

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

Benjamin P. Louis<sup>\*,1,2,3</sup>, Safya Menasseri-Aubry<sup>1,2,3</sup>, Philippe Leterme<sup>1,2,3</sup>, Pierre-Alain Maron<sup>4</sup> and Valérie Viaud<sup>2,1,3</sup>

<sup>1</sup>AGROCAMPUS OUEST, UMR 1069 SAS, F-35042 Rennes, France, <sup>2</sup>INRA, UMR 1069 SAS, F-35042 Rennes, France, <sup>3</sup>Université européenne de Bretagne, France, <sup>4</sup>INRA, Université de Bourgogne, UMR 1229 Microbiologie du Sol et de l'Environnement, Dijon Cedex, France  
\*benjamin.louis@agrocampus-ouest.fr



## 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

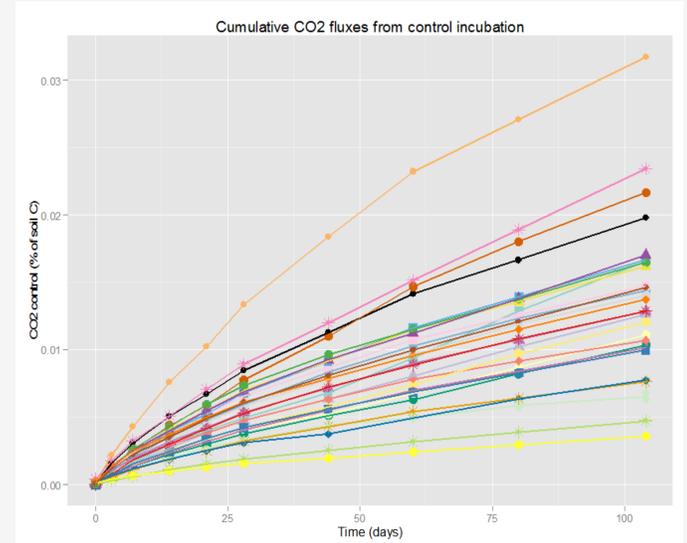
- Identification of relevant variables among the thematic ones and ranking of their contribution in predictive quality improvement
- Construction of functions between C dynamic model parameters and identified variables
- Assessment of predictive quality improvement after intergration of these functions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

- <sup>13</sup>C-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 CO<sub>2</sub> fluxes have been measured at 9 sampling times
- Diversity, structure and composition of microbial communities have been characterized before incubation time.



**Figure 1:** Control CO<sub>2</sub> 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

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

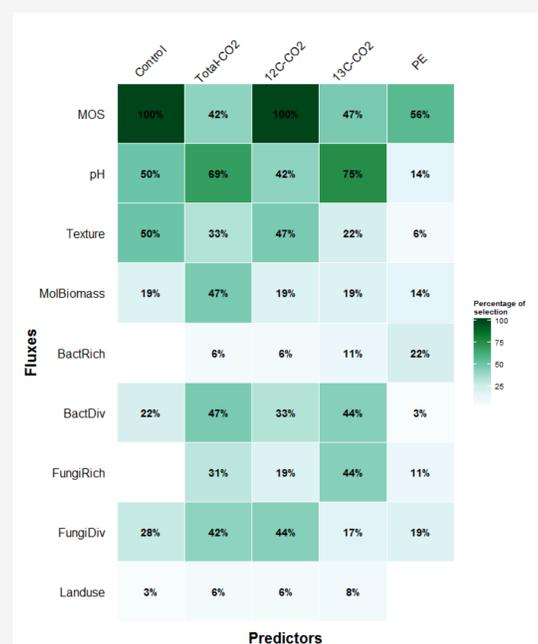
where  $\hat{y}_i$  is the flux prediction at one sampling time for the soil *i* with the model calibrated without soil *i*

- 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.