

Global soil carbon projections are improved by modelling microbial processes

Supplementary Table 1

Model parameter descriptions, values, and units used in the CLM microbial model

Supplementary Figures and Legends 1-4

Additional information detailing: the vertical distribution of soil C pools from the CLM microbial model, Arctic soil C distributions for observational estimates and the CLM microbial model, and CLM microbial model results using different enzyme kinetics parameters.

Supplementary Notes

Additional references from methods and SI figures.

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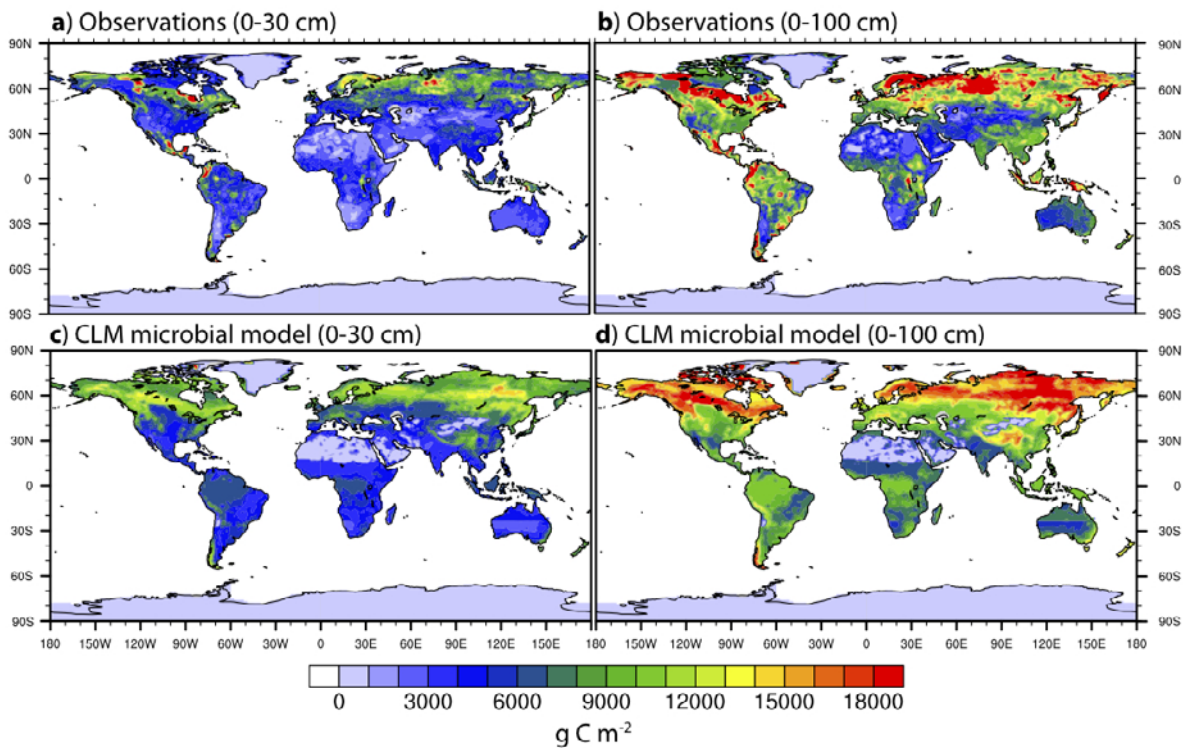
William R. Wieder, Gordon B. Bonan, & Steven D. Allison

SI Table 1 Model parameter descriptions, values, and units used in the CLM microbial model.

