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Convolutional neural network for the early identification of weeds: A technological support to biodiversity and yield losses mitigation

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ABSTRACT

Weeds are a major constraint for crop production and food security. Chemical management, the most utilized method for weed control, has serious drawbacks. In this context, the development of more sustainable methods like site-specific weed management (SSWM) is highly deemed. With this study, we assessed the possibility of applying two convolutional neural networks (CNN) for the recognition of different classes of weeds in a winter wheat (*T. aestivum*) cultivation based on RGB images. By using this methodology, we were able to recognize with a high average precision (AP > 0.6) some species whose abundance and distribution in the field was correlated with the final wheat yield. We demonstrated that where the presence of *R. raphanistrum, A. arvensis* and *P. rhoeas* was high at the tillering stage and weed biodiversity indexes were low (Menhinich's Index, Simpson's Reciprocal Index and Shannon's Index), wheat yield was significantly reduced. In contrast, higher weed biodiversity mitigated yield losses. Therefore, CNN is a useful tool for early evaluation of the impact that weeds may have on yield, and it can be used as SSWM classifier for an early mapping of weeds, which is critical to improve our understanding of weed ecology dynamics in agricultural fields.

Introduction

Among agricultural pests, weeds represent the main cause of yield loss worldwide [1]. The potential yield losses in wheat (*Triticum aestivum* L.) have been estimated around 23 % and attributed mainly to weeds among the most critical biotic stressors [2]. In wheat, as well as most other crops, weeds are controlled through applications of synthetic herbicides [3], which have been documented to be the most abundant class of pesticides used in global crop production from 1990 to 2020 [4]. Herbicides have numerous advantages compared to other weed control methods, including high efficacy and wide adaptability to different cropping systems. However, excessive use of herbicides has led to the contamination of surface and ground water, damages to non-target species, and development of resistance by weeds populations [5,6]. Moreover, the chemical weeding as well as intensive agriculture caused the over-simplification of the cropping systems, leading to the occurrence of few dominant, highly competitive weed species in the cultivated fields [7,8]. The negative impact of weed chemical control on the biodiversity of the cropping systems has therefore exacerbated the yield losses caused by this biotic constraint [8]. The ecological theories behind these findings point out that where the biodiversity is high, the competition for resources limits the prevalence of few dominant species in terms of number and biomass, possibly delaying the critical period of weed control (CPWC) and thus leading to lower weed-crop competition [8]. Understanding how weed diversity can mitigate yield losses is of critical importance in weed science [9]. Nevertheless, the implementation of biodiversity patterns/thresholds that may be functional to develop sustainable strategies for weed management have been restricted by technological limitations in weed identification, that impaired a thorough understanding of the ecological basis of weed infestations and its relationship with the crop performance [10]. Different methods for weed identification in the field have been proposed, including use of sensors to discriminate crop rows from weeds [11], and the use of multispectral images to identify differences between crops and weeds [12]. In contrast, a few attempts have been carried out with the aim to discriminate single weed species, an approach that is necessary to support the study of weed biodiversity in agricultural fields and expand our understanding on weed ecology [13]. Convolutional Neural

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Table 1
List of the weed species with their EPPO code and the number of individuals manually annotated with CVAT after slicing.

Weed species	EPPO	Number of annotations
Raphanus raphanistrum	RAPRA	11,721
Anthemis arvensis	ANTAR	10,316
Papaver rhoeas	PAPRH	6129
Chenopodium album	CHEAL	4977
Medicago polymorpha	MEDPO	1436
Polygonum aviculare	POLAV	2378
Veronica spp.	1VERG	871
Stellaria media	STEME	231
Fumaria officinalis	FUMOF	461
Ranunculus repens	RANRE	516
	Total	**39,006**

Network (CNN) is a particular application of neural networks generally used for object detection in computer vision [14,15]. Here we demonstrate that the application of CNN to weed identification can contribute to develop a flexible classifier for Multiple species of weeds in wheat field, enabling the identification of weed species composition at an early stage of infestation, giving important information on the weed biodiversity in the field.

