Probability functions to build composite indicators: a methodology to measure environmental impacts of genetically modified crops

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1. Introduction

Since the adoption of genetically modified (GM) crops in 1996 there has been an on-going debate about the impacts of GM crops. A vast scientific research on the agronomic, economic and environmental effects of GM crops has been conducted since their adoption. Most of this research is carried out at farm-level in specific countries for different crops. Recently, a number of reviews of both the agronomic and economic impacts of GM crops worldwide has been published (Areal et al., 2013a; Brookes and Barfoot, 2008, 2012, 2013; Carpenter, 2010; Park et al., 2011; Qaim, 2009). Brookes and Barfoot (2008, 2013) and Qaim (2009) provide an overview of agronomic and economic of insect resistant (Bt) and herbicide tolerant (HT) crops by using available impact studies. Areal et al. (2013a) and Carpenter (2010) compiled data from a number of peer-reviewed studies to carry out further statistical analysis (i.e. meta-analysis). The mentioned reviews indicate that GM crops overall tend to outperform conventional counterparts in agronomic (i.e. higher yields) and economic terms (i.e. higher gross margins per hectare), being results more evident for Bt traits. Areal et al. (2013a, 2013b) show that the agronomic and economic performance of GM crops occurs in both developing and developed countries, providing evidence that the adoption of GM crops in developing countries may contribute to increase global food security.

Potential environmental effects associated with the adoption of GM crops have been analysed at different levels: crop biodiversity, farm and landscape scales (Carpenter, 2011). Concerns on crop genetic biodiversity have been raised with the introduction of GM crops due to both the agricultural risks on cross-pollination between neighbouring GM and conventional fields through pollen transfer and seed (Bannert, 2006; Bonny, 2008; Breckling et al., 2011; Devos et al., 2005 and 2009; Graef et al., 2007; Hayes et al., 2004; Riesgo et al., 2010) and the fact that breeding programs are concentrated on a smaller number of high-value cultivars (Ammann, 2005). A reduction of crop genetic biodiversity may have significant consequences on the vulnerability of agricultural systems since crop diversity contributes to minimise the risk of harvest failures due to climate change, especially in poor farming systems (Frison et al., 2011; Padulosi et al., 2011). Declining crop genetic biodiversity may also erode the nutritional enrichment of diets based on greater supply diversity and increases potential risks for health (Jacobsen et al., 2013). However, despite the concerns on crop diversity several studies show that GM crops have not negatively affected genetic crop diversity in a significant manner (Bowman et al., 2003; Gepts and Papa, 2003; Sneller, 2003; Palaudelmás et al., 2009) or even that GM crops have actually increased crop diversity (Bhattacharjee, 2009; Gressel, 2008).

GM crops impacts at farm and landscape levels include any effects on organisms that live within or outside the farm (i.e. non-target soil organisms, weeds, non-target above-ground invertebrates and birds) and effects on pesticide[1] use. Potential environmental benefits of the adoption of HT crops have been raised by some authors, such as the substitution of selective herbicides (usually harmful for the environment) for less toxic broad-spectrum herbicides (e.g. glyphosate), savings associated with low herbicide use and the adoption of conservation tillage practices (Devos et al., 2008; Deward et al., 2003; Ervin et al., 2000; Nelson and Bullock, 2003; Smyth et al., 2011; Sydorovych and Qaim, 2009; Wolfenbarger and Phifer, 2000). However, the decrease in the total quantity of herbicides applied per unit surface area only occurs at early stages of HT crops adoption (Bonny, 2008; Owen and Zelaya, 2005; Shaner, 2000), but a rise in the quantity of herbicides is expected in late stages of adoption due to the presence of resistant weeds. It is worth mentioning that some of these potential impacts such as the substitution of selective herbicides and the adoption of conservation tillage practices are not directly caused by the GM plant but by the farm management practices associated with the cultivation of HT crops. In the case of Bt crops some authors pointed out a positive impact caused through the reduction of pesticide use not only on GM fields but also on neighbouring conventional fields ("halo effect") (Carriére et al., 2003; Wan et al., 2012; Mannion and Morse, 2012). One of the earliest studies on farm biodiversity was the UK Farm Scale Evaluations (FSE) of genetically modified herbicide tolerant (GMHT) crops, which included analysis on sugar beet, winter oilseed rape (WOSR), spring oilseed rape (SOSR) and maize (Squire et al., 2003; Heard et al., 2003a, 2003b; Haughton et al., 2003). The main results from the UK FSE regarding invertebrates indicate that whereas certain species such as butterflies may be negatively affected by the adoption of some GMHT crops (HT sugar beet and HT SOSR) other species such as springtails and some of their predators were more abundant. Also butterflies were positively affected by the adoption of HT maize (Haughton et al., 2003). With respect to plant densities less densities were found in HT beet and HT oilseed rape whereas more plant density was found in HT maize than in their

[1] Pesticide use includes both herbicides and insecticides use.

conventional counterparts (Heard et al., 2003a). As a result of research studying the environmental effects associated with the adoption of GM crops a number of reviews have been published compiling data and given an overview of environmental impacts of GM crops (Amman, 2006; Carpenter, 2011; Sanvido et al., 2007; Wesseler et al., 2011).

Environmental effects of GM crops when compared to their conventional counterparts are diverse in the literature, being measured those impacts using an array of indicators such as number of individuals, number of individuals per 100 plants, mg per square meter, number of sprays, kg of active ingredient, kg of pesticide per ha and litre per ha. Considering the type of impact, these eight indicators can be grouped into: a) indicators related to measuring impacts on non-target key species richness ((see Table A1 in the Appendix) and b) indicators related to the pesticide[2] use (see Table A2 in the Appendix).

