HoliSoils
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D5.4. Mechanistic representation of soil resilience in models

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

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Deliverable D5.4: Mechanistic representation of soil resilience in models with ORCHIDEE-KEYLINK		
In this deliverable, we run the new version of the ORCHIDEE model with a soil module coming from the KEYLINK model to study the resilience of forest to disturbances and the role of soil biodiversity on forest stability.		
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1. Introduction

Enhanced predictions of soil processes will serve society in multiple ways, including sustainable management of soil productivity, efficient CC mitigation, assessment of soil vulnerability to disturbances, and soil recovery capacity, also accounting for soil functional resilience under future conditions. Currently, the major challenge is to optimise soil and forest management practices in order to achieve GHG emission reduction targets, while simultaneously improving long-term carbon (C) sequestration in soil and maintaining provision of ecosystem services (e.g. timber production, production of non-woody materials, and biodiversity conservation). This can be achieved by developing understanding of soil processes and implementing it in ecosystem and soil models, which serve sustainable forest management decision and policymaking in Europe. Another of the great challenges of science is to understand the capacity for recovery (resilience) of soils in the face of the enormous environmental challenges they face. In this context, it is urgent to integrate the mechanistic knowledge that regulates a system's resilience into predictive models that are capable of providing more detailed information on soil response thresholds and their recovery capacity. Systems can absorb, rebound, or adjust to disturbances through capacities known as ecosystem resistance and resilience[1]. These capacities help ecosystems to maintain their functions and provision of multiple ecosystem services, including in future climate conditions in which forest resilience is likely to be challenged[2,3]. Understanding how these unprecedented climatic and biological conditions[4] will affect biodiversity and functioning of soil systems is especially important, since soils—particularly soil biota inhabiting soils (microorganisms, fauna) and their functional diversity—are key contributors to the function and resilience of terrestrial ecosystems[5]. Links between soil biodiversity and ecosystem processes have been recently found[6,7,8,9], but lack of mechanistic understanding of the contribution of soil

biodiversity to ecosystem functioning currently limits our ability to integrate soil biodiversity into models.

To be able to properly represent soil properties and soil biota in models and predict future forest performance, both standardisation of methods and appreciation of the roles of different components of forest soil biota are urgently needed. Furthermore—given that Europe is expected to become warmer and drier[10, 11,12]— interplay between water and C cycles and how they could be jointly managed stands out as an important research priority[13]. Comprehensive integration of the understanding of water, C, and nutrient cycling into tools and guidance used by decision makers will enable them to assess, mitigate, or adapt to impacts of changing land management and climate[13]. Currently, the major challenge is to optimise soil and forest management practices in order to achieve GHG emission reduction targets, while simultaneously maintaining provision of ecosystem services (e.g. timber production, fresh water supply, production of non-woody materials, recreation, aesthetic values and biodiversity). This can be achieved by developing understanding of soil processes and implementing it in ecosystem and soil models, which serve sustainable forest management decision and policymaking in Europe

The KEYLINK model embraces this new paradigm by linking the formation of soil pore space, decomposition, the stabilization of soil organic matter (SOM) and soil hydrology to all major microbial and faunal groups[14,15]. The soil biota transforms its physical and chemical environment, thus modifying soil structure and hydrology[16]. Soil structure determines the soil carbon turnover[17] and whether water infiltrates into the soil matrix and remains available for decomposers. For example, the hyphae produced by mycorrhizal and saprophytic fungi enhance the occlusion of organic matter in stable structures called aggregates[18], which in turn determine the porosity and connectivity of pores, as well as the infiltration and retention of water. Moreover, under the appropriate conditions, fungal hyphae and specific bacterial groups produce amphiphilic compounds (organic acids and waxes) associated with soil water repellency[19], which also affect overall soil hydrology[20]. Other highly diverse faunal groups, so-called ecosystem engineers, such as termites or earthworms, have an enormous impact not only on the production of aggregates by ingestion and defecation of sediment grains (casts[21]) but also on the formation of burrows (biopores), which promotes water infiltration[22]. Detritivores, including enchytraeids, collembolans, and large groups of mites[7], feed on decomposing litter, hence modifying water infiltration and evaporation from the soil surface. Along with taxonomic and functional diversity, the trophic structure of the soil biota affects the flow of matter and energy through different trophic levels (Figure 1), with far reaching consequences for carbon sequestration.

The objective of this deliverable is to provide the mechanistic basis that describes soil responses to disturbances (functional vulnerability after disturbances and recovery capacity). In order to study the resilience of forest to disturbance the new version of the land surface model ORCHIDEE has been run coupled to the soil carbon cycling model KEYLINK (see D2.10). Coupling KEYLINK with ORCHIDEE will substantially improve representation of soil biodiversity that affect soil resilience (e.g. exploring tipping points of resilience) and predictions of feedbacks of forest management, resilience, and even their effects on climate. This could

also represent a major step forward in future forest management aimed at conserving the vast biodiversity found in the soil.

