder@ucar.edu

address: TSS, CGD/NCAR

PO Box 3000

Boulder, CO 80307-3000

Society relies on Earth system models (ESMs) to predict future climate and carbon (C) cycle feedbacks. However, the soil C response to climate change is highly uncertain in these models^{1,2}, and they omit key biogeochemical mechanisms³⁻⁵. Specifically, the traditional approach in ESMs lack direct microbial control over soil C dynamics⁶⁻⁸. Thus, we tested a new model that explicitly represents microbial mechanisms of soil C cycling at the global scale. Compared to traditional models, the microbial model simulates soil C pools that more closely match contemporary observations. It also predicts a much wider range of soil C responses to climate change over the twenty-first century. Global soils accumulate C if microbial growth efficiency declines with warming in the microbial model. If growth efficiency adapts to warming, the microbial model predicts large soil C losses. By comparison, traditional models predict modest soil C losses with global warming. Microbes also change the soil response to increased C inputs, as might occur with CO₂ or nutrient fertilization. In the microbial model, microbes consume these additional inputs; whereas in traditional models, additional inputs lead to C storage. Our results indicate that ESMs should simulate microbial physiology in order to more accurately project climate change feedbacks.

Contemporary ESMs use traditional soil C models, which implicitly simulate microbial decomposition via first-order kinetics that determine turnover rates of soil C pools^{1,2}. Although such models can replicate extant soil C pools at various scales^{9,10}, their ability to predict soil C response in a changing environment remains unresolved^{11,12}. In the past 30 years, researchers have identified key processes and feedbacks that could be important for accurately simulating future C cycle—climate feedbacks. For example, traditional models neglect microbial physiological processes that transform and stabilize soil C inputs³⁻⁵. In contrast, recent microbial models explicitly simulate microbial biomass pools that catalyze soil C mineralization^{6,8} and

produce notably different results in transient simulations⁶. By representing microbial physiological responses, such models may provide a better fit to observations, especially in a changing environment^{13,14}. Yet to date, no modeling studies have tested the relevance of microbial mechanisms for soil C responses to climate change at the global scale.

We created a new soil biogeochemistry module for use in the Community Land Model that explicitly simulates microbial biomass pools (hereafter referred to as the CLM microbial model; Fig. 1; modified from ref.⁶). The CLM microbial model represents aboveground and belowground processes and separates belowground pools into surface (0-30 cm) and subsurface (30-100 cm) horizons. Microbes in this model directly catalyze the mineralization of litter and soil C pools according to Michaelis-Menten kinetics. In this formulation, decomposition losses can be limited by both substrate availability (the organic C pools) and the microbial biomass, which is assumed to be the source of enzymatic activity. This structure differs from traditional models in which decomposition losses depend only on first-order decay of substrate (soil C) pools⁶.

Temperature affects three key microbial parameters in our model. The Michaelis-Menten relationship requires two parameters: K_m , the substrate half-saturation constant, and V_{max} , the maximal reaction velocity (Fig. 1). We used observational data to constrain these parameters and their temperature sensitivities, which generally follow an exponential form¹⁵. The third key parameter is microbial growth efficiency (MGE), which determines how much microbial biomass is produced per unit of substrate consumed¹⁶. MGE probably declines with increasing temperature, although the magnitude of the response is uncertain¹⁷. Consequently, C decomposition depends on temperature, substrate availability, and the size of the microbial biomass pool.

After running to steady-state, we compared soil C pools from the CLM microbial model to soil C pools from two traditional models (illustrated with model parameterizations from CLM4cn¹⁸ and DAYCENT¹⁰). We also compared model outputs to observations from the globally gridded Harmonized World Soils Database¹⁹. Global simulations were forced with observationally-derived litter inputs (see methods) and with soil temperature and moisture from a 20th century simulation¹⁸. Overall, the CLM microbial model explained 50% of the spatial variation in the soil C observations, whereas the traditional models explained 28-30% of the variation and showed greater average deviations from soil C observations (Fig. 2).

