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Assessing crop sequence diversity and agronomic quality in grassland regions

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ABSTRACT

Industrial inputs have replaced crop rotations for fertility and pest management in input-intensive agriculture, resulting in a high number of crop sequence permutations and negative impacts on ecosystems and human health. Strengthening diversified and agronomically optimised crop sequences is critical to promoting sustainable practices. Comprehensive crop sequence diagnosis methods play an important role in evaluating and improving current crop sequence practices. However, recent literature has focused on annual crops, leading to biased results in crop sequence analysis for organic farming and livestock regions, where multiannual temporary fodder crops are a key aspect of crop sequences. This paper extends two methods of crop sequence analysis by including multiannual temporary fodder crops. By applying these generalised methods to a case study in the beef grassland regions of Belgium, using IACS crop data from 2015 to 2020, we reveal significant differences in the agronomic quality of the crop sequences across the territory and between organic and non-organic fields. In contrast to the existing literature, the inclusion of multiannual temporary fodder crops highlights the prevalence of high diversity and high agronomic quality sequences in livestock farming regions. Maize monoculture (of low agronomic quality), temporary grasslands (associated with high quality crop sequences) and organic certification are the main drivers of crop sequence quality in the regions studied.

1. Introduction

While mixed crop-livestock farming with crop rotations was dominant in pre-war Europe (Mazoyer and Roudart, 2017), industrial inputs have gradually replaced rotations for fertility and pest management during the agricultural intensification of the past century (Stone, 2022). Together with the mechanisation of production processes and genetic improvement, this intensification led to shorter rotations and monocultures (Barbieri et al., 2017; Bullock, 1992; Wijnands, 1997). Overall, this has resulted in agricultural production becoming dependent on a limited number of high-yielding, lucrative crops (Khoury et al., 2014), with crop choices being driven more by policy and market incentives than by agronomic requirements (Song et al., 2021).

The high-input agricultural systems stemming from this intensification have been recognised as unsustainable for more than six decades (Carson, 1962; Cleaver, 1972; Meadows et al., 1972; Paddock, 1970). Despite this, they remain widespread in developed countries (van der Ploeg, 2018). They have been associated with global negative externalities, such as biodiversity loss and reduced ecosystem services (Leenhardt et al., 2023), as well as high social costs and food insecurity in both developed and developing countries (Alliot et al., 2022; Rasmussen et al., 2018). In response, the European Union's Common Agricultural Policy (CAP) is progressively implementing sustainability objectives (Directive 2009/128/EC of the European Parliament and of the Council, 2009; Regulation (EU) No 1307/2013 of the European Parliament and of the Council, 2013). Among these, Integrated Pest Management (IPM) practices favour diversified and agronomically optimised crop rotations to reduce the use of synthetic inputs such as fertilisers or pesticides, directly mitigating the negative externalities of high-input cropping systems (Francis and Clegg, 1990).

In its broadest sense, crop rotation refers to the agricultural practice of growing a cyclic succession of crops of different types on a single field over several seasons. This practice differs from monoculture where the same crop is grown repeatedly over the years. Crop rotations have many agronomic benefits due to the temporal diversity of the crops grown in the field. These include (Selim, 2019): (1) breaking pest/weed cycles (*e.g.*, Curl, 1963; Liebman and Dyck, 1993; Médiène et al., 2011; Puliga et al., 2021); (2) allelopathic suppression of pests/weeds (*e.g.*, Farooq

Abbreviations: CDT, crop diversity type; CSI, crop sequence indicator.

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et al., 2011; Khanh et al., 2005; Mahé et al., 2022; Weston, 1996); (3) improving soil health, structure, and fertility and reducing erosion (*e.g.*, Basso et al., 2019; Dogliotti et al., 2004; Edwards et al., 1992; King and Blesh, 2018); or (4) increasing biodiversity (*e.g.*, Beillouin et al., 2021; McLaughlin and Mineau, 1995; Puliga et al., 2021); and (5) prevent time-averaged yield decline (*e.g.*, Andrade et al., 2023; Bennett et al., 2012; Cernay et al., 2018).

Today's farmers face a complex decision-making process when planning their next crops, often adjusting crop successions from one season to the next and from one field to another, deviating from planned rotations (Dury et al., 2013; Rodriguez et al., 2021; Stein and Steinmann, 2018). As the choice of succeeding crops is less and less influenced by agronomic principles, rotations have disappeared and there are now thousands of different crop permutations to consider (Leteinturier et al., 2006). Rather than limiting our analysis to the concept of rotations, we therefore take a broader approach by considering the concept of crop sequences, which encompasses the entire succession of the crops grown on a field within a given time interval, regardless of any cyclicity (Leteinturier et al., 2006).

Setting aside models and predictions of the most likely next crop within a sequence (*e.g.*, Aurbacher and Dabbert, 2011; Bachinger and Zander, 2007; Basso et al., 2019; Castellazzi et al., 2008, 2010; Dogliotti et al., 2003; Dupuis et al., 2022; Liang et al., 2023; Osman et al., 2015; Schönhart et al., 2009; Sharp et al., 2021; Sorel et al., 2010), most studies on agronomic quality or diversity of crop sequences have mainly focused on annual crops (*e.g.*, Jänicke et al., 2022; Leteinturier et al., 2006, 2007; Nowak et al., 2022; Stein and Steinmann, 2018). This approach has led to an inadequate representation of organic and livestock cropping systems, where multiannual temporary crops play a key role (Barbieri et al., 2017). In particular, temporary grassland and multiannual temporary fodder legumes (such as lucerne or clover), which are sown once and left to grow for two to five years,[1] have been neglected.

Among the studies investigating the agronomic quality or diversity of crop sequences, two methods have caught our attention. Based on the same source of historical crop data at field-level from the European Integrated Administration and Control System (IACS), these methods offer distinctive perspectives on crop sequence analysis and are both regularly referenced in the literature on the subject, having been applied over large geographical areas, including French departments, Belgian regions and German Länder.

The first method, developed by Stein and Steinmann (2018), consists of a double diversity typification of the crop sequences. This approach combines structural and functional diversity, where the former classifies sequences according to the number of different crops and crop changes, and the latter compares the proportion of spring sown-crops with the proportion of leaf crops. While this method proposes an easy-to-apply general typology of crop sequences and has been applied over large areas in Germany for 7-year sequences (Jänicke et al., 2022; Stein and Steinmann, 2018), it excludes all fields with sequences encompassing more than two (consecutive or distinct) years of temporary grassland. Furthermore, it does not include specific measures to account for multiannual temporary legumes, which are therefore automatically classified as (temporary) monocultures.

The second method, developed by Leteinturier et al., (2006, 2007), consists in calculating a crop sequence indicator (CSI) to assess the agronomic impact of the previous crops on the next, taking into account their influence on soil structure, disease, pest and weed proliferation risks, nitrogen residue characteristics, and includes an assessment of the return time of the crops and their diversity in the sequence. This method, which provides a more complex agro-environmental empirical diagnosis of crop sequences, was applied in the southern part of Belgium for sequences from 1997 to 2003 and is recognised as a pioneer work in numerous articles on crop sequence analysis. However, it excludes all fields containing even a single year of grassland (Leteinturier et al., 2007) and does not take into account fodder legumes.

We believe that both methods would benefit from an extension to include multiannual temporary crops, thereby improving their ability to accurately capture the crop diversity within organic, mixed-farming, and livestock cropping systems. Therefore, the aim of this paper is to extend these two crop sequence diagnosis methods to organic and livestock cropping systems, by including temporary grassland and multiannual temporary fodder crops. We apply them to a case study in the beef grassland regions of Belgium (*i.e.*, Famenne, Ardenne and the Jurassic region) from 2015 to 2020 using historical IACS crop data at field level.