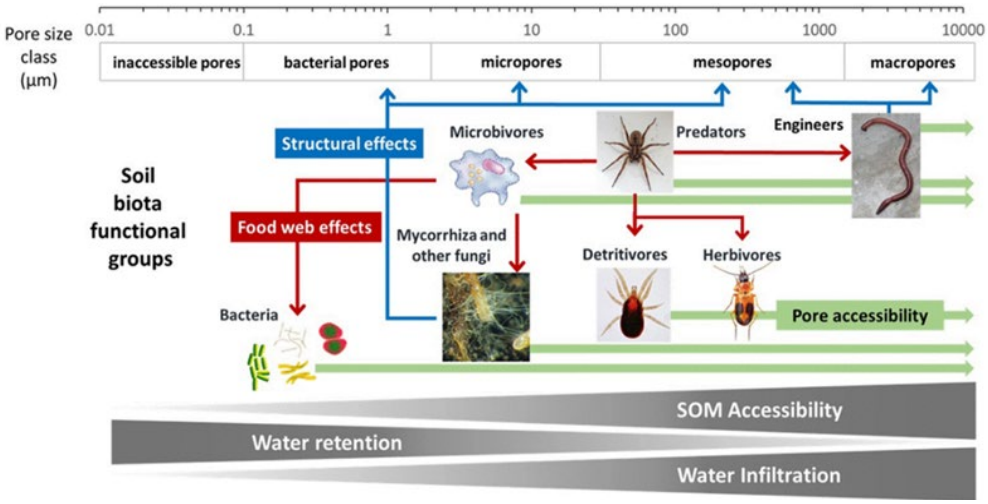

***Figure 1**. Trophic structure of soil biota functional groups and their relationships with soil structure (adapted from[7]). Pore size distribution is represented by five classes. Blue arrows indicate effects on soil structure; green arrows indicate the range of pore size classes accessible to each group; and red arrows indicate trophic effects by grazing and predation. Grey triangles show the expected responses of water retention, infiltration and SOM stabilization.*

2. ORCHIDEE

ORCHIDEE is a land surface model that computes fluxes of carbon (C), nitrogen (N), H2O, and heat exchanged between the land surface and the atmosphere at a 30 minutes time step, and the variations of C and N pools at a one-day time step[23]. Recently, some specific forest modules were implemented[24,25].

2.1 General description of the model

The ORCHIDEE model[26] calculates the exchange of energy, water, carbon and nitrogen at the atmosphere–surface interface and within the soil–plant continuum (Fig.2). The spatial discretisation depends on the modelled process. Water budgets are based on three tiles within each grid cell depending on the land cover: one for the bare soil, one for forest and one for herbaceous cover (grasslands and croplands). The energy budget is computed at the grid cell level, without accounting for differences between tiles, at least in the version (svn r7922) used for the coupling presented in this deliverable (although new versions of ORCHIDEE have energy

balances for each tile[35]). The carbon and nitrogen budget and related fluxes are computed for each vegetated tile within a grid cell. In ORCHIDEE, the carbon and nitrogen are split into 15 plant cover classes based on the concept of plant functional type (PFT). Different species, which share similar characteristics regarding their architecture, phenology or location, are gathered in a single PFT.

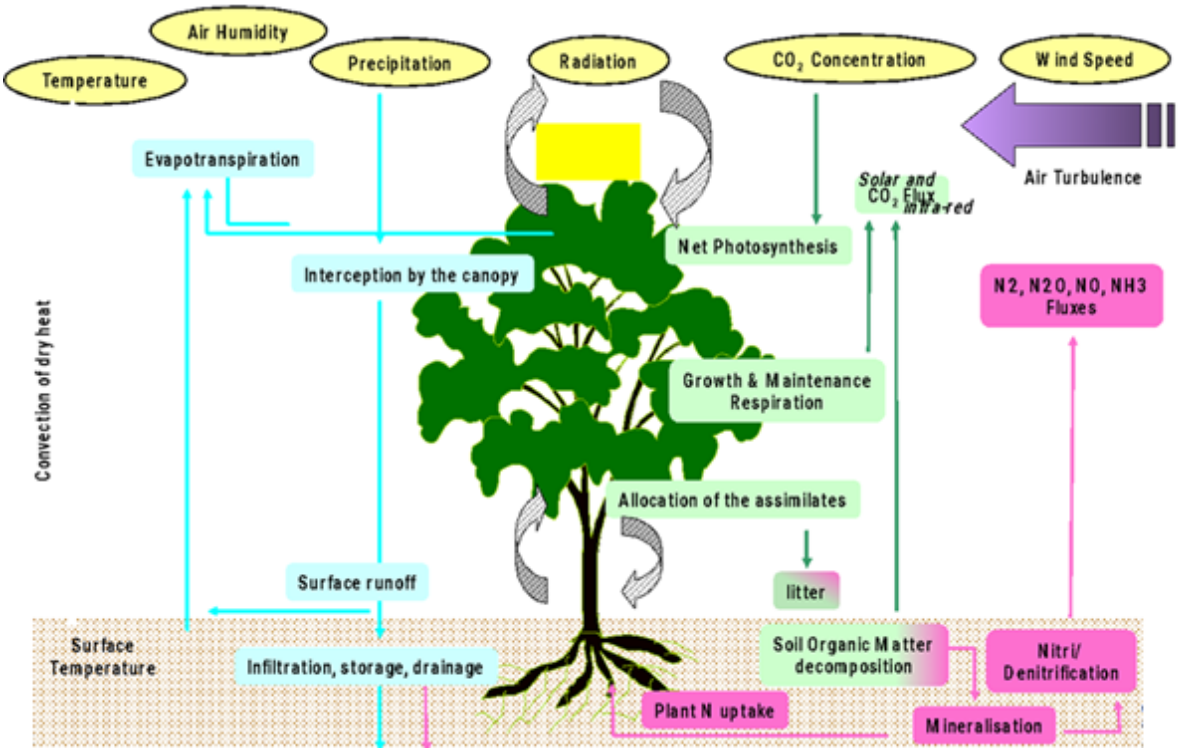

***Figure 2**. Schematic of the ORCHIDEE model (adapted from [26]).*

Recent developments performed specifically on the nitrogen dynamics within the soil–plant–atmosphere continuum and done before the start of Holisoils are based on a previous nitrogen implementation into a former ORCHIDEE version[27]. The nitrogen cycle is added at the PFT level as for the carbon cycle, and for each carbon pool there is a corresponding nitrogen pool, with C/N ratios evolving through time. The leaf C/N ratio is dynamic and varies as a result of the nitrogen supply by roots and demand for biomass allocation. The C/N stoichiometry of the other living biomass pools (i.e. belowground and aboveground sapwood, belowground and aboveground heartwood, fruit, and fine roots) is driven by the C/N ratio of the leaves but scaled by a pool-dependent factor. The dynamic of mineral nitrogen in the soil follows the formalism based on the DNDC model[28–30]. Nitrogen inputs in the soil–plant system are related to (i) atmospheric nitrogen deposition in the form of NHx and NOy components, (ii) biological nitrogen fixation (BNF) on any land category, and (iii) nitrogen fertilization over managed grasslands and croplands.