Other traditional models perform even worse than the two reported here. For example, a prior version of CLM4cn, using modeled litter inputs, explained only ~2% of the spatial variation in observed soil C stocks at the 1° grid scale, and no other ESM explained more than 16% of the variation². Some of this poor performance may be due to ESM errors in simulating litter inputs. We avoided these errors by using litterfall observations for our current analysis. Still, the CLM microbial model explained 20% more soil C variation than traditional CLM4cn with observed litterfall, an improvement rivaling the entire explanatory power of previous models. Moreover, the CLM microbial model accurately simulates observed soil C pools in both surface soil layers (0-30 cm) and total soil profiles (0-100 cm; $r = 0.75$ and 0.71 , respectively; SI Fig. 1).

A closer examination of regional patterns illustrates specific gaps in our representation of processes driving soil C cycling (Fig. 2). Some regions, especially in the tropics, have low predicted soil C densities compared to soil C observations. These low biases suggest systematic problems with modeling the physiochemical soil environment. Specifically, the CLM microbial model does not simulate the physical protection of soil C or pH effects on soil microbial activity.

These mechanisms should be a focus for future model development, especially in tropical soils. Additionally, simulating processes that build and maintain organic soils remains a challenge in ESMs²⁰. In the Arctic, the CLM microbial model generates higher soil C densities than traditional modeling approaches (Fig. 2). However, there are poor spatial correlations between our modeled soil C pools and observational datasets (SI Fig. 2). Also, all of the Arctic datasets show a high degree of spatial heterogeneity in soil C, a feature clearly absent from our model simulations (SI Fig. 2). Improved hydrologic and moisture controls over soil C turnover will likely be needed to simulate this heterogeneity in the Arctic. In addition to model improvements, measurement efforts should address the wide discrepancies in empirical estimates of Arctic soil C (SI Fig. 2).

Accurate simulation of current soil C stocks is essential, but the main goal of ESMs is to project carbon – climate feedbacks in the future. When the environment changes, the CLM microbial model makes projections that differ from traditional soil biogeochemistry models (Fig. 3). For example, perturbations like elevated CO₂ or N deposition may increase plant productivity and C inputs to soils. In the CLM microbial model, increasing global litter inputs by 20% results in an ephemeral accumulation of soil C, which concurrently increases microbial biomass. Larger microbial biomass pools then accelerate rates of soil C turnover and increase rates of heterotrophic respiration. The net effect is no change in soil C pools after 30 years (Fig. 3a). In contrast, increasing litterfall inputs to traditional models causes soil C accumulation. The difference is due to the joint dependence of soil C loss on substrate pool size and microbial biomass in the microbial model.

On balance, projections from the CLM microbial model show better agreement with observations from leaf litter manipulations^{21,22} and CO₂ enrichment studies²³. Increasing litter

inputs generally increase rates of soil respiration, but elicit no change in soil C storage (but see ref.²⁴). Although the mechanisms underlying these observations are not well understood, several studies emphasize the importance of the priming effect. Priming occurs when increased inputs of fresh organic substrates accelerate microbial decomposition of existing soil C²⁵. Typically, priming is driven by increased microbial demand for nutrients from soil organic matter, or increased microbial growth and enzyme production in response to substrate addition. Only the latter mechanism operated in our simulations because the CLM microbial model does not include C-N interactions.

We use both microbial and traditional models to simulate soil C responses to global warming (Fig. 3b). In the microbial model, elevated temperatures accelerate enzyme kinetics, which generally leads to soil C loss. However, this effect can be completely offset if MGE declines with warming and reduces the microbial biomass that controls decomposition. If MGE does not change with warming, then enzyme kinetics dominate and soils lose up to 300 Pg C. Consequently, global soil C losses over the 21st century could be negligible, or massive, depending on the thermal response of MGE. Empirical studies suggest that MGE declines with increasing temperature, at least in the short term^{16,17}. Still, the MGE response to temperature is poorly constrained, and adaptive processes in microbial communities could stabilize MGE in a warming world. In traditional models, MGE is a fixed constant. Accordingly, warming temperatures only affect kinetic constants in traditional models, which predict modest and similar soil C losses in the warming scenario (Fig. 3b). Thus, traditional ESMs miss an important element of global climate sensitivity driven by microbial control over soil C cycling.