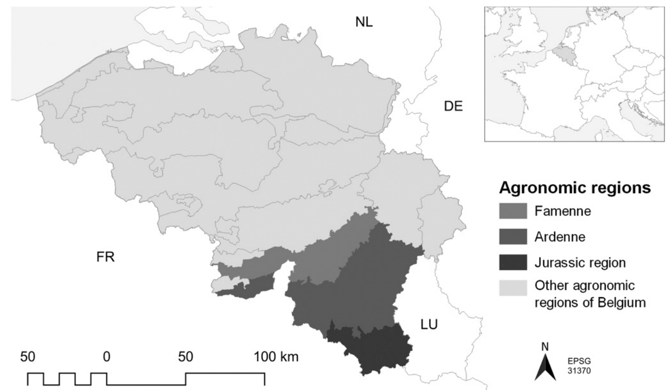

Fig. 1. The three southeastern beef-livestock agronomic regions of Belgium: Famenne, Ardenne, and the Jurassic region.

2. Materials and methods

2.1. Study area

The Belgian territory is traditionally divided into agronomic regions (Ministry of Agriculture, 1951), which are widely used to distinguish regions with specific agronomic practices. The three southeastern agronomic regions of Belgium (Famenne, Ardenne, and the Jurassic region; Fig. 1 and Table 1) make up our study area and cover a total utilised agricultural area (UAA) of roughly 210,000 ha (all figures are extracted from the IACS data). These regions are specialised in extensive beef-livestock farming, with an average 77% of the UAA covered by grasslands —65.5% by permanent and 11.5% by temporary grassland, where 79% of the temporary grassland surfaces are left in place for 3–5 years. The remaining UAA is divided between arable crops (mainly maize and winter cereals) and Christmas tree plantations (Table 2). 16% of the UAA is certified organic in Famenne, 17% in Ardenne and 33% in the Jurassic region (Table 1), which is significantly higher than the average organic share in Belgium (7%; Beaudelot et al., 2022).

It should be stressed that 'non-organic' systems do not always mean 'conventional' high-input industrial systems, as a diversity of farming practices (with or without alternative labels and certifications) exist (Sumberg and Giller, 2022). However, the distinction between organic and non-organic is the only accessible information we have from our dataset to compare different farming models.

2.2. Data source and processing

Geographical crop data were obtained from the anonymised Integrated Administration and Control System (IACS) of the European

[1] According to the classification criteria for temporary / permanent crops and grassland cover (*cf.* Supplementary material C), crops are either annual, multiannual temporary (2–5 years) or permanent (6+ years). We refrain from using the word 'perennial' as it does not permit to distinguish between multiannual temporary and permanent crops.

Table 1
Utilised agricultural area (UAA) in the curated IACS dataset. All areas are expressed in hectares (ha).

	Famenne	Ardenne	Jurassic region
Total UAA	62,844	102,310	34,692
Total organic UAA	9,745	17,693	11,378
Total arable land	21,543	23,911	8,452
Organic arable land	2,429	5,115	2,098

Common Agricultural Policy (CAP; European Commission n.d.), from the year 2010–2020. Anonymised databases on organic fields complement the IACS data from 2015 onwards. All data courtesy of the Public Services of Wallonia (PSW). In Belgium, anonymised IACS records allow information to be extracted for individual fields, including their geometry and the main crop grown that year (*i.e.*, the crop grown on 31 May; PSW, 2022), but the anonymised data do not include information at farm level.

The IACS data were collected on the basis of farmers' declarations for CAP subsidies, consolidated by the PSW, and therefore only include fields cultivated by farmers who apply for such subsidies. Over the years, declared fields may overlap, merge or split. We therefore established an automated procedure to subdivide declared fields into artificial polygons with unique crop sequence definitions (see Supplementary Material A). This procedure retains only differences and valid intersections of field geometries, and deletes all field overlaps with multiple declared crops, as well as duplicates. To simplify the computation process, the procedure also discards all fields and resulting polygons covering less than 0.1 ha. Fields that did not systematically apply for CAP subsidies and had missing crop declarations in some years were similarly removed from the dataset.

This data curation process led to the loss of 6% of the total UAA: from a yearly maximum of 81,186 fields covering a total of 213,037 ha, the final curated dataset contains a total of 157,781 polygons covering 199,846 ha of agricultural land (Table 1).

2.3. Crops of interest

240 different crops and land uses are listed in the IACS data during the studied period (Supplementary Material B). Following CAP reforms at European and member state levels, new crop codes are regularly added and some are abandoned. Following the Good Agricultural and Environmental Conditions (GAEC) and the greening conditionality of the CAP (Regulation (EU) No 1307/2013 of the European Parliament and of the Council, 2013), each crop is also classified into a crop diversification group (PSW, 2022). These groups are defined according to the botanical family of the crop and its sowing season. 66 different crop diversification groups are listed in the IACS data for the study area (Supplementary Material B).

Table 2
Average distribution (in %) of the utilised agricultural area (UAA) and arable land (AL) in the curated IACS dataset. Data on Christmas tree plantations are a low estimate based on the 2015 cartography by Lejeune (2018).

Crop group	Famenne		Ardenne		Jurassic region	
	UAA	*AL*	*UAA*	*AL*	*UAA*	*AL*
Permanent grassland	61.1	—	66.5	—	69.3	—
Temporary grassland	6.9	17.8	15.0	47.2	9.5	31.0
Lucerne and legume	0.8	2.0	0.6	1.9	0.8	2.6
Meslin	1.4	3.6	1.5	4.9	2.2	7.4
Maize	8.5	22.1	4.4	13.8	7.8	25.5
Winter spelt	3.1	8.2	2.9	9.1	1.8	5.9
Winter wheat	6.8	17,6	1.0	3.0	3.3	10.7
Winter triticale	1.0	2.6	0.9	2.7	1.1	3.7
Winter barley	4.0	10.3	1.2	3.7	0.9	3.0
Spring barley	0.3	0.8	1.0	3.2	0.5	1.7
Spring oats	0.5	1.4	1.1	3.5	0.7	2.3
Winter rapeseed	2.2	5.7	0.5	1.5	0.8	2.6
Christmas tree	0.3	—	1.8	—	0.2	—
Other	3.0	7.8	1.7	5.5	1.1	3.7

Over the studied period, the declaration rules for distinguishing temporary and permanent grassland for CAP subsidies have evolved. Furthermore, some farmers did not declare their permanent grassland as such in an attempt to avoid restrictions on grassland ploughing (Leteinturier et al., 2006, 2007). We therefore dedicated the first five years of the dataset (2010–2014) to determine the age of the grasslands. From 2015 onwards, all grasslands of 6+ years were classified as permanent, while grasslands of 1–5 years were classified as temporary (*cf.* Supplementary Material C). This underpins the focus of our case study, which concentrates on 6-year sequences from 2015 to 2020.

When working with crop diversity (*i.e.*, method #1, see below), we refer to the 66 crop diversification groups. However, to limit the number of possible crop sequences examined in the assessment of their agronomic quality (*i.e.*, method #2, see below), we have grouped the 240 crop codes into 14 different crop groups, depending on the relative importance of the crops in the agronomic regions under study and their botanical families (Table 2). The criteria for defining the crop groups are given in Supplementary Material C.

2.4. Method #1: crop diversity typification

The method of Stein and Steinmann (2018) offers a descriptive analysis of crop sequences in terms of a double (structural and functional) diversity typification.