Moreover, the allocation of carbon to leaf, root, wood, fruit and reserve pools; the transmittance, absorbance and reflectance of radiation within the canopy; and the vertical

discretisation of the energy budget calculations were recently modified[24]. In addition, conceptual changes were introduced towards a better process representation for the interaction of radiation with snow, the hydraulic architecture of plants, the representation of forest management and a numerical solution for the photosynthesis formalism of Farquhar, von Caemmerer and Berry.

2.2 The soil module

The soil carbon module in ORCHIDEE comes from the soil carbon and nitrogen cycling model CENTURY[31] 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:

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

where I is the input of organic matter into each pool and k is the soil organic matter decomposition rate. θ, τ, and γ are the soil moisture function, the temperature function, and the texture function modulating decomposition, respectively. Then, the decomposed organic matter is partially redistributed in other pools or respired (resp. mineralized) if C (resp. N) exists in the system.

3. The KEYLINK model

The KEYLINK model has been conceptually designed integrating the structure of the soil by its porosity, the hydrology and the C cycle through the soil food web[14,15]. Those key parts of the soil interact (Fig. 1) determining the rates of SOM stabilization and CO_2 emissions from soil. The functions developed to represent and simulate those processes are presented here.

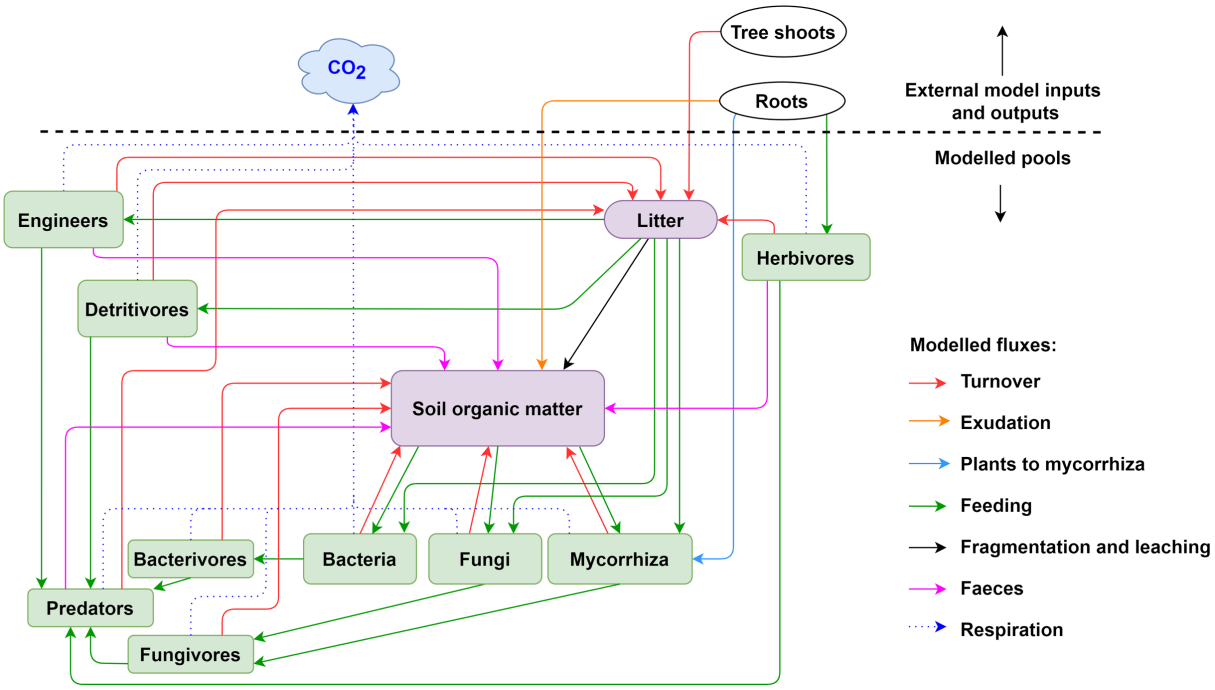

Figure 3: Schematic of the KEYLINK model from [15]

In the original version of KEYLINK the different pools described in Fig. 3 exchange carbon between each other. The growth of each living group is described using a Monod kinetics shown in eq. 2.

$$G = g_{max} B \sum_{n=1}^{N} \left(\frac{Sf_a}{K_s+S}\right)_n \qquad (2)$$

where g_{max} (g C g C^{-1} day^{-1}) is the maximal rate of growth, to which several modifiers are applied driven by environmental variables (temperature, pH, etc.). Substrate (S, g C m^{-3}) is the consumable pool, litter, SOM or biomass of the n-th soil organism, that the consumer (B) can use but corrected by its available fraction (f_a). K_s is the "half-velocity constant" from the Monod equation, representing the amount of S required to get half the maximal growth.