In addition to these indicators, some studies used some indicators to assess the risk of pesticides on humans and animals in order to evaluate the environmental impact of GM crops. The biocide index (Jansen et al., 1995) and the field use rating of the Environmental Impact Quotient (EIQ) developed by Kovach et al. (1992) are usually used to measure and compare the relative environmental impacts of GM crops (Morse et al, 2006; Brookes and Barfoot, 2005, 2008, 2013; Smyth, 2011). The EIQ is a tool to assess specific pesticide risk to farmers, consumers and the environment. More specifically environmental and health impacts of pesticides are calculated by incorporating potential toxicity values for specific pesticides considering the degradation and transportation rates (Knox et al., 2012). The main difficulty to use these indicators is data requirements on the type and rate use of pesticides.

In this paper we are interested on taking advantage of the information published to date on some environmental effects of GM crops when compared to conventional crops, in order to obtain some conclusions on the potential environmental impacts of GM crops adoption[3]. We propose first to build a composite indicator that allows to aggregate data published by several authors on environmental effects of GM and conventional crops[4]. Different normalisation

[2] Pesticide use include both herbicide and insecticide use.

[3] Please note that this paper only compares the environmental effects of GM and conventional crops, but organic crops are not included in the analysis. An analysis including organic crops cannot be performed since there is no enough published data available to perform the statistical analysis (data on non-target species richness and pesticide use for both organic and GM crops in similar edafoclimatic conditions). However, a comparative analysis of the environmental performance of both organic and GM crops would be of interest. Some meta-analysis conduct a comparative analysis of the environmental effects caused by organic and conventional crops (Mondelaers et al., 2009; Azadi and Ho, 2010; Tuomiso et al., 2012). Results show that organic farming has generally lower environmental impacts per unit of area than conventional farming.

[4] This paper is focused on the environmental impacts associated with the cultivation of GM crops at farm level.

procedures are analysed in order to aggregate the different indicators forming the composite indicator. Robustness of the constructed composite indicators is assessed by assigning different weights to the indicators and changing the aggregation method. Secondly, a meta-analysis of environmental impacts of GM and non-GM crops is conducted to examine whether GM crops performs environmentally better than their conventional counterparts.

2. Methods

Composite indicators aim to aggregate indicators that measure impacts on different fields (e.g. economic, social and/or environmental dimensions) in order to obtain a unique value. In this paper we are not interested in measuring dimensions like economic or social impacts of GM crops but environmental. Taking advantage of how a composite indicator is built we develop a methodology to aggregate data on some key environmental impacts of GM crops that have been published in a number of scientific articles.

The main issues in building a composite indicator are related to normalization, weighting and aggregation of indicators as well as the robustness of the composite indicator. Nardo et al. (2005) and OECD (2008) suggest a number of alternative techniques for this purpose, explaining their pros and cons. The most popular methods are based on the weighted sum of indicators (Andreoli and Tellarini, 2000; Rigby et al., 2001; Gómez-Limón and Riesgo, 2009), principal component analysis (Sands and Podmore, 2000), analytic hierarchy process (Pirazzoli and Castellini, 2000), geometric average (Qiu et al., 2007, Gómez-Limón and Sánchez-Fernández, 2010) or multiattribute utility functions (van Calker et al., 2006). The weight given to each indicator shows their contribution to the final composite indicator. We use here two aggregation rules of individual indicators: additive and multiplicative aggregation. The additive approach[5] is based on a linear weighted aggregation rule implying total compensation among indicators (i.e. allow to compensate one indicator with bad score with another with good score), whereas the multiplicative approach is based on the product of weighted indicators[6] allowing only partial compensation (i.e. still bad scores can be compensated with good scores but not linearly, thus only partial compensation is accounted for) (OECD, 2008).

[5] $CI_a = \sum_i w_i \cdot I_i$, where CI is the composite indicator following an additive approach, I_i is the indicator and w_i is the weight.

[6] $CI_m = \prod_i {I_i}^{w_i}$, where CI is the composite indicator following a multiplicative approach, I_i is the indicator and w_i is the weight.

Normalization is a prerequisite for any aggregation of indicators because they are usually measured in different units. Taking into account the indicators found in the literature review on the environmental impact measures/indicators of GM crops and conventional crops we use two different normalisation methods: a) the min-max and b) the distance to a reference point.

The min-max method normalises the indicator by subtracting the minimum value and dividing by the range of indicator values as shown in the following equation:

$$I_i = \frac{x_i - min(x)}{max(x) - min(x)} \qquad [1]$$

where x is an indicator vector that contains values of environmental impact (e.g. number of individuals (arthropods)).

The distance method normalises the indicator by measuring the relative position of an indicator to a reference point, which in this case is the maximum value of the sample as shown in equation 2.

