

Evaluating field-scale sampling methods for the estimation of mean plant densities of weeds

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Summary

The weed flora (comprising seven species) of a field continuously grown with soyabean was simulated for 4 years, using semivariograms established from previous field observations. Various sampling methods were applied and compared for accurately estimating mean plant densities, for differing weed species and years. The tested methods were based on (a) random selection wherein samples were chosen either entirely randomly, randomly with at least 10 or 20 m between samples, or randomly after stratifying the field; (b) systematic selection where samples were placed along diagonals or along zig-zagged lines across the field; (c) predicted *Setaria viridis* (L.) P. Beauv seedling maps which were used to divide the field into low- and high-density areas and to choose the largest sample proportion in the high-density area. For each method, sampling was performed with 5–40 samples. Systematic methods generally resulted in the lowest estimation error, followed by the random methods and finally by the predicted-map methods. In case of species over- or under-represented along the diagonals or the zig-zag sampling line, the systematic methods performed badly, especially with low sample numbers. In those instances, random methods were best, especially those imposing a minimal distance between samples. Even for *S. viridis*, the methods based on predicted *S. viridis* maps were not satisfactory, except with low sample numbers. The relationships between sampling error and species characteristics (mean density, variability, spatial structures) were also studied.

Keywords: semivariogram, Gaussian simulations, kriging, spatial distribution, sampling plans.

Introduction

Decision aid models based on damage thresholds and weed demography models are developed to assist farm managers to make both short- and long-term choices for weed management. In the decision aid models based on damage thresholds, weed densities observed in the field are compared with a density threshold to determine whether weed control measures are needed. This threshold value is the weed density that causes a crop yield whereby the associated financial loss

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exceeds the cost of control measures (Zadoks, 1985). If the observed weed density is larger than the threshold value, then herbicides are applied, whereas no action is taken if the weed density is below the threshold. In weed demography models, weed population characteristics such as seedling densities or seed production are estimated in fields and then used to initialize the model to simulate long-term weed population growth and to make decisions (Colbach & Debaeke, 1998). These kinds of models require accurate estimates of weed density to make correct decisions, even if a certain margin of error is acceptable for long-term weed control programmes (Wallinga *et al.*, 1999).

Most of the techniques used to estimate weed density are based on field surveys. A typical protocol for sampling weeds for research purposes consists of selecting a given number of quadrats of a certain size, located on a grid, and counting the number of weeds of each species within each quadrat. The mean quadrat density for each weed species is then assumed to represent the field. This approach is appropriate when there is no other information about the variable to estimate. However, weeds tend to cluster together in patches and they are not distributed randomly in the field (Marshall, 1988; Van Groenendael, 1988; Thornton *et al.*, 1990; Wiles *et al.*, 1992; Johnson *et al.*, 1995; 1996). This patchiness decreases the accuracy of yield loss estimates based on weed density (Auld & Tisdell, 1987; Dent *et al.*, 1989; Brain & Cousens, 1990) and of the mean density estimation for a given level of scouting effort (Gold *et al.*, 1996), as samples obtained close to one another vary less than samples obtained at greater distances (Legendre & Fortin, 1989).

Sampling strategies that account for spatial distribution may increase sampling efficiency (Cardina *et al.*, 1997). For instance, a sampling protocol may consist of dividing a field into parts with a separate determination of the mean density within these parts. Such an approach may reduce variability in weed density estimates compared with a single estimate for an entire field and a reduction in variability may improve the density estimate.

In recent years, a number of studies have been developed to optimize weed sampling, to gather enough information on weed densities and distributions and to make correct estimates that are not excessively expensive or time consuming. The search for optimal strategies that are cost effective in specific circumstances has been improved by the optimal use of prior information. This gave rise to devices like stratified, cluster, systematic and sequential sampling, which can be combined and specialized in many ways (Conn *et al.*, 1982).

The aim of this paper was to compare sampling methods in terms of estimation accuracy of mean weed seedling densities. The development of an optimal sampling procedure to make weed management decisions is still underway. The various sampling methods were not applied to the weed flora of a real field, but to the simulated flora of a field continuously grown with soybean conceived from semivariograms.

Materials and methods

In previous work (Colbach *et al.*, 2000), the seedling densities of seven weed species [*Amaranthus retroflexus* L.; *Asclepias syriaca* L.; *Chenopodium album* L.; *Cirsium arvense* (L.) Scop.; *Elytrigia repens* (L.) Nevski; *Setaria viridis* (L.) P. Beauv.; *Sinapis arvensis* L.] were counted in a continuously grown soybean [*Glycine max* (L.) Merr.] field (244 m × 54 m) at the Swan Lake Research Farm, Stevens Co., Minnesota, USA. From 1993 to 1997, the densities of the seven weed species were counted on 0.1-m² quadrats at 410 permanently marked locations within a 6.1-m (20-foot) grid system. The field received standard weed management practices, which

resulted in good to excellent control each year. Empirical semivariograms, i.e. a description of the variance between weed densities as a function of distance between sampling locations, were established for each species and year. Equations were fitted to the observations to predict variances of weed densities at unsampled distances.

In this work, the semivariograms were used to establish seedling maps for each year and species. Two different methods were used to generate these maps: ordinary kriging and stochastic simulation. Ordinary kriging based on the semivariograms was used to estimate weed densities at unsampled locations of the field by interpolation between the sampled points for each year and species, thus a single map was generated. However, kriging is often deemed unsuitable for evaluating sampling schemes, as it is known to smooth the actual variation of the mapped variable (Cressie, 1991; Deutsch & Journel, 1998). Consequently, another way of generating maps was necessary. Any statistical property depending only on the second-order moments of the model (semivariogram or covariance function) may be studied numerically on synthetic data displaying the same second-order moments. A common way to perform this kind of investigation is to simulate Gaussian random functions which are very easily simulated and can be used with any semivariogram models. In contrast to the kriged maps, the maps obtained with Gaussian simulations display the same variance as the data used to establish the semivariograms. Gaussian-type field maps were generated with the 'turning band' method which is known to be the most numerically efficient (Lantuejoul, 1994).