The net rate of change of a biomass pool is the sum of growth (G), respiration (R) and turnover (death, D_t), and possibly predation (P_d), all in g C m^{-3} day^{-1}:

$$\frac{dB}{dt} = G - R - D_t - P_d \qquad (3)$$

R is a function (Eq. 4) of temperature, and is calculated as the product of the biomass specific respiration rate (r, g C g C^{-1} day^{-1}) and biomass (g C m^{-3}), assuming the same temperature sensitivity as growth; this is somewhat different to how it is seen in many models where a food source is turned over with a specific efficiency.

From a more faunal point of view, this makes sense: a food source is "consumed"; the consumed material is partly excreted and partly assimilated and spent on respiration and growth (i.e., biomass formation).

$R = rB$ (4) where the respiration rate (r) is calculated as an exponential function of temperature for each functional group:

$$r = r_{opt} Q_{10}^{\frac{T-T_{opt}}{10}} \quad (5)$$

Eq. 5 is the classical equation of the temperature coefficient (Q_{10}) transformed to calculate r in function of temperature (T), while the other terms are constant parameters defined for each functional group, including the respiration rate of the group at its optimal temperature (r_{opt}, g C g C^{-1} day^{-1}). Q_{10} is normally assumed to have values between 2 and 3.

The mentioned sensitivity of growth to temperature is defined by three parameters for each functional group: minimum (T_{min}), optimum (T_{opt}) and maximum (T_{max}) temperatures. This is calculated through a modifier of growth (m_T), that is null below T_{min}, and also at T_{max} or higher temperatures, m_T equals one between T_{opt} and T_{max}, and any value between T_{min} and T_{opt} is calculated by Eq. 6:

$$m_T = Q_{10}^{\frac{T-T_{opt}}{10}} \quad (6)$$

with T being temperature during the simulation.

Such explicit calculation of growth and respiration depending on temperature and biomass, with different functions (i.e. growth has a plateau and a top limit, while respiration always increases with temperature) result in a more dynamic simulation of the efficiency of C assimilation by soil biota without needing any fixed efficiency parameter. Conversely, the death rate d (g C g C^{-1} day^{-1}) is constant.

$$D_t = dB \quad (7)$$

Predation depends on biomass of predator or microbivore and is calculated from the growth of the predator (G_{pred}, from Eq. (2)) plus the fraction of the prey allocated to faeces (f_{faec}).

$$P_{d_{Prey}} = G_{pred}(1 + f_{faec}) \quad (8)$$

In the original version of KEYLINK, the porosity is modulated by the size of the living biomass pools that modify the distribution between the pore size classes. As a consequence, the hydrology of the model is modified and the model reproduce some feedbacks between the soil biology and the soil hydrology.

4. New developments for the coupled version

Most of the new developments of KEYLINK for coupling it with ORCHIDEE were already explained in the deliverable 2.10. Since then, a major advance has been to merge ORCHIDEE-KEYLINK with a more dynamic simulation of soil hydrology[32], which will also allow to simulate the impact on the hydrology of the soil engineering by biota modifying soil porosity.

Moreover, while the soil food web is still simulated as if it occupies one soil layer, the new dynamic hydrology is based on several soil layers dividing the layer of the food web at different

depths. Those soil layers were already part of ORCHIDEE, therefore the new hydrology module allows to better link the KEYLINK module of the soil food web with the physical processes of the soil simulated by ORCHIDEE.

One important aspect of that new development is that it improves the simulation of one of the key concepts of KEYLINK, which is the availability of food sources conditioned by the aeration and humidity of the soil. In the KEYLINK model, within each soil layer, the soil water content is assumed to fill pores from the smallest to the largest, being those pores completely filled and those completely dry unavailable for biological activity, while all activity is concentrated normally in two pore classes: the one that is partially filled with water, and also the next pore class larger than the previous, which is assumed to be not completely dry but to have some moisture due to the water in the previous class[15].

If only one soil layer is used for hydrology, that limits the biological activity to only two pore classes. Therefore, the subdivision of soil depth into different layers allows for a more realistic representation of trophic interactions, since at different depths the soil water content might be different, changing in which pores there is both water and air to support biological activity. In the current version, the fluxes resulting from trophic interactions use a modifier of C availability that is calculated for each pore class as the sum of all the volumes among all the soil layers that have availability for that pore class; for example, if micropores are completely full of water in 5 out of 11 soil layers, and completely dry in another 2 layers, the availability calculated in micropores for the remaining 4 layers, those with both moisture and aeration, will be added together as the availability within micropores in all the soil.

5. Model run

Two parallel simulations have been run for this deliverable, one using the old hydrology with one single soil layer (hereinafter referred to as 'fixed hydrology'), and another one using the new more dynamic hydrology that also subdivides the soil into different layers (hereinafter referred to as 'dynamic hydrology'). Both were run at a single pixel in France (46-48ºN, 2-4ºE), using two plant functional types (PFT) of the temperate zone: evergreen conifers, and deciduous broadleaved trees.

An initial run of 20 years was used to get equilibrium within the pools, avoiding the instability of the initial years. Then three extra years were simulated in each case, producing daily output values: i) the first year was a continuation of the initial conditions without any perturbation; ii) on the second year, a clear-cut was applied, to simulate a perturbation that increases the litter input to the soil; and iii) a final third year was simulated after the perturbation.

6. Results

The following figures illustrate the results from the simulations explained in the previous section. Each figure corresponds to one variable for the two comparative simulations, with the "fixed hydrology" on the left and the "dynamic hydrology" on the right; and within each figure, the two PFT are represented, in which the black lines represent the conifers, and the red lines

represent the deciduous trees. The x-axis represents the time (T) in days, with the perturbation (clear-cut) happening at the end of the second year (T = 730).

