

## Research Paper

# From patterns to prediction: detecting crop sequence and interpreting crop selection with explainable AI at field level in Denmark

João G. Serra<sup>a,b,c</sup>, Edwin Haas<sup>d</sup>, Diego Abalos<sup>c</sup>, Søren Kolind Hvid<sup>e</sup>, Tommy Dalgaard<sup>a,c</sup>, Lars Uldall-Jessen<sup>c</sup>, Franca Giannini-Kurina<sup>c</sup>, Meshach Ojo Aderele<sup>a</sup>, Bo Thieson<sup>f</sup>, Jørgen Eivind Olesen<sup>c</sup>, Klaus Butterbach-Bahl<sup>a,d</sup>, Jaber Rahimi<sup>a,d,\*</sup>

<sup>a</sup> Pioneer Center Land-CRAFT, Department of Agroecology, Aarhus University, 8000 Aarhus, Denmark

<sup>b</sup> Forest Research Centre, Associate Laboratory TERRA, School of Agriculture, University of Lisbon, 1349-017 Lisbon, Portugal

<sup>c</sup> Department of Agroecology, Aarhus University, Blichers Allé 20, 8830 Tjele, Denmark

<sup>d</sup> Karlsruhe Institute of Technology (KIT), Institute of Meteorology and Climate Research, Atmospheric Environmental Research (IMK-IFU), Garmisch-Partenkirchen, Germany

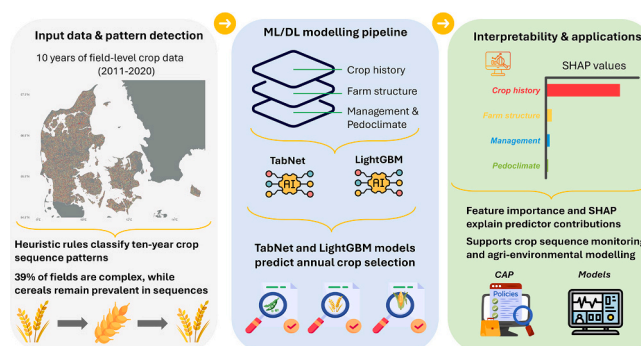
<sup>e</sup> SEGES, Agro Food Park, 8200 Aarhus, Denmark

<sup>f</sup> Agriculture and Digitalization, Danish Technological Institute, Denmark

## HIGHLIGHTS

- Field-level crop sequences across Denmark were characterised using a 10-year dataset.
- A heuristic algorithm detected recurring sequence patterns from longitudinal data.
- ML and DL models predicted annual crop choice using lagged structural and management predictors.
- Crop selection patterns were strongly associated with short-term crop sequences and farm typology.
- Pedoclimatic and management variables contributed minimally to model predictions.

## GRAPHICAL ABSTRACT



## ARTICLE INFO

Editor name: T Schut

## Keywords:

Machine learning  
Crop detection  
Crop rotation  
Crop sequence  
Decision-making  
Prediction

## ABSTRACT

**CONTEXT:** Crop sequences are important for sustainable agriculture, yet we know relatively little about how they recur across individual fields or which information best predicts the crop grown each year. Denmark's national field records allow both questions to be examined over time.

**OBJECTIVE:** We identified recurrent crop sequences across Denmark and tested how well annual crop-family selection could be predicted from crop history, farm characteristics, management, prices, soil and climate.

**METHODS:** Using 10 years (2011–2020) of national field-level crop data ( $\sim 600,000$  fields  $\text{yr}^{-1}$ ), we developed a heuristic algorithm to detect recurring crop sequence patterns. We then trained machine learning (LightGBM) and deep learning (TabNet) models to predict annual crop choices based on preceding crops and lagged management and farm structure predictors, and pedoclimatic conditions. Models were evaluated through forward-

\* Corresponding author at: Pioneer Center Land-CRAFT, Department of Agroecology, Aarhus University, 8000 Aarhus, Denmark.

E-mail address: [Jaber.rahimi@ago.au.dk](mailto:Jaber.rahimi@ago.au.dk) (J. Rahimi).

chaining validation and temporal holdout tests, and SHAP values were used to examine how LightGBM used each predictor.

**RESULTS AND DISCUSSION:** Crop sequences were largely dominated by cereals, with little diversification even in longer sequences. Crop selection patterns were strongly associated with the previous crops and farm typology, but pedoclimatic conditions and previous management played a minor role. The DL model achieved a slightly higher overall accuracy, particularly for dominant crops, while the ML model provided a more balanced performance across different crops and enabled interpretation through SHAP.

**SIGNIFICANCE:** The analysis separates two distinct tasks: identifying multi-year crop sequences and predicting the crop family grown each year. The sequence analysis shows why diversification cannot be assessed from sequence length or crop counts alone. The predictive models could help generate locally plausible sequences for agri-environmental simulations, reducing reliance on standard rotations that poorly reflect observed field histories.

## 1. Introduction

Crop rotations are one of the most effective management strategies for reconciling agricultural productivity with environmental sustainability. By alternating crops in sequence, rotations can increase yields (Gan et al., 2015), improve soil structure and fertility (Zotarelli et al., 2007) and reduce greenhouse gas (GHG) emissions (Yang et al., 2024). Rotations also enhance the resilience of farming systems to climatic and biological stresses (Peltonen-Sainio et al., 2017), influencing nutrient flows and cropping system dynamics from field (Sun et al., 2023) to landscape scales (Schiller et al., 2024).

Despite their agronomic and ecological importance (Rahimi et al., 2024), the temporal structure of crop rotations at national and regional scales remains poorly understood. The lack of long-term, field observations limits the realism of models used for yield forecasting (van Bussel et al., 2015), nutrient budgeting (Serra et al., 2019) and GHG mitigation (Michailidis et al., 2025). Models therefore rely on static crop calendars, survey data or remote sensing snapshots (Antle et al., 2017; Franke et al., 2020), which fail to capture farmers' sequential decision-making.

Advances in machine learning (ML), deep learning (DL) and explainable artificial intelligence (XAI) provide new opportunities to analyse large-scale datasets. These can uncover temporal, nonlinear and management signals in crop selection patterns (Blickensdörfer et al., 2022; Dupuis et al., 2022; Upcott et al., 2023). XAI approaches such as SHAP (Shapley Additive Explanations; Lundberg et al., 2020) support this by providing interpretable analyses and quantifying the contribution of different drivers, such as cropping history, nitrogen use and farm typology.

National farm registers provide an opportunity to apply these methods, and a growing body of literature has used such data to characterise (Chopin et al., 2026; Jänicke et al., 2022, 2025; Schaak et al., 2023; Whippo et al., 2026) and predict crop rotations (Dupuis et al., 2022; Palka et al., 2026). Denmark provides a particularly suitable testbed, as farmers are required to report crop and management information annually (Bligaard, 2014), enabling the reconstruction of longitudinal crop sequences linked to structural and management information at field-level, allowing a detailed characterisation of their patterns. This combination of field and management data, which is often not available in large-scale crop sequence studies, supports a more detailed assessment of the factors associated with crop selection.

Here we use long-term field records of almost 600,000 fields  $\text{yr}^{-1}$  in Denmark and apply data-driven modelling between 2011 and 2020. We characterise the dominant crop sequence patterns and their variability across fields, deriving their structure directly from longitudinal field data rather than from an assumed rotational design. We also assess the predictors most strongly associated with crop selection using ML and DL models complemented by XAI, which reveals statistical signals in reported practices, a dimension that is rarely represented in conventional crop modelling at this scale.

Our aim was to establish a data-driven, interpretable framework for representing crop sequence dynamics across agricultural landscapes in

Denmark. We first identified which ten-year field histories could be described by recurring crop family patterns, and which could not. We then evaluated whether annual crop family transitions could be predicted from recent crop history and recorded field, farm, management, economic and pedoclimatic predictors, and examined how the interpretable model used these predictors. The identified sequences provide empirically grounded alternatives to generic placeholder rotations in agri-environmental models. Where no recurrent patterns are identified, the observed ten-year patterns can instead be retained as non-repeating inputs rather than replaced by artificial rotations. The predictive models may help describe short-term crop selection in similar conditions. This has direct applications in agricultural systems modelling, environmental policy and digital advisory tools.

## 2. Methods

Our analysis involved four steps: (i) preprocessing and cleaning field-level crop data, (ii) identifying recurring crop sequence patterns, (iii) training the ML and DL models to predict crop choices, and (iv) using explainable AI to quantify key predictors of crop choice. We provide an overview of Denmark as a study case in Fig. S1.

### 2.1. Crop data

This study uses national-level data in the form of farm registers, accessible via the Danish Ministry of Green Transition (<https://mgtp.dk>). Information on crops and farmland boundaries was obtained from the EU Common Application (Fællesskemaet), implemented within the Integrated Administration and Control System (IACS) as the Geospatial Aid Application (GSA), through which farmers annually report crop and land-use information for CAP support applications (Leonhardt et al., 2024). This was supplemented by data on fertiliser usage from the national Fertiliser accounts (Gødningsregnskabet), which are not part of IACS but come from Danish regulatory requirements.

We harmonised spatial discrepancies at field edges using the 2020 polygons as the spatial reference, matching earlier years using unique field crop IDs. This procedure entailed selecting the dominant crop in fields with further sub-parcelling that were sub-parcelled over time. In other words, if a field with a dominant crop contained smaller edge crops (e.g. a wheat field with a small row of peas on the edge), we filtered out the latter. Alternative approaches exist, such as via the rasterizing of polygons (e.g. to 25  $\text{m}^2$ ; Jänicke et al., 2022) or using geographical intersection (Levavasseur et al., 2016). However, these approaches would substantially increase the computational complexity of multi-year national simulations. Given our focus on dominant crop sequence patterns, we consider the adopted approach to be a pragmatic compromise, although it introduces some uncertainty when representing fine-scale spatial variability.

This resulted in consistent 10 calendar-year crop sequences for each reference field, allowing us to reconstruct field-level crop trajectories over time. These sequences form the core input for modelling farmer decision-making and analysing crop sequence dynamics. We note how

there was a decrease in the number of fields, from more than 623,000 in 2011 to 583,000 in 2020. Although this is consistent with the trend for farm consolidation across the European Union (Boccaletti et al., 2024), which may influence field size and crop allocations, its causes and consequences were not examined here.