Despite better agreement with soil C observations, nearly 50% of the spatial variation in global soil C pools remains to be explained. Our work is just the first step toward a new

generation of models that includes key biological and physical mechanisms in the soil C cycle. For example, shifts in microbial community structure could alter the temperature sensitivity of heterotrophic respiration²⁶, such that soils respire less CO₂ than expected for a given amount of warming. Enzyme K_m, and enzyme V_{max} could also adapt to climate warming, such that enzyme catalytic rates increase more than expected at warmer temperatures^{14,15}. Some of these parameters may also shift with changes in N availability, possibly as a result of shifts in microbial community structure²⁷. Accounting for these mechanisms not only holds promise for improved simulation of current soil C distributions, but should also increase confidence in the prediction of soil C responses to future climate change. However, the magnitude of microbial adaptation to climate change remains controversial²⁸, and more empirical studies are needed to determine the mechanisms underlying adaptation, including physiological acclimation, microbial community shifts, and evolutionary processes. Nonetheless our analysis suggests that soil C predictions from current ESMs will remain questionable until they can account for critical microbial mechanisms that affect soil carbon dynamics.

Another key shortcoming in the CLM microbial model is the lack of soil mineral interactions. In particular, there is no physiochemical protection of soil organic matter on mineral surfaces or within aggregates, yet physical protection is known to affect soil C storage^{4,7,29}. This omission is also relevant because minerals and aggregates are involved in soil C responses to perturbations^{3,7,29}. For example, soil mineralogy may influence the stabilization of microbial byproducts and the temperature sensitivity of organic matter sorption and desorption. These mechanisms should be high priorities for future model development.

Our results have broad implications because society relies on ESMs to predict future atmospheric CO₂ levels and climate. Our model comparison shows that traditional ESMs omit

key microbial mechanisms that determine soil C responses to global climate change. Clearly additional mechanisms should be included, but our model is a crucial first step toward a new generation of global models that integrates microbial physiology. Soil biogeochemistry models in ESMs deserve further investigation, development, and more rigorous benchmarking with data, but we contend that an explicitly microbial approach, like the one presented here, has several advantages. Simple microbial models should help bring ESMs into better alignment with our theoretical understanding of processes controlling turnover and stabilization of soil C, without adding undue computational expense. Additionally, key parameters in the CLM microbial model can be measured, a feature that should facilitate future model development, evaluation, and validation. Finally, this approach represents biological mechanisms responsible for carbon turnover in soils and will likely generate more accurate predictions of soil C feedbacks on climate change.

Methods

Equilibrium soil C pools were calculated for CLM4cn and DAYCENT models using an analytical solution³⁰ with globally gridded input datasets for mean annual soil moisture and temperature¹⁸, soil texture and pH¹⁹, litter chemistry³¹, and litterfall inputs derived from observations³² (described in ref.³³). We forced the model with these litterfall data to reduce error and biases associated with ESMs' predictions of net primary productivity, plant C allocation, and associated litter fluxes. This modification substantially improves soil C estimates in conventional soil biogeochemistry models³³. Additionally, DAYCENT parameterizations were modified to simulate deeper soil horizons and minimize error between modeled and observed soil C pools³³. In its current configuration, the CLM microbial model has no structure allowing

for the decomposition of coarse woody debris. Accordingly, coarse woody debris inputs were omitted from the litterfall inputs used to force all three models evaluated here. For conventional models, soil C pools reported here are the sums of all pools (Fig. 2b, 2c).

Using the same soil temperature and litterfall inputs, we calculated equilibrium soil C pools for the CLM microbial model using a traditional spin-up (~1500 y run at hourly time steps). For vertically resolved soils in the CLM microbial model, we allocated 65% of root litter inputs to surface soils (0-30 cm) and the remaining 35% to subsurface horizons (30-100 cm). Soil C pools reported for the CLM microbial model represent the sum of SOC and microbial biomass, although at equilibrium, microbial biomass pools are only ~1% of total soil C pools. We compared modeled soil C pools with observations from the Harmonized World Soils Database¹⁹ using sample cross-correlation and area weighted root-mean-square-error (RMSE).

We assumed Michaelis-Menten kinetics parameters (V_{\max} and K_m) and MGE were temperature sensitive, using parameter values reported in refs.^{6,15}. Median values used to calculate the relationship between temperature and enzyme kinetics produced plausible global soil C pools (SI Fig. 3), although high RMSE, large litter pools, and large soil C pools suggested that C turnover was too slow, especially at high latitudes. Therefore we used the upper and lower bounds for the temperature sensitivity of V_{\max} and K_m , respectively, in the CLM microbial model to simulate equilibrium soil C pools that minimized RMSE with observations (Fig. 2d, SI Fig. 1).