Materials and methods

Plant material and experimental design

The experiment was conducted during the growing season of 2021–2022 at the experimental field of the Department of Agricultural Science of the University of Naples Federico II (Portici, IT, 40°48′52’’N, 14°20′48’’E). The soil of the field presented a sandy-loam texture with the following characteristics: sand 77.9 %, clay 6.5 %, silt 15.6 %, 71 ppm available P_2O_5, and 841 ppm exchangeable K_2O. A mixture of different varieties of wheat from APSOV Sementi S.p.a (Lombardy, Italy), named “Don Carmine”, was used. The experimental plots were 4 m^2 arranged in a completely randomized design with two treatments: weed-free (eight replicates) and weedy plot (14 replicates). Sowing was performed on December 15th, 2021, with a density of 450 seeds per m^2 with an inter-row distance of 10 cm. Fertilization was made following the guidelines of the Campania region, with the application of phosphorus at sowing, and two applications of nitrogen at tillering and stem elongation for a total of 150 kg ha^{-1} of nitrogen. Weed control in the weed-free plot was performed by the application of *Timeline Trio*®, a selective herbicide with three different active molecules (*pinoxaden, clodinafop-propargyl* and *florasulam*) for the control of dicotyledonous and monocotyledonous weeds. The selectivity toward wheat was guaranteed by the presence of the safener molecule *cloquintocet-mexyl*. The application was carried out at the tillering stage of wheat with a dose of 1 L ha^{-1}. Wheat was harvested on June 22nd, 2022, 189 days after sowing (DAS).

Agronomic measurement on wheat

At the heading stage (145 DAS) and at harvest (189 DAS), 1 m^2 per plot was used for the determination of different agronomic traits on wheat. At the heading stage, wheat plants were collected and counted for the determination of their density per m^2. Plants were then separated into their vegetative and reproductive portions and weighted for fresh shoot biomass determination and spike fresh biomass determination. At harvest (189 DAS), plants were counted for the determination of their density per plot. Then, wheat plants were divided in spikes and vegetative portions for the determination of shoot and spikes dry weights. Spikes were then subjected to threshing with a bench thresher to separate the kernels from husks for yield determination.

Determination of weed density

Weed density was evaluated at the tillering stage (43 DAS), and at the heading stage of wheat (145 DAS). At tillering stage, weed density per single species was evaluated on pictures acquired with a commercial RGB camera (Huawei Mate 20 Pro, 16-megapixel, resolution of 3968 × 2976 px) between 10:00AM and 12:00PM. Three pictures per plot were acquired at ~60 cm from the top of the canopy, for an area of ~0.5 m^2 per plot. In this phase, the herbicide treatment was not yet performed. Therefore, the pictures were acquired on all the plots of the field ($n = 24$). The acquisition height was measured with a roll meter from the soil to the camera. In every picture, a scale was present to make comparable the densities throughout the dataset. The weeds in the pictures were manually annotated with an online free tool “*Computer Vision Annotation Tool*” [16]. The total weed density was calculated as the sum of the number of individuals per plot independently from their species. In total, the dataset consisted of 72 images with a total of 39,006 elements manually annotated (i.e., weed individual plants) as reported in Table 1. Twelve different classes (i.e., weed species) were identified: *Raphanus raphanistrum, Anthemis arvensis, Papaver rhoeas, Chenopodium album, Melilotus officinalis, Medicago polymorpha, Polygonum aviculare, Veronica persica, Veronica hederifolia, Stellaria media, Fumaria officinalis, Ranunculus repens.*

The classes “*V. persica*” and “*V. hederifolia*” were merged in one single class “*Veronica* spp.” due to the morphological similarity that did not allow their discrimination at early stages of growth, as well as their low density found in the field. Similarly, “*Melilotus officinalis”* and “*Medicago polymorpha”* were merged in one single class. At the heading stage, weeds were cut at the collar, counted, and identified to calculate the density per single species (145 DAS) in the 1 m^2 sampling area used for agronomic measurements on wheat.

Biodiversity index

At tillering stage (43 DAS) and heading stage (145 DAS) were assessed also several biodiversity index such as the Menhinick’s Index, Simpson’s Reciprocal Index and Shannon’s Diversity index according to Kitikidou et al. [17].

Statistical analysis

Correlation matrices and all other statistical analyses were carried out with the open-source RStudio, correlation matrices were performed with the package “*corrplot*” [18]. Other graphics were obtained with SigmaPlot (Palo Alto, CA, USA).

Training of the convolutional neural network and model goodness evaluation

A convolutional neural network (CNN) was trained on the basis of the annotations performed on weeds at wheat tillering stage. All pictures were sliced in smaller images with a resolution of 640 × 640 pixels for a total of 3456 images use to train the CNN. For this operation it was utilized an open-source framework called “*Slicing Hyper Aided Inference*” [19]. The final dataset was composed by the number of annotations reported in Table 1.