Soil pore volumes are shown for the three largest classes: micropores, mesopores and macropores. Inaccessible pores are not shown because their volume is not affected by these processes, and bacterial pores are not shown because they have the same values as those of micropores. Porosity is common for the pixel and independent from PFT, so volumes are represented only with black lines.

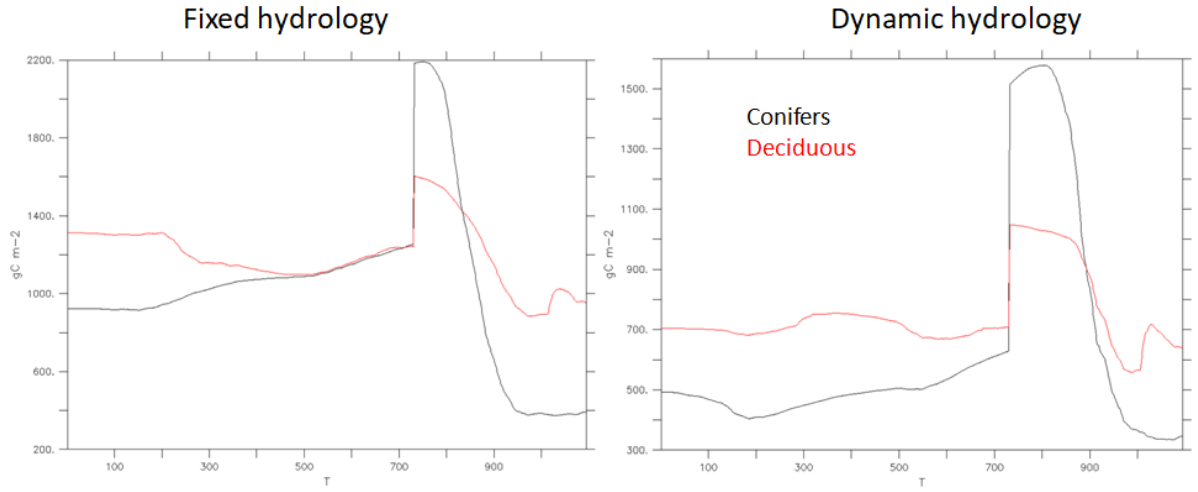

Figure 4: Total litter C in the soil.

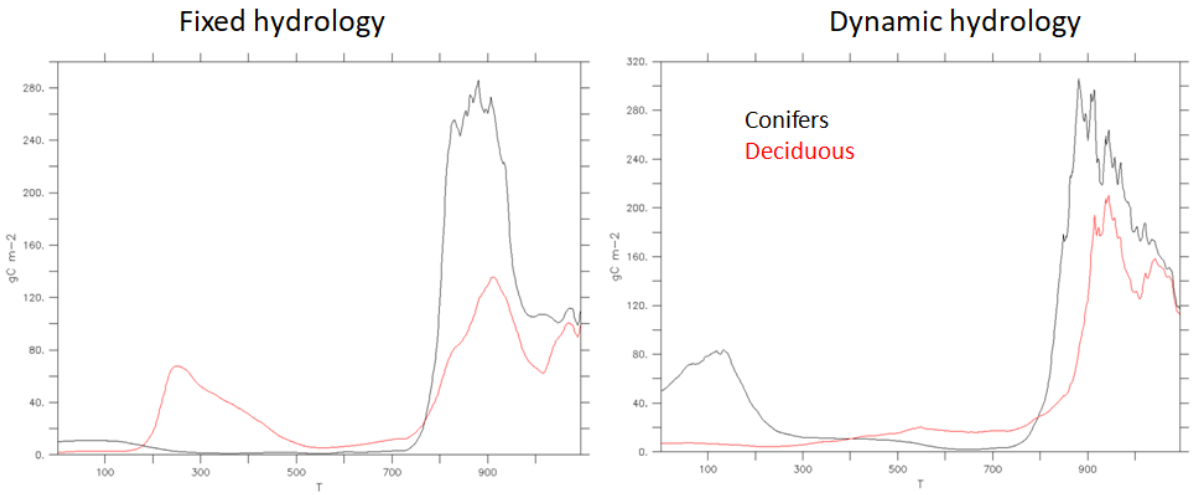

Figure 5: C biomass of bacteria populations.

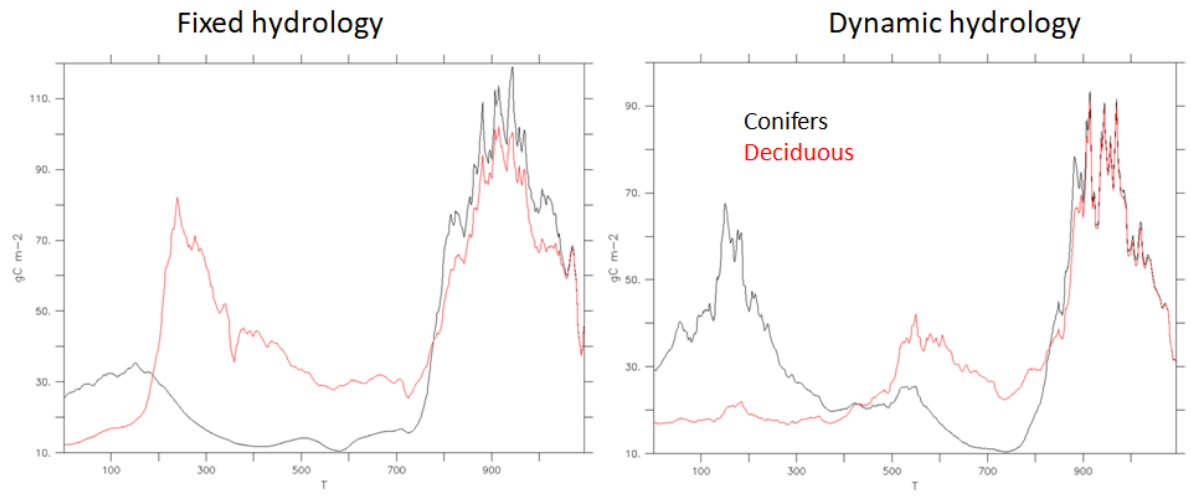

Figure 6: C biomass of bacterivore populations.

