Dear Topical Editor,

Please find bellow a point-by-point reply to referees' comments.

We hope the improvements proposed in the revised manuscript will address all issues that were raised.

Sincerely yours,

Rémy Ballot, on behalf of the authors

Referee #2

<u>Comment:</u> L. 165 : To which figure do the references to Figures S1, S2 and S3 refer? I can't find them in the illustrations.

<u>Response:</u> Figures S1, S2 and S3 are provided as supplementary information, which was uploaded as a separate file.

Referee #3

<u>Comment:</u> The manuscript developed the first map of dominant crop sequences in Europe for 2012-2018 using temporally-incomplete land cover information. Obviously, this is an important work. I have reviewed the revised manuscript and the point-by-point responses to the comments from the other two reviewers. Overall, the authors have done a good job in addressing these comments and revised the manuscript. However, I still have concerns about the data processing and quality assessment.

<u>Response:</u> We thank the referee for this positive feedback and hope the revisions proposed will address all concerns raised.

<u>Comment:</u> 1. According to the description in Section 2.3.1, two crop sequences can be derived based on the LUCAS dataset in 2012, 2015, and 2018 for each field among the 31159 points (Line 116). So, the two crop sequences can be different in each field. How many points have different crop sequences?

In the following section, a principle component analysis (PCA) was performed and eight groups (crop rotations) were selected to represent the primary crop sequence. So, if one of two different crop sequences in a field doesn't exist in the eight groups, will it be discarded? If you process the dataset like this, it will result in some uncertainties.

<u>Response:</u> For each point considered, a unique land cover is given for 2012, 2015 and 2018. Thus, a unique 2012-2015-2018 crop sequence is associated to each point. We added a sentence lines 116-117 in the revised manuscript to make this explicit: "Thus, each point is associated with a single (temporally incomplete) crop sequence.".

The PCA and hierarchical clustering performed aimed at distributing all points within the eight groups: no points were discarded here. We added a sentence lines 143-144 in the revised manuscript "A crop sequence type has thus been assigned to all points considered.".

Finally, line 114 in the revised manuscript, we specified how many points were added, identified as permanent grassland in 2018, but as a non-permanent agricultural use in 2012 or 2015. While adding this information and despite all previous verifications done, we identified a code mistake in lines 55-57 from the "1_LUCASD_formating.R" file. This mistake resulted in keeping in the analysis all points under permanent grassland in 2012, 2015, 2018. A corrected version of the script was shared on Zenodo and all relevant figures, tables and manuscript sections were corrected accordingly. This change leads to drop one third of Lucas points previously considered and crop sequences with temporary grasslands were no longer overestimated, but crop sequence types characteristics remains stable, as well as conclusions of this work.

Comment: *2. Dataset validation still needs to be improved for the manuscript. Though the authors have conducted comparisons analysis with LPIS and Eurostat datasets, the data accuracy outside of France has yet convinced me. Moreover, I did not see any new efforts to prove the reliability of the crop sequence in the revised manuscript. For example, they can collect crop sequence information from agricultural field studies to validate their dataset.*

Response: We agree the validation step is a critical step. However, collecting crop sequence information from agricultural fields as suggested to further validate our results may not provide a robust comparison because it would provide additional information about crop sequences cultivated on a limited number of fields, with a high risk of sampling bias. Moreover, for France, it would not improve the validation already performed by comparison with the LPIS, which provides an almost exhaustive knowledge about actual crop sequences in farmers' fields. We added a sentence lines 148-151 in the revised manuscript to strengthen this validation "The French LPIS represents the best available data for spatial distribution of crops in France in terms of spatial and temporal resolutions, spatial coverage, and disaggregation by crop type, , with a coverage higher than 98% for all field crops or 92% for temporary grasslands (Cantelaube et Lardot, 2022, Guilpart et al., 2022).". For other countries than France, we acknowledge that the validation could benefits from a comparison with datasets equivalent to the French LPIS : "the quality assessment of our map of crop sequence types in the EU would benefit from comparisons with other datasets at national or subnational levels in other countries" (lines 307-308 in the revised manuscript). But so far, we do not have access to such datasets.

Comment: *3. Random Forest (RF) model was applied to evaluate the accuracy of the crop sequence map for France. It is critical for the quality assessment, so detailed explanations about the RF model should be included in section 2.3.3. For example, how many samples were selected to train and validate the RF model? How the model performs for the model training and validation? Table 4 shows the confusion matrix of the Random Forest model, but it needs to be clarified that the results were calculated based on training data or validation data.*

Response: We thank the reviewer for giving the opportunity to clarify this point. Default settings were specified line 154 in the revised manuscript : "i.e. 500 trees, two variables randomly sampled as candidates at each split". The out-of-bag error is a metric commonly used to evaluate random forests classifiers, and is considered to yield similar results than cross-validation. To make this more explicit in the text, we added the following sentence and reference in lines 155-159 of the revised manuscript: "Each tree of our RF model is constructed based on a random sample of the observations generated by bootstrap. The observations that are not part of the bootstrap sample are referred to as OOB observations, which are being used for estimating the prediction error, the so-called OOB error. The OOB error is considered as a good measure of the true prediction error (Matthew, 2011; Janitza and Hornung, 2018)."

