

Identifying relevant soil microbial diversity metrics to integrate in soil carbon dynamic models



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Introduction

- A large quantity of carbon dynamic models has been developed during the last century
- Microbial diversity is mostly missing in these models, although evidences of its significant role in soil carbon dynamic
- These characteristics could be integrated in models through functions for adjustment of parameters
- One major issue is to identify which microbial diversity metrics are relevant to explain soil carbon dynamics

Objective

To identify if microbial diversity metrics, together with classical edaphic variables, are relevant to explain carbon fluxes from an incubation experiment

Thematic variables used

MOS Total Carbon, Nitrogen

pH

Texture Clay, Silt, Sand

MolBiomass ADN quantity at 0 and 3 days

BactRich OTU number, Chao1 index, ACE index, Rare OTU number for bacteria

BactDiv Shannon index, Evenness index, Simpson index inverse Simpson index, Abundant OTU number for bacteria

FungiRich OTU number, Chao1 index, ACE index, Rare OTU number for fungi

FungiDiv Shannon index, Evenness index, Simpson index inverse Simpson index, Abundant OTU number for fungi

Landuse (either pasture or cropland)

Discussion

For modelling :

- Classical abiotic variables have been revealed good predictors suggesting that the method used gives consistent results
- Microbial diversity appears relevant to improve predictive quality of carbon dynamic
- The useful metrics of microbial diversity depend on the flux considered and on the time of incubation

Limits :

- Due to high correlation, only thematic variables have been identified
- The contribution of each variable is not known

Ongoing work

- Identification of relevant variables among the thematic ones and ranking of their contribution in predictive quality improvement
- Construction of functions between C dynamic model parameters and identified variables
- Assessment of predictive quality improvement after intergration of these functions in models

Materials and Methods

Available data

Data come from an experimental results from a French National Research Agency program called DIMIMOS (ANR-08-STRA-06) :

- ¹³C-labelled wheat residue has been incorporated into 28 soils with different known pedological characteristics and land use history
- Amended and non-amended (control) soils have been incubated during 104 days and labelled and non-labelled CO₂ fluxes have been measured at 9 sampling times
- Diversity, structure and composition of microbial communities have been characterized before incubation time.