In the original method, structural diversity is addressed by plotting the number of transitions between different crop diversity groups against the number of crop diversity groups, for each polygon in the dataset (Fig. 2, left). Functional diversity compares the proportion of spring-sown crops (as opposed to winter-sown crops) to the proportion of leaf crops (as opposed to cereal crops[2]) in the sequences (Fig. 2, right).

Following Stein and Steinmann (2018), we distinguish nine main types of structural crop diversity (denoted by letters from A to I) and nine sub-types of functional crop diversity (denoted by numbers from 1 to 9; Fig. 2). The two diversity classifications define 76[3] possible crop diversity types (CDT), from A1 to I9, not all of which are observed in the data.

Within the main types, the (structural) diversity increases from A to I. Structural diversity type A, with only one crop diversity group, regroups all the monocultures. Sequences with less than three crop diversity groups (A–D) are considered of poor structural diversity: "*these types of sequences entailed a higher risk for pests and diseases and are therefore stronger dependent on plant protection products*" (Stein and Steinmann, 2018). Sequences with three crop diversity groups (E–F) are considered of moderate structural diversity, while those with more than three crop diversity groups (G–I) are considered of high structural diversity.

Within the sub-types, the (functional) diversity increases towards the central functionally balanced sub-type 5. Functional diversity groups distinguish either pure winter crop sequences (1, 4, and 7), sequences with moderate share of winter crops (less than 50%; 2, 5, and 8), and spring crop dominated sequences (3, 6, and 9), or they distinguish pure cereal sequences (no leaf crop; 1–3), moderate cereal/leaf ratio sequences (4–6), and leaf dominated sequences (7–9).

We propose the following amendments to the method. Although populated by a majority of *Gramineae/Poaceae* (*i.e.*, monocots; *cf.* our definition of grassland in Supplementary material C), multiannual grasslands usually serve similar functions to cover crops or green

[2] As in Stein and Steinmann (2018), we classify maize as a cereal crop.
[3] Each structural main type has nine functional sub-types, except for the monoculture structural main type A, where only the A1, A3, A7 and A9 can exist.

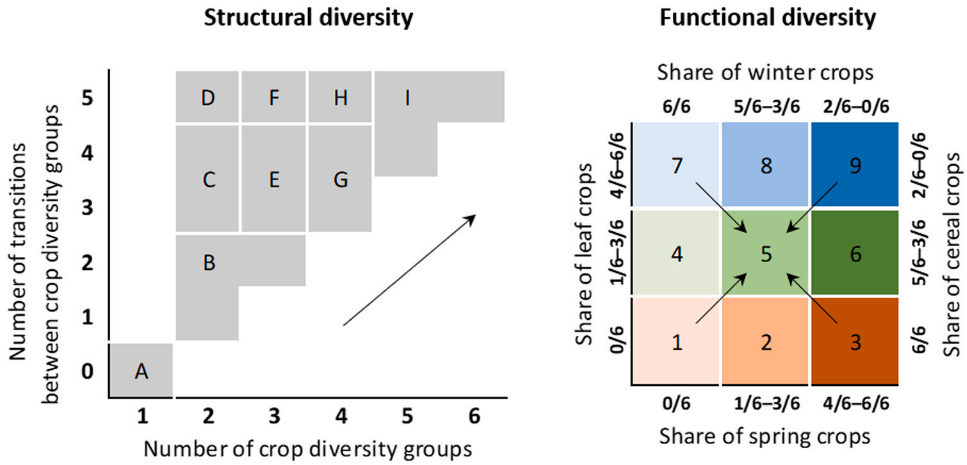

Fig. 2. Crop succession typification for a 6-year period. **Left:** letters A–I denote the nine structural diversity types. **Right:** numbers 1–9 denote the nine functional diversity types. The nine functional diversity types are defined for each structural diversity type. The black arrows show the direction of increasing diversity. Adapted from Stein and Steinmann (2018) and Jänicke et al. (2022).

manure, enhancing diversity within cereal crop sequences. Therefore, we categorized multiannual temporary grasslands as 'leaf crops', diverging from the original proposal of Stein and Steinmann (2018).

Furthermore, we do not define temporary grassland as either a spring or a winter-sown crop (*cf.* Supplementary material B) as both alternatives exist and the IACS data do not provide information on sowing dates. Therefore, instead of looking only at the share of spring crops in the functional diversity, we consider the ratio of spring to winter crops for the crop with specified sowing dates.

For multiannual temporary crops (*i.e.*, temporary grasslands or lucerne and legumes), to account for the positive impact on soil seed bank depletion (*e.g.*, Dominschek et al., 2021; Meiss et al., 2010; Munier-Jolain et al., 2012; Schuster et al., 2020), on soil organic matter increase (Crème et al., 2020) and nitrogen fixing (Nevens and Reheul, 2002; Palmero et al., 2022), we have structured our generalisation of the method as follows. For the structural diversity, the first three years are counted as different crop diversity groups, then each additional year is assigned the same diversity group as the third year (*e.g.*, for temporary grassland: 'tg1′, 'tg2′, 'tg3+'). The three-year timespan is deduced from the literature as the time needed for the optimal effects of the multiannual temporary crops to manifest themselves (*e.g.*, Hoeffner et al., 2021; Kelner et al., 1997; Nevens and Reheul, 2002).

2.5. Method #2: crop sequence indicator

The method of Leteinturier et al. (2006), based on the method of Bockstaller and Girardin (1996, 2008), constructs an empirical crop sequence indicator (CSI) to assess the agronomic quality of crop sequences on a given polygon, in line with the principles of IPM.

Although the principle of the method described here is the same as in the paper by Leteinturier et al. (details on our modifications are discussed in Section 4.1), the mathematical equation formulation is ours. This new formulation allowed us to expand the method to sequences of any length, rather than being restricted to 7-year sequences.

For a given polygon, we define the crop sequence indicator CSI_{ab}, calculated from an initial year a to a final year b, as the product of three factors:

$$CSI_{ab} = \underbrace{\frac{1}{b-a}\sum_{n=1}^{b-a}\alpha_{i(n)j(n)}}_{\text{Effect of the previous crops}} \times \underbrace{\frac{1}{N(\beta)}\sum_{n=0}^{b-a}\beta_i(n)}_{\text{Respect of the return times}} \times \underbrace{\gamma(\{i(n)|=0,...,b-a\})}_{\text{Crop diversity}}$$

where $i(n)$ is the crop grown in year $a+n$, and $j(n)$ is the crop grown in year $a+n-1$ (*i.e.*, the previous crop), with $n \in \{0,\ldots,b-a\}$. The three parameters α_{ij}, β_i and γ are discussed below in Sections 2.5.1, 2.5.2, and 2.5.3 respectively.

As in Leteinturier et al. (2006), the first factor, with values ranging from 1 to 6, averages the empiric agronomic effect of the previous crop on the next over the period considered; it is the core of the CSI. The second factor, ranging from 0.2 to 1.2, gives a penalty to the CSI if the recommended crop return times are not respected. The third factor, ranging from 1.0 to 1.4, gives a bonus to the CSI if the crop diversity within the sequence is high. The three factors are designed to produce a CSI scale ranging from 0 to 10.

As a slight change from the original method, sequences with CSI values from 0 to 3 are considered of low agronomic quality; sequences with values from 3 to 5 are considered of moderate agronomic quality; sequences with values from 5 to 10 are considered of high agronomic quality.

