

## D2.8 New version of ORCHIDEE and EFISCEN-Space

### Holistic management practices, modelling and monitoring for European forest soils, HoliSoils

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<b>Deliverable D2.8: New version of ORCHIDEE and EFISCEN-SPACE</b>		
Here we show the implementation of the biodiversity function developed in D2.3 into ORCHIDEE and EFISCEN-Space and how it impacts the model outputs.		
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R	Document, report	X
DEM	Demonstration, pilot, prototype, plan design	
DEC	Websites, patents filing, market studies, press & media actions, videos etc.	
OTHER	Software, technical diagram etc.	
Ethics	Ethics deliverables	

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## 1. Introduction

Soil micro-organisms are the main drivers in the decomposition of soil organic matter. For this reason, the literature is increasingly recommending an accurate representation of their activities in large scale models (Wieder *et al.* 2014). However, an explicit representation of microorganisms is not easy, notably because microbial dynamics are complex and their description requires mathematical approaches that are difficult to use on a large scale (Huang *et al.* 2021). With this in mind, in the HoliSoils project we set out to propose innovative solutions that would allow microbial dynamics to be taken into account, but in a mathematical approach that is compatible with large-scale simulations. The proposed approach is based on the idea that, rather than explicitly representing microbial populations, large-scale models need to represent the resulting effects of microbial dynamics on SOM decomposition fluxes. In other words, microbial processes are described implicitly with a empirical or semi-empirical function or set of functions via suitable parameterizations—a pragmatic approach that has proven effective for modelling large-scale, long-term dynamics.

To this end, we have chosen a simple approach still based on first-order kinetics for describing SOC decomposition, but with the addition of a decomposition rate modifier that drives decomposition as a function of biodiversity index. This modifier varies between 0 and 1 and is based on D2.2.a published by Khurana *et al.* (2023). This rate modifier accounts for any interaction between microbial groups and their substrates, as well as among microbial groups in the community. Generally, such interactions lead to increased decomposition rates in more diverse communities, thanks to complementarity effects. The positive effect of microbial diversity predicted by Khurana *et al.* (2023) is consistent with findings from empirical studies

where community richness was manipulated, though the effect becomes less important in highly diverse communities (Bell *et al.* 2005; Domeignoz-Horta *et al.* 2020). The main advantage of this approach is that with this rate modifier, we can capture complex microbial processes in a way that is consistent with the mathematical formulations of soil C models.

In this report, we describe how this function is currently integrated into ORCHIDEE and EFISCEN-Space and we demonstrate the effect of integrating this function into ORCHIDEE. Moreover, since the soil carbon scheme of EFISCEN-Space is based on Yasso and within the project we developed a new soil moisture function for Yasso (Tupek *et al.* 2023) a description of the new Yasso implementation into EFISCEN-Space is also included.

## 2. The ORCHIDEE model

### 2.1 The structure of the model

ORCHIDEE is a terrestrial ecosystem model that calculates the fluxes of carbon (C), nitrogen (N), H<sub>2</sub>O, and heat exchanged between the land surface and the atmosphere on a half-hourly basis, and the variations of C and N pools on a daily basis (Vuichard *et al.* 2018). Recently, some specific forest modules were implemented from Naudts *et al.* (2015). The soil carbon module comes from CENTURY (Parton *et al.* 1987) and describes soil carbon using three pools called active, slow and passive, with different residence times. The dynamics of soil organic carbon (SOC) for each pool is controlled by first order equations:

$$\frac{\partial SOM}{\partial t} = I - k \times SOM \times \theta \times \tau \times \gamma \quad (1)$$

where  $I$  is the input of OM into each pool and  $k$  is the soil organic matter decomposition rate.  $\theta$ ,  $\tau$ , and  $\gamma$  are the soil moisture function, the temperature function, and the texture function modulating decomposition, respectively. Then, the decomposed organic matter is partially redistributed on others pools or respired (reps. mineralized) if C (resp. N) exists in the system. To describe microbial diversity effects, here we modified eq. 1 into eq. 2

$$\frac{\partial SOM}{\partial t} = I - k \times SOM \times \theta \times \tau \times \gamma \times f_{FD} \quad (2)$$

where  $f_{FD}$  is the rate modifiers coming from Khurana *et al.* (2023) described in eq. 3.

