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Biological Mechanisms May Contribute to Soil Carbon Saturation Patterns: Modeling Archive

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Summary:

This Modeling Archive is in support of a TES-SFA publication “Biological Mechanisms May Contribute to Soil Carbon Saturation Patterns” (Craig et al., 2021).

We ran and evaluated a multi-assumption soil organic carbon (SOC) model to investigate whether alternative assumptions regarding constraints on soil microbial biomass could lead to soil carbon saturation patterns. We developed this model in the Multi-Assumption Architecture and Testbed (MAAT, https://github.com/walkeranthonyp/MAAT, tag: v1.2.1_Craig2021; Walker et al. 2018).

Using MAAT, we embedded three alternative hypotheses in a microbially explicit three-pool SOC model: 1) the efficiency of mineral-associated SOC formation decreases as mineral-associated SOC approaches a maximum value (“Mineral saturation”), 2) the microbial biomass turnover rate increases with increasing microbial biomass (“Density-dependent turnover”), and 3) community carbon use efficiency decreases as microbial biomass increases toward an upper limit (“Density-dependent growth”). We ran a factorial combination of these hypotheses resulting in eight models for three different classes of model (linear decay, Michaelis-Menten decay, or reverse Michaelis-Menten decay), resulting in 24 models, 12 of which are presented or discussed in the related publication. Models were parameterized using values from previous studies with similar models (Wang et al. 2013, Wieder et al. 2014, Li et al. 2014, Georgiou et al. 2017, Hassink and Whitmore 1997) and ran to an approximate steady state (200 years) at six (6) different C input rates corresponding to 0.5, 1, 2, 4, 7, and 10 times the default input value. Further model details are available in the related publication.

This archive contains output from three MAAT simulations, and scripts to run these simulations and process and plot the data. Simulations are labeled “lin”, “MM_highKm”, and “RMM_highKm” reflecting factorial runs for linear, Michealis-Menten, and reverse Michaelis-Menten models, respectively.

This archive contains:

- 3 R scripts prepended with "init_MAAT_" to initialize runs (1 for each simulation),
- 1 csv file containing years over which to run simulations ("met_year.csv"),
- 1 bash script (.bs) to run MAAT,
- 6 XML files that are output from MAAT describing a run (2 for each simulation),
- 3 model output csv files prepended by "out_" (1 for each simulation), and
- 1 analysis R script for reproducing figures 3 and 4 in Craig et al. 2021.

Related TES-SFA Publication:

A thorough description of the models and analysis is presented in the following publication: Craig ME, Mayes MA, Sulman BN, Walker AP. Biological mechanisms may contribute to soil carbon saturation patterns. *Global Change Biology*

Related TES SFA Datasets:

Matthew E. Craig, Anthony P. Walker. 2021. **Microbial Biomass in Soils Receiving Varying Levels of Organic Inputs - A Data Compilation.** Oak Ridge National Laboratory, TES SFA, U.S. Department of Energy, Oak Ridge, Tennessee, U.S.A. https://doi.org/10.25581/ornlsfa.021/1768047

Acknowledgments:

Modeling and analyses were performed by Matthew E. Craig (Postdoctoral Research Associate at Oak Ridge National Laboratory, Environmental Sciences Division and Climate Change Science Institute) in collaboration with Dr. Anthony P. Walker (walkerap@ornl.gov). Direct correspondence to Matthew Craig (craigmatthewe@gmail.com; ORCID: https://orcid.org/0000-0002-8890-7920).

Data and Documentation Access:

For public access to data from the US Department of Energy Terrestrial Ecosystem Science Scientific Focus Area (TES-SFA), please visit: **https://tes-sfa.ornl.gov/**

ORNL TES-SFA Data Policy: Archiving, Sharing, and Fair-Use

Overview of Terrestrial Ecosystem Science Scientific Focus Area

The TES SFA supports research to understand and predict the interaction of Earth's terrestrial ecosystems and climate, and to assess vulnerability of terrestrial ecosystems to projected environmental change. The research focuses on how terrestrial ecosystems affect atmospheric CO_2 and other greenhouse gases (e.g., CH_4) and how the responsible ecosystem processes interact with climate and with anthropogenic forcing factors.

- Targeted experiments are conducted to quantify and predict ecosystem responses to warming and elevated CO_2 (eCO_2) and the feedbacks from ecosystems to the atmosphere and climate.
- Other process research aims to accurately quantify the exchange of CO_2, water vapor, and energy between the atmosphere and land ecosystems through processes such as photosynthesis, evapotranspiration, net production, storage pools, and autotrophic and heterotrophic respiration.
- TES SFA research also includes efforts to provide comprehensive databases, above- and belowground, to benefit the analytical needs of Earth System Models.
- Understanding achieved by TES SFA tasks on the fundamental functions and interactions of vegetation, microbial community and soil is used to improve mechanistic representation of ecosystem processes within terrestrial biosphere models.