2.5.1. Previous crop parameter α_{ij}

Through the previous crop parameter α_{ij}, the first factor of the CSI averages the first-order effect of the previous crops j on the next crops i for each pair of crops $\{i,j\}$ in the sequence.

The α parameter considers several aspects of the agronomic impact of the previous crop on the next: effect on soil structure, risk of disease, pest and weed proliferation, and nitrogen residue/fixation characteristics (see details in the Supplementary Material D). The resulting values of the previous crop parameter α, expressed as a score ranging from 1 (very unfavourable) to 6 (very favourable), are given in Table 3. Note that no value of α_{ij} can be assigned to the crop group 'other' as it merges crops of very different characteristics: no CSI value can therefore be calculated for the sequences cultivated with at least one year of 'other' crop.

As the specific details behind the derivation of the previous crop parameter are missing from Leteinturier's paper (2006), the assessments of the various impacts and the resulting α values presented in this paper are based on available literature (Gaborit, 2017; Mohler and Johnson, 2009) and consultation with public extension experts (*Fermes Universitaires de l'UCLouvain* and *Centre de Michamps*). Some values differ from those proposed in the original method.

2.5.2. Return time parameter β_i

Through the return time parameter β_i, the second factor gives an average weight that checks whether the recommended return time interval t_i^r of each crop is respected.

Let $t_{i(n)}$ be the time interval (in years) between the year n and the previous cropping of crop $i(n)$ in the sequence and let $t_{i(n)}^r$ be its rec-

Table 3
Previous crop parameter α_{ij} for our crops of interest. Successions in white are either impossible or forbidden by the Walloon Nitrate Management Plan (*Plan de gestion de l'azote*, PGDA, 2014). The values for α are based on available literature and consultation with public extension experts.

Crop \ Previous crop	Permanent grassland	Temporary grassland (year 1)	Temporary grassland (year 2)	Temporary grassland (year 3)	Temporary grassland (year 4)	Temporary grassland (year 5)	Lucerne (year 1)	Lucerne (year 2)	Lucerne (year 3)	Lucerne (year 4)	Lucerne (year 5)	Lucerne (year 5+)	Meslins	Maize	Winter spelt	Winter wheat	Winter triticale	Winter barley	Spring barley	Spring oats	Winter rapeseed
Permanent grassland	5	4	5	6	6	6	5	6	6	6	6	6	5	3	4	4	4	4	4	4	3
Temporary grassland	6	4	5	6	6	6	5	6	6	6	6	5	5	3	4	4	4	4	4	4	3
Lucerne	6	4	5	6	6	6	5	6	6	6	5	4	5	3	4	4	4	4	4	4	3
Meslins	4	4	5	6	6	6	5	6	6	6	6	5	4	2	3	3	3	3	3	3	3
Maize	4	4	5	5	5	5	5	6	6	5	5	4	4	1	2	2	3	3	2	2	3
Winter spelt	4	4	5	6	6	6	5	6	6	6	6	5	4	2	1	2	2	3	2	2	3
Winter wheat	4	4	5	6	6	6	5	6	6	6	6	5	4	2	2	1	2	2	2	2	3
Winter triticale	4	4	5	6	6	6	5	6	6	6	6	5	4	2	2	2	1	3	2	3	3
Winter barley	4	4	5	6	6	6	5	6	6	6	6	5	4	2	3	2	3	1	1	3	3
Spring barley	4	4	5	6	6	6	5	6	6	6	6	5	4	2	2	2	2	1	1	2	3
Spring oats	4	4	5	6	6	6	5	6	6	6	6	5	4	2	2	2	3	3	2	1	3
Winter rapeseed	6	4	5	6	6	6	5	6	6	6	6	5	5	3	4	4	4	4	4	4	1

very unfavourable 1 2 3 4 5 6 very favourable

ommended return time interval (Table 4). The return period parameter $\beta_{i(n)}$ is a first-order estimate of the effect of replanting the crop $i(n)$ before its recommended return time interval. Its values are linearly dependent on the difference $t_i - t_i^r$ and are intended to over- or under-weight the values of the α_{ij} parameter depending on whether the recommended return time interval is respected. The values of β_i are set to range linearly from 0.2 for crops with $t_i - t_i^r \leq -4$, to 1.2 for crops with $t_i - t_i^r \geq 1$.

We extend the method as follows. For multiannual temporary crops (*i.e.*, temporary grasslands or lucerne and legumes), the return time is checked only between the last year of a multiannual cropping and the first year of the next. For crops $i(n)$ that have not been grown before in the succession and that have reached their recommended return time period (*i.e.*, with $(n+1) - t_{i(n)}^r \geq 0$), we further assume that they were grown in year $a-1$, *i.e.* we set $t_{i(n)} \equiv (n+1)$, in order to be able to calculate a β value. If the recommended return time period has not been achieved (*i.e.*, $(n+1) - t_{i(n)}^r < 0$), no value of $\beta_{i(n)}$ is assigned to the crop as we lack information to do so. To calculate the CSI, the return period parameters $\beta_{i(n)}$ are averaged over n, and the sum is divided by a partition function $N(\beta)$: this function counts the number of defined values of $\beta_{i(n)}$, with $N(\beta) \leq b - a + 1$.

As noted in Leteinturier et al. (2006), to ensure that the full length of the recommended return time interval $t_{i(b)}^r$ for the last crop $i(b)$ in the sequence can be checked, the length $b-a$ of the sequence should be at least equal to $\max_n\left(t_{i(n)}^r\right) + 1$. In our selection of crops of interest, we have $\max_n\left(t_{i(n)}^r\right) = 4$ (Table 4), which fits in the 6-year period 2015–2020.

2.5.3. *Diversity parameter* γ

The third factor, the diversity parameter γ, is a first-order estimate of the effect of having a high crop diversity along the sequence.[4] Its values are weighted counts of the number of different crop groups in the sequence and are intended to over-weight the values of the α parameter when the crop diversity is high. It is set to range linearly from 1.0 for a sequence with only one crop, to 1.4 in a sequence with $b-a+1$ different crops (*i.e.*, the maximum possible number of different crops).

We extend the method as follows. For temporary grassland of more than a year and permanent grassland, in order to account for the positive impact on soil seed bank depletion (*e.g.*, Dominschek et al., 2021; Meiss et al., 2010; Munier-Jolain et al., 2012; Schuster et al., 2020) and on soil organic matter increase (Crème et al., 2020), additional years count as 0.5 in the number of different crop groups. For multiannual temporary lucerne and legumes, to further include the fixing of atmospheric nitrogen (Nevens and Reheul, 2002; Palmero et al., 2022), the first two years count as 1, then each additional year counts as 0.5 in the number of different crop groups.

3. Results

3.1. *Crop rotations and crop sequences*

Based on our 14 crop groups (Table 1), we identified 13,964 different crop sequences in the total UAA of the studied regions (5,682 in Famenne, 7,091 in Ardenne, and 3,106 in the Jurassic region). Within these sequences, certain specific rotations may be counted more than once. For example, a biannual rotation is counted twice, once as 'ABAB…' and once as 'BABA…'. Nevertheless, recognisable crop rotations are rare in the regions studied. On arable land and excluding polygons with three or more years of temporary grassland, only five rotations[5] cover more than 100 ha each and account together for less than 10% of the arable land (including maize monoculture, 5.2%). Here, a detailed analysis has been

[4] It is analogous to the *x*-axis of the structural diversity of method #1 (Fig. 2).

[5] (1) maize monoculture, 5.2% of the arable land; (2–3) the biannual rotations of maize and winter wheat or winter spelt, 1.4% and 1.6% respectively; (4) the three-year rotation of maize, winter wheat and winter barley, 0.2%; (5) and the four-year rotation of maize, winter wheat, winter rapeseed and a second winter wheat, 0.7%.