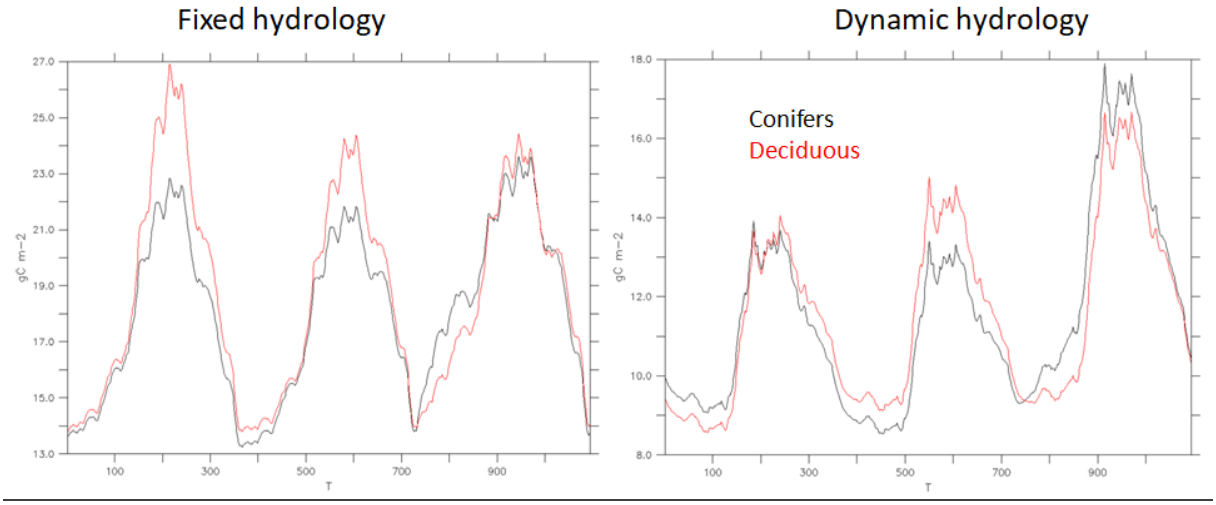

Figure 7: C biomass of the engineer populations.

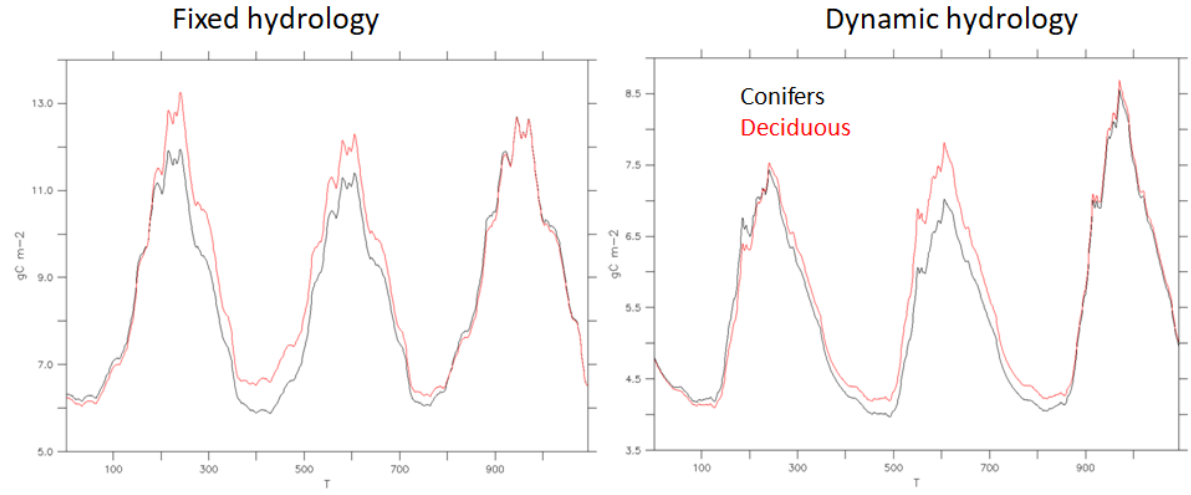

Figure 8: C biomass of predator populations.