For both mapping approaches, the basic unit was $1\text{ m} \times 1\text{ m}$. Consequently, the field consisted of 13 176 units. Table 1 shows the means and semivariogram parameters used for the mapping processes for each species and year. For each year, the generated weed maps were considered as the 'real' weed populations on which various sampling plans (sampling methods \times number of samples) were tested. Three general types of sampling methods were considered in this paper: (a) those selecting the samples randomly, (b) those using systematic selection, and (c) those using prior knowledge of the weed distribution in the field. The sample size was 1 m^2 and gave the weed densities for the seven above-mentioned weed species.

Methods based on random selection

Four random selection methods were tested. (a) The first of these methods (henceforth, 'random method') consisted of choosing samples entirely randomly from the simulated field and is often used in weed research. (b) In the second method ('10-m-minimal-distance method' or 'distance10 method'), samples were required to be separated by at least 10 m. The sampling process was as follows: the i^{th} sample was chosen randomly from the simulated field and its distance to each of the $(i-1)$ first samples was calculated; if any of these distances was smaller than 10 m, then the sample was discarded and a new one chosen; otherwise, the $(i+1)^{\text{th}}$ sample was selected. (c) The next method ('20-m-minimal-distance method' or 'distance20 method') used the same procedure, but with a minimal sampling distance of 20 m. These minimal distances between samples were introduced to limit dependence between samples. The values for the minimum distances were chosen below or above the range values found for the sampled species (Table 1) while still being small enough to ensure the possibility of placing large numbers of samples in the field. (d) For the fourth method ('stratified method'), the field was divided into five equal parts and then, a fifth of the required samples was selected randomly in each of these parts. This method is commonly used to divide the field into homogeneous parts with little internal variation for the measured variable (Scherrer, 1983); if no prior knowledge on the variable distribution exists before

Table 1 Means and semivariogram parameters for nested spherical models of seven weed species calculated by Colbach *et al.* (2000), using the weed densities observed in a continuous soyabean field from 1993 to 1997 in Morris, Minnesota, USA

Species	Mean density (plants m ⁻²)	c ₀ (m)	s ₀ (m)	c ₁ /s ₀	c ₂ /s ₀	a ₁₋₀ (m)	a ₁₋₉₀ (m)
1993							
<i>Amaranthus retroflexus</i>	3.28	1.75	2.09	0.16	0.11	38	1.00
<i>Asclepias syriaca</i> *	0	0	0				
<i>Chenopodium album</i>	0.89	0.24	0.74	0.67	0.32	12	19.63
<i>Cirsium arvense</i>	1.28	0.63	1.32	0.52	0.08	19	8.69
<i>Elytrigia repens</i> *	0.30	0.54	0.59	0.08	0.23	33	0.25
<i>Setaria viridis</i>	40.97	0.90	2.41	0.63	1.26	39	30.11
<i>Sinapis arvensis</i> *	3.31	8.67	8.67	0	0.07		
1994							
<i>Amaranthus retroflexus</i>	0.38	0.23	0.56	0.59	0.019	12	1.00
<i>Asclepias syriaca</i>	0.08	0.11	0.16	0.31	1.55·10 ⁻⁰⁷	13	1.26
<i>Chenopodium album</i>	0.27	0	0.42	1	0.059	9	0.98
<i>Cirsium arvense</i>	2.40	0.97	2.00	0.51	0.181	26	35.78
<i>Elytrigia repens</i> *	0	0	0				
<i>Setaria viridis</i>	14.67	0.93	2.26	0.59	0.793	43	25.00
<i>Sinapis arvensis</i>	0.11	0.24	0.24	≈0	0.044	38	13.58
1996							
<i>Amaranthus retroflexus</i>	0.01	1.31	2.94	0.55	0.033	19	6.69
<i>Asclepias syriaca</i>	0.18	0.29	0.38	0.22	0.008	12	0
<i>Chenopodium album</i>	0.30	0	0.53	1.00	0.053	11	≈0
<i>Cirsium arvense</i>	0.60	0.42	0.83	0.49	0.018	12	11.22
<i>Elytrigia repens</i> *	0	0	0				
<i>Setaria viridis</i>	56.71	0.30	2.30	0.86	1.042	34	10.02
<i>Sinapis arvensis</i> *	0	0	0				
1997							
<i>Amaranthus retroflexus</i>	0.07	0.12	0.16	0.26	0.10	12	1.00
<i>Asclepias syriaca</i>	0.31	0.38	0.51	0.25	0.21	12	0.96
<i>Chenopodium album</i>	0.05	0.008	0.08	0.89	≈0	10	2.97
<i>Cirsium arvense</i>	0.49	0.36	0.78	0.53	≈0	28	≈0
<i>Elytrigia repens</i>	0.44	0.25	0.53	0.52	1.18	47	1.00
<i>Setaria viridis</i>	4.40	0.77	2.19	0.64	0.24	30	30.00
<i>Sinapis arvensis</i> *	0	0	0				

Semivariance:

$$\gamma(h) = c_0 + \gamma_1(h) + \gamma_2(h)$$

$$\text{if } h < a_1 \quad \gamma_1(h) = c_1 \cdot \left[\frac{3}{2} \cdot \frac{h}{a_1} - \frac{1}{2} \cdot \left(\frac{h}{a_1} \right)^3 \right]$$

$$\text{if } h \geq a_1 \quad \gamma_1(h) = c_1$$

$$\text{if } h < a_2 \quad \gamma_2(h) = c_2 \cdot \left[\frac{3}{2} \cdot \frac{h}{a_2} - \frac{1}{2} \cdot \left(\frac{h}{a_2} \right)^3 \right]$$

$$\text{if } h \geq a_2 \quad \gamma_2(h) = c_2$$

h, distance between samples; *c*₀, nugget (unexplained variability); *s*₀, sill in the direction of the crop rows (0 direction); *c*₁, contribution of the first spatial structure (*s*₀-*c*₀); *c*₂, contribution of the second spatial structure [difference in sills between the 0 and 90 directions (= direction perpendicular to the crop rows)]; *a*₁₋₀ and *a*₁₋₉₀ are the ranges of the first spatial structure, for the 0 and the 90 directions, respectively; the ranges of the second spatial structure, *a*₂₋₀ and *a*₂₋₉₀, are infinite and nil respectively. The density data of all species (except those marked*) were transformed with $\log(z + 1)$ before geostatistical analysis to decrease dissymmetry of distribution.

sampling, fields are often divided arbitrarily to ensure that samples are more evenly distributed in the field.