Table 4
Recommended return time intervals t_i^r (in years) for our crop groups of interest. The values given here are adapted from Leteinturier et al. (2006) by consultation with public extension experts (*Fermes Universitaires de l'UCLouvain* and *Centre de Michamps*).

Permanent grassland	Temporary grassland	Lucerne and legumes	Meslins	Maize	Winter spelt	Winter wheat	Winter triticale	Winter barley	Spring barley	Spring oats	Winter rapeseed
1	3	3	3	2	3	3	3	4	3	3	4

carried out to sum up all possible permutations of the rotations, although they also include polygons that followed these 'rotations' for two or three cycles during the period under study, but that did not necessarily follow them before 2015 and/or after 2020. With such a large number of different sequences and low number of rotations, each covering such a small area, it is impossible to characterise the dominant rotations/sequences; this highlights the need for crop sequence analysis at wider scales.

3.2. Two crop sequence diagnosis

3.2.1. Method #1: crop diversity typification

The structural diversity of the sequences shows a wide range of variation, from pure monocultures to highly diverse sequences, with 58% of the arable land being cultivated with the five largest CDTs (I5, G8, I8, H5, and G5 in descending order; Fig. 3). Overall, high structural diversity dominates the arable land (69%), reflecting the abundance of temporary grasslands. Functional diversity shows a similarly wide spectrum: a high share of the arable land is cultivated with winter/spring balanced sequences (sub-types 2, 5, and 8; 81%), among which 39% of functionally balanced sequences (sub-type 5); however, a total of 22% of the arable land is cultivated with pure cereal sequences, half of which with pure spring cereal typical of maize monoculture.

There is a significant contrast in the spatial distribution of the CDTs, both between agronomic regions and between conventional and organic polygons. On non-organic arable land (Fig. 3, top), the sequences of high structural diversity cover 59%, 79%, and 48% in Famenne, Ardenne, and the Jurassic region respectively, with a dominance of leaf crops due to a high proportion of temporary grassland. However, lower diversity sequences also cover an important share of the arable land, with 20%, 14%, and 40% of the respective arable land of the three agronomic regions cultivated with pure cereal sequences (within which 4%, 4%, and 8% are cultivated with maize monoculture). On organically certified arable land (Fig. 3, bottom), sequences of high structural diversity cover between 77% (Jurassic region) and 87% (Ardenne), and balanced winter-to-spring sequences cover between 91% (Jurassic region) and 95% (Famenne). Between 8% (Ardenne) and 12% (Famenne) of the certified arable land is cultivated with pure cereal sequences. In the Jurassic region, 12% of the certified arable land is cultivated with sequences of poor structural diversity, while in Famenne and Ardenne this falls to 7% and 5% respectively.

3.2.2. Method #2: crop sequence indicator

The values of the CSI for the arable land vary widely, ranging from 0.2 to 8.0 (Fig. 4), while permanent grasslands have a value of 7.0. On average (organic and non-organic), sequences of low agronomic quality cover 21% of the arable land, sequences of moderate agronomic quality cover 30%, and sequences of high agronomic quality cover 24% (Fig. 5). No CSI values could be assigned to the remaining 25% of the arable land, where the sequences contain at least one year of 'other' crops, for which we could not assess the impact on the next crop nor assign a recommended return time period.

There is a significant contrast in the spatial distribution of the CSI values, both between agronomic regions and between conventional and organic polygons. For non-organic arable land (Fig. 5, top) low agronomic quality sequences cover 28% of the surfaces in Famenne, 16% in Ardenne and 43% in the Jurassic region. Moderate agronomic quality sequences cover 36%, 25%, and 30% of the surfaces respectively, and high agronomic quality cover 8%, 37%, and 14% of the surfaces respectively. For organic polygons, the regional differences tend to disappear (Fig. 5, bottom). Sequences of low agronomic quality occupy 3% (Famenne) to 6% (Jurassic region) of the certified arable land, sequences of moderate agronomic quality occupy 22% (Famenne and Ardenne) to 37% (Jurassic region), and sequences of high agronomic quality occupy from 31% (Famenne) to 40% (Ardenne) of the certified arable land.

The spatial distribution of the CSI shows a correlation with the different agronomic regions (Fig. 4). Famenne and the Jurassic region have a lower quality of non-organic cropping patterns compared to Ardenne (Fig. 6, blue lines). In organic sequences, territorial differences tend to disappear, with Ardenne showing the best agricultural quality of sequences (Fig. 6, green lines).

4. Discussion: crop sequence diagnosis in grassland regions

We proposed the extension to organic and livestock cropping systems of two methods of crop sequence diagnosis based on IACS historical crop data at field level. Method #1, by Stein and Steinmann (2018), is easy to implement and provides a qualitative diversity typification of crop sequences. Method #2, by Leteinturier et al. (2006), is more time-consuming to implement and provides a quantitative empirical indicator of the agronomic quality of sequences. We applied them to a case-study in Belgium's beef livestock grassland agronomic regions (*i.e.*, Famenne, Ardenne, and the Jurassic region), where arable land is dominated by temporary grassland and fodder crops, from 2015 to 2020.

Our findings showed a high number of crop sequences, counting over 10,000 different sequences between 2015 and 2020. This high number of different crop sequences is in line with previous results in Belgium and Germany (Leteinturier et al., 2006; Steinmann and Dobers, 2013). Within these sequences, the five main exact cyclic rotations covered less than 10% of the arable land (including maize monoculture, 5.2%). This confirms the observation of Leteinturier et al. (2006) that rotations have largely disappeared in southern Belgium.

Our results showed that most of the arable land is cultivated with sequences of moderate and high agronomic quality and diversity. Non-organic crop sequences are dominated by cereals (mostly maize and winter cereals) and show a poorer agronomic quality than in organic crop sequences, especially when temporary grasslands are absent from the sequences.

4.1. Methodology

4.1.1. Improvements to existing methods

Most of the recent studies on crop sequence analysis have overlooked multiannual fodder and forage crops, in particular certain temporary grasslands and multiannual temporary fodder legumes such as lucerne and clover that are sown once and left to grow for two to five years (see *e.g.*, Jänicke et al., 2022; Leteinturier et al., 2006, 2007; Nowak et al., 2022; Stein and Steinmann, 2018). This has led to an incomplete understanding of crop sequences in mixed farming regions and to biased results in regions dominated by extensive livestock farming. To address this issue, we have extended both studied methods to include temporary grasslands and multiannual temporary crops of all age.