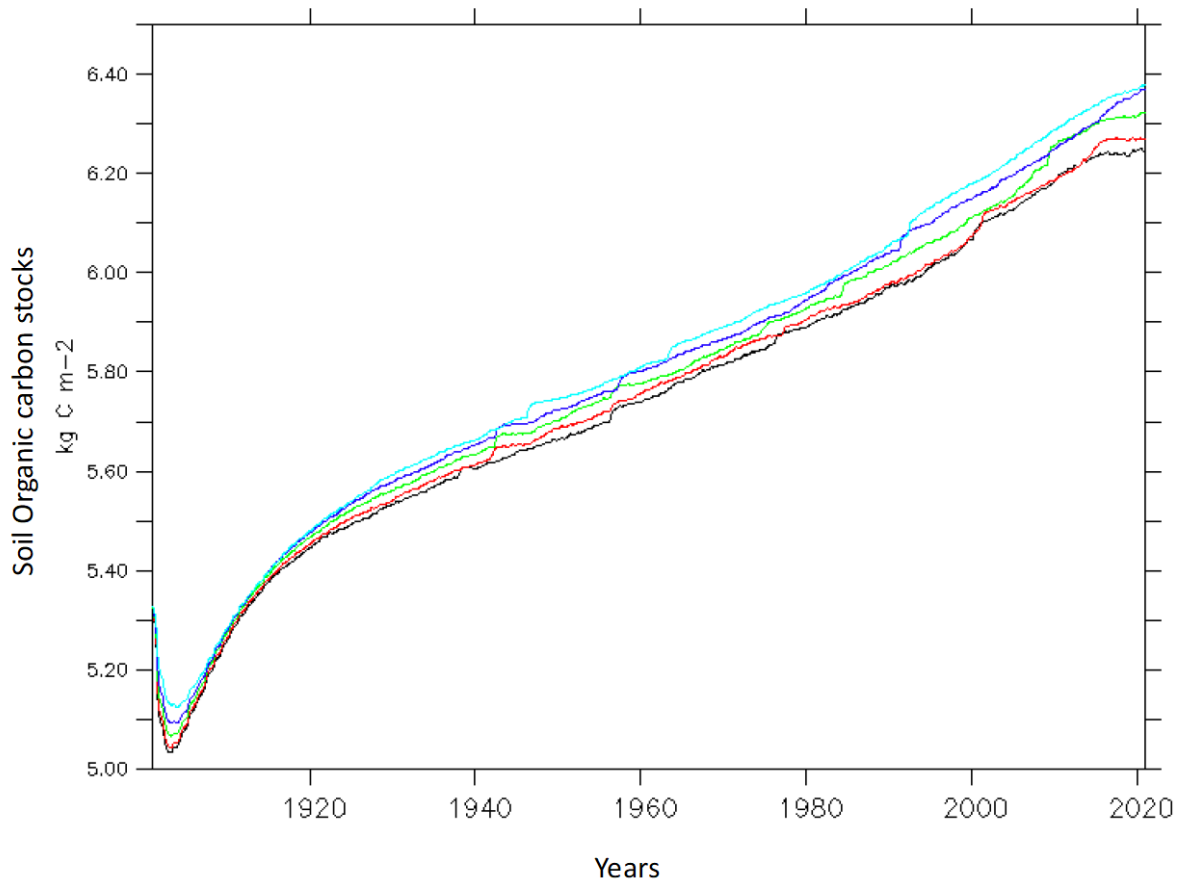
$$f_{FD} = \left( \frac{f_0}{f_{0,max}} \right)^\beta \quad (3)$$

where  $f_0$  is the microbial diversity index,  $f_{0,max}$  is the maximum value that the microbial diversity index can take and  $\beta$  an exponent characterizing the shape of the curve. Positive values of  $\beta$  indicate a positive diversity effect; negative values a negative effect. In the model analysis of Khurana *et al.* (2023)  $\beta$  was 0.1, implying that decomposition rates increase with increasing diversity, but with lower sensitivity to changes in diversity at high values of the diversity index—i.e., in highly diverse communities. Because  $\frac{f_0}{f_{0,max}} < 1$ , higher values of  $\beta$  for a given  $\frac{f_0}{f_{0,max}}$  actually decrease the value of  $f_{FD}$ , because the  $f_{FD}$  function has a stronger curvature at low  $\beta$ .

### 2.2 The simulations

For this report, we run idealized simulations over a pixel in France (47.0N, 9.0E) for 120 years. We use atmospheric CO<sub>2</sub> values corresponding to the global average over the years considered and we used climate data from CRU-JRA product for the 1901-2020 period. Similarly, the N deposition is coming from the products provided for the CMIP6 exercise and is also changing with time. The initial SOC value was 5 kg C m<sup>-2</sup> and the trees were planted at the beginning of the simulation. We run a sensitivity analysis over the microbial diversity index ( $f_0$ ) and the exponential ( $\beta$ ). Note that the nature of the microbial diversity index was not specified in Khurana *et al.* (2023). Thus, here we consider a theoretical diversity index and evaluate two situations, one where the diversity is maximal ( $f_0 = f_{0,max}$ ), i.e.,  $f_{FD} = 1$ , and