The CNNs chosen for the identification of weed species have been *“You only look once version 5″* (YOLO v5) [20] and “*You only look once version 8″* (YOLO v8) [21]. For the training it was utilized a GPU-sharing platform for data science Kaggle (Kaggle Inc, Delaware, USA). The images present in the final dataset were allocated for the 60 % to the training dataset, 20 % to the validation dataset and 20 % to test dataset. The main metrics utilized for the evaluation of the goodness model were average precision (AP) and mean average precision (mAP) on the basis of the intersection over union (IoU), that represent the ratio of the shared area between the annotation from the model and the ground

Table 2

Density for singular weed species present in weedy plot at tillering and heading stage. Asterisks indicate statistical differences according to the test-t (ns = not significant, * = $p < 0.05$; *** = $p < 0.001$).

Weed species	Tillering	Heading	Percent variation	Significance
	Number of plants m^{-2}			
R. raphanistrum	286.4	64	−77 %	***
A. arvensis	299.1	148	−50 %	***
P. rhoeas	175.4	36.9	−78 %	***
C. album	134.6	0.1	−99 %	*
M. polymorpha	28.5	53.4	87 %	*
P. aviculare	54.9	44	−19 %	ns
Veronica spp.	18.4	5.2	−71 %	***
S. media	6.18	6.2	1 %	ns
F. officinalis	3.25	0.2	−91 %	***
R. repens	13.1	2.7	−79 %	***
Total	**1101.5**	**425.6**	**−61 %**	***

Table 3

Average precision value obtained on test dataset at the end of training.

Weed species	Average Precision (0.5)	
	YOLOv5	YOLOv8
Raphanus raphanistrum	0.80	0.81
Anthemis arvensis	0.84	0.85
Papaver rhoeas	0.67	0.71
Chenopodium album	0.29	0.39
Medicago polymorpha	0.34	0.45
Polygonum aviculare	0.56	0.61
Veronica spp.	0.03	0.24
Stellaria media	0.002	0.01
Fumaria officinalis	0.32	0.44
Ranunculus repens	0.26	0.44
mAP	**0.41**	**0.50**

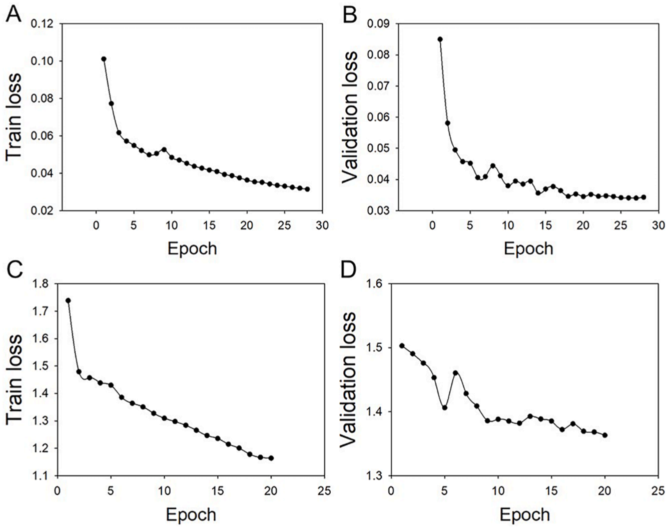


Fig. 1. Training and validation loss for YOLOv5 (A-B) and YOLOv8 (C-D).

truth annotation, and the total area from the union of the two annotations [22]. The IoU defines the threshold for three key categories:

- True positive (TP). Correct detection of a ground-truth annotation
- False positive (FP). Incorrect detection of a non-existing annotation or misplaced detection of an existing annotation

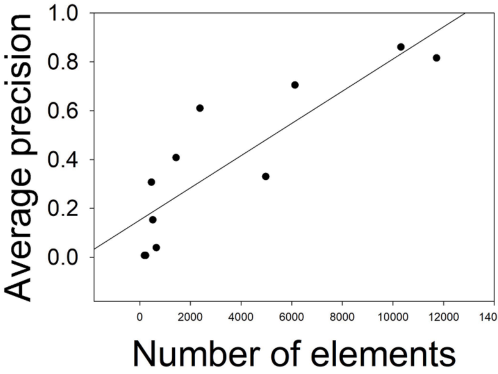


Fig. 2. Correlation between the average precision (AP) and the number of annotations per single species reported in Table 1.