Setting aside all other modifications within the methods, the inclusion of temporary grassland and multiannual temporary crops allowed

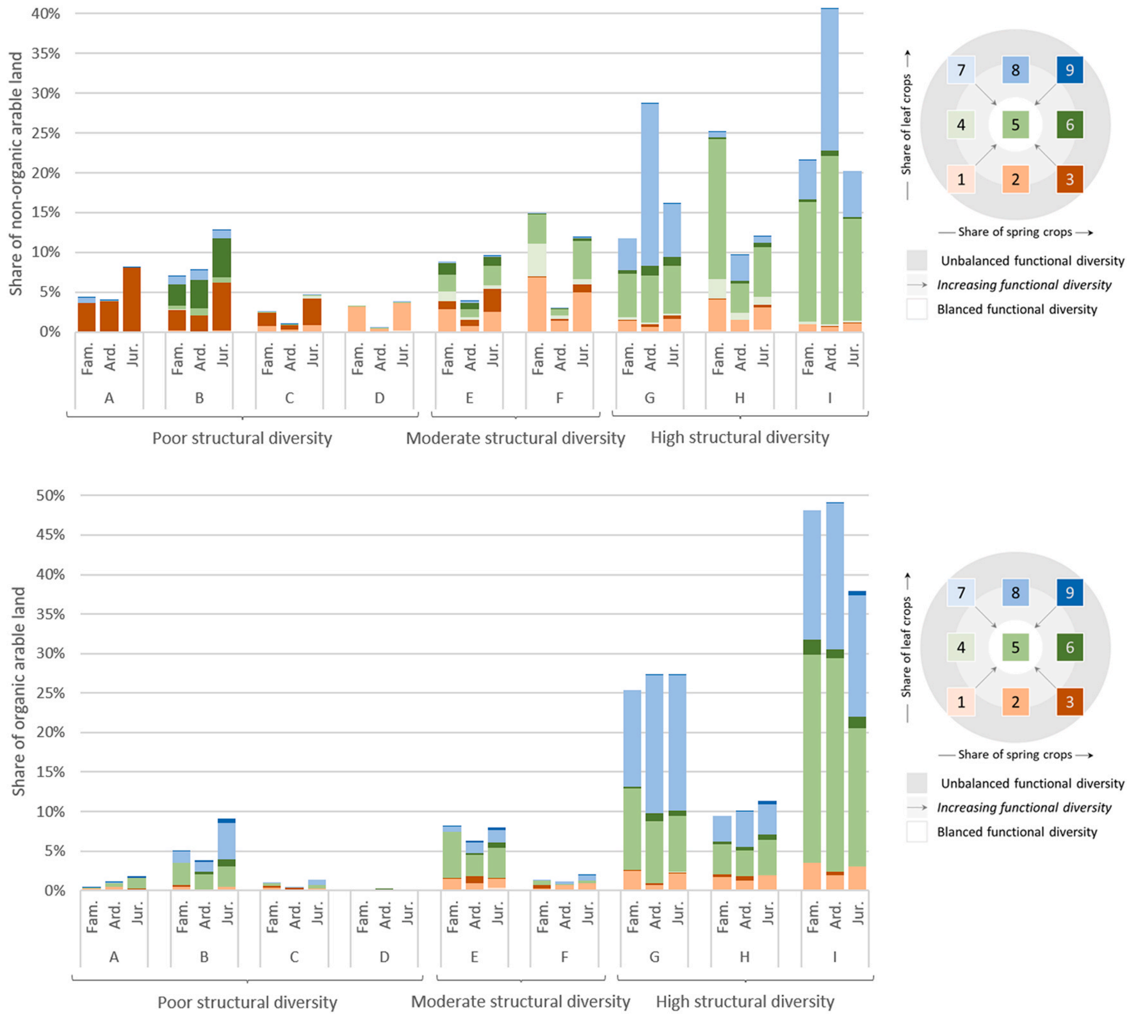

Fig. 3. Arable land distribution of the crop diversity types (CDT) in the different agronomic regions (Fam.: Famenne, Ard.: Ardenne, and Jur.: Jurassic region). The capital letters (A–I) represent the structural diversity and the colours (1−9) represent de functional diversity. **Top**: non-organic arable land; **bottom**: certified organic arable land.

us to analyse 100% of the arable land in our case study using method #1, compared to 68% under the original method of Stein and Steinmann (2018); where "*all sequences with more than two years of fallow or temporary grass* [...] *were not included in the typology*"). Similarly, with method #2, this generalisation enabled us to assess 75% of the arable land (setting aside all sequences containing at least one year of 'other' crop), compared to 31% under the original method of Leteinturier et al. (2006); where all temporary grassland, fodder legumes, and meslins were excluded). Furthermore, we also included permanent grasslands in method #2: this allowed us to apply the methods to 91% of the utilised agricultural area (UAA), compared to 8% under the original method of (Leteinturier et al., 2006).

Table 5 summarises the adaptations and improvements we have proposed for the CSI method of Bockstaller and Girardin (1996, 2008) and Leteinturier et al. (2006). First, we have generalised the method to accommodate any *n*-year crop sequence. Second, we introduced a calculation of the recommended return time parameter for crops that have exceeded their return time period, regardless of whether they were previously cultivated in the sequence. Finally, we included multiannual temporary crops, as well as temporary and permanent grasslands. Note that, as the specific details behind the derivation of the previous crop parameter are missing from the paper of Leteinturier et al. (2006), some values for the previous crop parameter α differ from those proposed in the original method.

Our modifications led to different results than Leteinturier et al., (2006, 2007). In particular, we conclude that crop sequences in Ardenne have a better overall agronomic quality than in Famenne or in the Jurassic region (*cf.* Fig. 4, Fig. 5 and Fig. 6), whereas Leteinturier et al. (2006, 2007) presented opposite results. This suggests that their study is not suited for assessing the agronomic quality of crop sequences in mixed farming and livestock cropping regions, as it overlooks the presence of both temporary grassland and multiannual crops, which are predominant in these farming systems. Therefore, the work of Leteinturier et al., (2006, 2007), carried out in southern Belgium on the basis of IACS data from 1997 to 2003, cannot be used as a time reference for the evolution of cropping practices for our case study.

In contrast to common practice in the literature, which often relies on raster fields to analyse crop data, we processed our crop data as vector data throughout the analysis (see Supplementary Material A). Using this approach, we were able to perform precise descriptive analyses without compromising data quality and avoided any additional data simplification after processing the initial crop dataset. Our method represents a significant improvement over other approaches used in the literature, including those from Habran et al. (2022) and Jänicke et al. (2022).

4.1.2. *Two complementary methods*

The double diversity typification method (method #1) is easier to implement as it only requires crops to be classified into botanical diversity groups and into categories (cereal/leaf crops and winter/spring

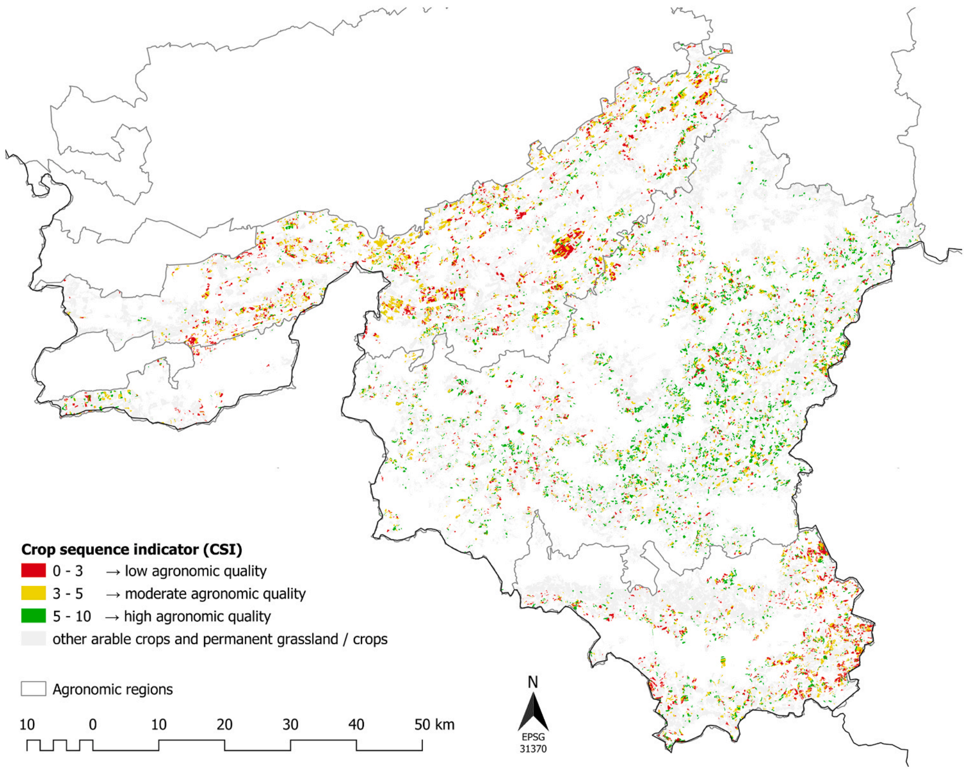

Fig. 4. Arable land crop sequence indicator (CSI) territorial distribution for the period 2015—2020 in Famenne, Ardenne, and the Jurassic region.