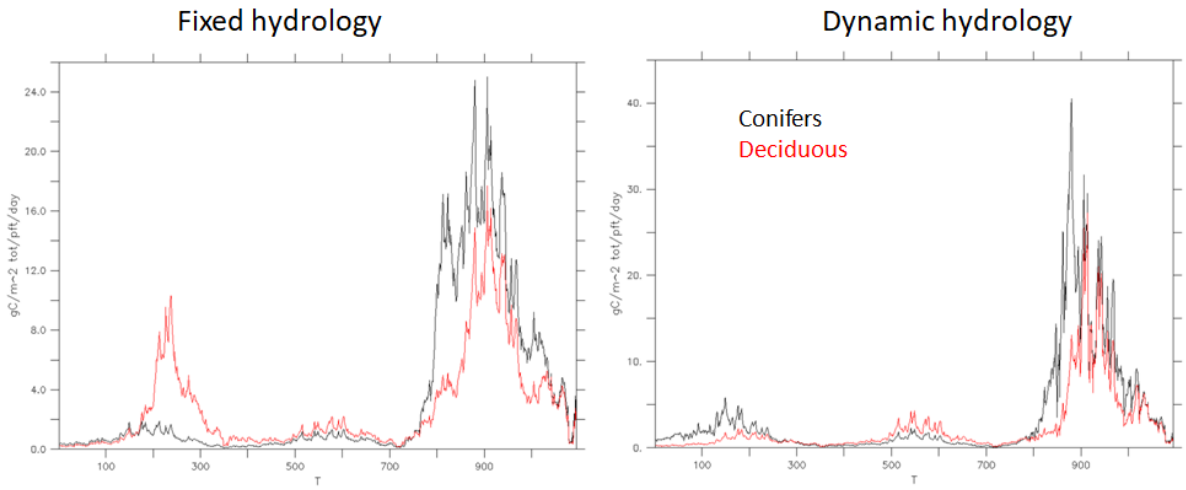

Figure 9: Heterotrophic respiration.

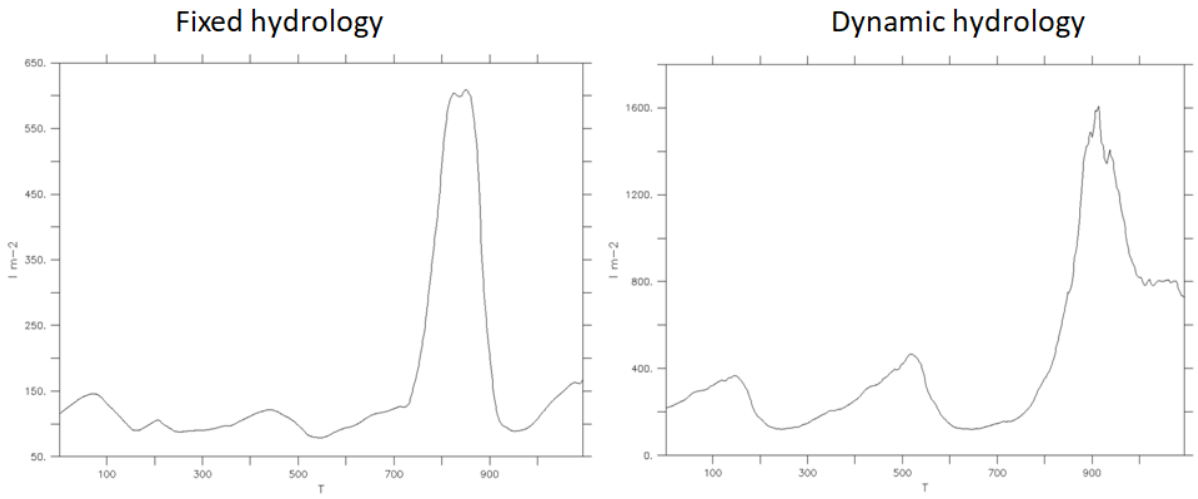

Figure 10: Total volume in micropores (same values as for bacterial pores).

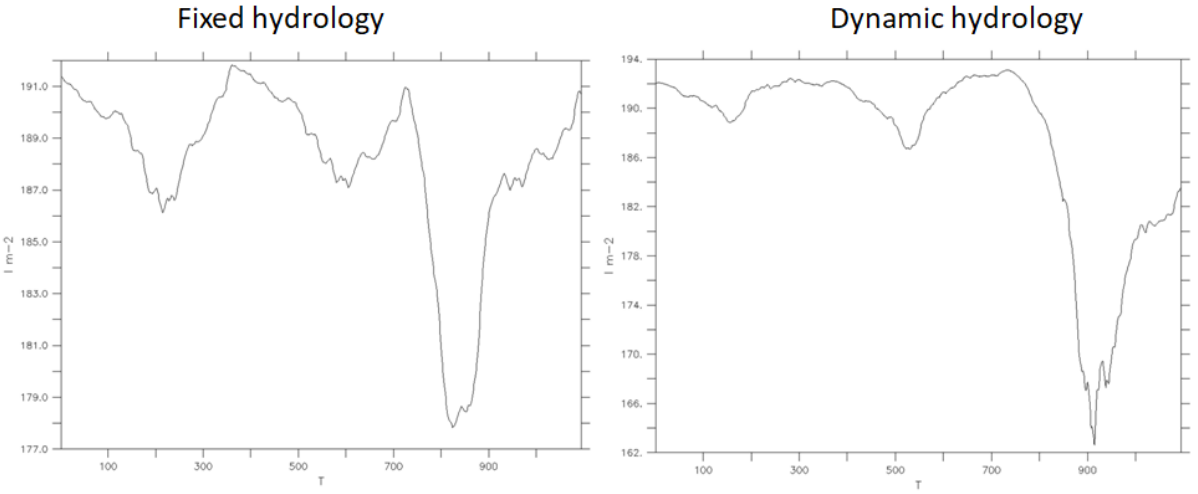

Figure 11: Total volume in mesopores.