Methods based on systematic selection

The systematic positioning of samples is often used to ensure that samples are placed independently of the experimenter avoiding or choosing unknowingly certain field areas while increasing the sampled field area (Scherrer, 1983). Systematic selection was examined by two methods. (a) With the first of these methods ('diagonal method'), the samples were selected on the two diagonals of the field. The sampling process for $N = 2n$ samples was as follows (Fig. 1): the field (of length l and width w) was divided into n^2 rectangles of $l/n \times w/n$ m²; the first sample was chosen randomly in the rectangle located on the field edge; if its co-ordinates were (x_1, y_1) , then the co-ordinates of the i^{th} sample taken on the same diagonal were $[x_1 + (i-1) \times w/n; y_1 + (i-1) \times l/n]$ and the co-ordinates of the i^{th} sample taken on the second diagonal were $[x_1 + (i-1) \times w/n; l - y_1 - (i-1) \times l/n]$. (b) With the second of the systematic methods ('zig-zag method'), the samples were taken from three lines assembled vaguely as an 'S'. The sampling process for $N = 3n - 2$ samples consisted of dividing the field into $n \times N$ rectangles of $w/n \times l/N$ m². The first sample of co-ordinates (x_1, y_1) was again chosen randomly in the rectangle located on the field edge and the subsequent samples were chosen according to a protocol similar to that for the diagonal method and shown in Fig. 2.

Methods based on predicted distribution maps

In this category, prior knowledge on weed distribution was used to define areas with low internal variability. To define these areas, we decided to predict *S. viridis* seedling maps of 1994 and 1997 from the *S. viridis* data sampled in 1993 and 1996, respectively, and cross-semivariograms

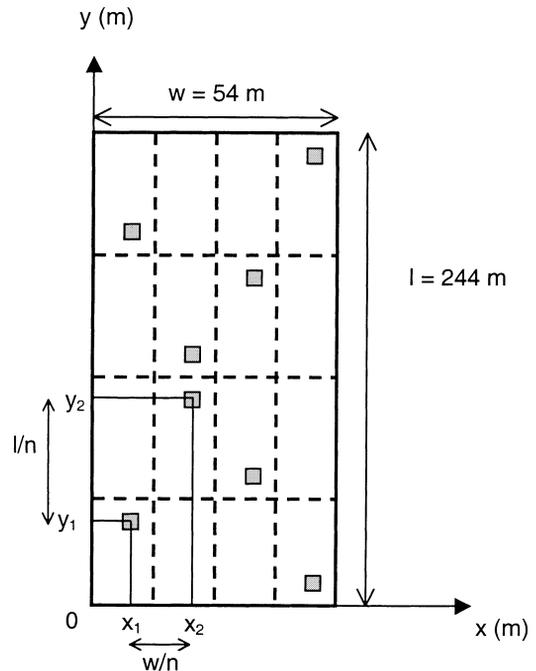


Fig. 1 Example of a systematic sampling plan ($n = 4$) selecting eight samples ($N = 2n = 8$) and using diagonals.

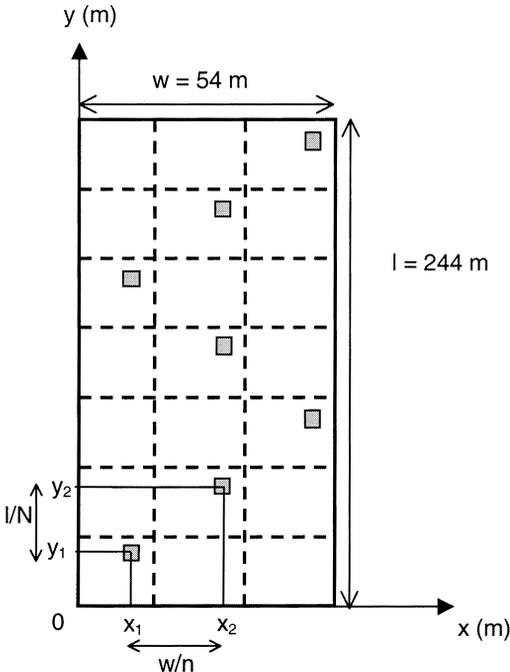


Fig. 2 Example of a systematic sampling plan ($n = 3$) selecting seven samples ($N = 3n - 2 = 7$) and using lines assembled as a zigzag.

describing the relationships between weed densities and locations of two successive years. These predicted maps composed of elementary units of 1 m^2 each, were calculated with ordinary co-kriging, using cross-semivariograms, i.e. the variability between samples of years j and $j + 1$ as a function of the distance between the samples. The details are given in Colbach *et al.* (2000). For each year, the field was divided into two parts: a high-density domain where the predicted (c-okriged) *S. viridis* density exceeded a threshold of d plants m^{-2} and a low-density domain with less than d plants m^{-2} . From both domains, those units of which any of the immediate eight neighbouring units did not belong to the same domain, were eliminated. Instead of choosing an identical number of samples in each area as in the 'stratified' method, a large percentage q of the samples were placed randomly in the high-density area and only a few samples were taken from the low-density field area. Four combinations of percentage q and threshold density d were tested for 1994 and 1997: (a) In the first method ('co1080 method'), a threshold value of $d = 10$ plants m^{-2} was chosen to separate the low- and high-density areas; $q = 80\%$ of samples were chosen in the high-density part of the 'real' field and 20% of the samples were taken from the low-density part; (b) with the 'co1090 method, as many as $q = 90\%$ of the samples were placed in the high-density area; (c) for the 'co2080 method', a $d = 20$ plant density was used for the distinction between high- and low-density domains and $q = 80\%$ of the samples came from the high-density area; and finally (d) the 'co2090 method' using a $d = 20$ plant threshold and a $q = 90\%$ proportion of high-density samples.

These methods were only tested on the kriged maps. They cannot be evaluated on the Gaussian maps which in this study were not conditional simulations. Consequently, the patch location did not depend on the raw weed data actually sampled in the real field but only on the inferred semivariograms.

Number of samples

For each method, sampling was simulated, using 5–40 samples. For some methods, not all sample numbers were possible; for the ‘stratified method’ for instance, sampling was done with 5, 10, ..., 40 samples because of the division of the field into five parts.