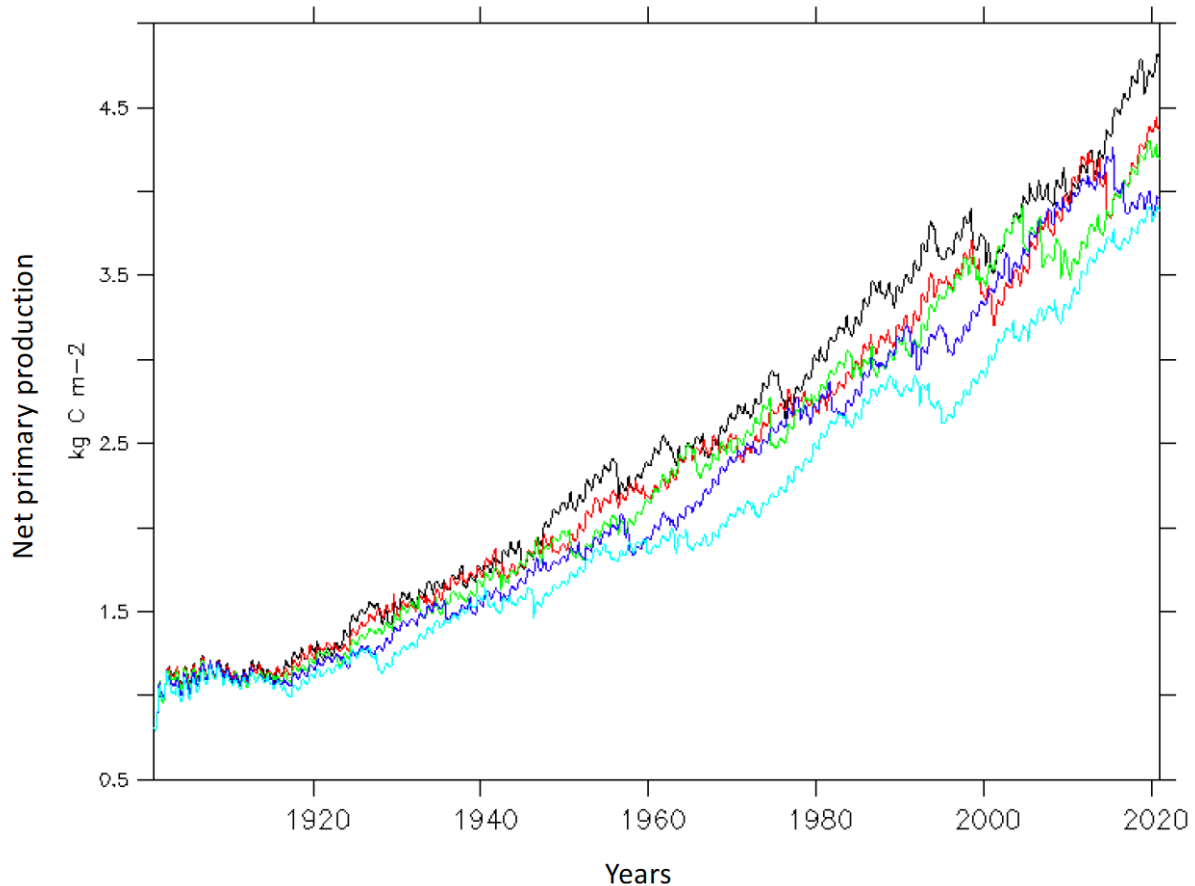
one where the diversity is half the maximal ( $f_0 = 0.5 \times f_{0,max}$ ), i.e.,  $f_{FD} = 0.5^\beta$ . We also run a sensitivity analysis with  $\beta = 0.1, 0.3, 0.5$  or  $0.8$ . For this sensitivity analysis, we used  $f_0 = 0.5 \times f_{0,max}$ . It is important to note that when  $f_0 = f_{0,max}$ ,  $f_{FD}$  takes the value of 1, being equivalent to the version of ORCHIDEE without the  $f_{FD}$  function implemented. The values chosen for the sensitivity analysis are similar to those chosen for D2.5.



**Figure 1:** Evolution of the soil organic carbon stocks ( $\text{kg C m}^{-2}$ ) for in  $f_0 = f_{0,max}$  in black,  $f_0 = 0.5 \times f_{0,max}$  in red, for  $\beta = 0.3$  in green,  $0.5$  in dark blue and  $0.8$  in light blue.