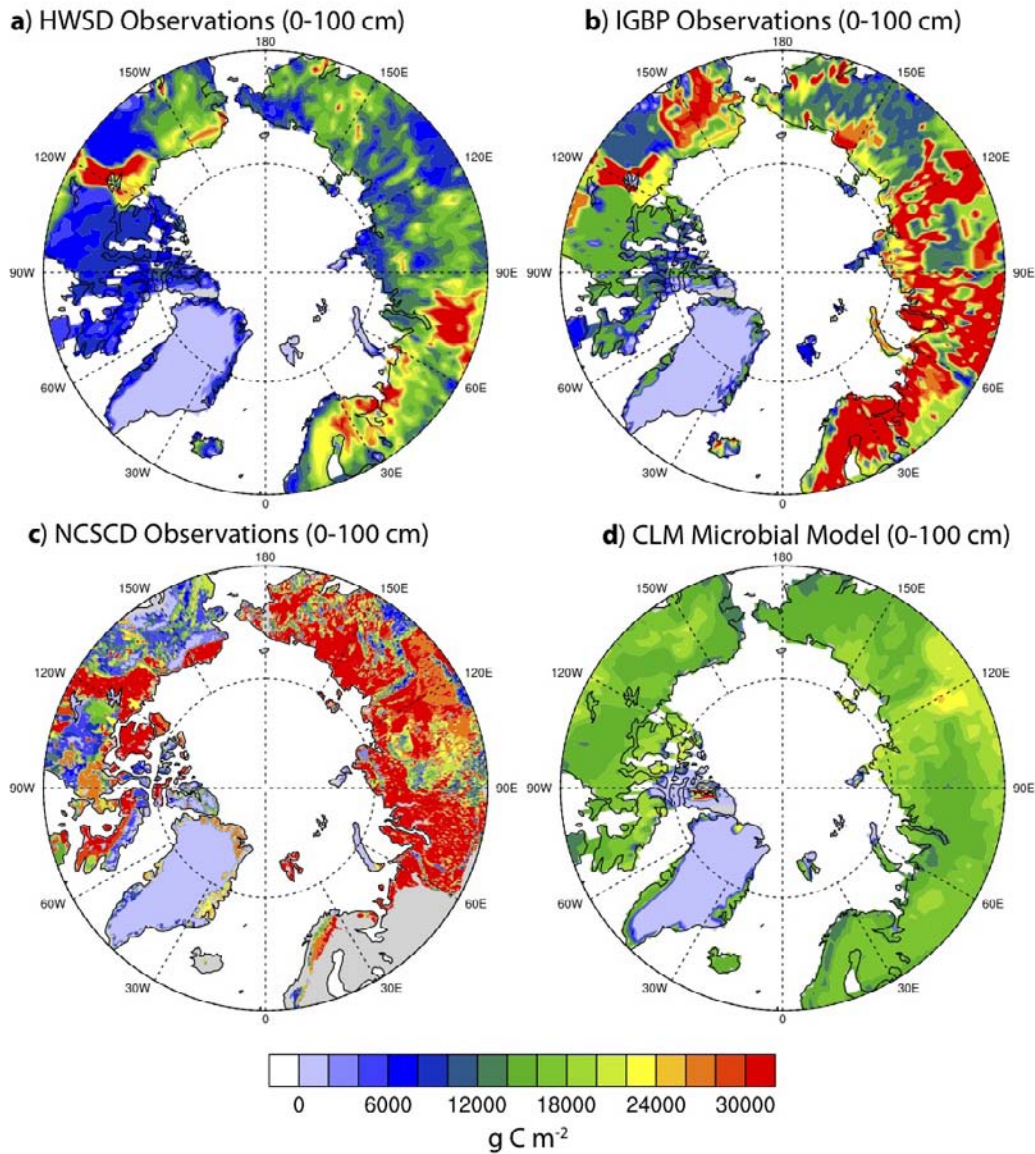
All values are from ref.¹⁵ except for F_i , a_v , and a_κ .

Parameter	Description	Value	Units
F_i	Fraction of litter inputs directly transferred to SOM	0.02	h^{-1}
τ	Microbial biomass turnover rate	0.0005	h^{-1}
$V_{\text{max-slope}}$	Regression coefficient	0.046-0.063	$\ln(\text{nmol g}^{-1} \text{h}^{-1})^\circ\text{C}^{-1}$
$V_{\text{max-int}}$	Regression intercept	5.47	$\ln(\text{nmol g}^{-1} \text{h}^{-1})$
a_v	Tuning coefficient	8.0, 1.5, 3.5*	$\text{mg}^{-1} \text{microbial biomass cm}^{-3} \text{h}^{-1}$
$K_{\text{m-slope}}$	Regression coefficient	0.007-0.034	$\ln(\mu\text{mol L}^{-1})^\circ\text{C}^{-1}$
$K_{\text{m-int}}$	Regression intercept	3.19	$\ln(\mu\text{mol L}^{-1})$
a_κ	Tuning coefficient	0.125, 0.667, 0.286*	mg cm^{-3}
ϵ_{slope}	Microbial growth efficiency temperature slope	-0.016	$\text{mg mg}^{-1} \text{ }^\circ\text{C}^{-1}$
ϵ_{int}	Microbial growth efficiency temperature intercept	0.63	mg mg^{-1}