Repetition of sampling plans

If the maps were generated with kriging, each sampling plan was carried out 200 times for each year to determine the estimation error with confidence, as this error is subject to considerable fluctuations from one realization to another. Similarly, the sampling plans were tested on 100 repetitions of the weed maps obtained for each year with the Gaussian simulations.

Calculation of mean plant densities

For each sampling method, number of samples, year and repetition, the means of each species density were calculated. For the methods based on predicted distribution maps, the following equation was used:

$$mean = w_{low} \times mean_{low} + w_{high} \times mean_{high}, \quad (1)$$

with:

w_{low} = weight of low-density area = $a_{low}/(a_{low} + a_{high})$

a_{low} = area of low-density area

$mean_{low}$ = mean density of low-density area

w_{high} = weight of high-density area = $a_{high}/(a_{low} + a_{high})$

a_{high} = area of high-density area

$mean_{high}$ = mean density of high-density area.

Quality indicators and their analysis

In the case of Gaussian maps, the variance of error was used as a quality indicator for each sampling plan (except the methods based on predicted distribution maps) and year and for every species, using the following equation:

$$Error = \frac{\Sigma(\bar{y} - \bar{y}_e)^2}{R} \quad (2)$$

with R = number of maps generated for each year and species

\bar{y} = real mean weed density

\bar{y}_e = mean weed density estimated with sampling method.

In the case of kriged maps, the variance of error was transformed to obtain the relative prediction error:

$$Error = \frac{1}{\bar{y}} \sqrt{\frac{\Sigma(\bar{y} - \bar{y}_e)^2}{R}} \quad (3)$$

with R = number of times a sampling plan was carried out for each year and species.

For each species, sampling method and year, a three-parameter non-linear equation was fitted to the error rates:

$$z = a \cdot e^{-b \cdot (x-5)^c} \quad (4)$$

with z = predicted variance of error (for Gaussian maps) or relative prediction error (for kriged maps)

x = number of samples

a , b and c = parameters.

To improve the level of fit and decrease parameter correlations, parameter b was replaced by $10^{-c} \ln(a/d)$. The parameters a , c and d were estimated using a non-linear fitting procedure. Equation 4 was then used to calculate the estimated values of $z_{x=5}$ ($= a$), $z_{x=15}$ ($= d$) and $z_{x=20}$ corresponding to $x = 5, 15$ and 20 samples. In the case of kriged maps, where the use of a relative error made the simultaneous analysis of all species interesting, these variables then were analysed with a linear model, using the year, the species and the sampling methods as input variables in order to rank the various methods. Whatever the mapping process, a simplified linear model, with only year and method as input variables, was used to rank the methods independently for each species. In this procedure, mean errors of the various methods were compared (least significant difference test, LSD, with $\alpha = 10\%$) separately for each species, assigned a LSD letter value (a, b, etc.), and methods followed by the same series of letters were given the same rank, ranging from 1 (lowest error) to 10 (highest error). Similarly, a linear model using species and method as input variables was used to rank the methods independently for each year. The fit of the non-linear equations was performed with the NLIN procedure and the analysis of the linear model with the GLM procedure of the SAS software (Statistical Analysis System, SAS Institute, Cary NC, USA).

Results

Fitting of the non-linear equation

Generally, the level of fit of eqn 4 was high. However, slight differences were observed between the sampling methods and mapping process. In the case of kriged maps, r^2 was slightly lower for those based on systematic sampling (mean r^2 of 0.98 and 0.96 for the 'diagonal' and the 'zig-zag' methods respectively) and among the methods based on predicted maps, the 'co2090' method, i.e. the one selecting 90% of the samples in the area with high *S. viridis* seedling densities (>20 seedlings m^{-2}), also presented slightly lower r^2 values (with a mean value of 0.98). The lower r^2 of the systematic and predicted map methods was due to a higher variability of observed relative prediction error as illustrated by Fig. 3 for the 'zig-zag' method; for the latter, the error predictors observed for the various sample numbers varied considerably compared with the 'random' method. This was, however, not the case if the maps were obtained by Gaussian simulation (Fig. 4).

Sampling with Gaussian maps

The methods based on systematic selection usually performed better than those based on random selection (Table 2), except with low sample numbers where was little difference between the

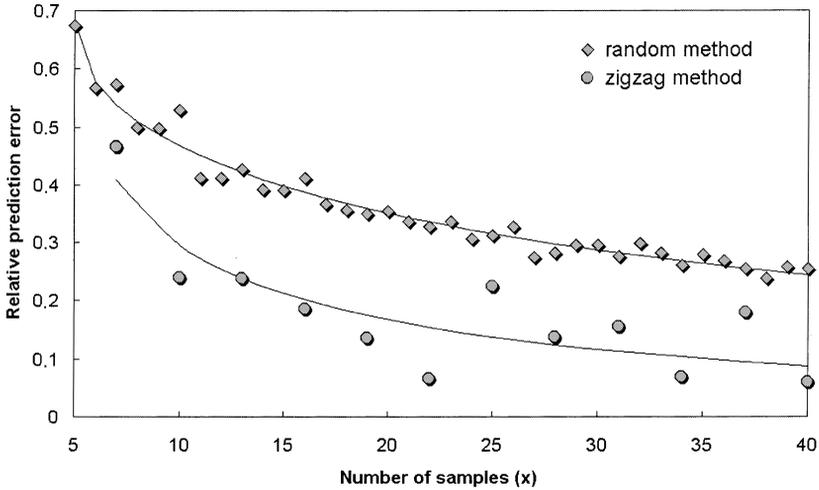


Fig. 3 Examples of fitting the non-linear eqn E4 to the relative prediction error for *S. viridis* and two sampling methods tested on kriged maps for 1997.