crops). It provides a broad qualitative typification of crop sequences that can be easily applied to all arable surfaces. The CSI method (method #2) enables a finer analysis of the agronomic quality of the sequences by providing a quantitative classification of sequences. However, it requires more detailed agronomic parameters to be contextualised to the study area, and is limited to the number of crops investigated.

As noted by Jänicke et al. (2022), diversity typification alone may sometimes be insufficient to provide an accurate representation of crop sequences, especially for temporal evolution analysis. Indeed, a reduction from high to moderate structural diversity does not necessarily lead to agronomic disadvantages, as high structural diversity may include unfavourable crop combinations, such as pure winter cereal sequences. Analysis of the co-evolution of both structural and functional diversity can help to reduce imprecisions, but we are convinced the CSI complements the diversity typification with a more direct and comprehensive picture of the crop sequences. While the first method can be used for an initial overview of crop sequence diversity, we recommend combining both methods for a comprehensive diagnosis.

4.2. Crop sequence diversity and agronomic quality in grassland regions

Our results showed that a significant proportion of the arable land in the studied regions is cultivated with simplified crop sequences. This is particularly noticeable in maize dominated sequences and to some extent in sequences characterized by moderate structural diversity or dominated by winter cereals without temporary grassland. Introduced in the 1970s, maize has progressively become the dominant crop in the livestock grassland regions (excluding temporary grasslands), covering nowadays 19% of the arable land in the beef livestock grassland regions of Belgium. Its wide adoption has contributed to the simplification of farming practices, and despite its potential to diversify sequences dominated by winter crops and interrupt the accumulation of weeds adapted to these crops (Stein and Steinmann, 2018), maize remains largely cultivated in (near) monocultures. In the regions under study, 20% of the arable land is cultivated with sequences composed of at least 50% maize, and 4% is cultivated as pure maize monocultures, in complete disregard of crop rotation recommendations.

This trend is not unique to the beef grassland regions of Belgium and has also been observed in livestock-specialised regions in Germany (Jänicke et al., 2022). Jänicke et al. (2022) and Stein and Steinmann (2018) suggested that intensive crop sequences of low agronomic, structural, and functional quality with a high prevalence of maize dominated sequences are common in livestock-specialised regions, where maize silage has become a major feed source. Our findings support this observation in regions where temporary grasslands are less common.

However, the inclusion of temporary grassland and multiannual temporary fodder crops in our crop sequence analysis revealed a prevalence of moderate and high crop sequence quality in our study area. This suggests that livestock cropping systems, when including grassland and legumes, can promote agronomic quality in crop sequences across regions.

4.3. Territorial variability and organic certification

The spatial distribution of the CSI showed a correlation with the different agronomic regions studied. Famenne and the Jurassic region, which have wider valleys, lower average altitudes and milder climates, showed a lower quality of non-organic cropping sequences compared to Ardenne, which has steeper valleys, higher plateaus and a colder climate (Fig. 6). In organic sequences, territorial differences tend to disappear. This can be attributed to the fact that certified organic agriculture does not allow the flexible choice of crop sequences that rely on synthetic inputs to be profitable, but rather requires stricter adherence to agronomic principles in crop sequences (Barbieri et al., 2017; Reckling et al., 2016). As a result, organic sequences have a higher agronomic quality.

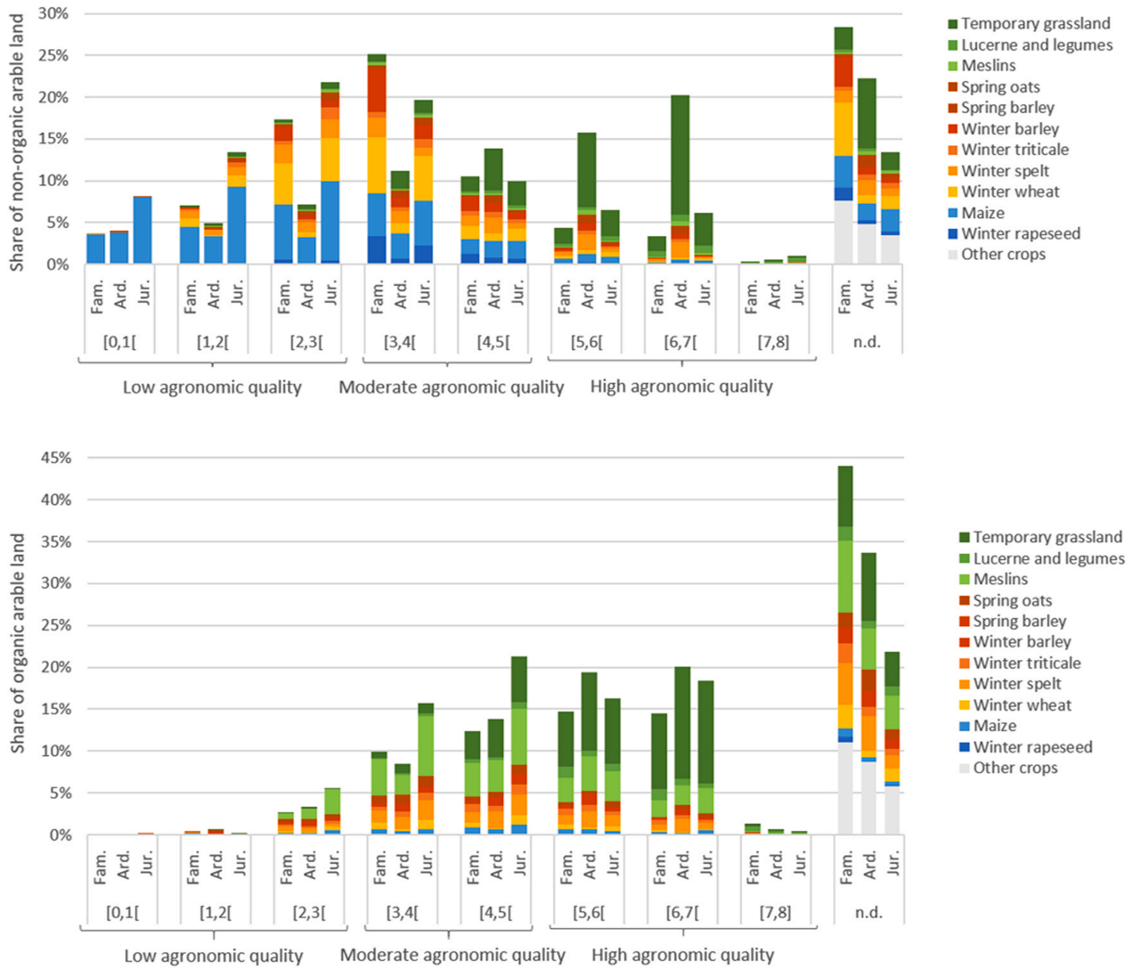

Fig. 5. Arable land distribution of the crop sequence indicator value (CSI) in the different agronomic regions (Fam.: Famenne, Ard.: Ardenne, and Jur.: Jurassic region). The colours represent the average share of crop groups per CSI value and per agronomic region for the period 2015–2020. The *n.d.* column regroups all surfaces cultivated with at least one year of 'other' crop, for which no CSI value could be calculated. **Top**: non-organic arable land; **bottom**: certified organic arable land.