Comment: *4. It confused me that why the RF-predicted crop sequence map was used to compare rather than directly using the newly developed crop sequence map.*

Response: We changed the sentence lines 160-161 in the revised manuscript to make it clearer "the crop sequence type distributions derived from the LUCAS dataset and predicted from

French LPIS dataset were compared". In other words, comparison was made between the newly developed crop sequence types map from LUCAS on the first hand, and the RF-predicted crop sequence types map from LPIS on the other hand, as shown in Figure 1.

Comment: *5. The newly developed crop sequence map is also compared with the Eurostat dataset by calculating their relative frequencies within the crop sequence types derived from the LUCAS dataset, the relative importance of crop sequence types, and the total arable land area. However, the newly developed crop sequence map is a point dataset, so how can the arable land area and the relative importance of each crop sequence type be calculated? Does the LUCAS data include field area information? I did check the Harmonized LUCAS data (https://developers.google.com/earth-engine/datasets/catalog/JRC_LUCAS_HARMO_THLOC_V1#table-schema), and I only found an attribute called "parcel_area_ha (i.e., Size of the surveyed parcel in hectares)". There is also no parcel area information in data shared on the Zenodo.*

Response: Relative importance was calculated regarding the number of points. We added an equation in lines 167-168 in the revised manuscript and justification in lines 171-172 "Relative importance of crop sequence types were calculated according to the number of points and without consideration to field area". Indeed, the harmonized LUCAS dataset provides information about size of the surveyed parcels in hectares, but this information is limited to four categories (i.e. < 0,5 ha, 0,5 – 1 ha, 1 – 10 ha, > 10 ha), which were not relevant to weight relative importance."

Comment: *6. Line 158. What's meaning of "relative importance" for LUCAS-based crop sequence? Is it calculated by dividing the total points by the number of points of each crop sequence? Does it include the parcel area information? I think the author need to clarify the calculation methods for "relative importance" through adding mathematical equations. The "relative frequency" also needs to be explained.*

Response: See response to the previous comment

Comment: *7. Figure 1 shows a step "Extrapolated surfaces from LUCAS data, crop surfaces per county". So how to extrapolate crop surfaces? Are the crop surfaces still point type, or did you upscale to a grid level and further calculated the crop area?*

Response: See response to the previous comment and equation added. For a given (group of) crop, the surface was calculated from total arable area, multiplied by the relative importance of crop sequence types including this (group of) crop and the temporal frequency of this (group of) crops within these crop sequence types.

Comment: *8. Line 252-257. I agree with the authors' point. These uncertainties resulted from the wrong records from LUCAS datasets.*

Comment: *9. Line 314-323. The authors discuss about the application of the newly developed crop sequence map in "crop diversity" issues. I suggest the authors can discuss the potential application of crop sequence/rotation map in terrestrial carbon, nitrogen, and hydrological cycles rather than limited in the "crop diversity" field.*

Response: We thank the reviewer for this very constructive comment. We modified the discussion section in lines 313-324 of the revised manuscript to include a broader perspective on the effects of crop rotations. Specifically, we added "soil carbon sequestration" and "water resources management" as crop rotation sensitive issues (lines 313-314), and added in lines

323-324 : “the share of summer and winter crops is relevant to water management as water demand is usually higher during the summer.”

Comment: *10. The authors highlight that the dataset was the first crop sequence map for Europe, but I did not find any information about the spatial resolution. So, I suggest that the authors can upscale the data from point to grid with a reasonable spatial resolution (e.g., 1 km or 0.05 degree), which will be more useful for agricultural studies.*

Response: This is an interesting suggestion, that has been considered. We agree that a gridded map of rotations over the EU would be of interest and would facilitate modeling studies if it could be used as a model input. However, we decided not to develop such a map because gridded agricultural/crop models vary in their spatial resolutions and crops/crop types simulated, which makes difficult to choose a single best spatial resolution and group of crops definition (for example, is soybean part of pulses or oilseeds?). Therefore, at this stage we decided to make publicly available the point-based map of dominant crop sequence types along with the corresponding observed crop (types) in 2012, 2015, and 2018 so that anyone could use these data to do different groupings and describe crop sequence in a way that is relevant to the question addressed.