To examine model behaviors in response to future global change, we took steady-state soil C estimates generated for each model and perturbed litter inputs or soil temperature. In both perturbation experiments, control simulations were forced with observationally-derived litter inputs evenly distributed throughout the year, and mean monthly soil temperature and soil

moisture data from 1985-2005 from a single Community Earth System Model (CESM) ensemble member from archived CMIP5 experiments (publically available online at <http://www.earthsystemgrid.org>). In year 5 of the litter manipulation experiment, we increased global litter fluxes 20% for 30 years, calculating the difference in global soil C pools between control and increased litter simulations (Fig. 3a). Using CESM soil temperature projections from an archived CMIP5 experiment for RCP 8.5 from 2006 to 2100, we calculated the change in soil C pools predicted by 4.8°C warming by the end of this century for each model (Fig. 3b). The CLM microbial model has temperature sensitive MGE. We explored the implications of assumptions made about changes in MGE with increasing soil temperatures, allowing: 1) instantaneous decreases in MGE with warming soil temperatures (Fig. 3b, solid green line); or 2) instantaneous adaptation of microbial community MGE, so that MGE does not decrease with warming (dashed green line). Data presented in Fig. 3b are a subset of results from these warming experiments showing the range of possible outcomes with different parameters and initial soil C pools. More information is available in SI Fig. 4.

Acknowledgements We appreciate the suggestions from three anonymous reviewers whose input clarified and improved this manuscript. The National Center for Atmospheric Research is sponsored by the National Science Foundation. This work was supported by National Science Foundation grant AGS-1020767, the NSF Advancing Theory in Biology Program, and the Office of Science (BER), US Department of Energy.

Author Contributions W.R.W and S.D.A. conceived the project and built the model. W.R.W. and G.B. assembled input and model evaluation data sets. W.R.W. conducted model runs. All authors contributed to writing the paper.

Additional Information The authors declare no competing financial interests. Correspondence and requests for materials should be addressed to W.R.W.

References

- 1 Friedlingstein, P. *et al.* Climate-Carbon Cycle Feedback Analysis: Results from the C4MIP Model Intercomparison. *J Climate* **19**, 3337-3353, doi:10.1175/jcli3800.1 (2006).
- 2 Todd-Brown, K. E. O. *et al.* Causes of variation in soil carbon predictions from CMIP5 Earth system models and comparison with observations. *Biogeosciences* **10**, 1717-1736, doi:10.5194/bg-10-1717-2013 (2013).
- 3 Conant, R. T. *et al.* Temperature and soil organic matter decomposition rates – synthesis of current knowledge and a way forward. *Global Change Biology* **17**, 3392-3404, doi:10.1111/j.1365-2486.2011.02496.x (2011).
- 4 Cotrufo, M. F., Wallenstein, M. D., Boot, C. M., Deneff, K. & Paul, E. The Microbial Efficiency-Matrix Stabilization (MEMS) framework integrates plant litter decomposition with soil organic matter stabilization: do labile plant inputs form stable soil organic matter? *Global Change Biology* **19**, 988-995, doi:10.1111/gcb.12113 (2013).
- 5 Schmidt, M. W. I. *et al.* Persistence of soil organic matter as an ecosystem property. *Nature* **478**, 49-56, doi:10.1038/nature10386 (2011).

228 6 Allison, S. D., Wallenstein, M. D. & Bradford, M. A. Soil-carbon response to warming
 229 dependent on microbial physiology. *Nat. Geosci.* **3**, 336-340, doi:10.1038/ngeo846
 230 (2010).

231 7 Six, J., Frey, S. D., Thiet, R. K. & Batten, K. M. Bacterial and fungal contributions to
 232 carbon sequestration in agroecosystems. *Soil Sci. Soc. Am. J.* **70**, 555-569,
 233 doi:10.2136/sssaj2004.0347 (2006).

234 8 Treseder, K. *et al.* Integrating microbial ecology into ecosystem models: challenges and
 235 priorities. *Biogeochemistry* **109**, 7-18, doi:10.1007/s10533-011-9636-5 (2012).