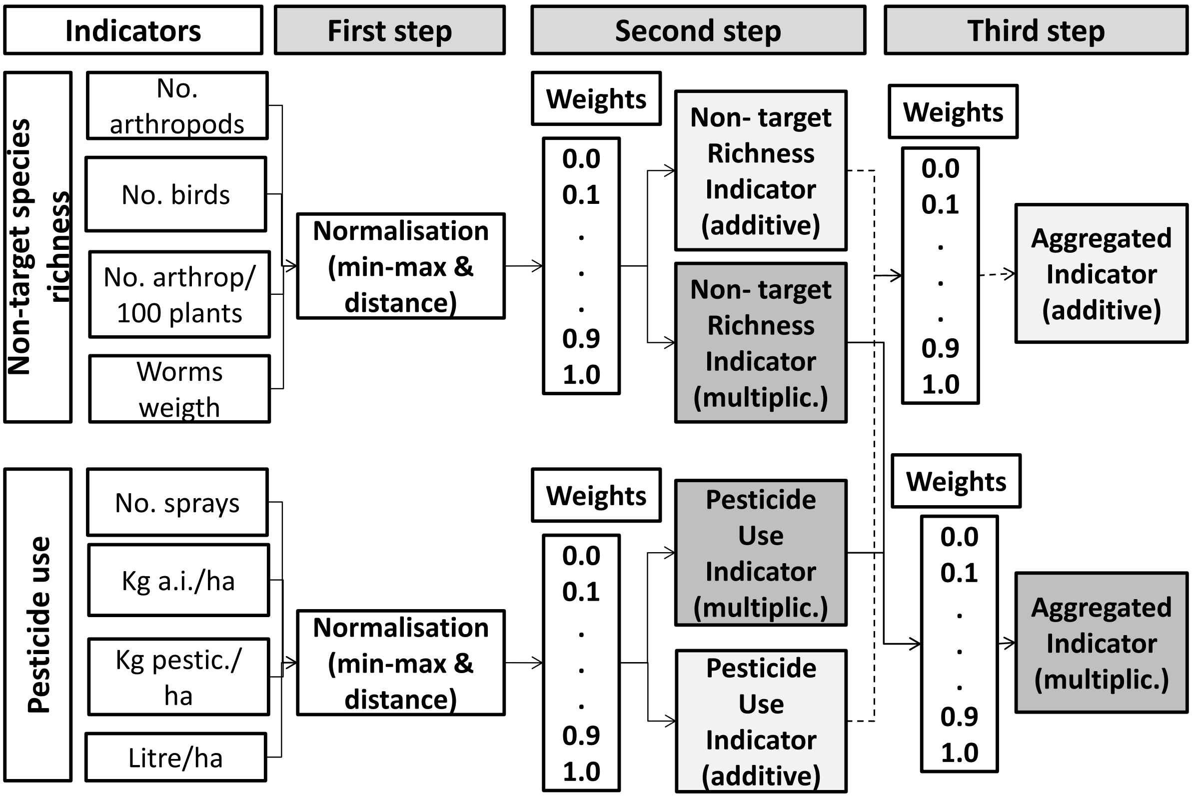
$$I_i = \frac{x_i}{max(x)} \qquad [2]$$

Both methods allows re-scaling indicators within a dimensionless range [0,1] for the min-max method and (0,1] for the distance normalisation method. Indicators can be classified into two groups: "more is better" indicators (e.g. indicators related with biodiversity richness: arthropods number, worms weight, birds) and "less is better" indicators[7] (e.g. indicators related with active ingredient use). In the case of a "less is better" indicator it will be transformed in "more is better indicator" by multiplying by -1. After normalization all indicators will have a value that range between 0 or close to 0 (the worst value, e.g. the minimum number of arthropods or the maximum quantity of active ingredient use) and 1 (the best value, e.g. the maximum number of arthropods or the minimum quantity of active ingredient use).

[7] All environmental indicators related with the pesticide use are of type "less is better". The use of these pesticides allows us to compare the use of the same pesticide among GM and conventional crops. We acknowledge that the use of some pesticides is more harmful (or toxic) for the environment than others (e.g. one kg of arsenic is more toxic than one kg of salt). This issue is of great importance in the case of HT crops, since this type of crop sometimes implies an increase in the amount of broad spectrum herbicides (pesticides) when compared with conventional counterparts, but with lower toxicity than specific herbicides against weeds used in conventional crops. This analysis does not take into account the toxicity of the pesticide in the environment, but assumes that it is better to use less pesticide than more.

A number of studies based on sample surveys compared the environmental impact of GM crops and conventional crops at farm level in different countries (see Tables A-1 and A-2). Data on environmental impacts were collated from peer-review studies and grouped into 8 different indicators (4 related to non-target key species richness and 4 related to pesticide use) to conduct the analysis (see Figure 1). As it is mentioned above we take advantage of the information published to date on some environmental effects of GM crops when compared to conventional crops. In this literature different indicators were used to analyse environmental impacts such as the number of individuals (arthropods); number of individuals (birds); number of individuals per 100 plants (arthropods); earthworm weight (in mg per square meter); number of sprays; kg of active ingredient per ha; kg of pesticide per ha; and litre of pesticide per ha. Data for non-target species richness were collated from studies based on field trials, where a number of plots were used to investigate the abundance of certain non-target species in fields grown with GM and conventional crops. Data for pesticide use were gathered from studies based on surveys at farm level and consequently no further information from farmers associations at market level or extension services are included in the analysis. Consequently, the environmental impacts are limited to farm level. The 8 indicators on environmental impacts were used to calculate two composite indicators: 1) one for the environmental impact related to non-target key species richness and 2) another for the environmental impact related to pesticide use. These two composite indicators are then used to calculate a third composite indicator that measures the aggregated environmental impact.

