



Effect of soil C model structural uncertainty on global projections

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Outline

- Uncertainty in carbon stocks estimates and projections by Earth System Models (ESMs)
- SOC modelling framework with changeable structure
- Parametrization and input data
- Sensitivity analysis and parameter uncertainty
- Results: structural uncertainty and model comparison
- Conclusions

Uncertainty in global soil C stock estimates and projections by ESMs

Carbon balance projections for 21 century vary from 72 GT C loss to 253 GT C gain (Todd-Brown et al., 2014)

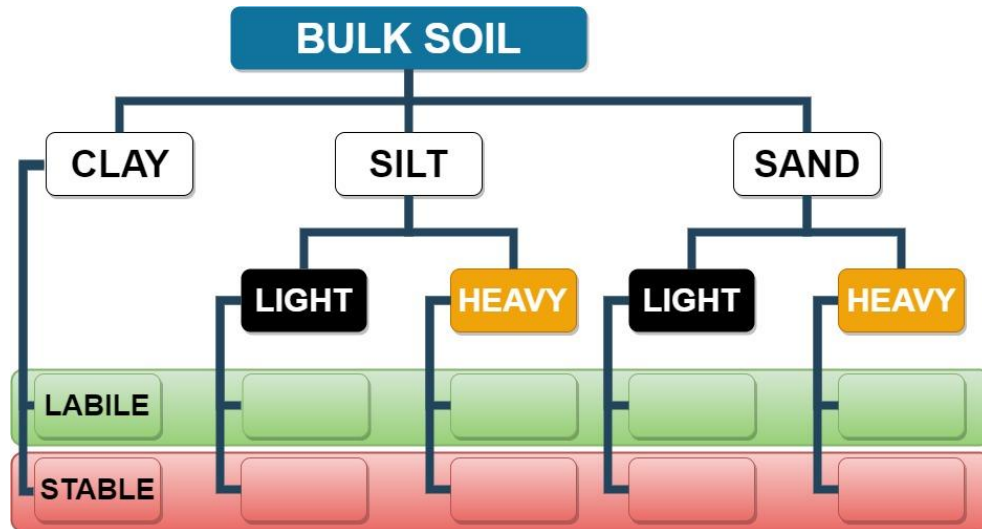
Estimates of future SOC dynamics range widely, and recent compilations of soil radiocarbon suggest that global models underestimate the transit time of C in soil, biasing estimates for soil C sequestration in future years (He et al., 2016).

Current carbon stock estimates are 425 – 2111 GT C (*Tian et al., 2015*, based on Multiscale Synthesis and Terrestrial Model Intercomparison Project (MsTMIP), 22 models) or **510 - 3040 GT C** (from *5th IPCC report based on results of Coupled Model Intercomparison Project CMIP5*, 11 models). 6th IPCC report coming in 2021 based on comparison project CMIP6 is expected to include nearly 100 models.