4.4. Limitations and further research

Both methods are first-order descriptive analyses, and we have limited the scope of this paper to arable land. On an annual basis, on average 5% of the arable land is cultivated with 'other' crops. However, the percentage of 6-year sequences containing at least one year of 'other' crops is higher, on average up to 25%, due to the temporal and spatial distribution of these crops in the sequences. This figure goes up to 44% on organic arable land in Famenne. Including more crops in the calculation of the CSI score, especially those grown in organic farming, would reduce the proportion of arable land with an undetermined CSI. Moreover, the conversion of permanent grassland to arable land at a territorial level could signal an intensification trend or a wider shift in cropping systems: a more comprehensive analysis of the whole UAA would be a valuable addition to this study.

In future work, we suggest extending the current 6-year study period to (at least) 7 years, as the inclusion of multiannual temporary crops and grassland, as well as the greater crop diversity in organic sequences, may

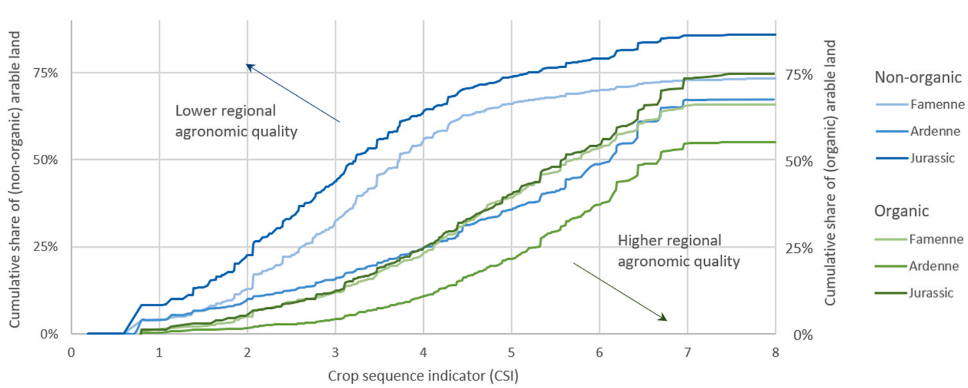

Fig. 6. Cumulative distribution of the share of crop sequence indicator (CSI) values in the agronomic region's (organic and non-organicy) arable land.

Table 5
Improvement of the crop sequence indicator (CSI) method from existing literature.

ROTATIONS / SEQUENCES STUDIED	Bockstaller and Girardin (1996, 2008)	Perfect cyclic rotations of maximum 4 years.
	Leteinturier et al., (2006, 2007)	Generic crop sequences of 7 years.
	In this paper	Generic crop sequences of any *n*-year length; applied to a 6-year case study.
CSI CALCULATION	Bockstaller and Girardin (1996, 2008)	The CSI value of the rotation is the average of the CSI values of each permutation of the rotation (*e.g.*, for a 4-year rotation, CSI values are calculated for 'ABCD', 'BCDA', 'CDAB', and 'DABC', and are then averaged).
	Leteinturier et al., (2006, 2007)	The sequence CSI value is calculated on the basis of: (1) the average of the 7 previous crop parameters α, (2) the average return time parameters β for crops that have already been grown in the sequence, averaged over the number of defined return time parameters, and (3) a general diversity parameter γ for the whole sequence.
	In this paper	The sequence CSI value is calculated on the basis of: (1) the average of the n previous crop parameters α, (2) the average return time parameters β for crops that have already been grown in the sequence and for crops that have exceeded their return time period (even if not grown previously), averaged over the number of defined return time parameters, and (3) a general diversity parameter γ for the whole sequence.
ADMISSIBLE CROPS	Bockstaller and Girardin (1996, 2008)	Annual arable crops; with parameters contextualised for Alsace (France).
	Leteinturier et al., (2006, 2007)	Annual arable crops; with parameters contextualised for Wallonia (Belgium).
	In this paper	Total UAA, including (1) annual arable crops, (2) multiannual arable crops and temporary grasslands, and (3) permanent grasslands; with parameters contextualised for the beef livestock grassland regions of Belgium.

require a longer period to fully capture the effects of crop diversity in the sequences. A 7-year period would also allow for an alignment with CAP reforms. Comparing historical crop data from earlier time periods would allow longer-term trends to be assessed. We also recommend carrying out case studies at a larger spatial scale, covering a variety of agronomic regions with different cropping and livestock systems.

Finally, the inclusion of data on intercrops, secondary crops, and cover-crops would broaden the scope of the analysis. They all play a key role in sustainable agriculture and the methods discussed would benefit greatly from taking them into account (as suggested in Bockstaller and Girardin, 2008, or in the second paper by Leteinturier et al., 2007). Furthermore, cover crops are becoming a common measure, in particular through the GAEC 7 of the CAP ("crop rotation in arable land"), and especially in maize monoculture. Unfortunately, IACS data do not include these crops.

Further cross-analysis with farm-level data (*e.g.*, Jänicke et al., 2022) and data on fertilizer and pesticide use (ideally at field level) would also prove informative (*e.g.*, Andert et al., 2016) as "*reliance on chemical and fertilizer use operates as a technological lock-in* [...] *unsustainably extending the viability of simplified systems*" (Spangler et al., 2022).

4.5. Policy recommendations

The territorial disparities observed, especially at the level of agronomic regions, highlight the need for tailored public extension support and regulations that consider specific local conditions. As suggested by Leteinturier et al. (2006), the local administration could identify farmers with low CSI values relative to their territory and provide them with free extension support to promote the adoption of IPM practices.

The benefits of crop sequence diversification, including reduced dependence on synthetic inputs, highlight the need for policy incentives to promote crop diversification, both at farm and value chain levels.

5. Conclusion

The aim of this paper was to propose the extension of two crop sequence diagnosis methods to organic and livestock cropping systems by including temporary grassland and multiannual temporary fodder crops, and apply them in a case study in Belgium's beef livestock grassland agronomic regions using historical crop data from the European Integrated Administration and Control System (IACS) between 2015 and 2020. Our results show a wide range of crop sequence diversity and agronomic quality, from low (*e.g.*, maize monoculture) to high (*e.g.*, diverse sequences with temporary grassland). Organic crop sequences show higher agronomic quality. Our results suggest that crop sequences in harsher environments, dictating the adherence to agronomic principles, have a higher agronomic quality. Including multiannual temporary fodder legumes and temporary grasslands in our analysis allowed a more comprehensive diagnosis of the region under study, highlighting the limitations of previous work in regions of mixed farming and livestock cropping. Further study including permanent grassland and farm-level data, as well as detailed input use data, would further improve the understanding of cropping systems diversity.

CRediT authorship contribution statement

Noé Vandevoorde: Conceptualisation, Methodology, Resources, Data curation, Software, Formal analysis, Visualisation, Writing – original draft, Writing – review & editing. **Philippe V. Baret:** Conceptualisation, Writing – review & editing, Supervision, Funding acquisition.

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.

Data availability

Data will be made available on request.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.eja.2023.126958.

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