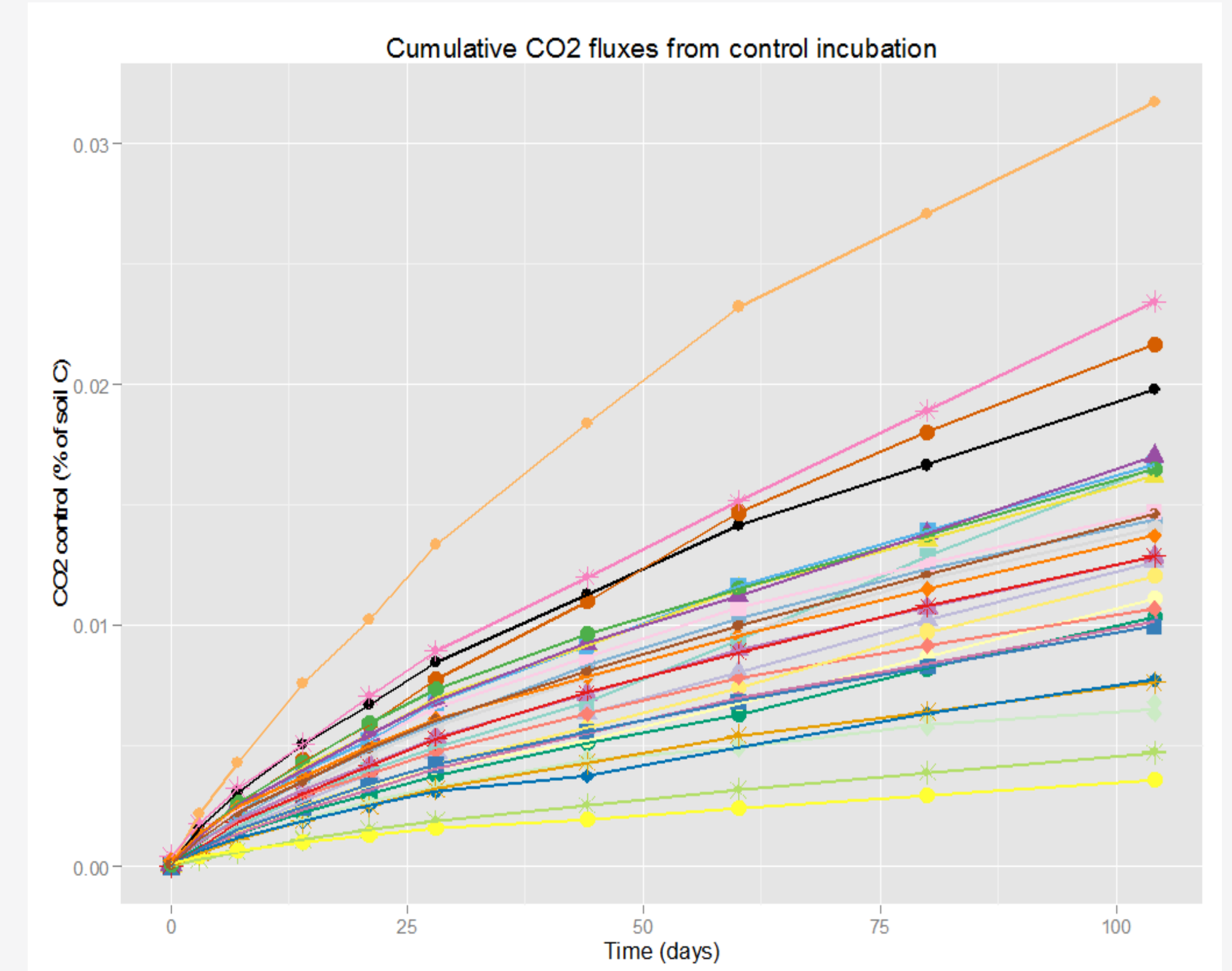


Figure 1: Control CO₂ flux

Statistical method

For each flux at each time of measure :

- 3 forward stepwise variable selections based on the *MSEP* minimisation of 3 *GAM*[1] models using i) spline smoothing, ii) loess fitting and iii) 3rd degree polynomial fitting are performed

$$MSEP = \frac{1}{n} \sum_{i=1}^n (\hat{y}_i - y_i)^2,$$

where \hat{y}_i is the flux prediction at one sampling time for the soil *i* with the model calibrated without soil *i*

- A variable selection based on random forest approach[2] is performed

Decision

Correlated metrics were grouped in thematic variables. We count the number of time that a thematic variables is selected in the 4 methods × 9 sampling times for each flux. The specific result at each sampling time for each flux is also considered.