## 2.2. Data preprocessing and crop family classification

We applied a common crop classification step followed by separate preprocessing pipelines for the heuristic crop sequence detection and ML/DL prediction of annual crop family selection. The initial dataset comprised 583,652 spatially harmonised fields with annual crop records for 2011–2020. Fields containing tree, fruit or flower crops were excluded ( $n = 43,535$  fields), leaving 540,117 fields.

The remaining crops were grouped into crop families according to their agronomic relevance in Denmark, adapted from Stein and Steinmann (2018). This classification preserves distinctions across broad crop families with different agronomic functions in a sequence, such as cereals, legumes and oil crops, while combining individual crops within these families. Retaining individual crops would have fragmented the observations into several low-frequency categories, reducing the number of repeated sequences available for pattern detection (Section 2.3) and predictive modelling (Section 2.4). The resulting patterns therefore represent recurrence at the crop family level rather than crop-specific rotations.

Subsequent preprocessing differed between the two analytical pipelines. For the heuristic sequence detection, fields dominated by permanent grass ( $\geq 6$  years) were removed ( $n = 86,621$ ), followed by fields meeting the criteria for non-arable patterns where a field was identified in at least 4 out of the 10 years as fallow, set-aside or permanent grass ( $n = 62,381$ ). The resulting dataset comprised 391,115 fields across 2011–2020, accounting for an annual average of 89% of Denmark's agricultural land.

These filters were not applied for the ML/DL modelling. Rather, 4014 fields lacking one or more predictors were excluded, leaving 536,103 fields  $\text{yr}^{-1}$ . These observations totalled an annual average of 96% of Denmark's agricultural land.

## 2.3. Identifying crop sequence patterns

We identified dominant crop sequence patterns using a heuristic pattern-detection algorithm applied to the full field-level crop history (2011–2020; see Fig. S2A). We used the aggregated crop families (Table 1) to stabilise the reported sequence data, while still capturing

**Table 1**

Crop family classification scheme for the identification of crop sequence patterns.

| Crop family           | Description                                         | Crops                                                |
|-----------------------|-----------------------------------------------------|------------------------------------------------------|
| Winter cereals (WC)   | Winter cereals/seed crops to produce grain/seed     | Winter wheat, winter barley, winter rye, triticale.  |
| Spring cereals (SC)   | Spring cereals/seed crops to produce grain/seed     | Spring wheat, spring barley, spring oat, spring rye. |
| Grain maize (FOCO)    | Grain maize (including corn on the cob)             |                                                      |
| Legumes (LEG)         | Spring grain legumes                                | Faba bean, pea, lupin                                |
| Oil crops (OIL)       | Oil seed crops                                      | Rapeseed, mustard                                    |
| Vegetables (VEG)      | Vegetables for fresh consumption or seed production | Miscellaneous vegetable crops                        |
| Root crops (ROOT)     | Roots and tuber crops                               | Potato, sugar beet                                   |
| Forage crops (FORAGE) | Crops harvested green                               | Silage maize, sorghum                                |
| Grass (GRASS)         | Grass in rotation for feed/seed production          | Grass, grass-clover, clover                          |
| Set-aside (/)         | Uncultivated                                        | Fields flagged as uncultivated fields                |

their functional roles within crop sequences. We further distinguished field size according to their empirical distribution using percentile thresholds: fields were classified as small ( $<1$  ha;  $<P25$ ), medium (1–6 ha;  $P25$ – $P75$ ), large (6–15 ha;  $P75$ – $P95$ ), and very large ( $>15$  ha;  $>P95$ ).

We first separated fields dominated by non-arable or structurally inactive land uses. Fields were classified as permanent grass when permanent grass was recorded in at least six of the ten study years. For the remaining fields, those with fallow, set-aside or permanent grass in at least 40% of years were classified as intermittent arable, reflecting an unstable arable use. These classes were not subjected to further crop sequence detection. All subsequent steps were applied only to agronomically active years, defined as years not classified as permanent grassland, fallow, set-aside, unknown, or missing.

We then screened each field for single-dominated sequences. A field was classified as such when two conditions were met: one crop family accounted for at least 85% of active sequence years and occurred in a continuous run of at least five years.

For the remaining fields, we searched for repeating crop sequence patterns between two and five years long. Longer patterns could not be reliably identified in the ten-year observation window. For each pattern length, the algorithm tested every possible starting point within the candidate pattern. For example, for a two-year pattern, the first, third and subsequent odd-numbered crop-years were assigned to the first position, while the even-numbered crop-years were assigned to the second crop (see Supplementary Methods; Fig. S2B). The most frequent crop family at each position defined the candidate pattern, which was repeated across the full crop history and compared with the observed crops. Testing every possible starting point allowed the same pattern to be detected regardless of where in the cycle the ten-year record began.

To evaluate whether a candidate rotation meaningfully represents the observed sequence, we quantified the pattern fit as the degree of agreement between the candidate pattern and the observed crop sequence history. Pattern fit was quantified using the mismatch rate, defined as the fraction of active crop-years in which the observed crop family differed from the repeating pattern.

Candidate patterns were accepted when the mismatch rate did not exceed 20%, thus allowing limited deviations from occasional break crops, reporting inconsistencies, or short-term management adjustments. To avoid accepting weakly defined patterns, we additionally required that the most common crop family at each step of the candidate pattern accounted for at least 50% of observations assigned to that position.

When several candidate patterns met these criteria, we first retained those with the lowest mismatch rate within a tolerance of 2% and then selected the shortest among them. This promoted parsimonious repeating patterns while avoiding unnecessary assignment of longer sequences. Patterns consisting of the same crop family at all positions were excluded from this step, as these were already captured by the single-dominated class.

Fields for which no candidate pattern satisfied these criteria were classified as complex, representing irregular crop sequences or sequences without a stable short- to medium-term recurring pattern.

## 2.4. Predicting crop selection with ML and DL

To analyse farmers' main crop sequencing decisions, we trained two supervised classification models, LightGBM and TabNet, hereafter mentioned as ML and DL models, respectively. LightGBM is a gradient-boosted ensemble of decision trees, offering fast training and high interpretability as it is compatible with an efficient SHAP computation (Ke et al., 2017). TabNet is a deep learning architecture optimised for structured, high-dimensional tabular data, and is designed to capture complex interactions between predictors (Arik and Pfister, 2020).

Both models were trained using data from 2011 to 2018. Predictions were evaluated using held-out data from 2019 and 2020. This analysis was independent of the heuristic sequence classification: fields classified

as intermittent arable, permanent grass or complex were retained.

#### 2.4.1. Defining target and feature variables

The target variable in both models was the crop cultivated at timestep  $t$  according to Table 1. Feature variables were next compiled to reflect factors hypothesised to influence crop selection (see Table S1). These included two sets of lagged features.

The first set captured short-term market and climate drivers preceding the crop decision at timestep  $t$  and were derived from the previous year ( $t-1$ ). This included producer price indices for major crop products, as in Palka et al. (2026).

The second set comprised of structural and management related features derived from the previous four years ( $t-1$  to  $t-4$ ). These included farm structure (field size, farm typology), crop sequence (previous crops, crop diversity according to the Shannon index; see Supplementary Methods), management (manure, compost and fertiliser nitrogen application rates, cover crop intensity, production systems). Since these predictors required data from the four previous years, data from 2007 to 2010 were used only to derive lagged features for the first prediction year, 2011, and were not themselves used in model training.

Additional features from timestep  $t$  included climate (seasonal temperature and precipitation for timestep  $t$ ) and soil (e.g., texture fractions in top- and sub-soil, soil pH, soil organic carbon).

#### 2.4.2. Preprocessing steps

Numeric features were standardised, and we did not impute or gap-fill fields lacking predictor overlap. Since the dataset presented had an unbalanced distribution of crop sequences, we applied random over-sampling of crop families with fewer than 15,000 observations within each fold to ensure a balanced training (Fig. S3).

After we harmonised crop families and filtered rare crops, the final dataset comprised of 4.3 million field-year observations for training (2011–2018), with 536,103 observations reserved for each holdout year (2019 and 2020).

#### 2.4.3. Forward-chaining cross-validation and hyperparameter optimisation

To assess temporal generalisability while preventing temporal leakage and repeated-field dependence during model development, we used a forward-chaining cross-validation with field-level separation.

Field-year observations from 2011 to 2018 were used for model training and hypertuning optimisation. Four successive validation folds were defined using 2015, 2016, 2017 and 2018 as validation years. For each validation year  $y$ , models were trained using observations from 2011 to  $y-1$ . Additionally, all earlier observations associated with fields in the validation year were removed from the corresponding training subset. Each fold thus evaluated crop predictions for a subsequent year using fields absent from that fold's training data.

Hyperparameters for both models were optimised using Optuna's Bayesian optimization framework (Akiba et al., 2019). The optimisation objective was the mean macro-averaged F1 score across the four validation folds, giving equal weight to each crop family despite differences in class frequency. The DL architecture included batch normalization, dropout regularization, and early stopping callbacks to prevent overfitting.

After hyperparameter selection, each model was refitted using the complete 2011–2018 dataset. The final performance was evaluated separately for 2019 and 2020, which were retained as temporal holdout years and were not used for model training or hyperparameter optimisation. When testing the final models on 2019 ( $n = 536,103$  fields each year), we used all field observations from those years.

#### 2.4.4. Model performance

Model performance was evaluated using multiple metrics derived from the confusion matrix: accuracy, macro-F1, weighted-F1 and area under the ROC curve (AUC). The F1 score (range: 0–1) is the harmonic mean of precision and recall. Macro F1 treats all classes equally by

averaging class-specific F1 scores, while weighted F1 accounts for class frequency. AUC measures the model's discriminative ability, where 0.5 indicates random classification and 1.0 represents perfect ranking. We computed these metrics on a crop- and yearly basis. Model performance was also calculated separately for the five field size bins using percentiles (<1, 1–3, 3–6, 6–15 and >15 ha) using all field-year observations in the holdout set.