*for litter pools, $\text{SOC}_{(1)}$, & $\text{SOC}_{(2)}$, respectively

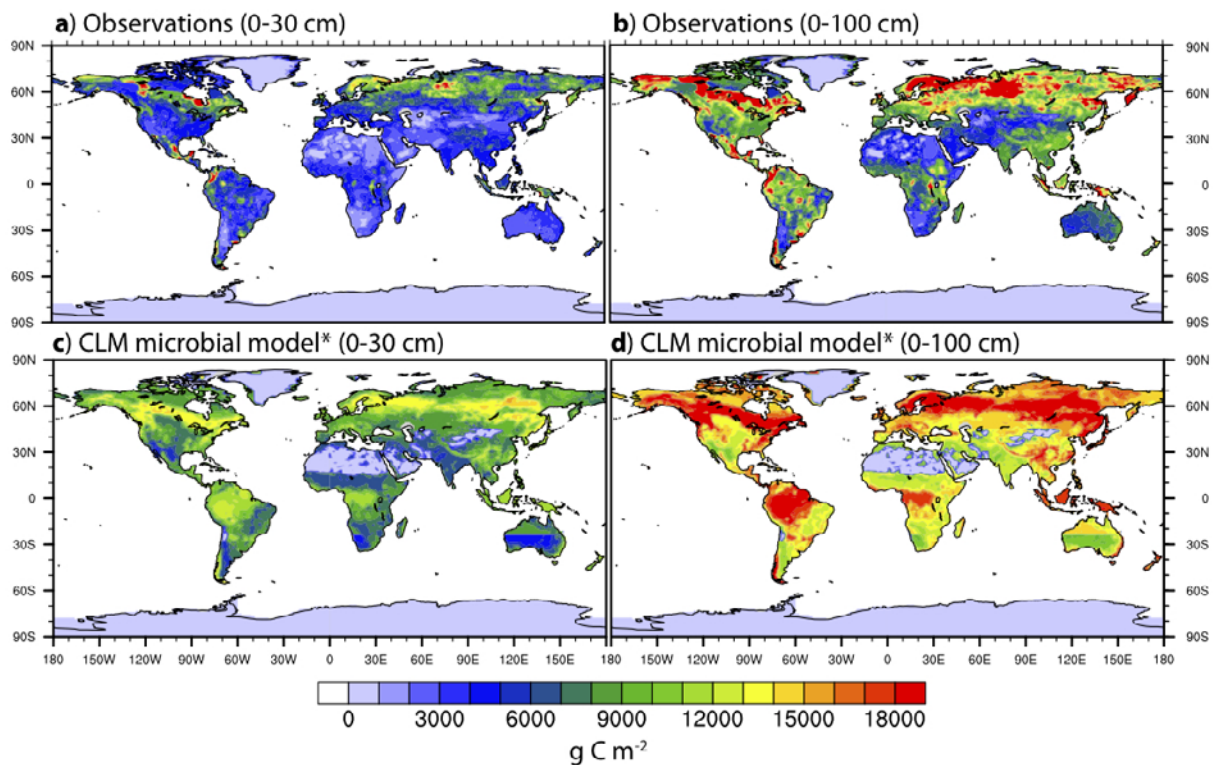


SI Figure 1 | Vertical distribution of global soil C pools from observations¹⁹ and the CLM microbial model. (a) Observed surface soils, global total = 660 Pg C; **(b)** Observed soil profile, global total = 1259 Pg C; **(c)** CLM microbial model surface soils, global total = 784 Pg C [spatial correlation with observations (r) = 0.75, model-weighted root mean square error (RMSE) = 2.9 kg C m^{-2}]; **(d)** CLM microbial model soil profile, global total = 1310 Pg C [r = 0.71, RMSE = 5.3].