Results

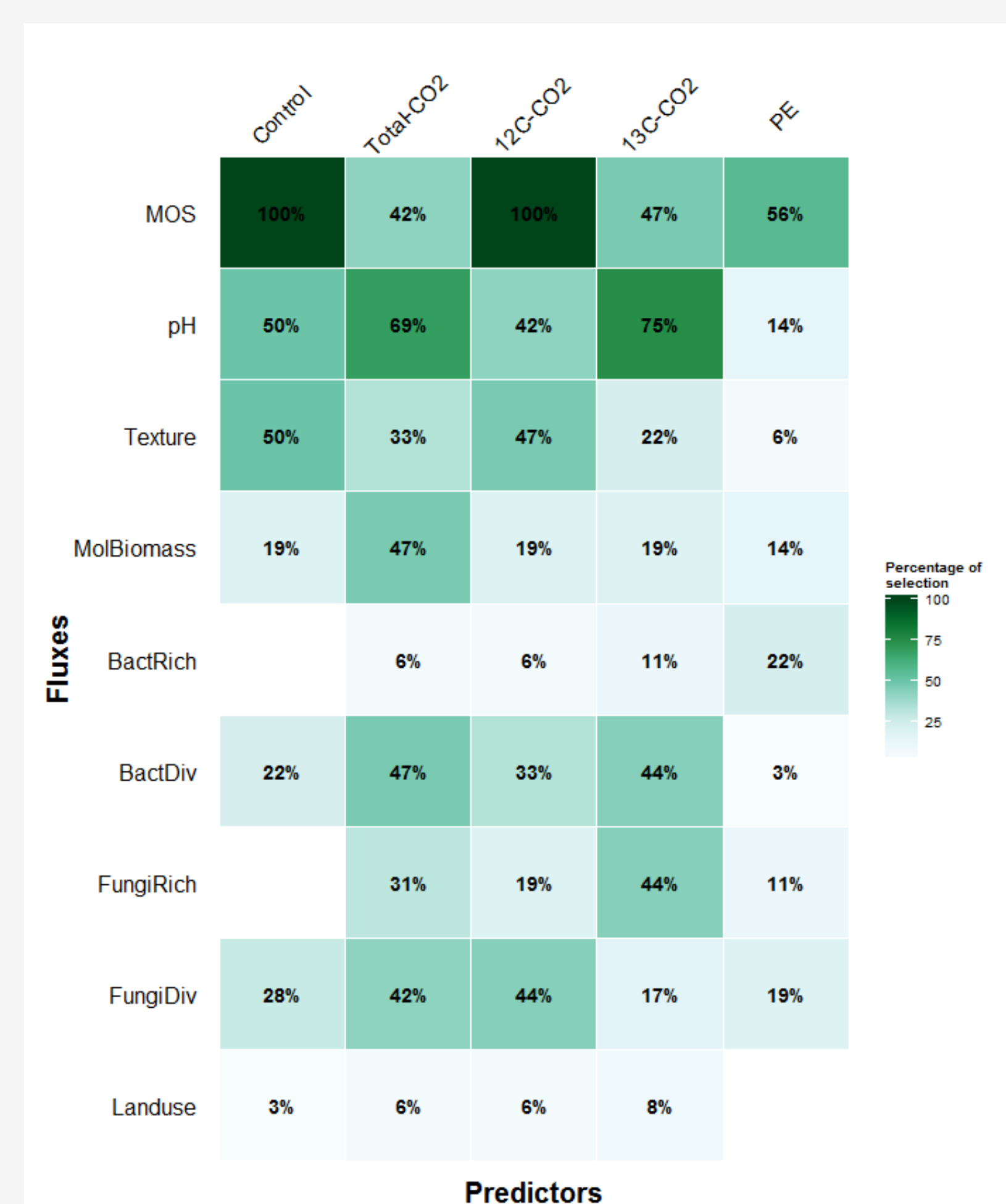


Figure 2: Proportion when thematic variables were selected by fluxes

Results on fluxes show :

- Classical abiotic variables (MOS, pH and texture) have been selected for all fluxes as expected
- Bacterial diversity and fungi richness have been selected for labelled fluxes
- Bacterial and Fungi diversity have been selected for non-labelled fluxes

The results observed at each sampling time show that :

- Bacterial diversity and fungi richness are rather selected for late sampling times of labelled fluxes (from 44 days)
- For non-labelled fluxes, fungi diversity is rather selected at early sampling times (up to 21 days) while bacterial diversity is rather selected for next sampling times

References

- [1] T.H. Hastie and R. Tibshirani. *Generalized Additive Models*. Chapman & Hall/CRC, 1990.
- [2] R. Genier, J-M. Poggi, and C. Tuleau-Malot. Variable selection using random forests. *Pattern Recognition Letters*, 31:2225–2236, 2010.