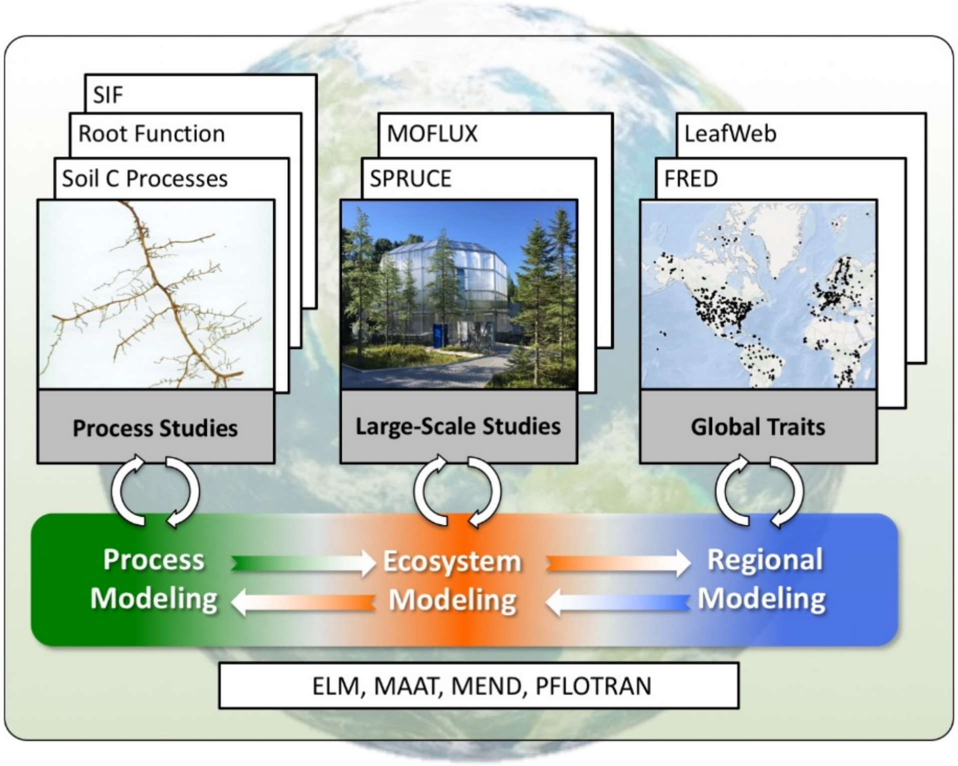

Diagram of the TES-SFA research philosophy and flow illustrating an iterative exchange between model projections, question or hypothesis development and the execution of observations and experiments to better understand impacts of multi-factor environmental changes on ecosystems.

Data Characteristics:

Temporal Coverage and Resolution:

The temporal aspects of the modeling activities were not essential to the analyses (Craig et al., 2021).

Spatial Coverage:

The spatial aspects of the modeling activities were not essential to the analyses (Craig et al., 2021). No geographic criteria were used during the modeling activities.

The location for this modeling archive will be listed as the Oak Ridge National Lab (ORNL): 35.9311 N, -84.3100 W.

Modeling Archive Contents:

Model

The model was developed in MAAT. Here is the public access and contact information for MATT.

Multi-Assumption Architecture and Testbed (MAAT), soil_decomp system model.
Contact: Anthony Walker (walkerap@ornl.gov)
Current version at: https://github.com/walkeranthonyp/MAAT
Version used for these simulations: tagged v1.2.1_Craig2021 at https://github.com/walkeranthonyp/MAAT

Input Files

- Environmental forcing (met_year.csv) during the run.
  - For these runs, this file merely acts as a time ticker. Soil water and temperature are included as dummy variables because >2 columns are needed to run MAAT.

Column Number	Column Name	Data Type	Description
1	year	integers (range: 1-200)	Year of simulation. This field defines the length of the model run and is appended to output data.
2	swc	numeric (dummy variable)	Soil water content (g/g). This field is irrelevant to these model runs which are unaffected by water.
3	temp	numeric (dummy variable)	Temperature (°C). This field is irrelevant to these model runs which are unaffected by temperature.

Output

This directory contains

- Output files for **three simulation configurations** as found in the paper (Craig et al. 2021):

1. “out_lin.csv” refers to the simulations using linear first-order decay kinetics.
2. “out_MM_highKm.csv” refers to the simulations using Michaelis-Menten decay kinetics.
3. “out_RMM_highKm.csv” refers to the simulations using reverse Michaelis-Menten decay kinetics.