#### 2.5. Interpreting crop selection with explainable AI

We extracted predictor importance for both the DL and ML models using model-agnostic permutation importance on the hold-out data, quantified as the decrease in macro F1 scores after randomly permuting each predictor while keeping all other predictors unchanged.

We then applied SHAP (SHapley Additive exPlanations; Lundberg et al., 2020), a game-theoretic method for feature attribution. SHAP expresses the output of a given model as a sum of feature-wise importance values relative to a reference value (typically the mean prediction over the training data). For each individual prediction, the importance value quantifies how much that feature, in the context of all others, shifts the model output away from the reference. In our multiclass classification setting, SHAP values are computed for each class-specific output (i.e., each crop family). This allows us to identify the most influential factors driving the predictions of farmers' crop choices.

Notice that SHAP explains the model, not the data-generating process. That is, SHAP values describe how variation in each predictor influences the model's predictions and should not be interpreted as causal effects of farmers' decisions. However, by consistently highlighting which predictors the model relies on across individual observations, SHAP can help identify plausible mechanisms and generate hypotheses about potential causal relationships that can later be tested with dedicated experimental or quasi-experimental designs.

We used the ML model (LightGBM) for SHAP analysis because it is compatible with TreeSHAP, an exact, tree-specific SHAP algorithm that allows efficient computation in  $O(TLD)$  time, where  $T$  is the number of trees,  $L$  the maximum number of leaves per tree, and  $D$  the maximum depth. In contrast, neural network models such as TabNet require kernel-based or sampling-based SHAP approximations that are substantially slower, less stable, and more difficult to scale to the number of observations in this study. We therefore restricted our XAI analysis to the ML model.

We computed SHAP values for every field observation and crop family, obtaining one vector of feature attributions per (observation, class) pair. Global feature importance was summarised as the mean absolute SHAP value across all observations, stratified by crop family (Table 1). For each crop family, the dominant predictor was defined as the feature with the largest mean absolute SHAP value. We also standardised all continuous predictors to zero mean and unit variance, and ordinal-encoded categorical predictors, prior to the SHAP analysis. For the SHAP waterfall plots, selected numeric variables were inverse-transformed to their original units for interpretability, without changing the underlying SHAP values.

This enabled both global (across the entire dataset) and local (field-level) interpretation of crop choice drivers, providing insight into how previous crop sequence, management intensity, and structural constraints shape crop selection.

### 3. Results

#### 3.1. Spatial and temporal variation of crop families

From 2011 to 2020, spring and winter cereals dominated Danish cropping systems, accounting for a combined total of 57% of arable land (Fig. S4). Spring cereals increased by ~60% (0.5 to 0.8 Mha; ~one-third of annual cropland by 2020), while winter cereals declined from 0.8 Mha to 0.6 Mha. The remaining portion of agricultural land was covered

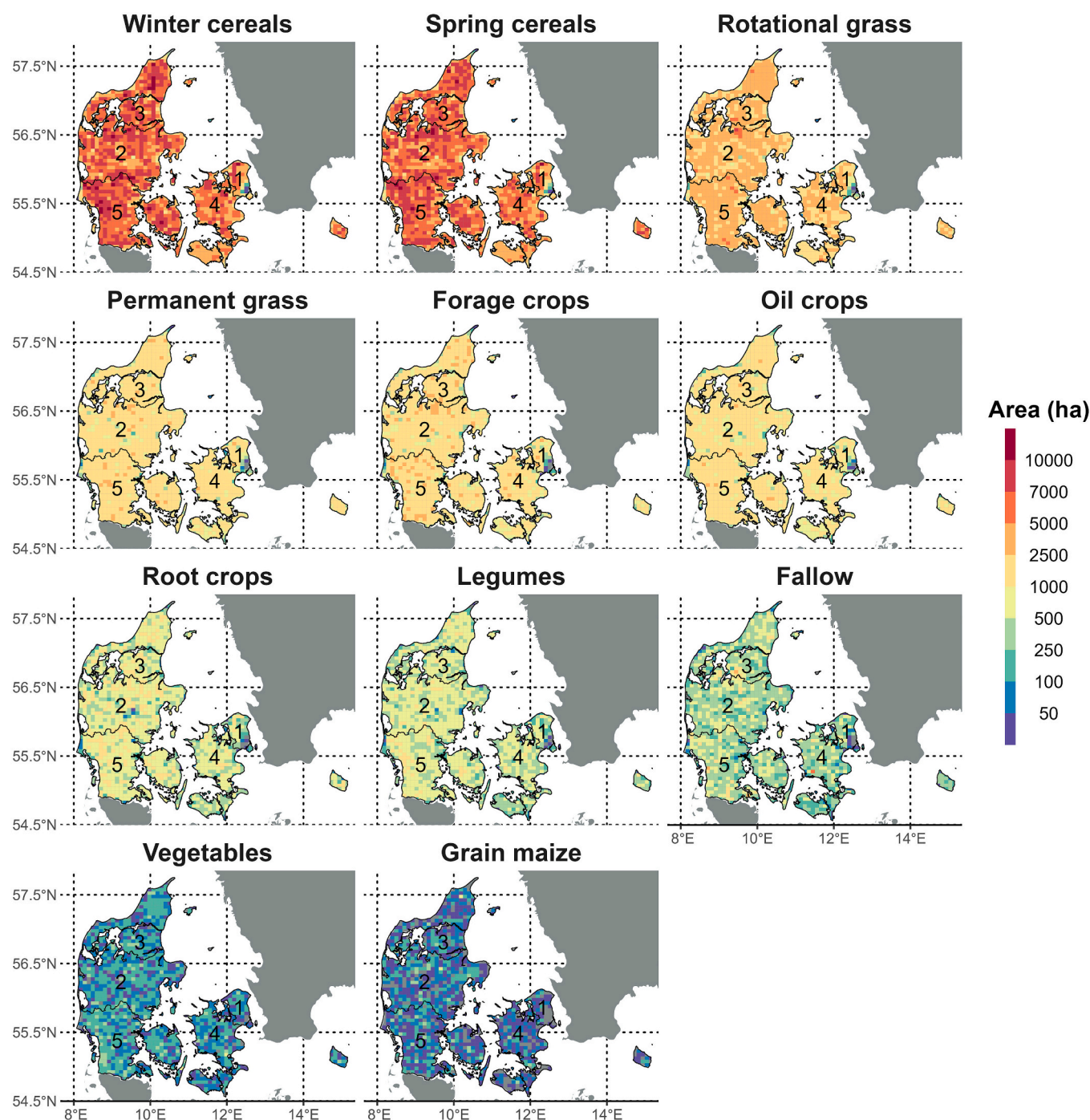
by other crops: rotational and permanent grass occupied around 14% and 7%, respectively. Forage and oil crops (7%), and legumes, root crops, and vegetables each occupied 1–3% but with modest upward trends in all cases.

Crop distributions also varied spatially across Denmark (Fig. 1). Several crop groups, including cereals, forage crops and grass, are more prevalent in western Jutland. Vegetables and root crops form more localised clusters, particularly in parts of central Jutland, whereas grain legumes showed a more dispersed pattern without strong clustering.

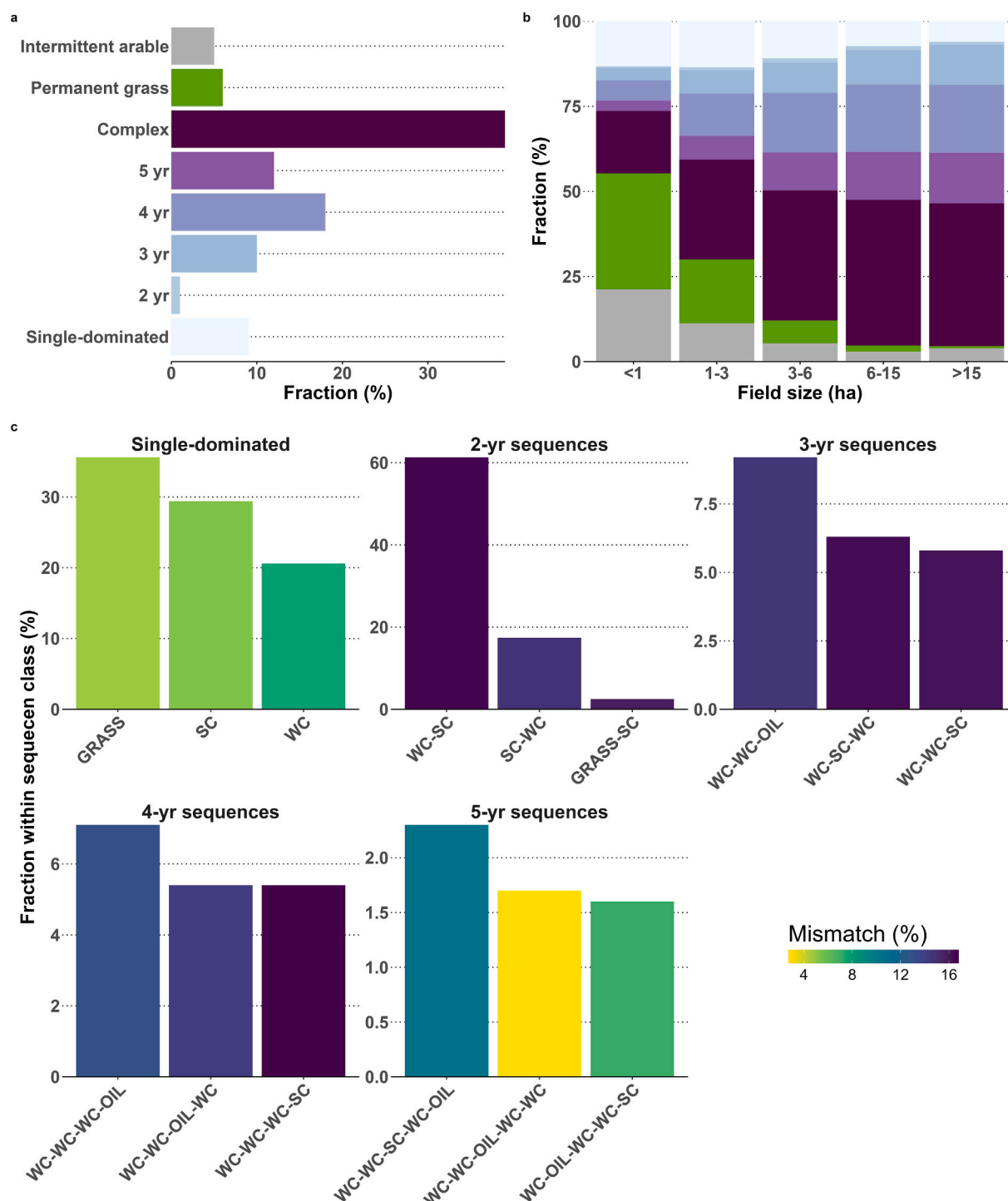
### 3.2. Detection of crop sequences

Building on the spatial and temporal variation described above, we analysed field-level crop sequences across an average annual cropland area of 2.1 Mha  $\text{yr}^{-1}$  and identified patterns varying in length and complexity. Complex sequences formed the largest class, accounting for 39% of field-year observations, lacking a clearly repeating pattern within the 10-year window. Fields dominated by only one crop family accounted for 9% of the area, while 2–5 year sequences were found in 41% of fields (Fig. 2a).