- False negative (FN). Undetected ground-truth annotation

Using these categories, it was possible to define the Precision (P) and Recall (R) values:

$$P = \frac{TP}{TP + FP} \quad R = \frac{TP}{TP + FN}$$

The AP with an IoU of 0.5 was defined as the area under the Precision/Recall curve [23]. The mAP was defined by the following equation:

$$mAP = \frac{1}{n} \times \sum_{i=1}^{n} AP_i$$

Where n is the number of classes. AP and mAP with an IoU of 0.5 are the most frequently utilized metrics for the evaluation of model goodness [22]. The results of metrics used here are referred to the test dataset.

Results

Training and metrics of convolutional neural network training

The CNNs were trained for an increasing number of epochs to establish the correct number to avoid overfitting as we can see from the validation loss (Fig. 4). The validation loss rapidly decreases in the early epochs for YOLOv5 (Fig. 4-**B**), meanwhile for YOLOv8 the decrease was more gradual (Fig. 4-**C**). The value of AP and mAP precision with an IOU of 0.5 taken at the end of the CNN training are reported in Table 3. The higher AP (> 0.6) have been obtained for *R. raphanistrum, A. arvensis, P. rhoeas*, with YOLOv5, and for *P. aviculare* with YOLOv8. For the other species the APs were smaller, ranging from 0.001 for *S. media* to 0.34 for *M. polymorpha* (Table 3). These results show a positive correlation ($r^2 = 0.73$) between the AP and the number of annotations per single species (Fig. 3).

Weed density and species distribution

The density of weed species from tillering to the heading stage showed significant variations (Table 2). At the heading stage, weed species such as *R. rapanistrum, A. arvensis*, and *C. album* showed a reduction of their density compared to the density at the tillering stage (−77 %, −50 %, and −99 %, respectively). *P. aviculare* and *S. media* densities were not reduced at the heading stage compared to the tillering stage, while the *M. polymorpha* class showed an increase of its density (+87 %) compared to the tillering stage.

Correlation between initial weed density and final wheat biometric parameters

Weed total density at tillering stage showed a high correlation with wheat yield at final stage ($r = -0.82$). This parameter was also positive correlated with *P. rhoeas* (PAPRH), *R. raphanistrum* (RAPRA) and A. arvensis (ANTAR) and negative correlated with three biodiversity indexes: Menhinick's Index ($r = -0.82$), Simpson's Reciprocal Index ($r = -0.51$) and Shannon Diversity Index ($r = -0.51$). All agronomical parameters of wheat at different phenological stages are reported in supplementary material (**Figs. S7–S9**). Moreover, correlation between biodiversity index and final harvest are reported in **Figs. S11, S12**.

Correlation between yield and biodiversity index at heading stage

Total weed density at heading stage showed a good correlation with wheat yield at final stage ($r = -0.65$). This parameter was also positively correlated with *P. rhoeas* (PAPRH), *R. raphanistrum* (RAPRA), *A. arvensis* (ANTAR), *P. aviculare* (POLAV) and *R. repens* (RANRE). The total weed density was negatively correlated only with Menhinick's Index ($r = -0.82$).

Discussion

Convolutional neural networks to support site-specific weed management

Real time identification of weed species on large areas has severely limited in-depth comprehension of weed ecology and relative implications of weed biodiversity on yield losses caused by weed-crop competition [24]. This limitation can be overcome by using convolutional neural networks (CNN), an efficient technology for object detection in different fields of application [25]. CNN have been applied for weed