Figure 1. Outline of the methodology



As far as we are concerned, all the studies using composite indicators are based on single values of the individual indicators. The analyses conducted consist of normalising and aggregating those single values to build a composite indicator. In this paper, we calculate two environmental composite indicators, one for GM and another for conventional crops by using data compiled from a number of peer-review studies[8]. Data collected from these studies show one observation (i.e. an average value) on either non-target key species richness or pesticide use per type of crop (i.e. one data for GM and another for conventional crops). Since data used are an average value we calculate each environmental composite indicator on the basis of the distribution of the mean of each indicator per crop information in order to take advantage of the information published on the sample size. This allows us to assign more (less) weight to the data provided by studies that contained more (less) information (i.e. studies with large (small) samples).

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[8] Large datasets on pesticide use at country level, such as national pesticide use surveys or the analyses published by Brookes and Barfoot (2012, 2013) on pesticide use and other environmental impacts, are not included in this analysis due to the different scale of analysis (this paper only collates data from papers analysing environmental impacts at farm level –real farms or field trials at farm level–).

The environmental indicators were selected on the basis of the literature on environmental impacts of GM and conventional crops, and no assumptions are made about the relative importance of each indicator within the environmental composite indicator. Hence, we calculate the mean of the posterior probability density function (pdf) of the composite indicator for the environmental impact of GM and conventional crops for all possible combinations of weighting (at one decimal level)[9].

Therefore we can a) compare the environmental impact related to non-target key species richness of GM vs. conventional crops (i.e. build a composite indicator for non-targeted key species richness for each crop and calculate afterwards the probability that GM crops perform better than conventional crops); b) compare the environmental impact related to pesticide use of GM vs. conventional crops (i.e. build a composite indicator for pesticide use for each crop and after that calculate the probability that GM crops perform better than conventional crop); and c) compare total environmental impact of GM vs. conventional crops using the two mentioned composite indicators (i.e. build an aggregated composite indicator considering both non-targeted key species richness and pesticide use composite indicators, and calculate afterwards the probability that GM crops perform environmentally better than conventional crops).

Bayesian and non-parametric methods were used to make inferences about the environmental performance of GM crops in comparison with conventional crops per indicator[10]. We tested for normality of the errors for each indicator per normalisation method and crop. We selected the method based on the results obtained from the normality tests[11]. Three possible approaches were possible: 1) if the normality assumption is not rejected a Bayesian linear analysis (BLA) assuming normally distributed errors is conducted; 2) if the normality assumption is rejected but the distribution is not skewed we assume a less restrictive Student´s t distribution for the errors than the Bayesian linear analysis; and 3) if the normality assumption is rejected and the distribution is skewed a non-parametric bootstrapping approach is conducted.

[9] A detailed explanation of the process can be found below under Section 2.4.

[10] For a detailed and comparative analysis of parametric and non-parametric statistical methods see Sheskin (2004).

[11] We tested for normality using the Jarque-Bera test. The sample skewness statistics is calculated by using: $= m_3/m_2^{3/2}$, where m_3 is the sample third central moment and m_2 is the sample variance. If the value of the estimate of skewness exceeds two times the standard error of skewness (calculated as $SES = \sqrt{6/N}$) then the sample distribution is regarded as skewed (Tabachnik and Fidell, 1996) and non-parametric bootstrap is carried out.

2.1. The Bayesian linear analysis

For each indicator there are N independent observations $y' = (y_1, y_2, \dots, y_N)$ which are assumed to be drawn from a Normal distribution with mean μ and variance ${\sigma^2}/{n_i}$ where n_i is the number of observations of study i. Therefore, each indicator equals its mean plus some zero-centred normally distributed error term $\varepsilon_i \sim N(0_N, h^{-1} I_N / n_i)$, where $h = 1/\sigma^2$ is the error precision and I_N is the $N \times N$ identity matrix. The linear regression model to be estimated is $y_i^* = \sqrt{n_i}\mu + v_i$, with $y_i^* = \sqrt{n_i} y_i$, $Var(v_i) = \sigma^2$ and $v_i = \varepsilon_i \sqrt{n_i}$.

Bayesian methods were used to infer the environmental impact of both GM and conventional crops in the case that errors distribution of the indicator I for the type crop was normally distributed. The Bayesian approach treats parameters as random variables and yields distributional information. The Bayes theorem can be represented in the following expression:

$$p(\theta|y) \propto p(\theta) p(y|\theta) \qquad [3]$$

where $p(\theta|y)$ is the posterior probability density function (pdf) for the parameter vector θ, given the sample information y; $p(\theta)$ is the prior information for the parameter vector θ; and $p(y|\theta)$ is the likelihood function, which is a pdf of the observations given the parameters. In the Bayesian approach inferences about the parameters are made using the posterior pdf. In this analysis our parameters of interest are the means of the indicators for environmental impact.

The likelihood function is defined by the assumption of normally distributed errors:

$$p(y^*|\mu, h) = \frac{h^{N/2}}{(2\pi)^{N/2}} exp\left(-\frac{h}{2}\left(\sum_{i=1}^{N} y_i^* - \sqrt{n_i}\mu\right)^2\right) \qquad [4]$$

The likelihood function shown in equation [4] is complemented with a prior distribution on parameters μ and h. We use natural conjugate priors that when combined with the likelihood distribution yields a posterior that falls under the same class of distributions. An independent Normal-Gamma prior was used for the mean μ and error precision h. Therefore the conditional posterior distributions for μ and h followed normal and gamma distributions. The prior distribution for the mean is:

$$p(\mu) \propto exp\left(\frac{h_0}{2}(\mu - \mu_0)^2\right) \qquad [5]$$

where μ_0 and h_0 are the mean prior and the inverse variance prior distributions with values 0.5 and 0.1, respectively, making the prior non-informative (i.e. the mean prior of each indicator was given a variance of 10 units which means that no prior information is given for this parameter). The prior distribution for the error precision is given by the following expression:

$$p(h) \propto h^{a-1} \exp\left(-\frac{a}{c}\right), h > 0 \qquad [6]$$

where a and c are hyperparameters with values 0.01 and 2,500 respectively[12]. These values put little weight to the prior information making the prior relatively non-informative. The Bayesian computation of the conditional posteriors was carried out using a Gibbs sampler (Geman and Geman, 1984). A total number of 1,200 random draws were generated from the conditional distributions with 200 draws discarded and 1,000 retained. These 1,000 draws could be considered a sample from the joint posterior density function of the parameters.