236 9 Jenkinson, D. S., Adams, D. E. & Wild, A. Model estimates of CO₂ emissions from soil
 237 in response to global warming. *Nature* **351**, 304-306 (1991).

238 10 Parton, W. J., Schimel, D. S., Cole, C. V. & Ojima, D. S. A general model for soil
 239 organic matter dynamics: sensitivity to litter chemistry, texture and management. (1994).

240 11 Ise, T. & Moorcroft, P. R. The global-scale temperature and moisture dependencies of
 241 soil organic carbon decomposition: an analysis using a mechanistic decomposition model.
 242 *Biogeochemistry* **80**, 217-231, doi:10.1007/s10533-006-9019-5 (2006).

243 12 Manzoni, S. & Porporato, A. Soil carbon and nitrogen mineralization: Theory and models
 244 across scales. *Soil Biology and Biochemistry* **41**, 1355-1379,
 245 doi:10.1016/j.soilbio.2009.02.031 (2009).

246 13 Lawrence, C. R., Neff, J. C. & Schimel, J. P. Does adding microbial mechanisms of
 247 decomposition improve soil organic matter models? A comparison of four models using
 248 data from a pulsed rewetting experiment. *Soil Biology and Biochemistry* **41**, 1923-1934,
 249 doi:10.1016/j.soilbio.2009.06.016 (2009).

250 14 Tucker, C. L., Bell, J., Pendall, E. & Ogle, K. Does declining carbon-use efficiency
251 explain thermal acclimation of soil respiration with warming? *Global Change Biology* **19**,
252 252-263, doi:10.1111/gcb.12036 (2013).

253 15 German, D. P., Marcelo, K. R. B., Stone, M. M. & Allison, S. D. The Michaelis–Menten
254 kinetics of soil extracellular enzymes in response to temperature: a cross-latitudinal study.
255 *Global Change Biology* **18**, 1468-1479, doi:10.1111/j.1365-2486.2011.02615.x (2012).

256 16 Manzoni, S., Taylor, P., Richter, A., Porporato, A. & Ågren, G. I. Environmental and
257 stoichiometric controls on microbial carbon-use efficiency in soils. *New Phytologist* **196**,
258 79-91, doi:10.1111/j.1469-8137.2012.04225.x (2012).

259 17 Frey, S. D., Lee, J., Melillo, J. M. & Six, J. The temperature response of soil microbial
260 efficiency and its feedback to climate. *Nature Clim. Change* **3**, 395–398
261 doi:10.1038/nclimate1796 (2013).

262 18 Lawrence, D. *et al.* Parameterization improvements and functional and structural
263 advances in version 4 of the Community Land Model. *Journal of Advances in Modeling*
264 *Earth Systems* **3**, 27 pp., doi:10.1029/2011ms000045 (2011).

265 19 FAO, IIASA, ISRIC, ISSCAS & JRC. *Harmonized World Soil Database* (version 1.2).
266 FAO. Rome, Italy and IIASA, Laxenburg, Austria (2012).

267 20 Koven, C. D. *et al.* Permafrost carbon-climate feedbacks accelerate global warming.
268 *Proceedings Of The National Academy Of Sciences Of The United States Of America* **108**,
269 14769-14774, doi:10.1073/pnas.1103910108 (2011).

270 21 Nadelhoffer, K. J. *et al.* The DIRT experiment: Litter and root influences on forest soil
271 organic matter stocks and function. In *Forests in time: the environmental consequences*

272 *of 1000 years of change in New England* (eds D. Foster & J. Aber) Ch. 15, 300-315
 273 (Yale University Press, 2004).

274 22 Sayer, E. J., Heard, M. S., Grant, H. K., Marthews, T. R. & Tanner, E. V. J. Soil carbon
 275 release enhanced by increased tropical forest litterfall. *Nature Climate Change* **1**, 304-
 276 307, doi:10.1038/nclimate1190 (2011).

277 23 Hungate, B. A. *et al.* Assessing the effect of elevated carbon dioxide on soil carbon: a
 278 comparison of four meta-analyses. *Global Change Biology* **15**, 2020-2034,
 279 doi:10.1111/j.1365-2486.2009.01866.x (2009).