We observe on Fig. 1 that the soil organic carbon stocks increase during the studied period. It is due to an increase in the litter inputs due to the tree growth. We also observed that the soil organic carbon stocks depends on the value of  $f_0$  and  $\beta$ . As expected, when  $f_0 = 0.5 \times f_{0,max}$  the soil organic matter decomposition (including C and N) is reduced leading to an increase in soil organic carbon stocks. When  $\beta$  increases it also decreases the value of  $f_{FD}$  leading to a reduction of the decomposition and therefore an increase of the soil organic matter. To understand this effect, recall that higher values of  $\beta$  imply a lower curvature and thus a less steep increase of  $f_{FD}$  with increasing diversity at  $f_0 < f_{0,max}$ . In ORCHIDEE, the soil

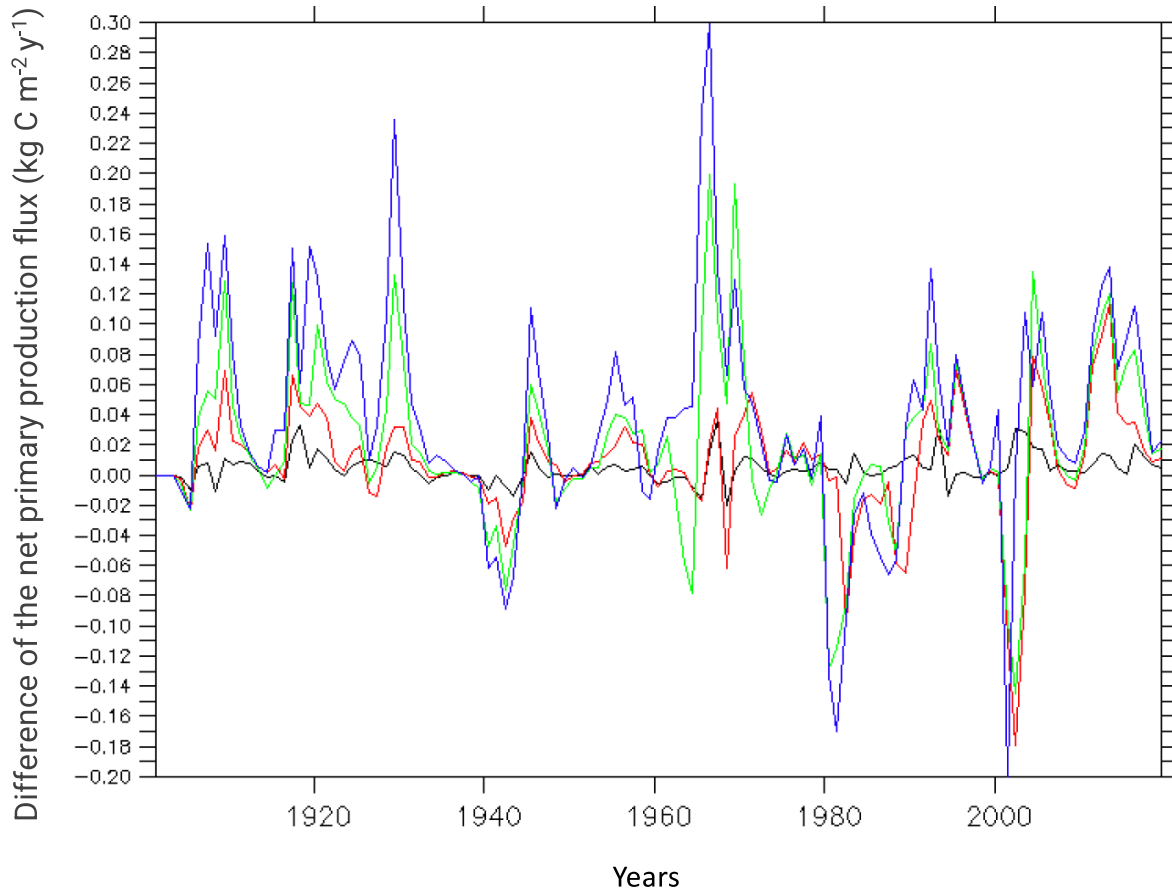
organic matter decomposition also controls the nitrogen release into the soil solution and therefore the nitrogen availability to plants.



**Figure 2:** Evolution of the carbon stocks in the tree biomass ( $\text{kg C m}^{-2}$ ) for  $f_0 = f_{0,max}$  in black,  $f_0 = 0.5 \times f_{0,max}$  in red, for  $\beta = 0.3$  in green, 0.5 in dark blue and 0.8 in light blue.