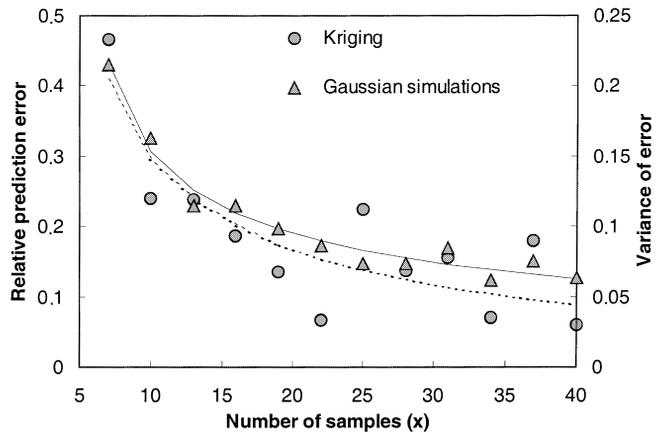


Fig. 4 Examples of fitting the non-linear eqn E4 to the relative prediction error and the variance of error, respectively, obtained with the 'zig-zag' method tested on kriged and Gaussian maps for *S. viridis* in 1997.

methods. There was less difference between the various methods of a given type than among types. However, slight differences emerged among the random methods, especially when analysing the ranking established for each species: the use of a minimum distance of 10 m or, even better, 20 m between samples; or, to a lesser degree, stratification decreased estimation error compared with the completely randomized method. This general ranking was not greatly affected by species. The analysis by species only shows that the systematic methods sometimes performed badly with low sample numbers as in the case of *A. syriaca*.

Sampling with kriged maps

The use of the relative error on the kriged maps and the evaluation of a third set of sampling methods, i.e. those based on the predicted *S. viridis* maps, confirmed and complemented the

Table 3 Level of significance (P) of factors sampling method, species, year and their interactions for their impact on sampling estimation error z_i in the case of sampling performed on kriged maps. Factors with probability values > 0.05 were not considered significant

Factors	Sampling estimation error z_i		
	z_5	z_{15}	z_{20}
Sampling method	0.0001	0.0001	0.0001
Species	0.0001	0.0001	0.0001
Year	0.0001	0.0001	0.0001
Sampling method*species	0.5144	0.7145	0.8148
Sampling method*year	0.5999	0.3230	0.2749
Species*year	0.0001	0.0001	0.0001
r^2	0.94	0.91	0.89

The tested linear model was: *mean relative prediction error* $z_1 = \text{constant} + \text{method effect} + \text{species effect} + \text{year effect} + \text{method*species interaction} + \text{method*year interaction} + \text{species*year interaction} + \text{error}$. In the case of z_5 , mean squares were weighted by the inverse of $(1 + \text{variance of } z_5)$ to take into account heterogeneity of variance.

results obtained with the Gaussian maps. The analysis of variance of the relative error permitted evaluation of the significance of effects and their interactions. It showed that in the case of sampling performed on kriged maps, all three primary factors, i.e. sampling method, species and year, had a significant effect on estimation error (Table 3). Only the interaction between species and year was significant; neither the method by species nor the method by year interactions were ever significant.

Those methods already evaluated with the Gaussian maps were similarly ranked when tested on the kriged maps (Tables 4 and 5). The other methods, i.e. the predicted-map methods, performed worst; among these, the use of the 10-plant instead of the 20-plant limit to distinguish high and low *S. viridis* density areas as well as the selection of only 80% (instead of 90%) of the samples in the high-density area decreased estimation error. In contrast to the Gaussian maps, the ranking of methods observed on the kriged maps varied more depending upon species (Table 5) and the systematic methods often performed poorly, especially for low sample numbers, even if the difference with the other methods was not always significant enough to appear in the synthetic ranking of Table 4. For instance, the 'diagonal' method was not adapted to *C. arvensis* and *S. arvensis* at low sample numbers or, generally, for *C. album*, whereas the 'zig-zag' method performed badly with *A. syriaca* even for high sample numbers. In the case of two other species (*S. viridis*, *S. arvensis*), its ranking deteriorated when the sample number increased from 15 to 20 samples. In many cases, the 'distance 20' and, to a lesser degree, the 'distance 10' method, were as good or even better than the systematic method (*C. arvensis*, *E. repens*, *S. arvensis*). Moreover, for *S. viridis*, two of the predicted-map methods, 'co2080' and 'co2090' performed better than the 'random' or the 'stratified' methods. At low sample numbers, the predicted-map methods were better than even the systematic methods (Fig. 5) which resulted in particularly high error.

The methods tended to be similarly ranked, regardless of the year (Table 6). However, the performance of the systematic methods varied considerably among years, especially with low sample numbers (z_5). The other exceptions were the minimum-distance methods, which performed worse than the 'random' or the 'stratified' methods in 1996.

In general, species ranking according to estimation error was almost similar irrespective of the number of samples (Table 7). For instance, errors were always highest when estimating densities of species such as *C. album* or *A. retroflexus*, whereas estimation of other species like *S. viridis* or

A. For five samples

Methods	Means of z_5				
Zigzag	0.571	a			
Diagonal	0.836		b		
Random	0.943		b		
Stratified	1.011		b		
Distance10	1.029		b		
Distance20	1.047		b	c	
Co1080	1.087		b	c	
Co1090	1.289			c	d
Co2080	1.411				d
Co2090	1.497				d

Table 4 General ranking of sampling methods according to their mean relative prediction error made when estimating weed densities with three sample numbers in the case of sampling performed on kriged maps

B. For 15 samples

Methods	Means of z_{15}					
Zigzag	0.463	a				
Diagonal	0.464	a				
Distance20	0.590	a	b			
Stratified	0.593	a	b			
Distance10	0.596	a	b	c		
Random	0.623	a	b	c	d	
Co1080	0.687		b	c	d	
Co2080	0.774			c	d	
Co1090	0.800				d	e
Co2090	0.959					e

C. For 20 samples

Methods	Means of z_{20}					
Zigzag	0.484	a				
Diagonal	0.486	a				
Distance20	0.608	a	b			
Distance10	0.616	a	b			
Stratified	0.636	a	b	c		
Random	0.661	a	b	c		
Co1080	0.703		b	c		
Co2080	0.808		b	c		
Co1090	0.835			c	d	
Co2090	1.027				d	

Comparison of means of the variables z_5 , z_{15} and z_{20} representing the relative prediction error estimated for 5, 15 and 20 samples, respectively, performed after the linear model *mean relative prediction error* $z_l = \text{constant} + \text{method effect} + \text{species effect} + \text{year effect} + \text{method*species interaction} + \text{method*year interaction} + \text{species*year interaction} + \text{error}$ (see Table 3). Means followed by the same letter are not significantly different at $P=0.05$ (least significant difference test).