280 24 Leff, J. W. *et al.* Experimental litterfall manipulation drives large and rapid changes in
 281 soil carbon cycling in a wet tropical forest. *Global Change Biology* **18**, 2969-2979,
 282 doi:10.1111/j.1365-2486.2012.02749.x (2012).

283 25 Kuzyakov, Y. Priming effects: Interactions between living and dead organic matter. *Soil*
 284 *Biology and Biochemistry* **42**, 1363-1371, doi:10.1016/j.soilbio.2010.04.003 (2010).

285 26 Bradford, M. A. *et al.* Thermal adaptation of soil microbial respiration to elevated
 286 temperature. *Ecology Letters* **11**, 1316-1327, doi:10.1111/j.1461-0248.2008.01251.x
 287 (2008).

288 27 Stone, M. M. *et al.* Temperature sensitivity of soil enzyme kinetics under N-fertilization
 289 in two temperate forests. *Global Change Biology* **18**, 1173-1184, doi:10.1111/j.1365-
 290 2486.2011.02545.x (2012).

291 28 Hartley, I. P., Hopkins, D. W., Garnett, M. H., Sommerkorn, M. & Wookey, P. A. Soil
 292 microbial respiration in arctic soil does not acclimate to temperature. *Ecology Letters* **11**,
 293 1092-1100, doi:10.1111/j.1461-0248.2008.01223.x (2008).

- 29 Dungait, J. A. J., Hopkins, D. W., Gregory, A. S. & Whitmore, A. P. Soil organic matter turnover is governed by accessibility not recalcitrance. *Global Change Biology* **18**, 1781-1796, doi:10.1111/j.1365-2486.2012.02665.x (2012).
- 30 Xia, J. Y., Luo, Y. Q., Wang, Y. P., Weng, E. S. & Hararuk, O. A semi-analytical solution to accelerate spin-up of a coupled carbon and nitrogen land model to steady state. *Geosci. Model Dev.* **5**, 1259-1271, doi:10.5194/gmd-5-1259-2012 (2012).

Figure 1 | Diagram of the CLM microbial model. The model explicitly simulates microbial-driven soil C cycling in above ground, surface (0-30 cm) and sub-surface (30-100 cm) soil horizons. Ovals represent pools for litter (Lit), microbial biomass (Mic), and soil organic carbon (SOC). Fluxes between pools are shown with arrows. Plant inputs enter leaf and root litter pools (solid black arrows). A small fraction of litter flux (F_i) enters SOC pools without passing through microbial biomass (dashed black arrows). Otherwise, litter and SOC pools pass through microbial biomass, with rates determined by the size of the microbial biomass pool and temperature sensitive Michaelis-Menten kinetic parameters (V_{\max} and K_m , red arrows), based on observations¹⁵ (SI Table 1). Microbial respiration is also assumed to be temperature sensitive, and equal to $1 - \text{MGE}$ (heavy black arrows). Currently, MGE declines linearly with soil temperature, but parameters for this relationship are not well constrained by observations (see also ref¹⁵). Microbial turnover (i.e., mortality; τ) converts microbial biomass to SOC pools (blue arrows). In the current parameterization, $\tau = 0.0005 \text{ h}^{-1}$ and $F_i = 0.02 \text{ h}^{-1}$ (SI Table 1).

Figure 2 | Global distribution of soil C pools (0-100 cm) from observations¹⁹ and models. (a) Observations, global total = 1259 Pg C, **(b)** CLM4cn, global total = 691 Pg C [spatial correlation

with observations (r) = 0.55, model-weighted root mean square error (RMSE) = 7.1 kg C m⁻²];

(c) DAYCENT, global total = 939 Pg C [r = 0.53, RMSE = 7.6]; and (d) the CLM microbial

model, global total = 1310 Pg C [r = 0.71, RMSE = 5.3].

Figure 3 | Divergent model responses of global soil C pools in global change simulations.