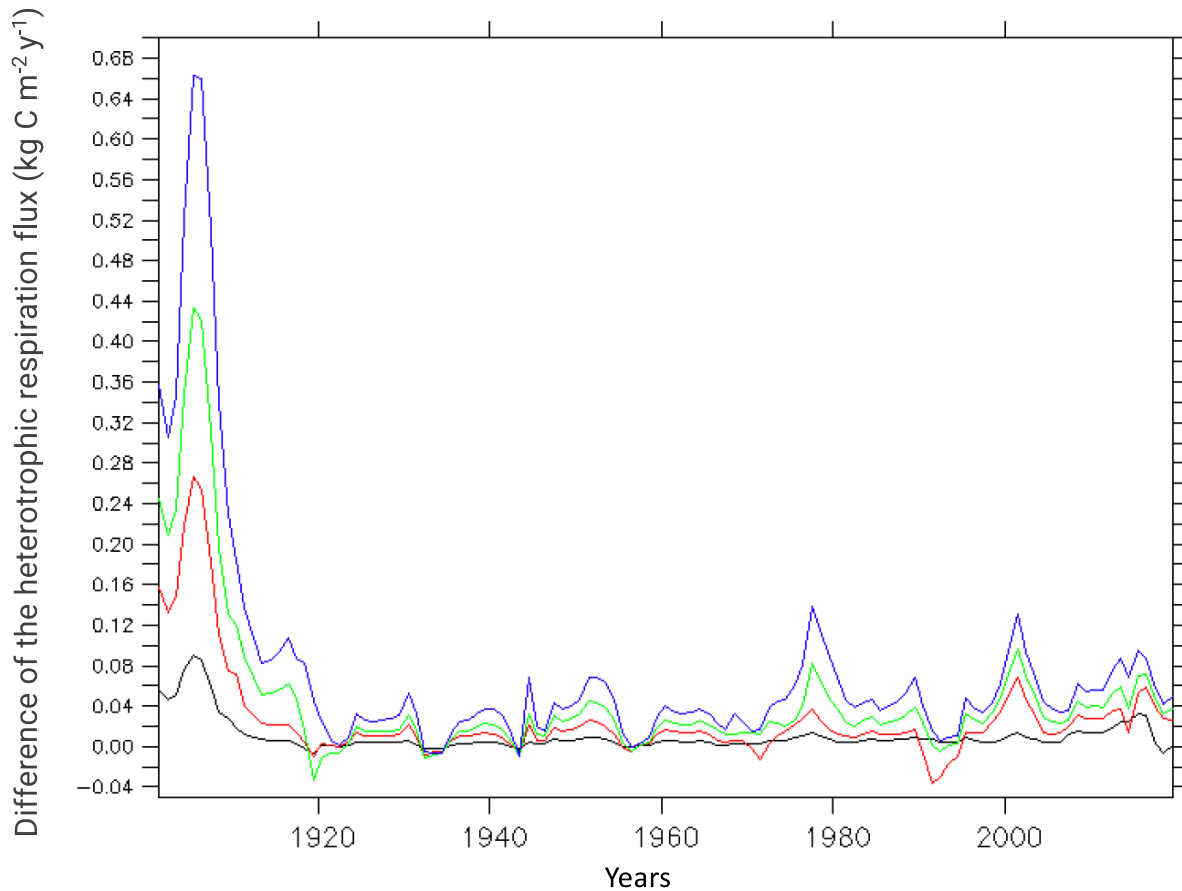
Consequently, the modification of the  $f_{FD}$  function not only impacts the soil organic matter dynamics (including C and N) but also the tree growth as shown in Fig. 2. Indeed, when  $f_0 = f_{0,max}$  soil organic matter mineralization is maximum (i.e., no reduction in the decay constants due to low diversity), leading to increase the N availability in the soil solution (black line in Fig. 2). As a consequence, the plant N uptake is relatively high and more tree growth is predicted by the model. When  $f_{FD}$  is reduced as it would occur when microbial diversity is negatively impacted by disturbance or management, the more it is reduced the less nitrogen is available and therefore the tree growth and the carbon in the biomass decrease. It is interesting to note that despite a decrease in the tree biomass induced by a decrease in  $f_{FD}$ , the soil organic carbon stocks increase with decreasing  $f_{FD}$ . It suggests that in the model the soil organic matter decomposition (i.e. the second term of eq. 1) is more reduced than the input (i.e. the first term of eq. 1) leading to a higher C storage in soils.

To study the effect on the exchange with the atmosphere we calculated for the soil heterotrophic respiration and for the net primary production the difference between the simulation with  $f_0 = f_{0,max}$  and the other simulations.



**Figure 3:** Difference of the net primary production flux ( $\text{kg C m}^{-2} \text{y}^{-1}$ ) between the simulation with  $f_0 = f_{0,max}$  ( $f_{FD} = 1$ ) and  $f_0 = 0.5 \times f_{0,max}$  in black and  $\beta = 0.1$ ,  $f_0 = 0.5 \times f_{0,max}$  and  $\beta = 0.3$  in red,  $f_0 = 0.5 \times f_{0,max}$  and  $\beta = 0.5$  in green, and  $f_0 = 0.5 \times f_{0,max}$  and  $\beta = 0.8$  in blue.