A. syriaca resulted low errors. To study this species effect further, the relationship was analysed between the relative prediction error and the weed distribution characteristics presented in Table 1:

- the mean annual species density *mean*,
- the relative variance, s_0/mean ,
- the relative contributions of the first (c_1/s_0) and second spatial structures (c_2/s_0) to the variability (see Colbach *et al.*, 2000),

Table 5 Ranking of sampling methods based on comparisons of means of relative error predictor performed separately for each species (1 = lowest error, 10 = highest error) in the case of sampling performed on kriged maps

Methods	Species																				
	A. retroflexus		A. sylvatica		C. album		C. arvense		E. repens		S. viridis		S. arvensis		Mean		Standard error		Median		
	Z ₅	Z ₁₅																			
Based on systematic sample selection																					
Diagonal	1	2	2	1	1	1	5	6	5	1	1	2	1	1	1	1	1	1	8	1	1
Zigzag	1	1	1	1	9	9	1	1	1	2	2	1	2	1	2	3	1	2	7	1	2
Based on random sample selection																					
Distance20	1	8	8	1	2	2	1	2	3	3	2	1	2	1	3	2	1	2	1	2	1
Distance10	1	8	8	1	2	2	1	1	2	4	3	3	2	1	2	1	6	4	1	2	3
Stratified	1	2	2	1	6	5	1	1	2	2	5	4	1	1	6	1	7	6	1	2	4
Random	1	2	2	1	6	7	1	5	2	6	5	5	2	1	2	1	7	6	1	2	5
Based on predicted seedling maps																					
Co1080	1	2	2	1	4	4	1	7	7	7	7	7	2	7	7	1	10	10	1	2	5
Co1090	1	2	2	1	4	5	1	8	9	9	8	8	2	8	9	10	9	6	1	2	7
Co2080	1	2	2	1	8	7	10	8	8	8	8	8	2	8	8	1	4	5	9	9	9
Co2090	1	8	8	10	10	10	1	8	9	9	10	10	1	8	10	1	5	6	9	10	10

Ranks were attributed, using comparison of means (with alpha = 10%) of relative error predictors for five (z₅), Fifteen (z₁₅) and 20 samples (z₂₀) performed separately for each species and variable (z_i). An identical rank was given to methods followed by the same series of letters.

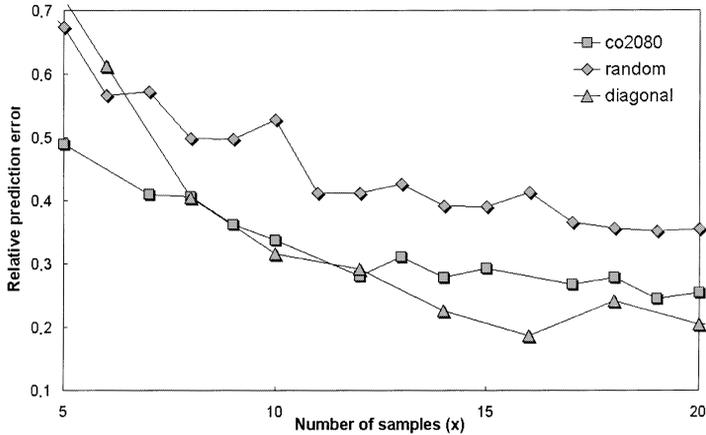


Fig. 5 Relative prediction error described by eqn E3 for *S. viridis* and three sampling methods in 1997.

- the ranges along (a_{1-0}) and across the crop rows (a_{1-90}) of the first spatial structure (see Colbach *et al.*, 2000).

These characteristics were used as input variables for a linear model, with the variables z_5 , z_{15} and z_{20} as output variables. The final models containing only effects and covariables significant at $P = 0.05$, were similar for the three tested output variables, but correlations were strongest for z_{15} . In the latter case, the final model was:

$$\begin{aligned}
 z_{15} = & \text{constant} + \text{method effect} + \text{year effect} \\
 & - 0.00802 \cdot \text{mean} + 0.0100 \cdot \frac{s_0}{\text{mean}} + 0.373 \cdot \frac{c_1}{s_0} + 0.247 \cdot \frac{c_2}{s_0} \\
 & - 0.00791 \cdot a_{1-90} + \text{error} \\
 & \text{with } r^2 = 0.67
 \end{aligned}
 \tag{5}$$

This model shows that the relative prediction error increased with the relative variance s_0/mean (or $s_0/(\log(1 + \text{mean}))$) if such a data transformation was necessary before the geostatistical analysis performed by Colbach *et al.*, 2000). The contributions c_1/s_0 and c_2/s_0 of the first and second spatial structures, respectively, were positively correlated with estimation error. Average annual mean density of species and the geostatistical range across the crop rows, a_{1-90} , of the first spatial structure were correlated negatively with estimation error.

Discussion

Despite small variations in the ranking of the sampling methods for some species, a general ranking of methods according to their estimation error can be established, independently of the species and the years. Indeed, with the Gaussian maps, the method ranking was nearly the same whatever the species; and with the kriged maps, the interaction between the ‘species’ and the ‘method’ factors was not significant. Therefore, choosing from this ranking one or more methods that adequately estimate the densities of all weed populations is possible, with one or two exceptions observed on the kriged maps, which will be discussed below. The interaction between

Table 6 Ranking of sampling methods based on comparisons of means of relative error predictor performed separately for each year (1 = lowest error, 10 = highest error) in the case of sampling performed on kriged maps

Methods	Year												Median					
	1993			1994			1996			1997					Z ₅	Z _{1.5}	Z ₂₀	
	Z ₅	Z _{1.5}	Z ₂₀	Z ₅	Z _{1.5}	Z ₂₀	Z ₅	Z _{1.5}	Z ₂₀	Z ₅	Z _{1.5}	Z ₂₀						
Based on systematic sample selection																		
Diagonal	6	1	1	7	1	1	2	2	6	1	1	1	1.3	1.3	0.5	0.5	1	1
Zigzag	1	1	1	1	4	5	1	1	1	1	1	4	1.0	1.8	0.0	1.5	1	1
Based on random sample selection																		
Distance20	1	1	1	2	2	2	1	5	4	2	1	1	1.5	2.3	0.6	1.9	1.5	1.5
Distance10	1	1	1	2	2	3	1	5	4	5	4	1	2.3	3.0	1.9	1.8	1.5	3
Stratified	1	1	1	2	4	4	1	2	2	2	4	4	1.5	2.8	0.6	1.5	1.5	3
Random	1	1	1	2	4	5	1	2	4	2	4	4	1.5	2.8	0.6	1.5	1.7	3
Based on predicted seedling maps																		
Co1080	2	7	5	2	7	5	6	7	7	6	7	7	4.0	7.0	2.8	0.0	1.4	4
Co1090	8	8	8	8	8	8	8	8	9	8	8	9	8.0	8.0	0.0	0.0	0.7	8
Co2080	8	9	9	8	9	9	8	8	8	8	8	8	8.0	8.5	0.0	0.7	0.7	8
Co2090	10	10	10	10	10	10	10	10	10	10	10	10	10	10	0.0	0.0	0.0	10