- 3 XML files (out_lin_setup_static.xml, out_MM_highKm_setup_static.xml, out_RMM_highKm_setup_static.xml) describing static components of each MAAT run (i.e. functions, parameters, and environmental variables that do not vary among models within a run).

- 3 XML files (out_lin_setup_dynamic.xml, out_MM_highKm_setup_dynamic.xml, out_RMM_highKm_setup_dynamic.xml) describing dynamic components of each MAAT run (i.e. functions, parameters, and environmental variables that vary among factorial MAAT model runs).

Data dictionary for each of the 3 simulation configuration output *.csv files:

Column Number	Column Name	Data Type	Description
1	time	integers (range: 1-200)	Appended from “year” in “met_year.csv”
2	soil_decomp.temp	numeric (dummy variable)	Appended from “temp” in “met_year.csv”
3	soil_decomp.swc	numeric (dummy variable)	Appended from “swc” “met_year.csv”
4	soil_decomp.litter	numeric	Carbon input rate (mg C g soil^{-1} yr^{-1})
5	soil_decomp.transfer.t2_to_3	character	Function controlling the transfer of C from pool 2 to 3 (microbial biomass to mineral-associated SOC). “f_transfer_cue” transfers a static percentage (in this case 100%). “f_transfer_cue_sat” applies the mineral saturation hypothesis described in Craig et al. (2021).

Column Number	Column Name	Data Type	Description
6	soil_decomp.transfer.t1_to_2	character	Function controlling the transfer of C from pool 1 to 2 (particulate SOC to microbial biomass). “f_transfer_cue” transfers a static percentage (in this case 47%). “f_transfer_cue_sat” applies the density-dependent growth hypothesis described in Craig et al. (2021).
7	soil_decomp.transfer.t3_to_2	character	Function controlling the transfer of C from pool 3 to 2 (mineral-associated SOC to microbial biomass). “f_transfer_cue” transfers a static percentage (in this case 47%). “f_transfer_cue_sat” applies the density-dependent growth hypothesis described in Craig et al. (2021).
8	soil_decomp.decomp.d2	character	Function controlling the decomposition of pool 2 (microbial biomass). “f_decomp_lin” is first-order linear decomposition. “f_decomp_dd” applies the density-dependent turnover hypothesis described in Craig et al. (2021).
9	cpools1	numeric	Particulate SOC pool (mg C g soil^{-1})
10	cpools2	numeric	Microbial biomass pool (mg C g soil^{-1})
11	cpools3	numeric	Mineral-associated SOC pool (mg C g soil^{-1})
12	cpools_n	integer	number of pools in the model structure (this is always 3 here).

Configurations

This directory contains

- Initialization files (init_MAAT_lin.R, init_MAAT_MM_highKm.R, init_MAAT_RMM_highKm)
    - These files specify static parameters and functions and set up factorial combinations of functions and input levels.
- Bash script (call_run_MAAT_inputlevs_althyp.bs) to run MAAT with the initialization and environmental forcing files.

Post-processing/Distillation and Analysis

- "Analysis.R" processes the three output csv files (e.g. renames variables, names models based on hypothesis combinations, reformats the data for analysis of steady-state values), and creates figures 3, 4, S3, and S4 from the related publication (Craig et al. 2021).

References:

Georgiou, K., Abramoff, R. Z., Harte, J., Torn, M. S. & Riley, W. J. Microbial community-level regulation explains soil carbon responses to long-term litter manipulations. *Nature Communications* **8**, 1–10 (2017).

Hassink, J. & Whitmore, A. A model of the physical protection of organic matter in soils. *Soil Science Society of America Journal* **61**, 131–139 (1997).

Li, J., Wang, G., Allison, S. D., Mayes, M. A. & Luo, Y. Soil carbon sensitivity to temperature and carbon use efficiency compared across microbial-ecosystem models of varying complexity. *Biogeochemistry* **119**, 67–84 (2014).

Wieder, W. R., Grandy, A. S., Kallenbach, C. M. & Bonan, G. B. Integrating microbial physiology and physio-chemical principles in soils with the MIcrobial-MIneral Carbon Stabilization (MIMICS) model. *Biogeosciences* **11**, 3899–3917 (2014).

Walker, A. P. *et al.* The multi-assumption architecture and testbed (MAAT v1.0): R code for generating ensembles with dynamic model structure and analysis of epistemic uncertainty from multiple sources. *Geosci. Model Dev.* **11**, 3159–3185 (2018).

Wang, G., Post, W. M. & Mayes, M. A. Development of microbial-enzyme-mediated decomposition model parameters through steady-state and dynamic analyses. *Ecological Applications* **23**, 255–272 (2013).

Data Access:

For public access to ORNL TES SFA data please visit the TES SFA Web Site: https://tes-sfa.ornl.gov/home

Contact for Data Access Information: https://mnspruce.ornl.gov/contact