In fig. 3 we observed a large variability in the net primary production difference between simulations at high ( $f_{FD} = 1$ ) and low microbial diversity ( $f_{FD} < 1$ ), in particular with higher values of the exponent  $\beta$ . Fig. 3 showed that when  $f_{FD}$  is reduced, the absolute value of the difference between net productivity at high and low diversity increases. Indeed, we observed important decrease of net primary production in the 60's when  $\beta = 0.8$  but also important increase for the same simulation in the 80's. In ORCHIDEE, NPP is sensitive to climatic conditions explaining the interannual variability but it is interesting to note that the climate sensitivity of the model seems to be partially controlled by the  $f_{FD}$  value.



**Figure 4:** Difference of the heterotrophic respiration flux ( $\text{kg C m}^{-2} \text{y}^{-1}$ ) between the simulation with  $f_0 = f_{0,max}$  and  $f_0 = 0.5 \times f_{0,max}$  in black, with  $f_0 = f_{0,max}$  and  $\beta = 0.3$  in red, with  $f_0 = f_{0,max}$  and  $\beta = 0.5$  in green and with  $f_0 = f_{0,max}$  and  $\beta = 0.8$  in blue.

In fig. 4 we observed that decreasing  $f_{FD}$  reduce heterotrophic respiration in the great majority of the cases, as indicated by positive differences between simulated respiration at high ( $f_{FD} = 1$ ) and low microbial diversity ( $f_{FD} < 1$ ). Indeed, only some years showed slightly negative differences suggesting an increase in heterotrophic respiration ( $\beta = 0.3$  in the 90's,  $\beta = 0.5$  in the late 10's, etc.). Fig. 4 showed that the effect of different  $f_{FD}$  is not the same during the simulation period with higher differences in the 70's and in the 80's. It suggests like for net primary production that the interannual variability of the heterotrophic respiration flux is affected by the  $f_{FD}$  function even though  $f_{FD}$  is considered constant throughout the simulation length. This indicated some combined effects between diversity and climate on the simulated fluxes.

## 2.3 Discussion and Perspective

Here we show how the  $f_{FD}$  function developed by Khurana *et al.* (2023) is adapted to and implemented in the ORCHIDEE model. The model represents the interaction between the



soil and the plant with important feedbacks due to the carbon and nitrogen cycles, and these interactions are altered by changes in the  $f_{FD}$  function. Such effects propagate from the soil organic carbon dynamics to the net primary production and the carbon storage in the tree biomass. This new model opens interesting avenue for future research in particular to study the feedbacks between soil microbial diversity and plant growth in systems where diversity has been altered by management or disturbance events.

In practice, the diversity effects amount to a time-invariant re-scaling of the decay constants in the model, which could be captured by a site-specific calibration. The advantage of linking the decay constants to microbial diversity (instead of re-calibrating them) is that we could use the modified ORCHIDEE model to describe soil and vegetation responses to disturbances that affect microbial communities in known ways—e.g., altering taxonomic richness or community composition. However, there remain three major challenges hampering progress in this direction: i) we still do not know if the new rate modifier is applicable in the proposed form in field settings (it was derived from mathematical modelling and confirmed by data from laboratory incubations with low-diversity communities); ii) we do not know if the exponent of the rate modifier (which we have shown here to play a major role) can be regarded as constant across ecosystems (preliminary analysis using data from García-Angulo *et al.* (2020) suggest that it might not be the case); and iii) it is still unclear what easily measurable diversity indices can be used as proxies for functional diversity.

Upcoming work in HoliSoils will start addressing these challenges. Now that the code is working, the next step will be to test the model outputs using the data obtained in the WP1,4 and 5 over the experimental sites and eventually recalibrate the  $f_{FD}$  function. Once the model is evaluated at site level, application at European scale might be considered. Indeed, the implementation of the  $f_{FD}$  function has been done in the model in a way that allow the  $f_0$  to be read from a map potentially coming from the outputs of the WP1. Thus, the importance of the spatial distribution of the microbial diversity index considered can be tested in the ORCHIDEE model. Nevertheless, temporal dynamic the  $f_0$  is probably as important as the spatial distribution no information regarding these aspects will be considered in the HoliSoils project.

### **3. EFISCEN-Space model**

#### **3.1 Current coupling with Yasso15**

EFISCEN-Space is a high-resolution empirical forest model which simulates the development of European forest resources (Schelhaas *et al.* 2022). It is a diameter-class model operating at the stand level with growth driven by an environmental dataset with pan-European coverage. Processes in EFISCEN-Space (growth, regeneration, mortality and management) are parameterised using tree-wise repeated observations coming from National Forest Inventories (NFIs) and monitoring networks in forest reserves. Model functionality allows estimation of various resource-related variables such as carbon in biomass, soil and harvested wood products, as well as biodiversity & ecosystem services indicators and economic indicators.