Ranks were attributed, using comparison of means (with alpha = 10%) of relative error predictors for five (z₅), 15 (z_{1.5}) and 20 samples (z₂₀) performed separately for each year and variable (z_i). An identical rank was given to methods followed by the same series of letters.

A. For five samples

Species	Means of z_5				
<i>S. arvensis</i>	0.519	a			
<i>A. syriaca</i>	0.754		b		
<i>S. viridis</i>	0.783		b		
<i>E. repens</i>	0.834		b		
<i>C. arvense</i>	1.141			c	
<i>C. album</i>	1.574				d
<i>A. retroflexus</i>	1.873				e

B. For 15 samples

Species	Means of z_{15}				
<i>S. arvensis</i>	0.324	a			
<i>S. viridis</i>	0.385	a			
<i>A. syriaca</i>	0.425	a	b		
<i>E. repens</i>	0.548		b	c	
<i>C. arvense</i>	0.615			c	
<i>C. album</i>	0.947				d
<i>A. retroflexus</i>	1.081				d

C. For 20 samples

Species	Means of z_{20}				
<i>S. viridis</i>	0.333	a			
<i>A. syriaca</i>	0.451	a	b		
<i>C. arvense</i>	0.533		b		
<i>S. arvensis</i>	0.562		b		
<i>C. album</i>	0.848			c	
<i>A. retroflexus</i>	0.935			c	
<i>E. repens</i>	0.959			c	

Comparison of means of the variables z_5 , z_{15} and z_{20} representing the relative prediction error estimated for 5, 15 and 20 samples, respectively, performed after the linear model *mean relative prediction error* $z_j = \text{constant} + \text{method effect} + \text{species effect} + \text{year effect} + \text{method} * \text{species interaction} + \text{method} * \text{year interaction} + \text{species} * \text{year interaction} + \text{error}$ (see Table 3). Means followed by the same letter are not significantly different at $P=0.05$ (Least significant difference test).

the 'method' and 'year' was not significant, and the detailed ranking of methods for each year was relatively similar. The slight variations in the methods' ranking could be due to the differences in densities and patch locations for the different years. As a consequence, the ranking of methods does not depend on the year, and one method is better or worse than another, regardless of the year.

The systematic methods, i.e. the 'diagonal' and the 'zig-zag' methods performed best globally. However, irrespective of the mapping process, their performance was not always satisfactory with low sample numbers. This result is consistent with former weed seedling sampling studies performed in set-aside fields with different species (Chauvel *et al.*, 1998). The reason for poor performance does not depend on the actual nature of the sampled species, but rather on the distribution of the weed patches in a field. With a low sample number, the systematic methods could oversample the field edges and undersample the field interior and, thus, poorly estimate

Table 7 Effect of species on the relative prediction error made when estimating weed densities with various sample numbers in the case of sampling performed on kriged maps

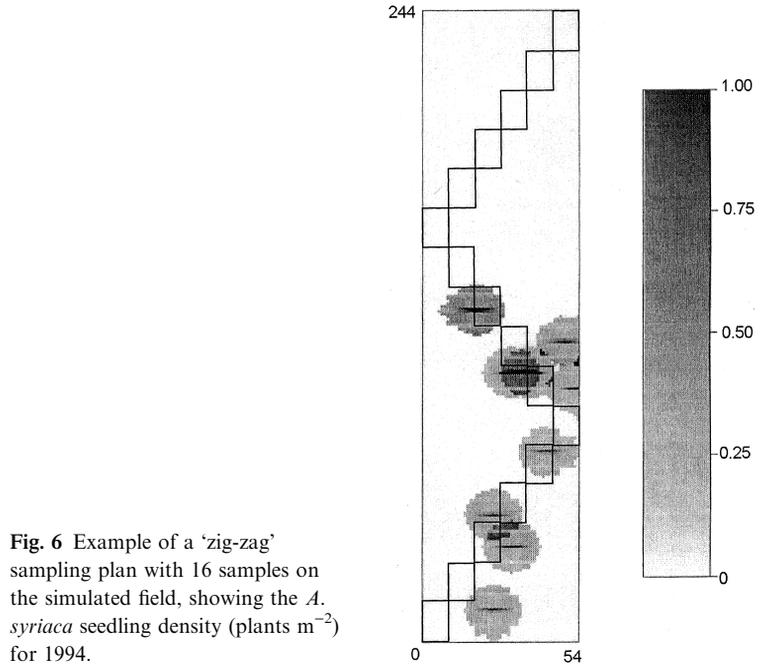


Fig. 6 Example of a 'zig-zag' sampling plan with 16 samples on the simulated field, showing the *A. syriaca* seedling density (plants m^{-2}) for 1994.

densities for species over- or under-represented along the field edges. This bias disappears when the sample number increases. Furthermore, the systematic location of these samples ensures that a large part of the field is covered, comprising both field edges and interior, thereby explaining why the systematic methods are usually the best methods with 15 or 20 samples. Nevertheless, the unsampled proportion of the field is still considerable and even with a large sample number, estimation can be poor if most weed patches are concentrated in the unsampled part of the field or, inversely, in the sampled part of the field. This phenomenon was not visible on the Gaussian maps based solely on the semivariograms, independent of actual patch location, where each of the 100 maps generated for a given year showed a different patch distribution. However, the kriging process also uses the actual raw weed data for generating the maps and, thus, only produced one map for each year on which each sample plan was repeated 200 times. This permitted the study of the impact of a particular patch location, for instance, as in the case of *A. syriaca* in 1994 (Fig. 6). In this situation, about half of the 16 samples had a high probability of hitting a patch whereas less than 20% of the field was infested. This explains the high estimation error of the 'zig-zag' method in this particular configuration. If the sample number was increased, still another deficiency of the systematic methods appeared for some species. Indeed, the distance between two successive samples would fall below the semivariogram ranges and the samples would become dependent, thereby leading to a systematic estimation bias. For instance, with 30 samples used in a 'diagonal' system, the distance between samples is only 18 m, which is lower than many geostatistical ranges of the species sampled in this study (Table 1). With the 'zig-zag' method where samples are even closer together, this problem would appear with even lower sample numbers; already with 20 samples, the intersample distance would only be 16 m. This might explain why for species with high geostatistical ranges such as *S. viridis* or *S. arvensis*, the performance of the 'zig-zag' method decreased with 20 samples compared with 15 samples.