2.2. The Student´s t distributed errors

This approach is the same as for the normally distributed errors case, with the exception that now $v_i \sim N(0_N, h^{-1}\lambda_i^{-1})$ for $i = 1, \ldots, N$ is assumed, where $\lambda = (\lambda_1, \lambda_2, \ldots, \lambda_N)'$ is a vector of error precisions. Following Koop (2003) we incorporate the new parameter λ into the Bayesian analysis. The prior for λ is $(\lambda) = \prod_{i=1}^{N} f_G(\lambda_i|1, \tau_\lambda)$, which is the exponential distribution with hyperparameter τ_λ. We set $\tau_\lambda = 25$ which allocated substantial prior weight to both fat-tailed error distributions as well as error distributions which were roughly Normal (Koop, 2003). The conditional posterior distribution of the new parameters λ_i had the form of a Gamma density, whereas the conditional posterior distribution for τ_λ was not a standard one

[12] These values are based on the expectation that the errors in the environmental indicators are of the order of magnitude of 0.1 to 0.2 units. We set a value for the standard deviation of h of 0.2 which gives a mean for the prior distribution of h of 25. We assign little weight to the prior information about h by setting the variance of the prior distribution of h in 62,500.

and a Random Walk Chain Metropolis–Hastings algorithm (Hastings, 1970; Chib and Greenberg, 1995) was used to obtain the distribution.

$$p(\lambda_i|y^*,\mu,h,\tau_\lambda) = f_G\left(\lambda_i|\frac{\tau_\lambda+1}{v_i^2+\tau_\lambda},\tau_\lambda+1\right) \quad [7]$$

$$p(\tau_\lambda|y^*,\mu,h,\lambda) \propto \left(\frac{\tau_\lambda}{2}\right)^{\frac{N\tau_\lambda}{2}} \Gamma\left(\frac{\tau_\lambda}{2}\right)^{-N} \exp(-\eta\tau_\lambda) \quad [8]$$

where $\eta = \frac{1}{\tau_\lambda} + \frac{1}{2}\sum_{i=1}^{N}[\ln(\lambda_i)^{-1} + \lambda_i]$. The conditional posterior distribution for μ, h and λ were obtained using a Gibbs sampler in the same way as in the linear analysis.

2.3. The non-parametric Bootstrapping residuals method

The non-parametric Bootstrapping residuals method (Efron and Tibshirani, 1993) is a resampling method for statistical inference where no distributional parameters are given. This is used to estimate the mean of the distribution of each indicator μ for both types of crops (i.e. GM and conventional). The method has three steps: (1) calculating approximate errors using the least square estimate of μ $(\hat{\mu})$; (2) drawing the approximate errors 1,000 times with replacement to obtain v_i^{**}; and (3) using these to generate $y_i^{**} = \hat{\mu} + v_i^{**}$.

2.4. Building composite indicators

Regardless of the approach used we obtained a density function with 1,000 elements for each indicator vector which allowed us to construct composite environmental indicators for each type of crop (i.e. GM and conventional). Therefore we build a $1{,}000 \times 4$ matrix RI_j with the 4 indicators associated with non-target key species richness per crop type j (GM crop, conventional crop) and a $1{,}000 \times 4$ matrix PI_j with the 4 indicators associated with pesticide use per crop type j. In order to build a composite indicator we need to weight and aggregate the individual indicators matrices RI_j and PI_j. We generated a weighting matrix W_1 with the following characteristics: each element of W_1 can take any of the following values $\{0, 0.1, 0.2, \dots, 1\}$, and the rows of the weighting matrix are combinations of elements (weights) where the sum of the elements of each row of the weighting matrix equals 1. The total number of combinations under these characteristics of the weighting matrix W_1 is 286. Therefore W_1 is a 286×4 (i.e. one column per indicator) weighting matrix.

We construct two $1{,}000 \times 286$ composite indicator matrices, one for non-target key species richness $\left(CRI_j\right)$ and another for pesticide use $\left(CPI_j\right)$ per crop j, each containing 286 columns (i.e. composite indicators) as below:

$$CRI_j = RI_j \times W_1' \qquad [9]$$

$$CPI_j = PI_j \times W_1' \qquad [10]$$

The matrices CRI_j and CPI_j effectively have: (a) 286 composite indicators (mean values of the distribution function) for environmental impact related to non-target key species richness and (b) 286 composite indicators for environmental impact related to pesticide use.