Crop sequence length showed a clear gradient with field size



**Fig. 1.** Spatial distribution of crop family presence across Denmark (2011–2020), expressed in annual average area for each 10 km × 10 km grid. Crop families are ordered according to total area, from highest (winter cereals; 743,000 ha) to lowest (grain maize; 83,000 ha). For a brief overview of Denmark, the reader is referred to Fig. S1. NUTS2 regions are denoted per their number (1–5): 1 - Capital (Copenhagen), 2 - Central Jutland, 3 - North Jutland, 4 - Zealand and 5 - South Denmark.



**Fig. 2.** Crop sequence distribution in Denmark. a) distribution of different crop sequences lengths per total area; b) distribution of different crop sequence lengths per field size. Field size classes were defined based on the empirical distribution of field areas, using percentile thresholds. Fields were classified as small (<1 ha; <P25), medium (1–6 ha; P25–P75), large (6–15 ha; P75–P95), and very large (>15 ha; >P95). (c) Detection of dominant (top 3) crop sequence from monocropping to 5 years, with fraction representing the share of a given crop sequence relative to its sequence length. Fields classified as intermittent arable and permanent grass were not used in the heuristics although they are also visualised here. Colour palette represents the mismatch rate, defined as the fraction of active crop-years in which the observed crop family differed from the repeating pattern.

(Fig. 2b). Small fields (<1 ha) were predominantly classified as permanent grass or intermittent arable. This share declined sharply from 1 to 6 ha and remained low thereafter. Conversely, complex sequences became increasingly dominant with increasing field size, particularly above 3 ha. Longer crop sequences (3–5 years) showed a similar pattern, with their frequency increasing with field size. Single-dominated

sequences were more frequent in small fields (<3 ha) but decreased rapidly with size, remaining marginal in larger fields.

Cereal-dominated sequences prevailed across all detected pattern lengths (Fig. 2c). In single-dominated classes, grass was present in almost 50% of fields, followed by spring and winter cereals and forage crops. Among 2-year sequences, spring and winter cereals dominated,

accounting for over 60% of the total. For 3-year sequences, cereal combinations remained dominant, with the inclusion of oil crops but, to a lesser extent, forage or root crops. Even longer patterns (4–5 years) continued to be dominated by cereals. Sequences involving similar variations of spring and winter cereals represented the most frequent long-term patterns.

Mismatch rates for the most common patterns averaged 5% for single-dominated sequences, and 12% for five-year sequences and 15% across two- to four-year sequences (Fig. 2c). The crop family observed in 85–95% of field-years thus matched the pattern assigned to that field, although individual fields did not always repeat the sequence exactly.

### 3.3. Data-driven prediction of crop family choices

Given the variability in sequence patterns, we evaluated whether annual crop family choices at the field level (i.e., crop in year  $t$ ) can be reliably predicted at field level using ML and DL models (Fig. 3). This analysis is independent of the heuristic algorithm used to classify crop sequence patterns and focusses on the predictability of annual decisions rather than on reconstructing full crop sequences.

**Model skill and generalisability.** The DL model achieved a higher performance overall, with a hold-out accuracy of 0.65, macro F1 of 0.47, and weighted F1 of 0.65. The ML model performed slightly worse, with an accuracy of 0.63, macro F1 of 0.51 and weighted F1 of 0.64. Performance evaluated separately by crop family (AUC around 0.91;

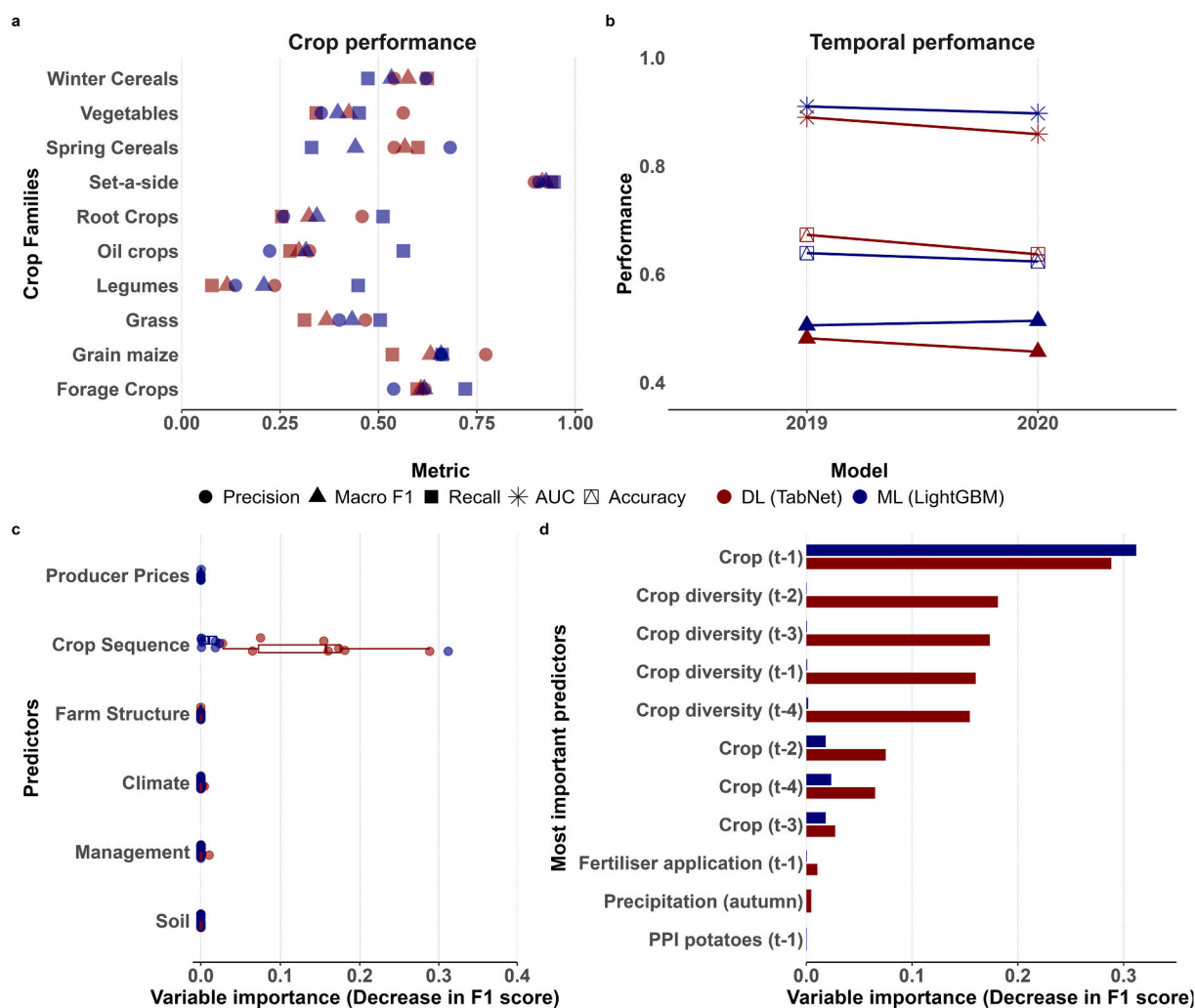
Fig. 3a) and years (Fig. 3b) confirmed a strong predictive capacity, although balancing precision and recall remained challenging for minority crops.

**Crop-specific performance.** The DL model consistently outperformed the ML model for spring and winter cereal crop families, which dominate Danish agriculture. However, its performance dropped for less common or rotationally irregular crops (grain legumes, root crops), where both models had low predictive skill (Tables S3–4).

The ML model showed greater variability in crop-specific performances, with a strong precision-recall trade-offs. While it occasionally achieved higher precision for underrepresented crops like vegetables and legumes, this often came at the cost of lower recalls. This suggests that the model often failed to detect these crops, underestimating their extent.

These patterns were confirmed through confusion matrices (Fig. S5), where both models struggled to correctly identify underrepresented crop families. Specifically, grain legumes, oil crops and vegetables were often misclassified as dominant crop groups, especially spring and winter cereals.

**Temporal performance.** Both models showed a high and stable AUC across the holdout years (Fig. 3b). Accuracy and F1 scores were slightly lower in 2020 compared to 2019, particularly for the ML model, whereas the DL performance was more stable. Despite this, the consistently high AUC suggests that both models were able to distinguish between crop families over time, even when classification accuracy



**Fig. 3.** Performance metrics for the hold-out fold across crop families (a) and (b) years for both models, where 2019 and 2020 were the holdout years, exclusively used in model evaluation. Aggregated (c) and top individual predictor importance (d) in both models.

declined slightly.