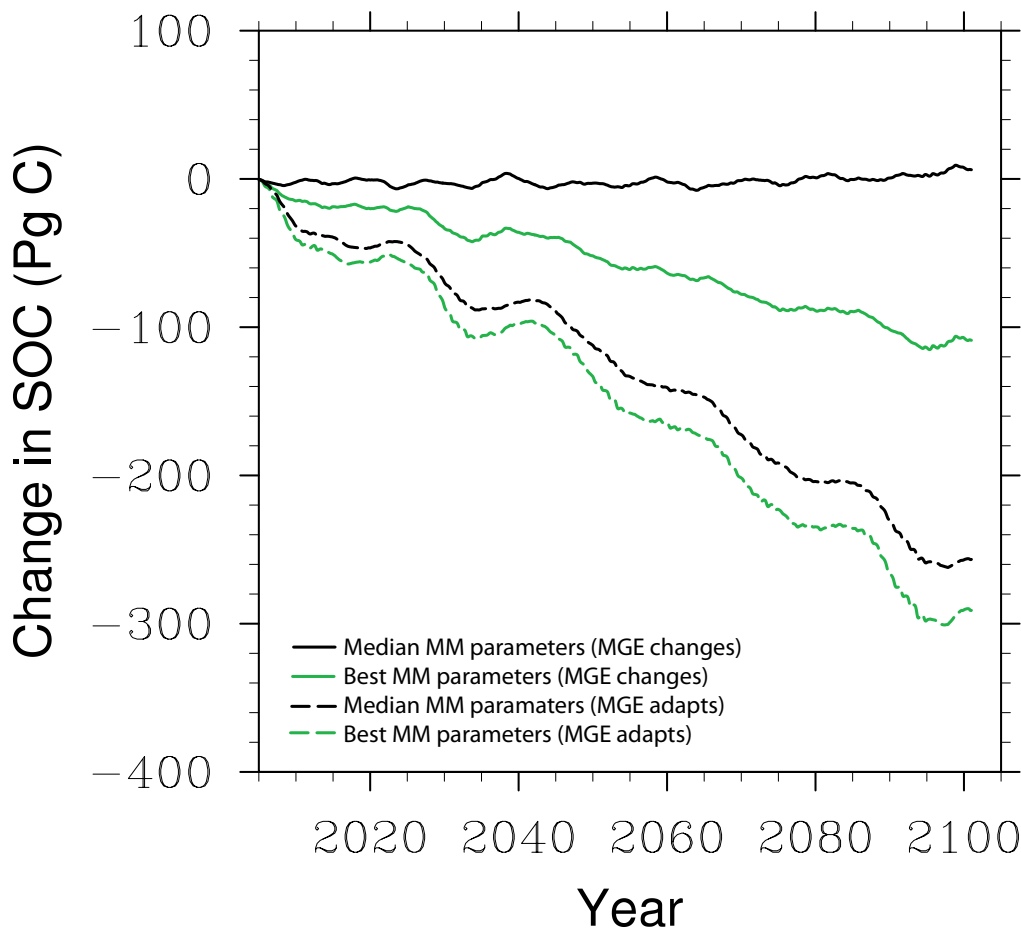


SI Figure 2 | Arctic SOM pools from gridded observations and the CLM microbial model.

Total SOC pools (0-100 cm, Pg C) in soils north of 60° N: **(a)** Harmonized Word Soils Database (HWSD)¹⁹, 219 Pg C; **(b)** International Geosphere-Biosphere Programme (IGBP)³⁴, 340 Pg C; **(c)** Northern Circumpolar Soil Carbon Database (NCSDC)³⁵, 496 Pg C (totals for the entire permafrost region, including regions below the Arctic circle that are not shown here); **(d)** CLM microbial model, 251 Pg C. Note change in color bar from global SOC maps.



SI Figure 3 | Vertical distribution of global soil C pools from observations¹⁹ and the CLM microbial model. Model results calculated using median values for enzyme kinetic parameters (from ref.¹⁵). **(a)** Observed surface soils, global total = 660 Pg C; **(b)** Observed soil profile, global total = 1259 Pg C; **(c)** CLM microbial model surface soils, global total = 1085 Pg C [spatial correlation with observations (r) = 0.75, model-weighted root mean square error (RMSE) = 4.2 kg C m⁻²]; **(d)** CLM microbial model soil profile, global total = 1812 Pg C [r = 0.71, RMSE = 6.8].



SI Figure 4 | Divergent CLM microbial model responses to warming temperatures.

Response of steady-state soil C pools from the CLM microbial model to 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. Steady-state soil C pools calculated with median values for temperature – enzyme kinetic parameter relationships (black lines; SI Figure 3), and the “best” enzyme kinetic parameter values that minimized RMSE (green lines; Fig. 2). Solid versus dashed lines highlight the CLM microbial model sensitivity to assumptions about MGE: MGE declines with temperature (solid lines) or microbial communities adapt to increasing temperatures without changing MGE (dashed lines). Highest and lowest lines from this figure are shown in Fig. 3 to illustrate the range of possible results from the CLM microbial model.

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