SOC modelling framework with changeable structure

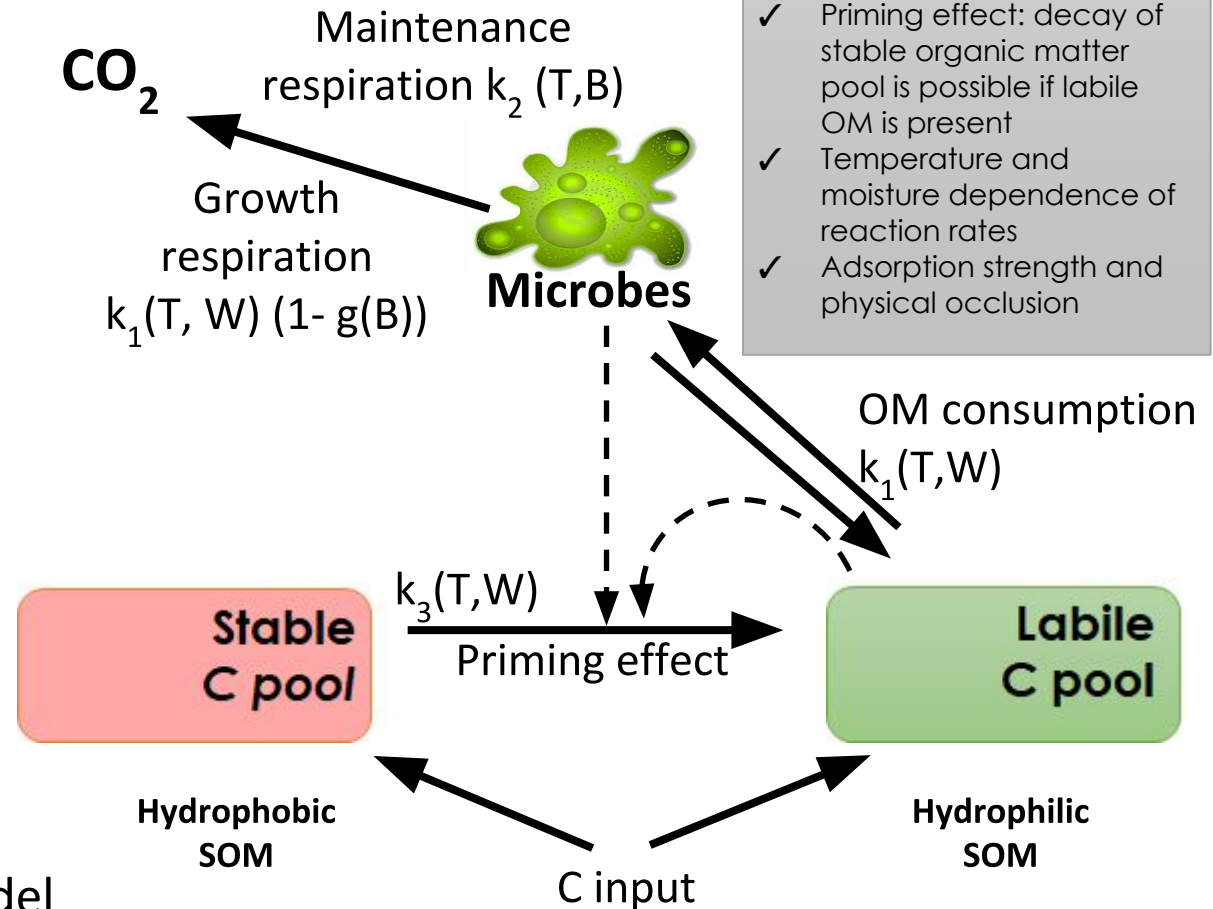
C pools

Soil organic matter (SOM) is divided into pools by it's biochemical availability and location in measurable physical size and density fractions.



- ★ Total of 10 organic matter pools are used in the model
- ★ C input is distributed among these pools
- ★ C cycle in each physical fraction differs in decay rates for size and density location
- ★ Modeling framework allows **switching off and on** each of the mechanism in C cycle

C cycle



Model input data, simulation and parametrization

Model input data:

- litter fall
 - soil surface temperature
 - soil moisture
- Input data for parametrization were taken from historic time series of mean annual values for LTBF sites.
- Input data for projections were taken from Earth System Model.

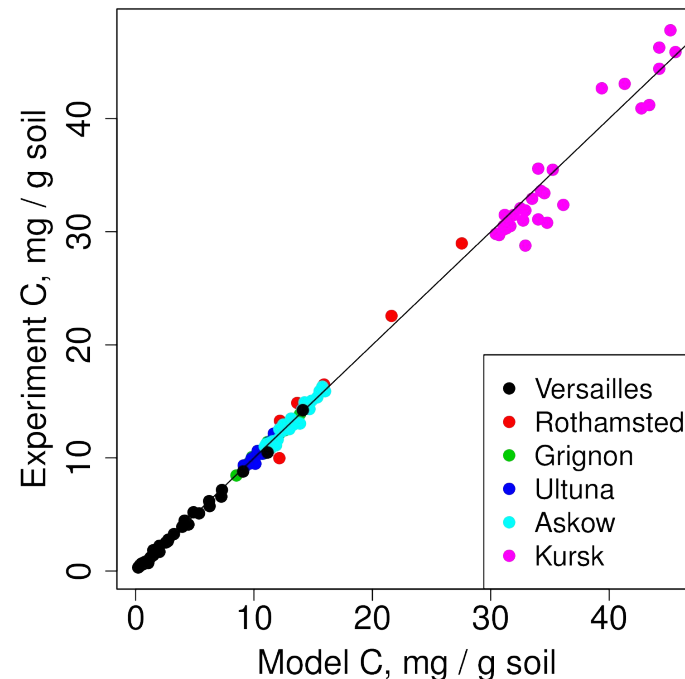
Community Earth System Model (CESM 4.0)
Scenario: 1deg_GSWP3v1_CMIP6_SSP3-7
Global Soil Wetness Project Phase 3
Grid $1.25 \times 0.94^\circ$