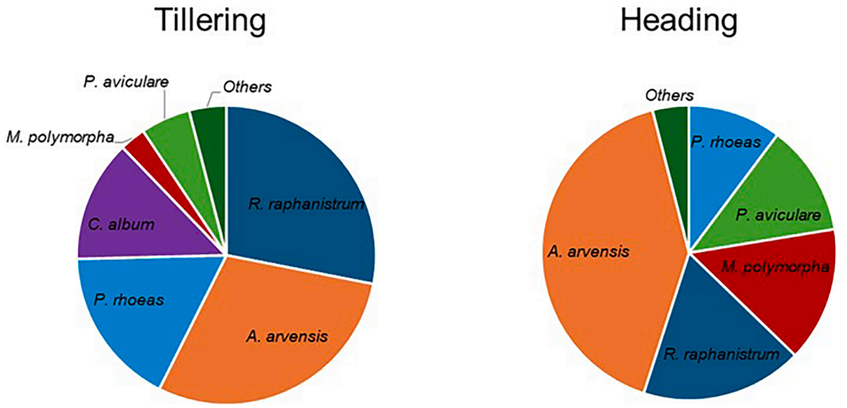
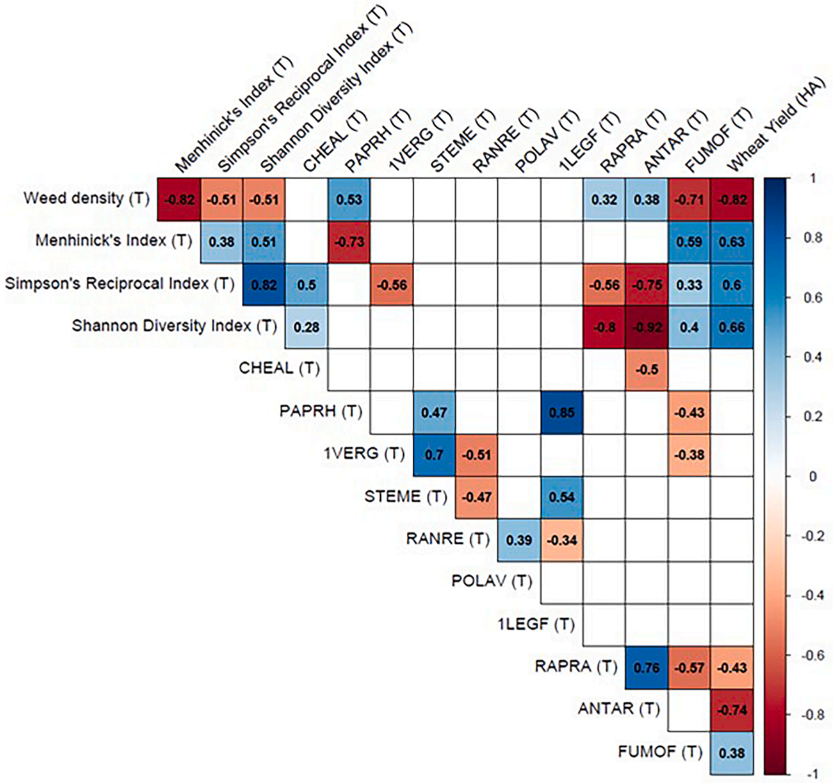
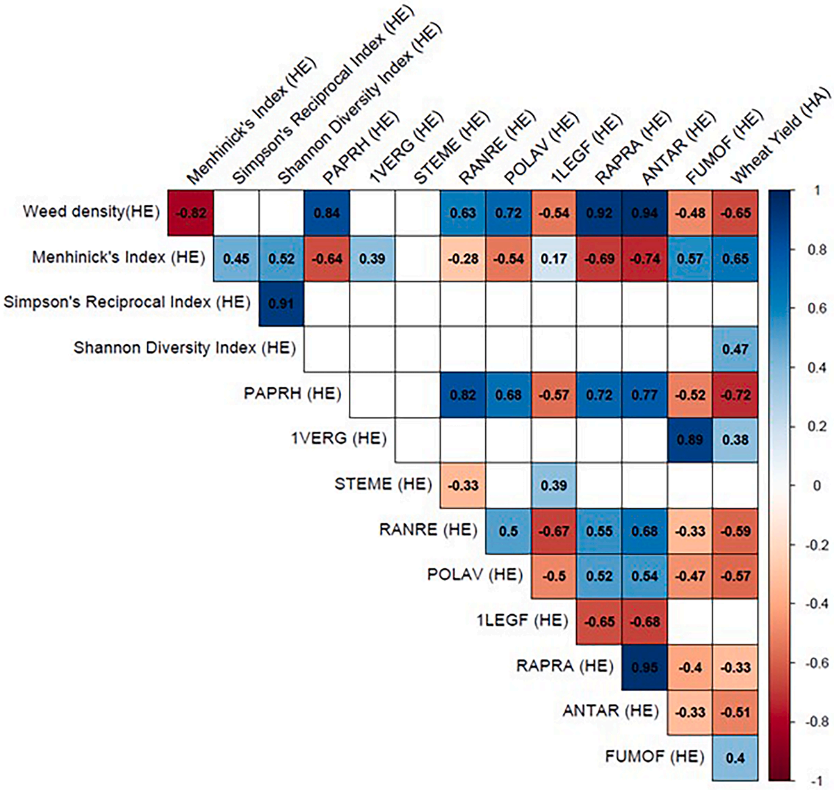


Fig. 3. Weed distribution at the tillering and the heading stage of wheat. "Others" represent the species within the 2 % of the total density.



