Numerical comparison of five soil microbial models, in relation to measurable soil organic matter fractions

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1 What did we do?

- **MCM – minimum consensus model approach: Build a «skeleton» biogeochemical model with features common to** various biogeochemical models
- consider measurable **soil matter pools** only
- **Plugins to extend the skeleton model**

2 Why?

1. Main driver for soil organic carbon (SOC) cycling is the soil microbial community
2. soil "microbiomes" differ in structure and functions across ecosystems
3. Various biogeochemical models exist, each representing different structures and functions of the microbiomes
4. difficult to compare them and hard to understand which behaviour/processes of the microbial community most releant and in which conditions

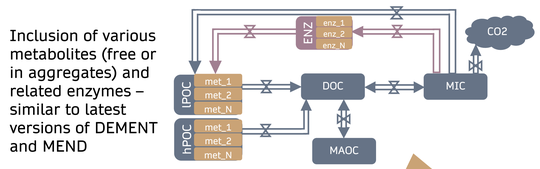
Example: Sulman et al. 2018 → How do we solve the uncertainty problem?

4 MCM approach

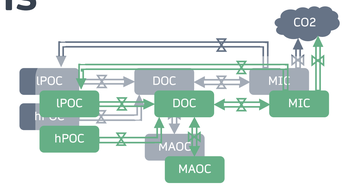
1. Five different biogeochemical models selected from literature: MEND, RESOM, CORPSE, MIMICS, DEMENT
2. Equations sets for each of them was extracted, and used to find the intersection of equations sets
3. Used intersection to build the "skeleton", fixed to be able to work by itself
4. Remaining equations adapted to build "plugins" representing original models
5. Plugins tested: do they give the same results as original models with same parameters? → YES
6. Skeleton models and plugins implemented in: Vensim (System Dynamics), R, Python

Plugins

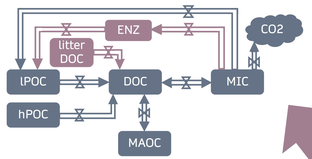
Inclusion of various metabolites (free or in aggregates) and related enzymes – similar to latest versions of DEMENT and MEND



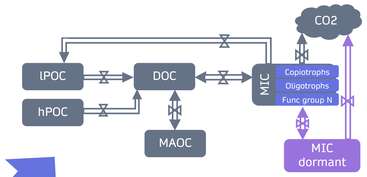
Inclusion of "duplicates" of the system to represent separated communities (e.g. rhyzosphere, hot spots in aggregates)



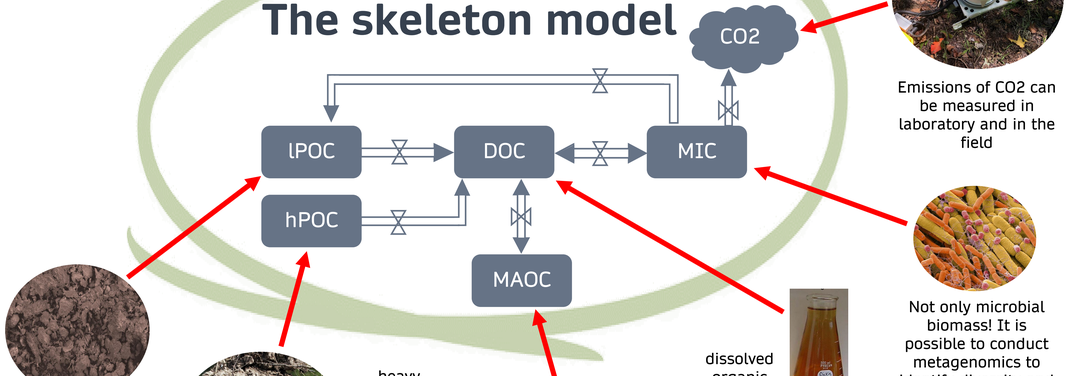
Inclusion of enzymes and dissolved organic carbon infiltrating from litter – similar to DEMENT



Inclusion of microbial functional groups and dormancy – similar to MIMICS and MEND

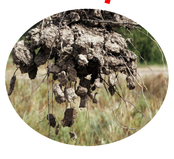


Emissions of CO2 can be measured in laboratory and in the field

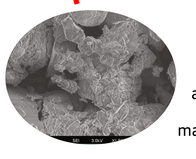


Not only microbial biomass! It is possible to conduct metagenomics to identify diversity and abundances of the soil microbiome

light particulate organic matter carbon – carbon contained larger molecules and vegetable material



heavy particulate organic matter carbon – carbon contained in aggregates



mineral associated organic matter carbon

dissolved organic carbon

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Sharing is encouraged

5 Preliminary results

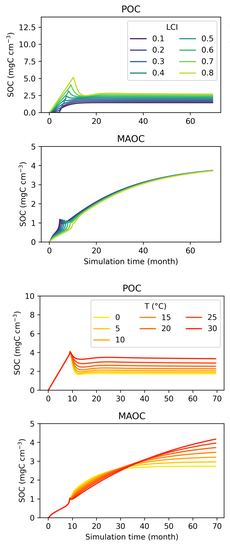
SOC value and dynamics similar among original models **but** we can see the difference in the plugin results in response to:

- Change in soil carbon input (lignocellulosic index)
- Change in soil temperature

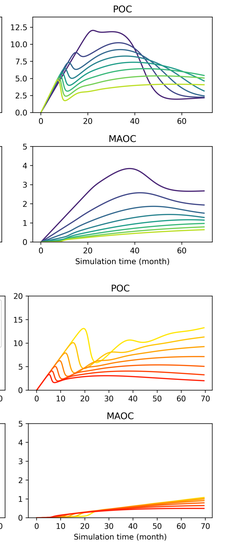
All difference large enough to be detectable in field experiments

Conclusions:
1) Comparison among models
2) Plugins discriminate between effects on measurable carbon pools
3) Very robust – possible to determine parameters space of best fit

Enzymes and dormancy plugin



Functional groups plugin



6 Future developments

- MCM approach working in theory → what about reality? Conduct a series of test in different conditions
- Improve-expand the model: coupling with soil physical models, introduce biochar and nitrogen, adapt to metagenomic data input