EFISCEN-Space is coupled with the Yasso15 model which allows for simulation of soil carbon stock for mineral soils (Järvenpää et al. 2015). Yasso15 receives input from litterfall from living trees, slash produced after harvesting activities and biomass input as a consequence of natural mortality. These inputs are fractionated over four groups of organic fractions according to their resistance to decomposition, as represented by their solubility in different solvents (A – acid, W – water, E – ethanol, N – non-soluble). Decomposition products of each of these groups are redistributed to the same groups, or assigned to a stable humus compartment (H), or released as CO<sub>2</sub> to the atmosphere. Decomposition rate of different fractions depends on air temperature and precipitation and it also varies per tree species and biomass compartment (foliage, branch, stem and roots). In addition, a dependency on litter size was introduced in Yasso15. In EFISCEN-Space this new functionality is utilised by making the decomposition of stems dependent on the diameter class. Currently, Yasso15 is implemented as post-calculation after running EFISCEN-Space. Thus, contrary to the ORCHIDEE model, outcomes of Yasso15 do not influence the forest dynamics. More detailed information about implementation and formalisation of Yasso15 can be found in EFISCEN-Space v1.0 manual provided by Schelhaas et al. (2022).

## 3.2 Improvements made

### 3.2.1 Coupling with SoilR package

As part of the work done in HoliSoils WP2, EFISCEN-Space has been coupled directly to the SoilR multi-model package developed in T2.4. This new coupling allows for direct use of biomass litter outputs of EFISCEN-Space to simulate mineral and organic soils with any of the soil models included in the SoilR package. Furthermore, improvements made to the SoilR package, including the inclusion of rate modifiers for soil biota or for soil moisture (see section 3.3), can therefore be directly considered in EFISCEN-Space assessments.

As EFISCEN-Space and SoilR are developed by different developers and in different software packages, the two tools have been linked through a loose coupling. This loose coupling has been implemented by adding litterfall rates as an output variable. In EFISCEN-Space, three types of litter input are considered for the already existing coupling of EFISCEN-Space to Yasso15 (Järvenpää 2015). These include litter inputs from: 1) turnover of living trees, 2) dead trees, and 3) harvest residues and considering litter from stems, roots, branches, foliage. Litter input rates to the soils were calculated internally, but were not provided as output variables. Litter input rates are now added as an output variable, facilitating the linkage with other soil models in the SoilR package, as well as with ECOSSE that is used in WP6. In summary, the coupling of EFISCEN-Space with the SoilR package allows to study the effect of the newly developed rate modifiers in post-calculation mode.

### 3.2.2 Other improvements

Several other improvements have been made for the purposes of this deliverable and for simulating Climate-Smart-Forestry (CSF) management in WP6 general. These include:

- In EFISCEN-Space, Yasso15 was run as a post-calculation to the EFISCEN-Space calculations. Yasso15 can now optionally be applied to calculate soil carbon during EFISCEN-Space calculations during every step of simulation. This allows the use of litter and soil carbon estimates to dynamically influence the development of the forest as simulated by EFISCEN-Space. This may become important for the simulation of other processes in the model, for example to calculate the fuel load in case of wildfire or the availability of breeding material in case of bark beetles.
- The coupling of EFISCEN-Space to Yasso15 has been improved to increase overall performance. Calculations are now done in multi-plot batches and using process pool. These numbers are parameterized and can be fine-tuned to maximize the utilization of the target system, so these parameters affect positively and directly to the processing time per plot. Processing data in multi-plot batches minimizes the memory-allocation pressure and maximizes the data throughput of the CPU cores. As a rough estimate the default settings will process one plot (with 5 years of data) in around 25 milliseconds. The parallelization of Yasso15 post-calculations increased the performance time roughly from 0.4 plots/s to 20-40 plots/s. These processing numbers can be scaled even further when fine-tuning the parameters that affect the plot batch size and how many number of processor cores to use. The best performance gains are achieved when running the calculations using high-end PC or server cluster where data can be stored fully in memory and large amount of processor cores can be used. However, these optimizations will have positive impact on any kind of computer.
- Inclusion of forest management rules, as documented in deliverable D6.1 which allows for applying a range of CSF options like those which aim to increase carbon storage in forest soils.