Model parameters:

- Distribution ratio of litter fall C input between physical fractions
- Reaction rates of SOM decomposition for each physical fraction
- Microbial CUE, microbial maintenance respiration (turnover), SOM temperature and moisture sensitivity
- In total 18 parameters in the most complex model structure

Model simulation includes 400 years spin-up with average temperature, moisture and litter fall of historic input data, or first 15 years of ESM projection scenario, followed by model run with input data.

The model was validated by simulation of bulk soil C in several long-term experiments (experimental data from Barre et al., 2012) with best fit model parameterized on Versailles chronosequence fractionation data (see [SSS10.4](#)).



To simplify model fit to a given equilibrium carbon concentration we introduce scaling parameter: characteristic carbon concentration c_0 (related to nonlinear reaction terms of the system). c_0 effects all reaction rates in the model as a factor $c_0^{(1-x)}$ where x is reaction kinetics order.

Sensitivity analysis, parameter uncertainty

Different versions of the model (over 200) were fitted to experimental time series of carbon content in physical fractions and compared using Bayesian information criterion (BIC). Sensitivity analysis was used to obtain standard error for model parameters (see [SSS10.4](#)). A group of microbial models with dormant state gave better performance, while including physical occlusion and density-dependent adsorption strength gave no improvement. For further analysis of effect of structural uncertainty on global projections we consider the best fit model and it's simplified versions, as well as first order kinetics model.