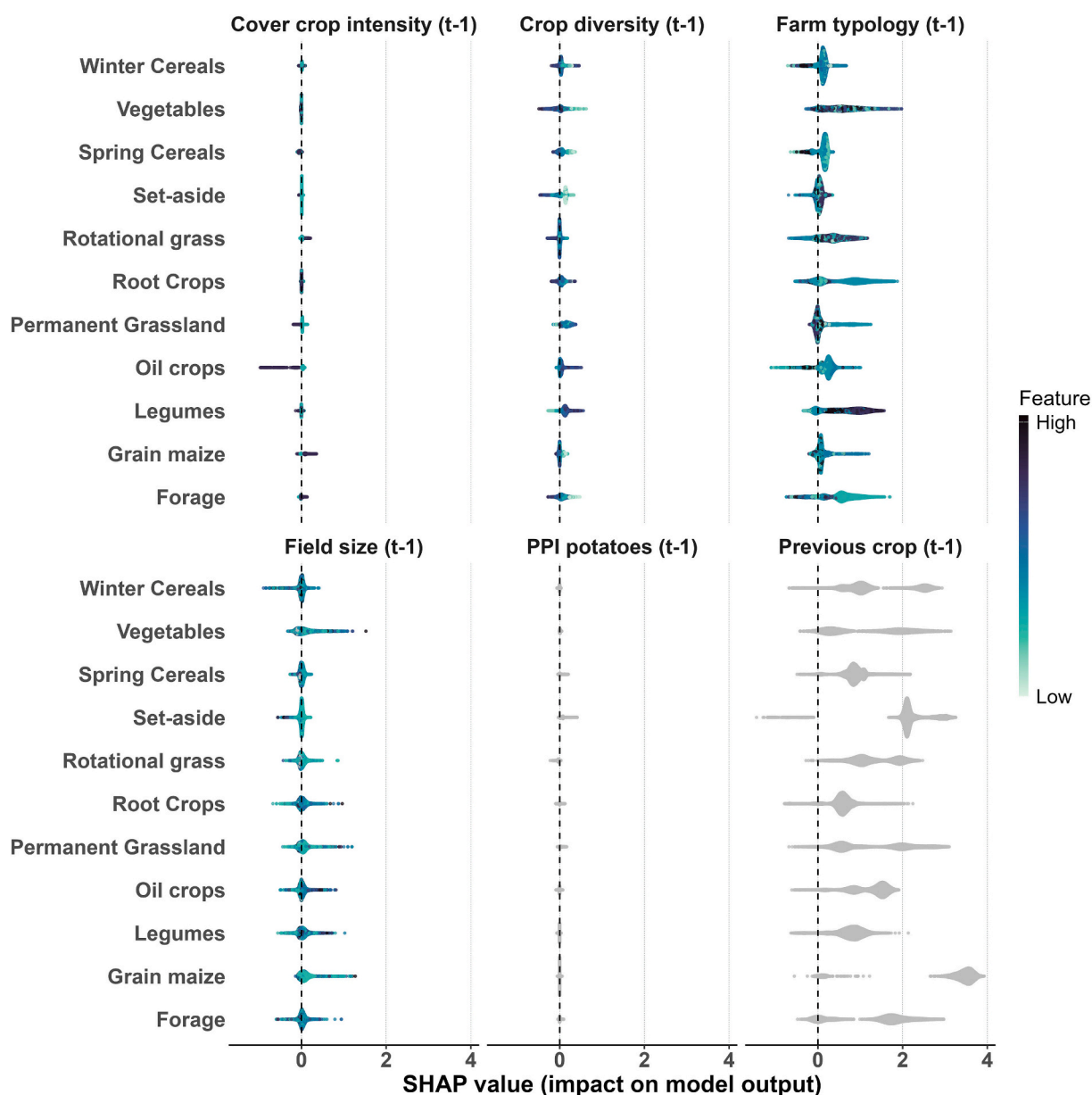
**Field size performance.** Model performance declined consistently with increasing field size (Fig. S6). Accuracy decreased from 0.78 in small fields (<1 ha) to 0.5 in large fields (>15 ha), with similar reductions in AUC (0.91 to 0.82) and macro F1 (0.48 to 0.41). The largest decrease occurred between 1 and 3 and 3–6 ha bins, after which the decline was more gradual. Predictive performance was highest in the most common field classes (<1 and 1–3 ha). Larger fields had substantially fewer observations and lower predictive performance and should therefore be interpreted with caution.

**Predictor importance.** Crop selection decisions (Fig. 3c-d) were primarily associated with sequence history and farm structure, while soil, climate and previous management practices had comparatively lower influence. Both models consistently identified recent crop sequences as the dominant driver, particularly the identity of the crop in

the previous year (t-1), followed by short-term crop diversity on a given field per the Shannon index.

The ML model predictions were strongly reliant on the identity of previous crops, particularly from the year before (t-1). Other predictors had a negligible effect, with no drop in F1 scores when removed. Conversely, the DL model distributed importance more evenly across different lagged predictors, particularly the previous crops and crop diversity on a given field.

Other predictors, such as fertiliser application and autumn precipitation, contributed modestly to the DL model but remained secondary. Soil properties, producer prices, and most management variables had minimal influence in both models.



**Fig. 4.** SHAP bee-swarm plots for the ML model showing how the most influential predictors contribute to the predicted probability of each crop family on the year 2020. Each point in the swarm represents a single field observation; its horizontal position is the SHAP value (positive values increase, negative values decrease the probability of assigning that observation to a given crop family), and its colour indicates the min-max normalised feature value (0 = low, 1 = high). We did not use this normalization for categorical features, namely previous crops (see Fig. S7). For example, a higher proportion of cover crops increases the predicted probability of the Forage class, whereas low cover intensity increases the probability of a Winter cereal classification. PPI represents the producer price index.

### 3.4. Interpreting model-based associations in crop selection

We next use SHAP values from the ML model to interpret the predictors associated with farmers' crop family selection at field level (Fig. 4). This shifts our analysis from prediction to interpretation, highlighting the associations that the model has learned between structural, sequence and management predictors and Danish farmers' crop sequencing decisions. It also provides a transition from global feature importance (Fig. 3c, d) to field-level drivers.

We interpret these results as model-based associations inferred from historical data, not as causal mechanisms. However, consistent and agronomically plausible SHAP patterns can be suggestive of underlying causal relationships and thus serve as a basis for formulating causal hypotheses.

**Previous crops.** Recent crop sequences showed, by far, the strongest association with model predictions across all crop families (Fig. 4). The identity of the previous crop (t-1) dominated model behaviour, with large SHAP contributions and clear separation between crop families. Crop diversity per the Shannon index (t-1) provided a secondary but consistent signal, with lower diversity associated with higher probability of vegetables and forage crops, while higher diversity was associated with legumes and oil crops (Fig. 4). These patterns point to how short-term sequences contain much of the information the ML model uses to distinguish crops.

SHAP analysis further revealed how the preceding crop contributed to the predictions of each crop family (Fig. S7). For cereals, grass systems and grain maize, the contributions were consistently positive when the same crop family had been grown in the previous year. This reveals to how the model learned the tendency for these crops to be grown in successive years. However, it does not necessarily indicate monocultures as consecutive repetitions may occur within a longer sequence. Other associations depended on crop order in a sequence: a preceding oil crop contributed positively to the prediction of winter cereals, but a preceding winter cereal did not equally contribute to the prediction of oil crops. A similar asymmetry was identified between root crops and spring cereals. The model therefore captured which crop tended to follow another.

Crops such as vegetables, grain maize and forage were more concentrated with fewer preceding crop associations, suggesting a more constrained or specialised sequence patterns. Conversely, grass systems (permanent grassland, rotational grass and forage) showed strong internal associations, forming a distinct sequence sub-system.

**Farm structure.** Farm typology was the most informative structural predictor (Fig. 4). Although its contribution varied by crop family, typology was an important structural cue for which crops were more likely within a given farm context. Dominant crop families (spring and winter cereals) had narrower SHAP distributions centred closer to zero and thus weaker associations with farm type. Conversely, less dominant crops such as vegetables or root crops showed broader and more asymmetric SHAP Distributions, suggesting stronger and more variable associations with farm typology.

Field size in the previous year (t-1) showed general weak associations with model predictions, with SHAP values tightly centre around zero across crop families. While some variability was identified, these effects were small and inconsistent, with no clear directional patterns. Occasional larger positive or negative contributions occurred: vegetables, oil crops and legumes are associated with larger fields, while set-aside and rotational grass with smaller field areas. Despite this, we could not find robust or clear associations between field size and specific crop families.

**Management.** Past management practices showed weaker associations (see also Fig. 3). Cover crop intensity in the previous year (share of cover crops on a given field) had the clearest crop-specific signals out of all management practices, but still substantially weaker than farm structure features. We identified marginally stronger associations in specific crop families: oil crops were negatively associated with a higher

share of cover crop in the previous year. A contrasting relationship was occasionally found in grain maize, forage crops and rotational grass in some fields.

The SHAP analyses of past nitrogen application rates (fertiliser, slurry and solid manure; Fig. S8) also showed very modest effects for different crops. Higher synthetic fertiliser rates in the past were linked to increased probabilities for winter cereals, oil crops and grain maize, while slurry and solid manure rates contributed minimally across all crops. These relationships are model-based associations rather than evidence that past management directly influenced the subsequent crop selection. Management predictors contributed only modestly to model performance, likely since much of their co-variation with previous crops and farming systems.

**Other predictors.** Producer price for different agricultural products (e.g. potatoes, meat, pulses) had a very small influence on the model predictions, although with small positive and negative effects on set-asides and rotational grass, respectively (Fig. 4). Pedoclimate predictors showed negligible contributions to the model predictions (Fig. S8).

To complement the global SHAP analysis, we next examine local explanations for two individual field predictions, one from a conventional and one from an organic production system (Fig. 5).

In the conventional field, the root crop cultivated in the preceding year provided, by far, the largest positive contribution to the prediction of spring cereals. Earlier crops contributed more modestly, with previous winter cereals and spring cereals supporting the prediction while root crops weakly opposed it. Farm typology reflected a transition from full-time mixed production at t-4 to full-time sugar beet production, with the latter contributing positively to the predictions. Previous crop diversity and share of cover crops made only minor contributions.