However, this decrease in performance was not observed with the Gaussian maps and might therefore not be a general phenomenon.

For low sample numbers, methods based on random selection are best; their performance is independent of species, they do not present any systematic risk of over- or under-sampling specific field regions and the probability of the samples being located farther than the semivariogram ranges is high. This last point explains why the use of a minimum distance between samples, or use of stratification, does not have much effect with five samples. However, with 15 or 20 samples, the situation changes. Imposing a distance constraint increases the probability of independent samples and thus decreases estimation bias. Logically therefore the 'distance 20' methods give better results than the 'distance 10' methods because in the former case the distance between samples exceeds the ranges of a larger number of species than in the latter case (Table 1). Species with the highest ranges, i.e. *S. viridis* and *S. arvensis*, are those where the 'distance 20' method performs as well (when sampling on the Gaussian maps) or better (sampling on the kriged maps) than the systematic methods. The distance constraint also leads to a larger sampling coverage of the field than with the 'random' method where the area covered by the samples can vary considerably. The stratification of the field also ensures that the whole field is more or less sampled, but imposes no minimum distance between samples; samples are therefore not necessarily independent. This explains why the 'stratified' method performs slightly worse than the 'distance 10' or 'distance 20' methods, especially as the stratification criterion is not based on any knowledge of spatial structure but consists simply of a division of the field into five equal parts.

Compared with the systematic methods, the randomized methods have another disadvantage that was not considered in this paper. Even if the chosen method is supposed to be a randomized selection of samples, this is actually rarely the case. Few researchers randomly select field co-ordinates before travelling to the field and then take their samples exactly at the prechosen co-ordinates. In practice, when sampling randomly, an experimenter is more likely to wander through a field, taking samples, here and there, which often leads to a subconscious selection or avoidance of certain types of situations. This risk is considerably reduced with the systematic methods where the samples are taken at defined intervals, even if this still leaves a certain margin of error in practice. Furthermore, the prior random selection of field co-ordinates adds time and cost to the methods based on random selection. Hence, more counts can be made with systematic methods in the same time, therefore leading to a greater accuracy per sampling hour.

The methods based on predicted seedling maps of one species (e.g. *S. viridis*) should be avoided for estimation of general weed populations. This is in fact not very surprising if various species with different distribution characteristics are present in a field, but are sampled using information relevant to only one of them. However, for some species, the predicted-map methods perform better than the systematic methods, probably because the former ensure a larger coverage of the field and do not oversample field edges like the latter. This would also explain why the 'co1080' method performs best among the four predicted-map methods; this method is indeed the one that selects the lowest proportion of samples in the high *S. viridis* density areas, thus ensuring a better sample distribution over the field than the other three methods of the same group. More generally, the same explanation would apply for the better performance of the methods using the 10-plant instead of the 20-plant limit to distinguish high and low *S. viridis* densities or of those choosing only 80% instead of 90% of the samples in the high-density area.

This reasoning, however, is not true for the species for which we originally designed these methods, i.e. *S. viridis*. In this case, the methods using the 20-plant boundary performed best because they limited the highly sampled portion of the field to those areas where the species is most abundant and sampling is most productive. However, even for *S. viridis* the predicted-map methods are really not satisfactory, especially considering the amount of work needed to prepare the sampling protocol, i.e. information on spatial distribution of the previous year and on interannual cross-semivariograms needed to predict the seedling maps (Colbach *et al.*, 2000). This is surprising in the sense that sampling plans taking into account information on spatial variability and structure are supposed to decrease estimation error (Scherrer, 1983; Cardina *et al.*, 1995). Therefore, either the prediction of the seedling distribution in the field was not sufficiently accurate for sampling purposes (which was not the objective of the map prediction conducted by Colbach *et al.*, 2000) or the delimitation of the high-density area and/or the proportion of samples chosen in this area were not adequate. Another possibility is that the methods were not evaluated correctly, as they were only tested on the kriged maps which tend to smooth variations.

Despite the general method ranking being valid for every species, more or less, the relative estimation error varied considerably for each species, depending on their distribution characteristics. As a consequence, for high-error species such as *A. retroflexus*, a high sample number would be necessary to limit the estimation error to the same level as that obtained for low-error species, such as *S. viridis*. Low-density species (as indicated in eqn 5 by the negative correlation between estimation error and mean plant density) and/or highly variable species (illustrated by the positive correlation between error and relative variance), of course, are difficult to sample correctly, irrespective of the method chosen for sampling (Dessaint *et al.*, 1992; Jones, 1998). Moreover, if the population is spatially structured (positive correlation between error and contributions of spatial structures to variability), the risk of spatially dependent samples increases, as does estimation error.

In conclusion, the use of two map generating processes, i.e. ordinary kriging and Gaussian simulations, resulted in a common ranking of sampling methods. This occurred despite the fact that kriging tends to smooth variations. The observed differences seemed to depend on whether the mapping was based solely on the semivariograms (Gaussian simulations) or also used the raw weed data actually sampled in the real field (kriging) and thus delineated certain risks related to the systematic sampling methods. Nevertheless, for a given number of samples, ranking the sampling methods was possible according to their performance, regardless of species and year. Depending on the time and effort the investigator can devote to the sampling process, this ranking allows identification of the optimal method, which leads to the lowest estimation error. This study does not consider other aspects of sampling design, such as sample area, which also are of critical importance. Moreover, determination of optimal sampling procedures for making the best weed management decisions as opposed to mere characterization of weed densities, awaits further analyses.

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