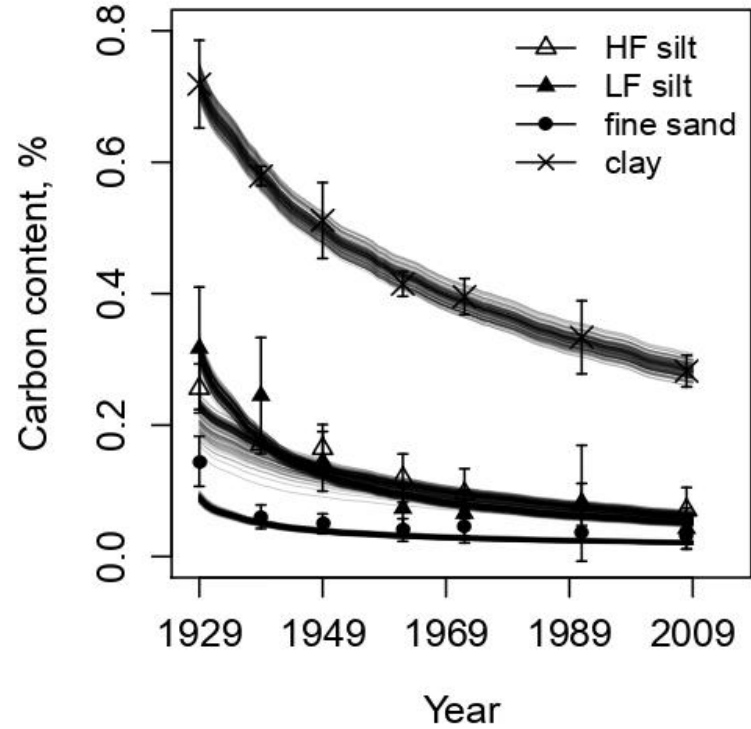
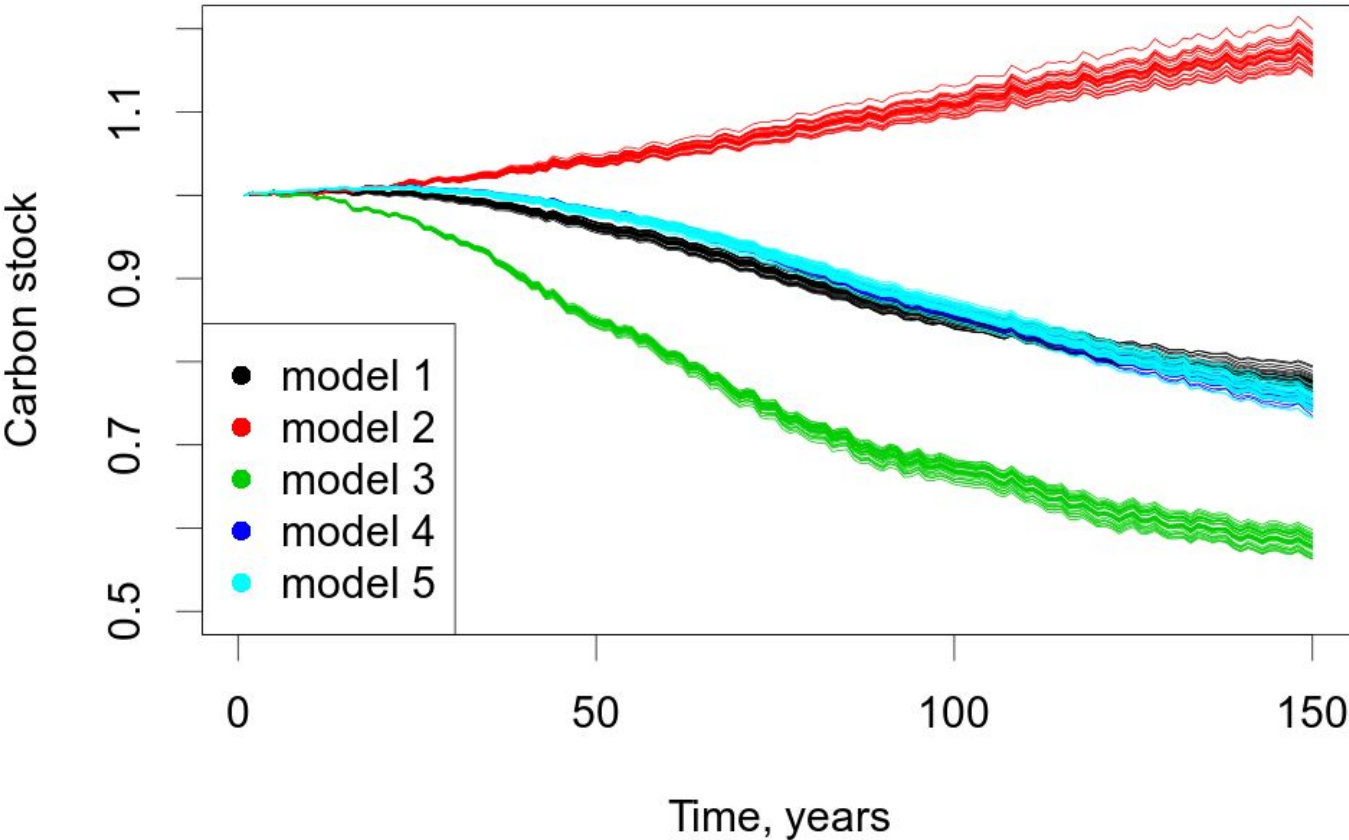


Figure shows carbon dynamics in physical fractions, obtained with model parameters sampled from normal distributions with estimated standard errors.

Model versions

	Model 1	Model 2	Model 3	Model 4	Model 5
Microbial growth, dynamic turnover rate (dormant state)	+	+	+	+	-
CUE	dynamic	constant	dynamic	constant	-
Priming effect	+	+	-	-	-
Model performance (BIC)	157	163	168	202	267

Results: comparison of model projections



Carbon stock, normalized to its initial value for different model versions.

Linear model, microbial model and microbial model with dynamic CUE and stable pool give similar result for overall carbon balance, but different spatial distribution and variance