Finally, in order to obtain an overall composite indicator matrix OCI_j per crop type j we conduct the following steps: (1) stacking the columns of CRI_j and CPI_j obtaining two $286{,}000 \times 1$ vectors: cri_j and cpi_j per crop type j; (2) forming a $286{,}000 \times 2$ matrix using cri_j and cpi_j; (3) generating a 11×2 (i.e. one column per indicator) weighting matrix[13] W_2 which elements can take $\{0, 0.1, 0.2, \dots, 1\}$ as values and the sum of the elements of each row equals 1; and (4) constructing OCI_j as follows:

$$OCI_j = \left[cri_j \; cpi_j\right] \times W_2' \qquad [11]$$

The resulting OCI_j is a $286{,}000 \times 11$ matrix per crop type j. This allows us to compare the environmental impact of both crops per composite indicator and calculate the probability that a GM crop performs environmentally better than its conventional counterpart.

3. Results

Results are organised as follows: first, the impacts of GM and conventional crops are presented by considering all environmental indicators individually. Secondly, the impacts of both crop types on the non-target key species richness and the pesticide use is presented through composite indicators and finally, the impact of both crops on the aggregated environmental indicator is shown.

[13] Taking into account that we consider all possible combinations of weighting at one decimal level (from 0.0 to 1.0) and that the sum of all that combinations must be 1.0, there are 11 possible weighting combinations when using two indicators.

3.1. Individual Environmental Impact Indicators

Table 1 shows the type of approach used based on the assumption about the errors to obtain a density function for each indicator.

Table 1. Type of approach

Indicator (Positive[a])	**Non-target key species richness** *GM*	*Conventional*	**Indicator (Negative[b])**	**Pesticide use** *GM*	*Conventional*
I1. No. of individuals (arthropods)	Bootstrapping	Bootstrapping	I5. No. of sprays	Bootstrapping	Bootstrapping
I2. No. of individuals (birds)	Linear	Bootstrapping	I6. Kg of active ingredient	Linear	Linear
I3. No. of individuals (arthropods)/100 plants[14]	Bootstrapping	Bootstrapping	I7. Kg of pesticides	Bootstrapping	Bootstrapping
I4. Earthworm weight	Bootstrapping	Bootstrapping	I8. Litre of pesticides per ha	Bootstrapping	Bootstrapping

[a] These indicators are positive in the sense that a high value of any of these indicators are considered beneficial for the environment, since they contribute to increase biodiversity.
[b] These indicators are negative in the sense that a high value of any of these indicators are considered harmful for the environment, since the use of pesticides can cause water pollution, reduction of biodiversity, etc. The use of some pesticides is more damaging for the environment than others, but the toxicity is not considered in this analysis. We assume that for the environment more pesticides are worse than less.

Figures A-1a (min-max normalising method) and A-1b (normalising method using distance) in the Appendix show the density functions for the 8 environmental impact indicators for GM and conventional crops. In addition, the probability that GM crops perform environmentally better than conventional crops per indicator is calculated in Tables 2 and A-3[15]. Results show that GM crops outperform conventional crops in three indicators related with pesticide use, such as number of sprays, kg of active ingredient and kg of pesticide per ha (i.e. probability higher than 98%), regardless of the normalisation approach. For the rest of indicators GM crops tend to perform better than conventional crops (probability higher than 50%) except for the number of arthropods (i.e. the probability that GM crops have a lower impact than conventional crops on non-target species is negligible) and the indicator litre per ha (i.e. GM crops are more harmful for the environment than conventional).

[14] Two indicators on the number of arthropods were selected in this study (I1 and I3). While I1 measures the absolute abundance of arthropods in a plot I3 measures a relative density of arthropods per number of plants. Since both indicators show different dimensions (and units of measures), they cannot be added together and consequently they were considered as different components of the composite indicator on non-target key species richness.
[15] Table A-1 can be found in the Appendix.

Table 2 shows the mean values of each normalised indicator for both GM and conventional crops. Values close to 1 for a specific indicator imply a high environmental performance of the crop whereas values close to 0 mean low performance of the crop in the indicator. For an indicator on non-target key species richness, e.g. number of birds, GM crops shows a value of 0.478 which is higher than the value for conventional crops (0.446). This means that GM crops are slightly better than conventional crops on bird richness, and consequently more beneficial for the environment. For an indicator on pesticide use, e.g. no. of sprays, GM crops show a higher value (0.925) than conventional crops (0.867), implying that GM crops requires on average less pesticide sprays than conventional crops[16], which is environmental preferable.

Table 2. Indicator results for GM and conventional crops (using the min max method)

Indicators	**GM**		**Conventional**		**Pr (GM>Conv)**
	Mean	*Std. Dev*	*Mean*	*Std. Dev*	
I1. No. of individuals (arthropods)	0.024	0.008	0.024	0.008	0.503
I2. No. of individuals (birds)	0.478	0.066	0.446	0.069	0.648
I3. No. of individuals (arthropods) per 100 plants	0.191	0.051	0.161	0.047	0.682
I4. Earthworm weight (mg/m^2)	0.211	0.054	0.190	0.042	0.611
I5. No. of sprays	0.925	0.013	0.867	0.030	0.984
I6. Kg active ingredient per ha	0.752	0.085	0.330	0.115	0.998
I7. Kg pesticide per ha	0.958	0.019	0.777	0.067	0.996
I8. Litre per ha	0.421	0.230	0.714	0.102	0.130

3.2. Environmental Impact Indicators on non-target key species richness and pesticide use

The next step consists of calculating a composite indicator to measure the environmental impact of both crops on non-target key species richness and pesticide use. Hence, for each indicator there are 286 composite indicators for GM crops (i.e. results obtained for all potential combinations of weights for individual environmental indicators) and 286 composite indicators for conventional crops, which allowed us to compare the difference in environmental impact of both crops as well as calculating the probability that one crop type performs environmentally better than the other (here we calculate the probability that GM crops perform environmentally better than conventional crops). Figure A-2 shows the densities for the composite indicators on non-target key species richness and pesticide use for

[16] The indicators on pesticide use are of type "less is better", but later is transformed in "more is better" indicator. So, 0 is the worst value (maximum number of pesticides) and 1 is the best value (minimum number of pesticides).

both GM and conventional crops. For each normalising approach, results for additive and multiplicative aggregation methods are also shown.