### 3.3 Further developments

Within HoliSoils, two rate modifiers have been developed: the **soil microbial diversity rate modifier** (reported in D2.2) and the **soil moisture rate modifier** (Tupek et al. 2023). Both rate modifiers have been implemented and studied in the SoilR package, which has been coupled with EFISCEN-Space, as explained in section 3.2.1. However, it is yet unclear if these modifiers can be parameterised at European scale, which limits the additional functionality in large-scale simulators like EFISCEN-Space (see section 2.3 and below). The new coupling of EFISCEN-Space with the SoilR package allows to study the effect of these modifiers in post-calculation mode. In case the rate modifiers can be parameterised at European scale, these modifiers can be built into the Yasso15 model that is hard linked with EFISCEN-Space, as the rate modifiers are relatively simple from mathematical point of view. In current stage of their development, they are scalars for given soil properties and normally applied as multiplication decomposition rates by given scalar value. This can be explained by same way as in eq. 1 with slightly different parameters:

$$\frac{\partial SOM}{\partial t} = I - k \times SOM \times \theta \times \tau \times \varepsilon \times \varphi \times \omega \quad (4)$$

where  $I$  is the input of OM into each pool and  $k$  is the soil organic matter decomposition rate.  $\theta$ ,  $\tau$ , and  $\varepsilon$  are the soil moisture function, the temperature function, and the litter size function modulating decomposition, respectively (current set of Yasso parameters) and  $\varphi$  is microbial diversity rate modifier,  $\omega$  - wetland related rate modifier.

### 3.3.1 Implementation of soil microbial diversity rate modifier in Yasso15

The modifier value calculation is explained by eq. 3. Once  $f_0$ ,  $f_{0,max}$  and  $\beta$  are defined then EFISCEN-Space should apply the modifiers to the 'original' Yasso decomposition rates. The actual application of the modifier at this stage of its development meets a few challenges. The 'roots' of the modifier comes from mathematical modelling and were tested against a few laboratory experiments, so we cannot rely on the proposed values for application at large scale with EFISCEN-Space simulations. Another challenge is a temporal behaviour of microbial diversity. Microbial diversity can dramatically change during a management (e.g. harvest) or natural disturbance event (Mäkipää et al., 2023), but yearly dynamics are still unclear as well as dependency on other environmental conditions such as weather variety. The most important issue is a lack of knowledge to build a mapping between site characteristics we know for simulated EFISCEN-Space units (usually forest inventory plot) and microbial diversity of its soil. So, we expect in coming work in HoliSoils to start with selecting a few EFISCEN-Space plots which are most close (by environmental characteristics) to natural communities where laboratory experiments were implemented to obtain first 'pilot' mapping to get candidates to be a proxy from known plot variables to microbial diversity. Also, we expect to use outputs of WP1 as possible spatial input to obtain this rate modifier for any plot in EFISCEN-Space set. As a first attempt we can assume the modifier as a 'static' in time. Then effect of disturbances can be applied, when microbial recovering dynamics will be investigated.

### 3.3.2 Implementation of soil moisture rate modifier in Yasso15

Yasso has been originally parametrised mostly for mineral soils. Tupek et al. (2023) propose a soil moisture rate modifier as a constant reduction of default Yasso decomposition rate for to improve the model's decomposition estimation for organic soils.

The soil moisture rate modifier proposed by Tupek et al. (2023) was studied by R code investigation (yasso07.sER\_function\_example.r) as a part of the SoilR package. We look at the so-named Environmental Modifier given in eq. 5

$$EM = a \times q^{\frac{T-10}{10}} \times SWC \times e^{-\frac{a \times SWC}{e}} \quad (5)$$

Where  $a$ ,  $q$ , are parameters of the environmental function;  $SWC$  and  $T$  are climate variables Soil Water Content and air Temperature respectively.

A main challenge is that both the Environmental Modifier and the moisture rate modifier were developed and tested using the Yasso7 implementation in the SoilR package. EFISCEN-Space is using Yasso15 (<https://github.com/JariLiski/Yasso15>), which is different from Yasso7 in terms of parameters used, with its own realisation of climate dependencies (analogue of Environmental Modifier). In addition, Tupek et al. (2023) tested the soil moisture rate modifier for Finland, the rate has not been tested outside Finland.

(4. Overall Discussion and perspective??)

## 4. Overall discussion and perspective

In this deliverable we showed how microbial responses can be implemented in spatialized models without necessary to have an explicit representation of the microbial populations. This promising avenue can help to better understand the role of microorganisms on the functioning of the ecosystems including plant growth. Nevertheless, this approach still suffers from a couple of draws. For instance, the biodiversity function emerged from a theoretical study not yet evaluated against observations. Some work is ongoing in the HoliSoils project to test the validity of the biodiversity function and depending on the results some adjustment might be necessary. Another limitation is the static view of the microbial diversity. Indeed, it is clear that microbial diversity evolved with time in particular in disturbed systems. So far, the microbial diversity index used in the function are not dynamic predicting its evolution with time would be an important next step. Finally, since the microbial diversity function is not model dependent we can easily take advantage of this approach to compare the response of ORCHIDEE and EFISCEN-Space and propose a multi model approach.

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