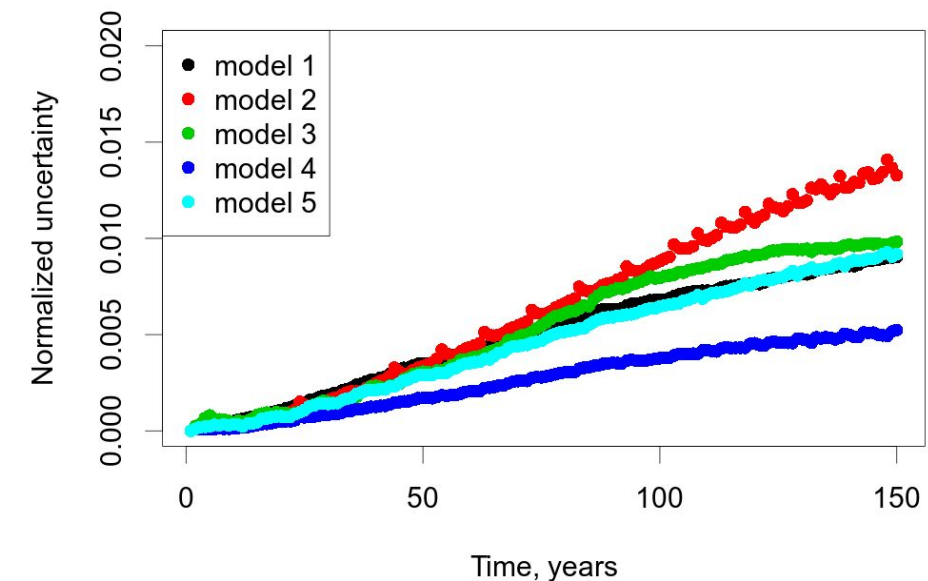
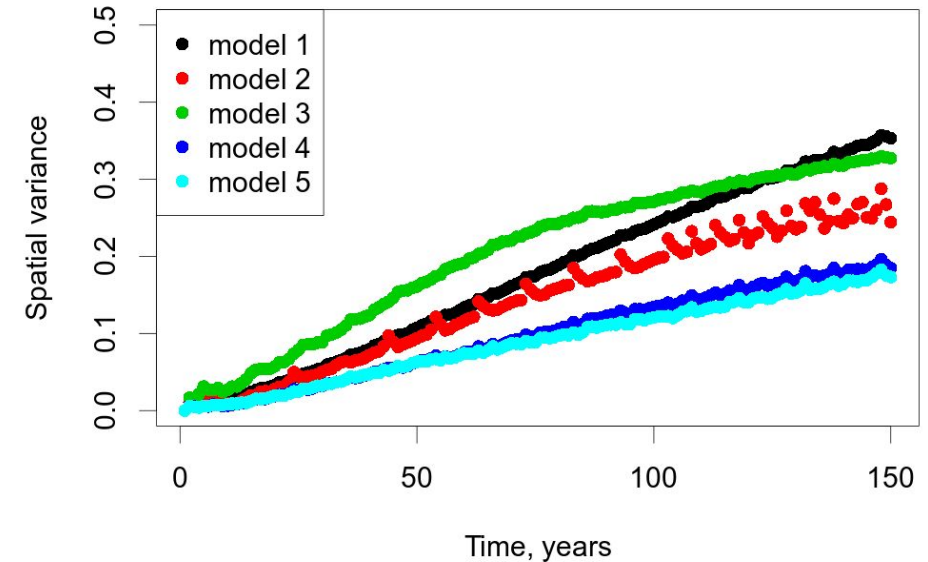
Effect of dynamic stable pool gives much faster decay in carbon stock, as all carbon can be consumed in this case.

Effect of dynamic CUE gives increase in carbon stock as decay rates grow slower with temperature and cannot compensate increasing litter input.

Results: structural uncertainty

To compare models with similar performance the following procedure was used:

- a) 100 spatial locations were randomly sampled from ESM grid, for each of them initial carbon content and time series of litter fall, temperature and moisture were extracted.
- b) Model parameters were adjusted by changing characteristic carbon content to give correct initial C value after spin up.
- c) Model parameters were sampled using normal distributions with standard errors, obtained by sensitivity analysis. Then a bunch of projection trajectories was produced for each spatial location.
 - From these trajectories spatial variance was calculated.
 - For each bunch standard deviation of carbon stock, normalized to its initial value was calculated at every time point, the result is plotted on the figure.



Conclusions

- Considering additional effects in the model structure results in better model performance (BIC), but may strongly change global carbon projections from gain to loss
- The simplest microbial model demonstrated the lowest uncertainty
- The simplest and the most complex microbial models produced similar projections for average carbon stock change, however its spatial distributions was very different (with higher spatial variation for complex model)
- Modeling chronosequence data from different locations is necessary to investigate relevant microbial feedbacks.

Thank you for your attention !