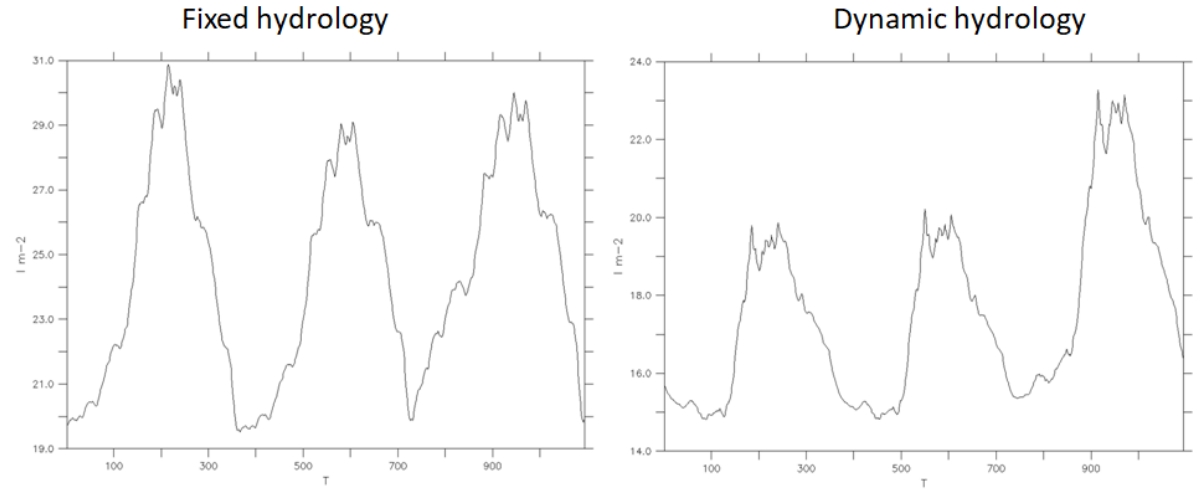

Figure 12: Total volume in macropores.

The increase in litter input resulting from the disturbance event (Fig. 4) was followed by a subsequent rise in microbial decomposer biomass (Fig. 5), which in turn stimulated an increase in the biomass of higher trophic-level consumers (Fig. 6). This trophic cascade was associated with an elevation in heterotrophic respiration, which remained elevated throughout the year following the clear-cut event (Fig. 9). The disturbance had a more pronounced impact on microbial communities and microfauna compared to larger soil fauna (Figs. 7–8), including ecosystem engineers that also rely on litter as a resource. This differential response suggests that organismal body size may influence the sensitivity and responsiveness of soil fauna to perturbations.

Regarding the pore volumes, the clear-cut had a clear effect on all accessible pores, except in macropores. In bacterial pores and micropores, the volume had a sharp increase after the perturbation (Fig. 10), while in mesopores it caused a fast decrease (Fig. 11). For macropores, the effect is not so clear (Fig. 12), mainly in the dynamic hydrology simulation it could explain the higher value reached after the perturbation within its normal dynamic fluctuation, which follows that of the engineers (Fig. 7), as those control the formation of macropores. The major effect on the smaller pores is also explained by the larger impact on smaller biota, since microbial biomass and its activity decomposing soil organic matter regulate soil particle aggregation, which modifies the volumes of those smaller pores.

7. Conclusions

In this study, we present a novel and integrative approach to elucidate the mechanisms underlying ecosystem responses to disturbances in complex systems such as soil, and to assess the consequent impacts on forest functioning. Our methodology involves the coupling of the mechanistic soil model KEYLINK with the dynamic global vegetation model ORCHIDEE, representing a pioneering framework for incorporating soil biodiversity into large-scale ecosystem response simulations. The model simulations reveal an abrupt system response following a high-intensity disturbance, exemplified by clear-cutting. This disturbance leads to a marked increase in the availability of dead organic matter (litter), which initiates a cascade of bottom-up effects throughout the soil food web. These effects, in turn, abruptly raised the biological CO_2 emissions and altered key soil physical properties, including porosity, with consequential impacts on soil hydrology. Notably, the system exhibits a relatively rapid return toward pre-disturbance equilibrium conditions, suggesting a high degree of resilience. However, ongoing and future work will extend these simulations to longer timescales and broader spatial contexts in order to investigate disturbance legacies and long-term ecosystem trajectories. Another important finding is the differential response magnitude between plant functional types (PFTs). Coniferous species demonstrated a greater sensitivity to disturbance compared to hardwood species. This observation is particularly relevant in light of current forestry trends favoring the expansion of fast-growing, but potentially more disturbance-sensitive, conifer plantations at the expense of hardwood-dominated systems[33]. These results underscore the necessity of evaluating soil system vulnerability across different PFTs, particularly in relation to future forest management strategies and climate change resilience.

This study has provided an opportunity to investigate and better understand the mechanisms through which soil systems recover following disturbance events. While the preliminary results are encouraging, they remain exploratory in nature and highlight the need for further refinement. In particular, future work will involve updating the model components to their most recent versions and calibrating the coupled system using empirical data, such as those obtained from the experimental plots of the HoliSoils project[34]. Looking ahead, we aim to extend these simulations both spatially—across the European scale—and temporally—over multi-decadal periods—in order to anticipate and characterize potential emergent responses to disturbances under varying environmental and management scenarios. Upon completion of these developments, the updated model code will be released and made publicly accessible to support broader research and application.

8. How to access to the model

Since the ORCHIDEE version is a v1 and not published yet, the code is only available upon request. To request access please send an email to guenet@geologie.ens.fr explaining your motivations to access the code.

Once you are authorized to access the code, you will receive a tar file with the code

If you want to run the model, please follow the procedures described here:

https://forge.ipsl.fr/orchidee/wiki/Documentation/UserGuide/InstallingORCHIDEEBasic

Please be aware that ORCHIDEE is a complex model and not user friendly. If you plan to use it for production or publication please contact guenet@geologie.ens.fr and read carefully the ORCHIDEE policy:

https://forge.ipsl.fr/orchidee/wiki/GroupActivities/UseOfORCHIDEEpolicy

And the ORCHIDEE strategic plan:

https://forge.ipsl.fr/orchidee/wiki/GroupActivities/VVM-

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