	Menhinick's Index (T)	Simpson's Reciprocal Index (T)	Shannon Diversity Index (T)	CHEAL (T)	PAPRH (T)	1VERG (T)	STEME (T)	RANRE (T)	POLAV (T)	1LEGF (T)	RAPRA (T)	ANTAR (T)	FUMOF (T)	Wheat Yield (HA)
Weed density (T)	-0.82	-0.51	-0.51		0.53						0.32	0.38	-0.71	-0.82
Menhinick's Index (T)		0.38	0.51		-0.73								0.59	0.63
Simpson's Reciprocal Index (T)			0.82	0.5		-0.56					-0.56	-0.75	0.33	0.6
Shannon Diversity Index (T)				0.28							-0.8	-0.92	0.4	0.66
CHEAL (T)												-0.5		
PAPRH (T)							0.47			0.85			-0.43	
1VERG (T)							0.7	-0.51					-0.38	
STEME (T)								-0.47		0.54				
RANRE (T)									0.39	-0.34				
POLAV (T)														
1LEGF (T)														
RAPRA (T)												0.76	-0.57	-0.43
ANTAR (T)														-0.74
FUMOF (T)														0.38

Fig. 4. Correlation matrix between weed species reported with EPPO code, biodiversity index and total density at tillering stage (T) and wheat productivity parameters at harvest stage (HA). In the boxes are reported the Pearson correlation value. Blank boxes are not statistically significant ($p < 0.05$).



	Menhinick's Index (HE)	Simpson's Reciprocal Index (HE)	Shannon Diversity Index (HE)	PAPRH (HE)	1VERG (HE)	STEME (HE)	RANRE (HE)	POLAV (HE)	1LEGF (HE)	RAPRA (HE)	ANTAR (HE)	FUMOF (HE)	Wheat Yield (HA)
Weed density(HE)	-0.82			0.84			0.63	0.72	-0.54	0.92	0.94	-0.48	-0.65
Menhinick's Index (HE)		0.45	0.52	-0.64	0.39		-0.28	-0.54	0.17	-0.69	-0.74	0.57	0.65
Simpson's Reciprocal Index (HE)			0.91										
Shannon Diversity Index (HE)													0.47
PAPRH (HE)							0.82	0.68	-0.57	0.72	0.77	-0.52	-0.72
1VERG (HE)												0.89	0.38
STEME (HE)							-0.33		0.39				
RANRE (HE)								0.5	-0.67	0.55	0.68	-0.33	-0.59
POLAV (HE)									-0.5	0.52	0.54	-0.47	-0.57
1LEGF (HE)										-0.65	-0.68		
RAPRA (HE)											0.95	-0.4	-0.33
ANTAR (HE)												-0.33	-0.51
FUMOF (HE)													0.4

Fig. 5. Correlation matrix between weed species reported with EPPO code, weed total density, biodiversity index at heading stage (HE) and wheat productivity parameters at harvest stage (HA). In the boxes are reported the Pearson correlation value. Blank boxes are not statistically significant ($p < 0.05$).

detection with good results for a generic discrimination of weeds from wheat and from other vegetable crops [26,27] or to detect single weed species in the field [28]. Other studies performed weeds species identification with the use of CNN, but in some cases the images were taken in laboratory [29], or the CNN was used for a classification task and not for an object detection [30,31]. In other cases, CNN have been used for weeds detection at advanced developmental stage [32–35]. In our experiment we compared the different performances of two CNN architectures, namely YOLOv5 and YOLOv8, which showed different capacity to recognize weeds. YOLOv8 improved the identification of all the weed classes compared to the previous version YOLOv5, with higher average precision for *A. arvensis* (ANTAR), *R. raphanistrum* (RAPRA), and *P. rhoeas* (PAPRH) (Table 3). It is worth to note that these weeds represented the most dominant species found in the experimental field (Table 2), and this is the main reason for the high average precision obtained for these weed species, which allowed us to use a high number of annotations for the CNN training (Fig. 2). The final dataset utilized for the training of the two CNN architectures was the largest in terms of number of objects among those used in the literature for similar analyses on weeds in the open field (**Table S4**). In addition, to the best of our knowledge, this is the first time that the most updated CNN architecture YOLOv8 has been used for weed identification. (**Table S4**). Moreover, this study provides a system for the identification of weeds at an early stage of development, which is the crucial moment for the evaluation of the intensity/magnitude of weed infestation. Several studies indicate that the initial weed density can be detrimental to crop development. Indeed, it has been reported that weed competition causes different levels of yield loss depending on the phenological stages of the crop. On corn, only weed competition occurring at the emergence stage causes significant yield losses, while it did not affect the yield when they were controlled until the fourth to sixth leaf stage [36]. Similarly, weed competition in rice after 29 to 32 days after sowing had negligible effects on crop yield [37]. On the basis of these evidence, the evaluation of weed presence at an early stage of wheat cultivation is a pivotal indicator of yield losses induced by weeds. We show that the early identification by CNNs allowed us to assess the levels of weed biodiversity and its implication on wheat productivity. This may help us to improve the sustainability of weed control and increase the ecological services provided by agriculture since, based on this knowledge, the sustainability-productivity trade-off can be better tuned [38–41].