Table 3 shows that GM crops tend to perform environmentally better than conventional crops in both composite indicators, regardless aggregation method used and for the min-max normalisation method. Results for the distance normalisation method can be found in the Appendix (Table A-4). It can be seen that when the individual indicators are aggregated in composite indicators, results tend to be more favourable for GM crops, regardless of the weights given to the individual indicators included in the composite indicator.

Table 3. Non-target key species richness and pesticides use composite indicators for GM and conventional crops (using min-max normalisation and the additive/multiplicative aggregation methods)

Composite indicators	GM		Conventional		Pr (GM>Conv)
	Mean	*Std. Dev*	*Mean*	*Std. Dev*	
Additive approach					
Non-target key species richness CI	0.23	0.09	0.21	0.08	0.68
Pesticide use CI	0.77	0.13	0.67	0.12	0.77
Multiplicative approach					
Non-target key species richness CI	0.17	0.09	0.15	0.08	0.63
Pesticide use CI	0.73	0.12	0.64	0.12	0.73

The additive aggregation method shows slightly higher results for GM crops than the multiplicative approach in both composite indicators. Since the additive approach allows total compensation amongst individual indicators within each composite indicator, this means that GM crops have on average better results for individual indicators included in each composite indicator than conventional crops.

3.3. Aggregated Environmental Impact Indicators

Finally, by aggregating the non-target key species richness and pesticide use composite indicators we obtain 11 environmental impact composite indicators per crop (i.e. GM and conventional) depending on the weights given to each composite indicator.

Figure A-3 in the Appendix shows the densities for the environmental composite indicators per crop for both the min-max normalisation and the additive aggregation methods (results for the distance normalisation method and the multiplicative aggregation approach are quite similar to results showed in Figure A-3).

Table 4. Overall environmental composite indicators for GM and conventional crops for each combination of weights*

Min-max	**GM**		**Conventional**		**Pr (GM>Conv)**	*Distance*	**GM**		**Conventional**		**Pr (GM>Conv)**
	Mean	*Std. Dev*	*Mean*	*Std. Dev*			Mean	Std. Dev	Mean	Std. Dev	
Additive						*Additive*					
C1[17]	0.77	0.13	0.67	0.12	0.77	C1	0.70	0.15	0.61	0.13	0.80
C2	0.72	0.12	0.63	0.11	0.77	C2	0.66	0.13	0.60	0.12	0.80
C3	0.66	0.11	0.58	0.10	0.78	C3	0.61	0.13	0.53	0.10	0.80
C4	0.61	0.10	0.53	0.09	0.78	C4	0.56	0.11	0.59	0.09	0.81
C5	0.55	0.09	0.49	0.08	0.79	C5	0.51	0.10	0.45	0.09	0.81
C6	0.50	0.08	0.44	0.08	0.79	C6	0.47	0.09	0.41	0.08	0.81
C7	0.44	0.08	0.39	0.07	0.79	C7	0.42	0.08	0.37	0.08	0.81
C8	0.39	0.08	0.35	0.07	0.79	C8	0.37	0.08	0.33	0.07	0.80
C9	0.33	0.08	0.30	0.07	0.78	C9	0.32	0.08	0.29	0.08	0.78
C10	0.28	0.08	0.25	0.08	0.75	C10	0.28	0.09	0.25	0.08	0.73
C11	0.23	0.09	0.21	0.09	0.68	C11	0.23	0.10	0.21	0.09	0.66
Multiplicative						*Multiplicative*					
C1	0.73	0.17	0.64	0.14	0.73	C1	0.65	0.18	0.57	0.14	0.72
C2	0.62	0.14	0.54	0.12	0.74	C2	0.56	0.14	0.49	0.12	0.73
C3	0.53	0.12	0.47	0.10	0.74	C3	0.48	0.12	0.42	0.10	0.73
C4	0.45	0.11	0.40	0.10	0.74	C4	0.42	0.11	0.37	0.09	0.73
C5	0.39	0.11	0.35	0.09	0.73	C5	0.37	0.11	0.32	0.09	0.73
C6	0.33	0.11	0.30	0.09	0.72	C6	0.32	0.10	0.28	0.09	0.72
C7	0.29	0.10	0.26	0.09	0.71	C7	0.28	0.10	0.25	0.09	0.71
C8	0.25	0.10	0.23	0.09	0.69	C8	0.24	0.10	0.22	0.09	0.69
C9	0.22	0.10	0.20	0.09	0.67	C9	0.21	0.10	0.20	0.09	0.67
C10	0.19	0.10	0.17	0.09	0.65	C10	0.19	0.10	0.17	0.09	0.65
C11	0.17	0.09	0.15	0.08	0.63	C11	0.17	0.09	0.16	0.09	0.63

* The test of equality of means (non-parametric Kruskal-Wallis test) shows that the average of the composite indicator of GM are statistically different from the mean value of the composite indicator for conventional crops at 95%, for any weighting combination (C1-C11) and aggregation method.