Response of steady-state soil C pools for conventional soil biogeochemistry models [CLM4cn

(black) and DAYCENT (blue)] and the CLM microbial model (green) to: (a) 20% global

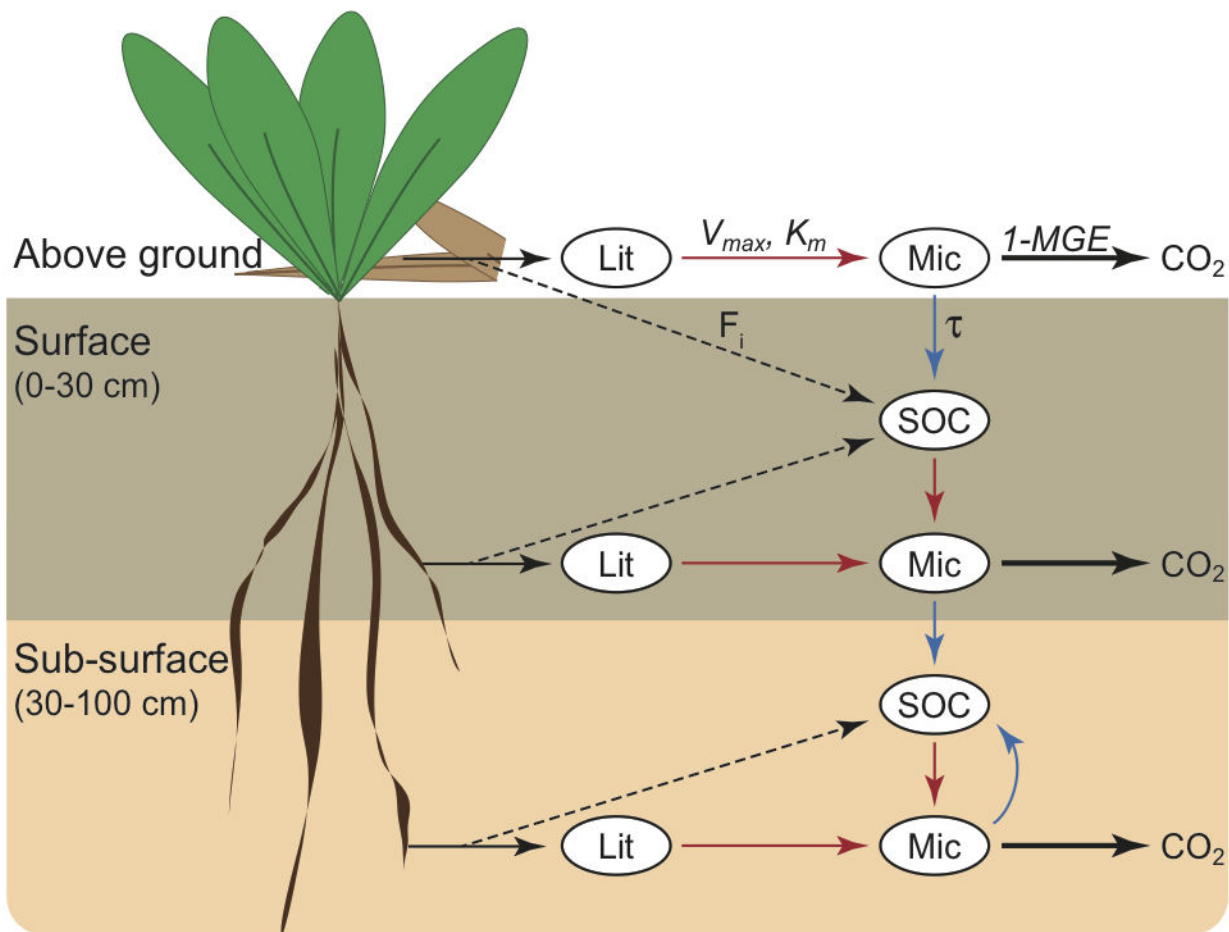
increase in litterfall beginning in year 5; (b) 4.8°C mean increase in global temperature by 2100,

predicted by ensemble member one of CESM simulations for RCP 8.5 used in CMIP5

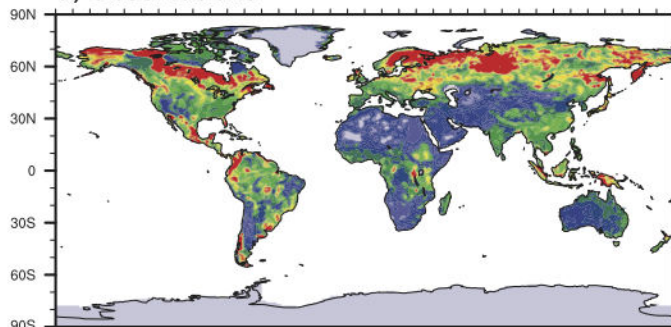
experiments from 2006-2100. For the microbial model, MGE changes with temperature (solid

line) or microbial communities adapt to increasing temperatures without changing MGE (dashed