Low biodiversity causes dominant species over-growth and higher yield losses

Early identification of weed species at the tillering stage allowed us to correlate the density of these species and wheat biometric and productive parameters (Fig. 4). Weed total density at the tillering stage was correlated with the presence of the most dominant species *R. raphanistrum* (RAPRA), *A. arvensis* (ANTAR) and *P. rhoaes* (PAPRH), and inversely correlated with weed biodiversity (Fig. 4). Moreover, biodiversity indices were positively correlated with yield (Fig. 4, **Figs. S11, S12**). This is highly relevant since it underlines that diversified weed communities can reduce the weed competitiveness, and thus crop yield losses [42]. Indeed, notwithstanding the impact that single weed species can have on crop productivity, it is pivotal to understand in which ecological dynamics these species become noxious, an aspect that has been linked with the over-simplification of agricultural cropping systems, and already highlighted in the literature [43]. Esposito et al., [44] found that the composition of weed communities can be an important factor in crop-weeds interaction. With a cluster analysis approach, they found two weed communities, one of which did not reduce the wheat production. Ferrero et al. [45] in a long-term study of 15 years analyzed the impact of weed diversity on soybean. Also in this case, an increase of weed diversity was positively associated with yield. Similarly, Adeux et al. [9] found that more biodiverse weed communities were correlated with lower yield losses. Indeed, where dominant

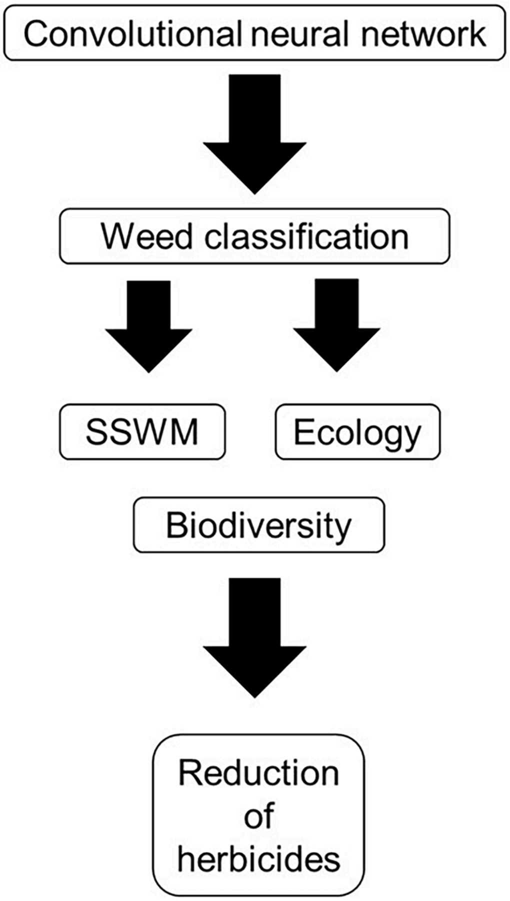


Fig. 6. Schematic representation of the possible output from the use of convolutional neural network. The weed classification can be useful to improve our knowledge about ecology of weeds and their biodiversity, and at same time is fundamental for the application of site-specific weed management.

species are present, they can easily reach high densities and biomass, exceeding the critical period for weed control [46]. Our results confirmed that where the biodiversity was low, the total weed density was high as well as the yield losses (Fig. 4). Likewise, dominant species were favored, as confirmed by the inverse correlation between biodiversity and *A. arvensis* (ANTAR), *R. raphanistrum* (RAPRA), and *P. rhoaes* (PAPRH) density (Table 2). It is therefore pivotal to find the best practices able to increase weed biodiversity in the agro-ecosystem that can favor species co-existence thus reducing yield loss caused by weeds [8, 44,47,48]. Artificial intelligence and robotics can represent a key tool to this aim. In order to guarantee both productivity and biodiversity, Zingsheim and Döring [10] stated that a robot should be technically capable to distinguish between crop plants vs weeds, and among weeds the single weed species. As previously pointed out, a species specific CNN can respond to this need since it can comprehensively track the initial weed density in crops both in terms of quantity and composition.