In the organic field, the oil crop cultivated in the preceding year was likewise the most important contributor to the prediction of winter cereals. This contribution was partly offset by rotational grass at t-2 and t-3 and by the dairy cattle farm typology in previous years. The organic production system made a small negative contribution, whereas field size and previous crop diversity made small positive contributions.

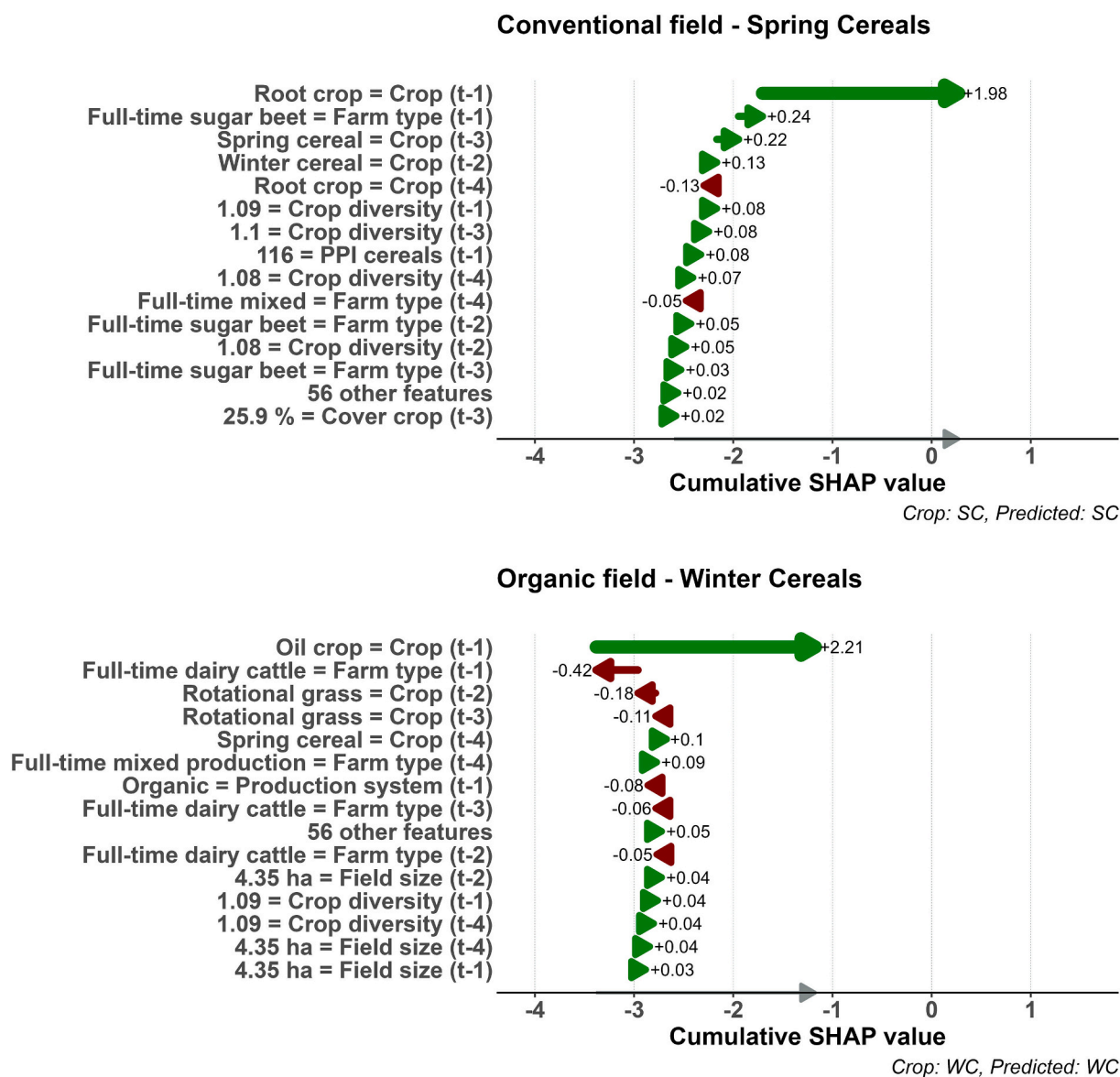
In both fields, the preceding crop dominated the prediction, but the local explanations revealed how its contribution was modified by the remaining predictors. This illustrates how local SHAP explanations can be used to interrogate predictions for individual fields and identify the predictors on which the model relied.

## 4. Discussion

### 4.1. Crop sequence patterns and their agronomic implications

Our analysis reveals a Danish cropping landscape anchored in cereal production, with winter and spring cereals dominating across all sequence lengths. These cereal crops were also cultivated, on average, 53% yr<sup>-1</sup> of fields classified as complex across 2011–2020. Even four- and five-year sequences included few grain legumes, root crops, or vegetables. Longer sequences did not necessarily represent a greater functional diversity but often different arrangements of functionally similar cereal crops. This distinction is agronomically important as increasing crop rotational diversity has generally increased spring and winter cereals' yields in long-term experiments (Smith et al., 2023). Our analysis did not quantify yield or environmental effects, however, so the observed cereal dominance indicates limited functional contrast rather than demonstrating that individual sequences were inefficient.

The dominance of cereals in crop sequences is not unique to Denmark. Declining crop diversity and increasing regional specialisation have also been documented in Sweden (Chopin et al., 2026; Schaak et al., 2023), whereas in Finland a similar prevalence of cereal monocultures despite a gradual decline in their share (Peltonen-Sainio et al., 2017). The Danish expansion of spring cereals and decline of winter cereals (Fig. S4) likewise appear to represent a reorganisation in the



**Fig. 5.** Example SHAP profiles for two individual fields, illustrating how the model combines crop, structural and management information when predicting crop families. SHAP values describe how predictors influence the model's output and may highlight patterns that are suggestive of causal relationships. Each plot starts from the baseline model output (the expected value across the observations) and shows how successive contributions shift the prediction towards the final output, as denoted by the arrow on the x axis. Contributions accumulate from bottom to top, with positive (green) and negative (red) values increasing or decreasing the predicted probability, respectively. The values explain the model prediction and do not identify causal effects. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

dominant cereal system rather than broader diversification. It is consistent with the tightening of governmental regulations that has required a greater use of cover crops. One of the ways to accommodate for this has been to prioritise spring cereals, leaving the autumn windows open for establishing mandatory cover crops. Additionally, increasingly wet autumns and winters have made cultivation of autumn sown crops difficult (Goncharov et al., 2023; Sjulgård et al., 2025). The register data cannot determine how much either factor contributed to the observed shift.

Fields classified as complex also require a careful interpretation. These accounted for 39% of all fields, for which no recurring one- to five-year pattern satisfied the classification criteria within the ten-year observation window, thus not describing a single type of cropping system. Complex fields may contain longer cycles, genuinely irregular sequences, changes in land use or management, or patterns only partly captured after the harmonisation of field boundaries. A similarly large

share of complex sequence patterns was reported for Great Britain (Upcott et al., 2023), although differences in the observation periods and classification rules preclude direct comparisons. The main inference is that many fields could not be reduced to a short repeating pattern, not that they were necessarily more diverse.

Crop sequences observed differed with field size, although the relationship was not linear. Small fields (<1 ha) were disproportionately associated with permanent grass, moved intermittently in and out of arable production, or were dominated by a single crop family. Conversely, larger fields were more often under longer repeating and complex sequence patterns. Possible explanations include differences in the stability of land uses across the observation window, machinery constraints, farm organisation and the allocation of crops among fields. Field area does not represent total farm area, and the register data contain no information about the reasoning behind these allocations. The relationship identifies where different sequence forms occurred, but

not why they occurred there.

#### 4.2. Predictors associated with annual crop family selection

Building on the multi-year classification, our predictive analyses examined how much the selection of different crop families could be reconstructed from recent crop history, and field- and farm-level predictor.

The identity of previous crops was the most informative predictor of annual crop family selection in both the feature importance and SHAP analysis, consistent with similar studies (Abernethy et al., 2023; Palka et al., 2026; Upcott et al., 2023). This is agronomically plausible as preceding crops affect which successor crops are suitable through recurrence restrictions, carry over effects and management timing. The predictor ranking does not, however, reveal how far ahead farmers planned their sequences. The smaller contributions of the identity of crop family in earlier years (t-2 and t-3) also do not necessarily imply that older crops were unimportant, because crop diversity summarised part of these previous sequences (Supplementary methods) and may therefore have absorbed some information about the underlying sequences. The prevalence of cereals, which generally permit shorter recurrence intervals than many specialised crops, may have reduced the apparent influence of longer-term sequence constraints.

Farm typology revealed contrasting global and local importance using permutation importance and SHAP analysis, respectively. Permuting farm typology had a negligible effect on overall model performance (Fig. 3c, d), whereas its SHAP values were broad and heterogeneous for several crop families. Disaggregating by farm typology showed that the strongest contributions were predicted to specialised production systems, such as vegetables with horticultural farms, forage and rotational grass with intensive dairy farms, legumes with organic dairy and plant production farms (Table S5). Conversely, the narrower SHAP distributions and smaller typology contributions for spring and winter cereals indicate that the model relied less on farm structure when predicting these dominant crops. Farm typology therefore helped refine predictions in specialised production contexts but added little unique information to overall performance.

Management predictors added little to predictions already informed by crop history and farm typology. Nitrogen inputs, for example, are closely linked to the crop grown and the production system and may therefore provide little information beyond crop history and farm typology. Farm typology may likewise capture persistent differences in management, soil and climate, reducing the additional contribution of individual pedoclimatic variables. These weaker contributions should therefore not be mistaken for evidence that nitrogen management, soil or climate are agronomically unimportant.

Producer prices in the previous year also contributed little, in contrast to their greater importance across Central Europe in Palka et al. (2026). This represents an imperfect proxy for the returns farmers expect when choosing their next crop. These decisions depend on relative expected margins, which also reflect input costs, contracts, policy support and farm-specific marketing conditions not captured by FAO-STAT prices. The wider spatial and temporal variation available to Palka et al. (2026) may partly explain the difference between the studies. Notwithstanding, our results do not imply that market conditions were unimportant to Danish farmers, only that the price variables used here added little predictive information.