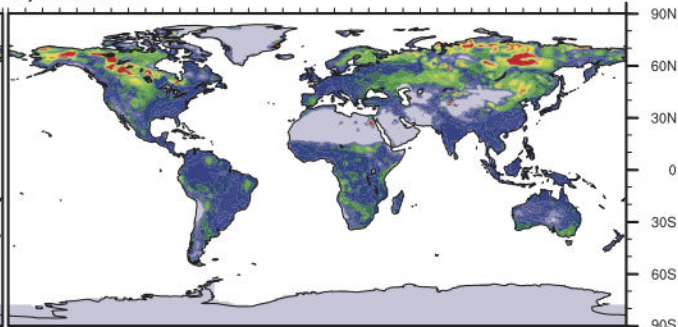
line).



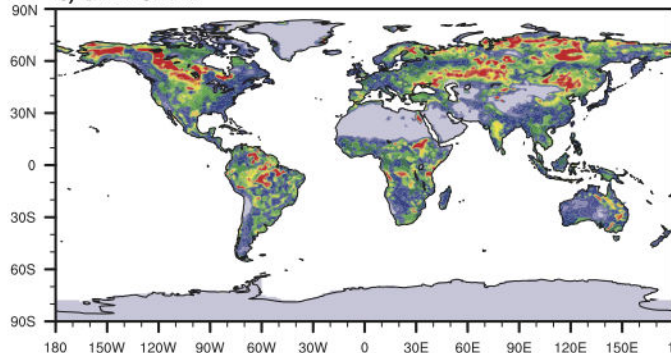
a) Observations



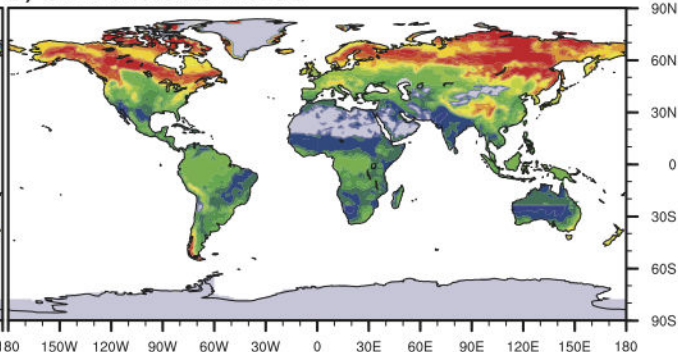
b) CLM4cn



c) DAYCENT

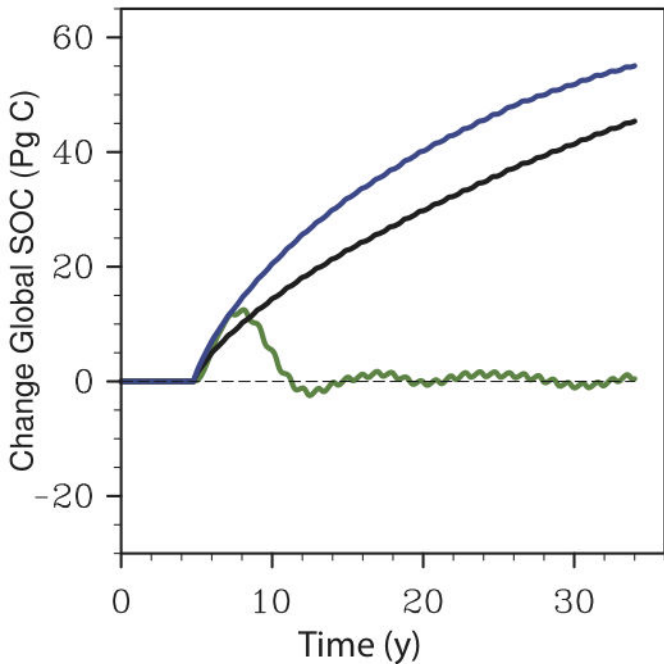


d) CLM microbial model



g C m^{-2}

a) Increasing Litterfall



b) Increasing temperature