Adaptive traits to understand weed dynamics and the implication on yield loss

The competitive traits of weeds are the main reason of their impact on crop productivity, depending on the factors for which crops and weeds compete in the open field. Resource scarcity (water, nutrients), as well as the competition for light, are the main drivers of weed induced yield losses, with negative impacts on quantitative and qualitative yield. In this experiment, weed dynamics could reason the effects of weed competition on wheat yield. At the early stage of wheat growth (tillering), three dominant weeds were present, namely *R. raphanistrum* (RAPRA), *A. arvensis* (ANTAR), and *P. rhoaes* (PAPRH) (Fig. 1, Table 2). *R. raphanistrum* is a well-established noxious weed for wheat [49–51] with the capacity to reduce yield even with a density of 15 plants m^{-2} [50]. Also, *A. arvensis* can be a problematic weed, with high plasticity and adaptability to different environmental constraints [52–54]. Similarly, *P. rhoaes* is one of the most problematic weeds in wheat fields, due to the competition for water and light, its high seed production, and its ability to persist in the field. It has been estimated that this species induces up to 32 % of yield loss in wheat [28]. Where the density of these species was high, the weed biodiversity was significantly reduced, and yield losses were higher. At the heading stage, the weed distribution showed an increase of the presence of *M. polymorpha* (1LEGF) and *P. aviculare* (POLAV) (Fig. 5). Also in this case, the different competitive traits of the two weeds can be related with the results on weed biodiversity, total weed density, and wheat yield (Fig. 5). Indeed, *M. polymorpha* was only present where the total weed density was low, thus where the dominant species found at the tillering stage were absent. This led to a low competition toward wheat, that can be explained by i) the late presence of these species, that had a minor impact on wheat yield loss, which further confirmed the higher detrimental impact of weed competition at early stages of plant cultivation; ii) the absence of competition for nitrogen, due to the ability to nitrogen fixation of this leguminous species. In contrast, *P. aviculare* did not show correlations with total weed density, with the dominant species density, and with wheat yield at the tillering stage (Fig. 4). At the heading stage, its density was negatively correlated with wheat yield (Fig. 5). This is probably due to the ability to tolerate the shading induced by the other species, allowing to maintain a similar density at the two time of assessment [55, 56]. Perthame et al. [57], found that nitrogen assimilation in *P. aviculare* was not affected by light scarcity, leading to enhanced performances of this weed underneath the canopy of competitor plants. The ability to intercept the sunlight underneath the competitor canopies is functional to the continuous production of propagules [58,59]. Differently from *M. polymorpha*, the presence of *P. aviculare* (i.e., a non nitrogen-fixing species) could have induced a high competition for nitrogen, thus exacerbating the competitiveness toward wheat. These aspects underline that an appropriate knowledge of the weed dynamics in the field is necessary to optimize weed management. It is also important to point out that these results derive from one single growing season, which could represent a limitation to the full understanding of weed dynamics. Moreover, the RGB recognition could be expanded and improved by using multispectral or hyperspectral images, which would allow us to better discriminate among morphologically similar species [60,61].

Conclusions

Weeds are the most problematic biotic constraints for wheat production. Herbicides have always been proven to be an effective solution for weeds management, but the shortcomings from their widespread use have been revealed overtime. Site-specific weed management is a valuable tool that may limit problems associated to herbicides and intensive use of chemicals in agriculture. Convolutional neural networks can be implemented to enhance the efficacy of this strategy because they can be used for early stage weed detection, improve our knowledge on weed ecology and so helping us to understand the effects of weed density, weed biodiversity, and their community composition on crop yield (Fig. 6).

Authorship

We confirm that the manuscript has been read and approved by all named authors.

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Ethics statement

Not applicable: This manuscript does not include human or animal research.

CRediT authorship contribution statement

Claudio Russo: Writing – original draft, Visualization, Software, Methodology, Investigation, Formal analysis, Data curation. **Valerio Cirillo:** Writing – review & editing, Validation, Supervision, Methodology, Investigation, Conceptualization. **Marco Esposito:** Methodology, Investigation. **Matteo Lentini:** Methodology, Investigation. **Nausicaa Pollaro:** Methodology, Investigation. **Albino Maggio:** Writing – review & editing, Validation, 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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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.atech.2024.100594.

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