#### 4.3. Methodological insights: balancing prediction and interpretation

The model comparison did not produce a clear winner in terms of performance. The DL model was more accurate and stable across years, particularly for spring and winter cereals, but it more often misclassified less frequent crop families to these dominant classes. Conversely, LightGBM obtained a slightly lower overall accuracy, but its predictions were less strongly drawn towards the dominant cereals, and its errors

more often involved agronomically similar crops. Neither model, however, reliably distinguished the rarest crop families. In this imbalanced dataset, the overall accuracy therefore favoured the model that best predicted dominant crops, while class-specific metrics provided a different assessment of performance for crops relevant to diversification.

The models were consequently useful for different purposes. The DL model better reconstructed dominant cropping patterns, whereas the LightGBM model enabled an estimation of predictor contributions via SHAP, as well as a more balanced representation of less common crops. This comparison showcases why model choice cannot depend only on overall performance metrics. SHAP values indicate how predictors contributed to the predictions, but they do not establish why farmers selected a crop or provide causal estimates of crop choice drivers.

These interpretations are also limited by the information available to the models. Although national producer prices from the preceding year were included, we lacked farm-specific information on expected margins, subsidy eligibility, land tenure and risk preferences. The models thus reconstruct crop selection from historical inferred associations rather than more directly representing farmers' decision-making.

The forward-chaining validation and temporal holdout testing provided evidence of near-term predictive performance, but only within the conditions represented in the Danish data. They do not establish performance following new policies, abrupt market changes or climatic and logistical shocks. Farmers' decisions can shift when facing unusual economic, climatic (Yaseen et al., 2025) or logistical pressures (Tyllianakis et al., 2024). Models trained only based on historical patterns may not capture these responses.

#### 4.4. Implications for crop diversification and agri-environmental modelling

Longitudinal field datasets allow crop change to be distinguished from agronomically meaningful diversification. Crop sequence length and stability describe how crops recur, whereas sequence composition shows whether successive crops provide different agronomic functions. Indicators based only on annual crop changes or crop counts may therefore register diversification within sequences that remain dominated by cereals. Monitoring should also consider cereal recurrence and the frequency and position of legumes, root crops and other break crops.

This distinction has immediate policy relevance in Europe, particularly as the amended Common Agricultural Policy now allows Member States to offer crop diversification as an alternative to crop rotations (Regulation EU 2024/1468). Our data predates this amendment and cannot evaluate its effects, but it shows why compliance based on crop counts should not automatically be interpreted as crop diversification. Farm typology could help distinguish how these patterns vary among production systems, although it cannot explain why they persist.

The same longitudinal data could also make regional agri-environmental simulations less dependent on generic rotations, whose use can substantially affect simulated yields and nitrogen losses (e.g., Rahimi et al., 2024). Where a recurring crop family sequence was detected, the underlying patterns could be used to reconstruct representative model inputs. For the 39% of fields classified as complex, where no recurring one- to five-year pattern was detected, the observed ten-year histories could instead be retained rather than replaced with artificial rotations. Crop sequence generators based on observed transitions and agronomic rules have already been coupled with agri-environmental models to explore productivity and environmental trade-offs (Metcalfe et al., 2024; Sharp et al., 2024). A future extension would be to test whether such generators can be improved by conditioning annual crop selection on several years of crop history, farm typology and field conditions, as in our predictive models, rather than primarily on the preceding crop.

Our classification models remain specific to the Danish agricultural context and the observation window. Applying this approach elsewhere would require locally meaningful crop groups, consistent field

identifiers, and local retraining and validation. Field-level data from the Integrated Administration and Control System (IACS) increasingly provide the annual field histories needed to do this across Europe (Jänicke et al., 2025). Our contribution is thus not simply a national model, but a way of moving from observed field histories to plausible crop sequences that can be examined through agri-environmental simulation.

## 5. Conclusion

By combining an algorithm to classify crop sequence patterns with machine and deep learning models of annual crop family, we examined how Danish cropping patterns were organised over ten years (2011–2020) and how reliably they could be predicted. The agricultural landscape showed a prevalence of winter and spring cereals, with longer and less regular sequences often providing little additional functional diversity. The previous field-level crop history contained most of the predictive information, while farm typology refined predictions for several specialised crops. The deep learning model (TabNet) reconstructed dominant cropping patterns more accurately, whereas the machine learning model (LightGBM) represented less common crops more evenly and allowed its predictions to be interpreted.

Our study highlights how longitudinal field datasets can go beyond describing past cropping patterns. They can reveal whether crop changes introduce meaningful agronomic diversity, while predictive models estimate annual crop-family selection under conditions represented in the training data. These sequences could replace generic rotations in agri-environmental models, allowing their effects on productivity, nitrogen cycling and environmental losses to be tested. As field-level data becomes more widely available, this workflow can be applied elsewhere using locally defined crop groups and locally trained and validated models.

## Declaration of generative AI use

During the preparation of this work the authors used ChatGPT to streamline the writing. After using this tool, the author reviewed and edited the content as needed and take full responsibility for the content of the published article.

## CRedit authorship contribution statement

**João G. Serra:** Writing – original draft, Visualization, Validation, Software, Resources, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Edwin Haas:** Writing – review & editing, Conceptualization. **Diego Abalos:** Writing – review & editing, Supervision, Project administration, Funding acquisition. **Søren Kolind Hvid:** Writing – review & editing, Project administration, Funding acquisition. **Tommy Dalgaard:** Writing – review & editing, Supervision, Project administration, Funding acquisition. **Lars Uldall-Jessen:** Writing – review & editing, Resources, Data curation. **Franca Giannini-Kurina:** Writing – review & editing, Visualization, Validation, Methodology. **Meshach Ojo Aderale:** Writing – review & editing, Software. **Bo Thiesson:** Writing – review & editing, Validation, Methodology, Formal analysis, Data curation. **Jørgen Eivind Olesen:** Writing – review & editing, Project administration, Funding acquisition. **Klaus Butterbach-Bahl:** Writing – original draft, Supervision, Project administration, Funding acquisition, Conceptualization. **Jaber Rahimi:** Writing – original draft, Visualization, Validation, Resources, Project administration, Methodology, Funding acquisition, Formal analysis, Data curation, Conceptualization.

## Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

## Acknowledgement

This study was supported by the Pioneer Center for Research in Sustainable Agricultural Futures (Land-CRAFT), DNR grant number P2, Aarhus University, Denmark. This research has been funded by the SmartField initiative (supported by Novo Nordisk Foundation under grant number NNF24SA0091172). We acknowledge [Flaticon.com](https://www.flaticon.com) for the images used to generate the Graphical Abstract.

## Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.agry.2026.104982>.

## Data availability

The authors do not have permission to share data.

## References

- Abernethy, J., Beeson, P., Boryan, C., Hunt, K., Sartore, L., 2023. Preseason crop type prediction using crop sequence boundaries. *Comput. Electron. Agric.* 208, 107768. <https://doi.org/10.1016/j.compag.2023.107768>.
- Akiba, T., Sano, S., Yanase, T., Ohta, T., Koyama, M., 2019. Optuna: A Next-generation Hyperparameter Optimization Framework. <https://doi.org/10.48550/arXiv.1907.10902>.
- Antle, J.M., Basso, B., Conant, R.T., Godfray, H.C.J., Jones, J.W., Herrero, M., Howitt, R. E., Keating, B.A., Munoz-Carpena, R., Rosenzweig, C., Tittmonell, P., Wheeler, T.R., 2017. Towards a new generation of agricultural system data, models and knowledge products: design and improvement. *Agric. Syst.* 155, 255–268. <https://doi.org/10.1016/j.agry.2016.10.002>.
- Arik, S.O., Pfister, T., 2020. TabNet: Attentive Interpretable Tabular Learning. <https://doi.org/10.48550/arXiv.1908.07442>.
- Blickensdörfer, L., Schwieder, M., Pflugmacher, D., Nendel, C., Erasmi, S., Hostert, P., 2022. Mapping of crop types and crop sequences with combined time series of Sentinel-1, Sentinel-2 and Landsat 8 data for Germany. *Remote Sens. Environ.* 269, 112831. <https://doi.org/10.1016/j.rse.2021.112831>.
- Bligaard, J., 2014. Mark online, a full scale GIS-based Danish farm management information system. *Int. J. Food Syst. Dyn.* <https://doi.org/10.22004/ag.econ.198969>.
- Boccaletti, S., Maranzano, P., Viegas, M., 2024. Inequality and Concentration in Farmland Production and Size: Regional Analysis for the European Union from 2010 to 2020. <https://doi.org/10.48550/arXiv.2409.00111>.
- Chopin, P., Hermouet, S., Watson, C., Öborn, I., Bergkvist, G., 2026. A novel framework to study the evolution of crop rotation diversity reveals changes towards regional crop type specialisation in Sweden. *Eur. J. Agron.* 172, 127848. <https://doi.org/10.1016/j.eja.2025.127848>.
- Dupuis, A., Dadouchi, C., Agard, B., 2022. Predicting crop rotations using process mining techniques and Markov principals. *Comput. Electron. Agric.* 194, 106686. <https://doi.org/10.1016/j.compag.2022.106686>.
- Franke, J.A., Müller, C., Elliott, J., Ruane, A.C., Jägermeyr, J., Balkovic, J., Ciais, P., Dury, M., Falloon, P.D., Folberth, C., François, L., Hank, T., Hoffmann, M., Izaurralde, R.C., Jacquemin, I., Jones, C., Khabarov, N., Koch, M., Li, M., Liu, W., Olin, S., Phillips, M., Pugh, T.A.M., Reddy, A., Wang, X., Williams, K., Zabel, F., Moyer, E.J., 2020. The GGCM Phase 2 experiment: global gridded crop model simulations under uniform changes in CO<sub>2</sub>, temperature, water, and nitrogen levels (protocol version 1.0). *Geosci. Model Dev.* 13, 2315–2336. <https://doi.org/10.5194/gmd-13-2315-2020>.
- Gan, Y., Hamel, C., O'Donovan, J.T., Cutforth, H., Zentner, R.P., Campbell, C.A., Niu, Y., Poppy, L., 2015. Diversifying crop rotations with pulses enhances system productivity. *Sci. Rep.* 5, 14625. <https://doi.org/10.1038/srep14625>.
- Goncharov, A.A., Safonov, T.A., Malko, A.M., Bocharov, G.A., Goncharov, S.V., 2023. Climate change expected to increase yield of spring cereals and reduce yield of winter cereals in the Western Siberian grain belt. *Field Crop Res.* 302, 109038. <https://doi.org/10.1016/j.fcr.2023.109038>.
- Jänicke, C., Goddard, A., Stein, S., Steinmann, H.-H., Lakes, T., Nendel, C., Müller, D., 2022. Field-level land-use data reveal heterogeneous crop sequences with distinct regional differences in Germany. *Eur. J. Agron.* 141, 126632. <https://doi.org/10.1016/j.eja.2022.126632>.
- Jänicke, C., Petersen, K.A., Schmidts, P., Müller, D., Jepsen, M.R., 2025. Field and farm-level data on agricultural land use for the European Union. *Sci. Data* 12, 1050. <https://doi.org/10.1038/s41597-025-05210-6>.
- Ke, G., Meng, Q., Finley, T., Wang, T., Chen, W., Ma, W., Ye, Q., Liu, T.-Y., 2017. LightGBM: a highly efficient gradient boosting decision tree. In: *Proceedings of the 31st International Conference on Neural Information Processing Systems, NIPS'17*. Curran Associates Inc., Red Hook, NY, USA, pp. 3149–3157.
- Leonhardt, H., Wesemeyer, M., Eder, A., Hüttel, S., Lakes, T., Schaak, H., Seifert, S., Wolff, S., 2024. Use cases and scientific potential of land use data from the EU's Integrated Administration and Control System: a systematic mapping review. *Ecol. Indic.* 167, 112709. <https://doi.org/10.1016/j.ecolind.2024.112709>.

- Levavasour, F., Martin, P., Bouty, C., Barbottin, A., Bretagnolle, V., Théron, O., Scheurer, O., Piskiewicz, N., 2016. RPG Explorer: a new tool to ease the analysis of agricultural landscape dynamics with the Land Parcel Identification System. *Comput. Electron. Agric.* 127, 541–552. <https://doi.org/10.1016/j.compag.2016.07.015>.
- Lundberg, S.M., Erion, G., Chen, H., DeGrave, A., Prutkin, J.M., Nair, B., Katz, R., Himmelfarb, J., Bansal, N., Lee, S.-I., 2020. From local explanations to global understanding with explainable AI for trees. *Nat. Mach. Intell.* 2, 56–67. <https://doi.org/10.1038/s42256-019-0138-9>.
- Metcalfe, H., Storkey, J., Hull, R., Bullock, J.M., Whitmore, A., Sharp, R.T., Milne, A.E., 2024. Trade-offs constrain the success of glyphosate-free farming. *Sci. Rep.* 14, 8001. <https://doi.org/10.1038/s41598-024-58183-8>.
- Michailidis, V., Lugato, E., Panagos, P., Freund, F., Abalos, D., 2025. Impact of healthy diet shifts on soil greenhouse gas emissions across Europe. *Glob. Chang. Biol.* 31, e70624. <https://doi.org/10.1111/gcb.70624>.
- Palka, M., Nendel, C., Weiß, L., Schiller, J., Jänicke, C., Gaviria, J.A., Ryo, M., 2026. Cropping history, agronomic rules, and commodity prices shape crop rotations across Central Europe. *Agric. Syst.* 231, 104522. <https://doi.org/10.1016/j.agry.2025.104522>.
- Peltonen-Sainio, P., Jauhiainen, L., Sorvali, J., 2017. Diversity of high-latitude agricultural landscapes and crop rotations: increased, decreased or back and forth? *Agric. Syst.* 154, 25–33. <https://doi.org/10.1016/j.agry.2017.02.011>.
- Rahimi, J., Haas, E., Scheer, C., Grados, D., Abalos, D., Aderle, M.O., Blicher-Mathiesen, G., Butterbach-Bahl, K., 2024. Aggregation of activity data on crop management can induce large uncertainties in estimates of regional nitrogen budgets. *Npj Sustain. Agric.* 2, 7. <https://doi.org/10.1038/s44264-024-00015-3>.
- Schaak, H., Bommarco, R., Hansson, H., Kuns, B., Nilsson, P., 2023. Long-term trends in functional crop diversity across Swedish farms. *Agric. Ecosyst. Environ.* 343, 108269. <https://doi.org/10.1016/j.agee.2022.108269>.
- Schiller, J., Jänicke, C., Reckling, M., Ryo, M., 2024. Higher crop rotational diversity in more simplified agricultural landscapes in Northeastern Germany. *Landsc. Ecol.* 39, 90. <https://doi.org/10.1007/s10980-024-01889-x>.
- Serra, J., Cordovil, C.M.d.S., Cruz, S., Cameira, M.R., Hutchings, N.J., 2019. Challenges and solutions in identifying agricultural pollution hotspots using gross nitrogen balances. *Agric. Ecosyst. Environ.* 283, 106568. <https://doi.org/10.1016/j.agee.2019.106568>.
- Sharp, R.T., Sanderson Bellamy, A., Clear, A., Mitchell Finnigan, S., Furness, E., Meador, E., Metcalfe, H., Mills, S., Coleman, K., Whitmore, A.P., Milne, A.E., 2024. Implications and impacts of aligning regional agriculture with a healthy diet. *J. Clean. Prod.* 449, 141375. <https://doi.org/10.1016/j.jclepro.2024.141375>.
- Sjulgård, H., Graf, L.V., Colombi, T., Hirte, J., Keller, T., Aasen, H., 2025. Earth observation reveals reduced winter wheat growth and the importance of plant available water during drought. *Biogeosciences* 22, 1341–1354. <https://doi.org/10.5194/bg-22-1341-2025>.
- Smith, M.E., Vico, G., Costa, A., Bowles, T., Gaudin, A.C.M., Hallin, S., Watson, C.A., Alarcón, R., Berti, A., Blecharczyk, A., Calderon, F.J., Culman, S., Deen, W., Drury, C. F., García, A.G. y, García-Díaz, A., Plaza, E.H., Jonczyk, K., Jäck, O., Lehman, R.M., Montemurro, F., Morari, F., Onofri, A., Osborne, S.L., Pasamón, J.L.T., Sandström, B., Santín-Montanyá, I., Sawinska, Z., Schmer, M.R., Stalenga, J., Strock, J., Tei, F., Topp, C.F.E., Ventrella, D., Walker, R.L., Bommarco, R., 2023. Increasing crop rotational diversity can enhance cereal yields. *Commun. Earth Environ.* 4, 89. <https://doi.org/10.1038/s43247-023-00746-0>.
- Stein, S., Steinmann, H.-H., 2018. Identifying crop rotation practice by the typification of crop sequence patterns for arable farming systems – a case study from Central Europe. *Eur. J. Agron.* 92, 30–40. <https://doi.org/10.1016/j.eja.2017.09.010>.
- Sun, C., Zhang, H., Xu, L., Ge, J., Jiang, J., Zuo, L., Wang, C., 2023. Twenty-meter annual paddy rice area map for mainland Southeast Asia using Sentinel-1 synthetic-aperture-radar data. *Earth Syst. Sci. Data* 15, 1501–1520. <https://doi.org/10.5194/essd-15-1501-2023>.
- Tyllianakis, E., Otokiti, K.V., Shahvi, S., Martin-Ortega, J., 2024. Farmers' perceived effect of the COVID-19 pandemic and its relationship to preparedness and risk perception. *J. Rural. Stud.* 109, 103318. <https://doi.org/10.1016/j.jrurstud.2024.103318>.
- Upcott, E.V., Henrys, P.A., Redhead, J.W., Jarvis, S.G., Pywell, R.F., 2023. A new approach to characterising and predicting crop rotations using national-scale annual crop maps. *Sci. Total Environ.* 860, 160471. <https://doi.org/10.1016/j.scitotenv.2022.160471>.
- van Bussel, L.G.J., Grassini, P., Van Wart, J., Wolf, J., Claessens, L., Yang, H., Boogaard, H., de Groot, H., Saito, K., Cassman, K.G., van Ittersum, M.K., 2015. From field to atlas: upscaling of location-specific yield gap estimates. *Field Crop Res.* 177, 98–108. <https://doi.org/10.1016/j.fcr.2015.03.005>.
- Whippo, C.W., Coale, E., Igathinathane, C., Heintzman, L., Friedrichsen, C., Archer, D. W., 2026. Crop sequence complexity of the major land resource areas (MLRA) in the contiguous United States (CONUS). *Agric. Ecosyst. Environ.* 396, 110003. <https://doi.org/10.1016/j.agee.2025.110003>.
- Yang, X., Xiong, J., Du, T., Ju, X., Gan, Y., Li, S., Xia, L., Shen, Y., Pacenka, S., Steenhuis, T.S., Siddique, K.H.M., Kang, S., Butterbach-Bahl, K., 2024. Diversifying crop rotation increases food production, reduces net greenhouse gas emissions and improves soil health. *Nat. Commun.* 15, 198. <https://doi.org/10.1038/s41467-023-44464-9>.
- Yaseen, M., Saqib, S.E., Zulfiqar, F., Ali, S., Visetnoi, S., 2025. Farmers' decisions under climate change: a field level empirical investigation of climate risk management strategies. *Sustain. Futur.* 10, 101390. <https://doi.org/10.1016/j.sfr.2025.101390>.
- Zotarelli, L., Alves, B.J.R., Urquiaga, S., Boddey, R.M., Six, J., 2007. Impact of tillage and crop rotation on light fraction and intra-aggregate soil organic matter in two Oxisols. *Soil Tillage Res.* 95, 196–206. <https://doi.org/10.1016/j.still.2007.01.002>.