[17] C1 implies that a weight of 1 is given to the composite indicator of pesticide use and a weight of 0 to the composite indicator of non-target key species richness, whereas C11 considers that a weight of 0 is given to the composite indicator of pesticide use and a weight of 1 to the composite indicator of non-target key species richness. Indicators from C1 to C11 consider a decrease of 0.1 of the weight given to the composite indicator given to pesticide use and an increase of 0.1 of the weight given to the composite indicator of non-target key species richness.

Table 4 shows the probability of GM crops performing environmentally better than conventional crops for each combination of weights given to the composite indicators of non-target key species richness and pesticide use. In addition, results show that the probability that GM crops outperform conventional crops from an environmental perspective is always greater than 63%, regardless of the weights given to each indicator (i.e. non-target key species richness and pesticide use) and the normalisation (i.e. min-max or distance) and aggregation (i.e. additive or multiplicative) methods. We can see that the probability diminishes as the weight given to the non-target key species richness is increasing (and consequently the weight given to pesticide use is decreasing). This is a consequence that on average GM crops outperforms their conventional counterparts on pesticide use to a great extent, whereas this is not so evident for non-target key species richness.

Table 5 shows the average probability that GM crops perform environmentally better than conventional crops. In accordance with the results of Table 4, when all the individual environmental indicators are considered GM crops outperform on average conventional crops from an environmental perspective, with a probability of 70% or 78% depending on the aggregation approach.

Table 5. Overall environmental composite indicator for GM and conventional crops

Overall composite indicator	**GM**		**Conventional**		**Pr (GM>Conv)**[a]
	Mean	*Std. Dev*	*Mean*	*Std. Dev*	
Min-max normalisation					
Additive aggregation method	0.50	0.20	0.44	0.17	0.77
Multiplicative aggregation method	0.38	0.21	0.34	0.18	0.70
Distance normalisation					
Additive aggregation method	0.47	0.18	0.41	0.16	0.78
Multiplicative aggregation method	0.35	0.19	0.31	0.16	0.70

[a] The probability is the average probability for all the combinations of weights given to non-target key species richness and pesticide use.

4. Conclusions

The methodology developed in this paper allows researchers to make the most of published data on a particular topic. When there is information available on a particular topic, such as indicators on environmental impacts of GM and conventional crops, these can be collated and analysed allowing researchers to analyse any topic at a broad level. In this paper we collected data on environmental indicators of GM and conventional crops worldwide, allowing us to contribute to the open debate on which crop is less harmful from an environmental perspective. This approach can be applied to other topics such as agricultural sustainability, the efficiency of policy measures, etc.

Building composite indicators aims to establish a ranking of different options (e.g. crops, farm-types, policies, etc.) in order to elucidate which of those alternatives is the most adequate (e.g. the most sustainable crop or farm-type). Following the new approach developed in this paper, not only a ranking of alternatives can be obtained but the probability that some alternative outperforms the other(s). This information can be used to a) know up to what degree an option is better than another (i.e. knowing the level of certainty) and b) under what circumstances (i.e. what weighting combination(s)) one option is better than another. In the case of a ranking of options based on single values (e.g. average values, values calculated for a particular crop or farm, etc.) decisions are made as long as values differ and these decisions may be taken with little knowledge on the level of certainty on that decision. Hence, by using distributions instead of values overlapping amongst indicators is allowed (i.e. distributions may overlap) and not only a ranking of alternatives can be obtained, based on the average values of the distribution, but the probability that one alternative is better than another can be obtained. This can be then used to rank options differently than under a single value approach. For instance, let us have two composite indicators for GM and conventional environmental performance with values 0.30 for GM and 0.27 for conventional but probability of GM performing better than conventional of 51% (e.g. assuming a positive skewed distribution for GM and normal distribution with small standard deviation). Under a single value we would say that GM performs better than conventional. Under our approach there would be little evidence that one performs better than the other and we would consider them equal.

One of the main drawbacks of composite indicators is related with the weights given to each indicator. Our approach makes no assumptions concerning the importance of each indicator within the composite indicator. In fact, a set of weights that includes all the options is considered (i.e. from a weight zero assigned to indicators related with non-target key species richness to a weight equal to one, and vice versa for the pesticide use). This approach is useful in situations where we are uncertain about what specific weights should be given to each indicator used. In addition, we conducted sensitivity analysis by applying two aggregation methodologies. Regardless of the methodology used, and the weights given to indicators, results show that GM crops tend to cause lower negative environmental impacts than conventional crops when a number of indicators related with and pesticide use are considered. However, it is worth mentioning that the outperformance of GM crops from an environmental perspective is lower when the weight of pesticide use is lower and consequently the weight of non-target key species richness is higher. The variability in the value of the environmental composite indicator is expected since GM crops outperform conventional crops in most of the pesticide use indicators, whereas for the indicators related with non-target key species richness GM and conventional crops show relatively similar results. One of the limitations of the analysis of environmental impacts of both GM and conventional crops is related with the indicators on pesticide use. These indicators are based on the quantity of pesticides and the number of sprays, so the analysis does not take into account the toxicity of each type of pesticide (e.g. selective vs. broad spectrum pesticides) in the environment. An extension of this work based on the toxicity of pesticide use by using EIQ, would be valuable as further research.

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6. Appendix

Table A1- Dataset of non-target species richness for GM and conventional crops

Scientific Reference	Year	Country	Non- Target Species	Trait/ Crop	Mean GM	Mean Conv.	No. observations	Units
Rauschen et al. (2008)	2003	Germany	Auchenorrhyncha (arthropods)	Bt maize	116.9	116.9	192	No. of individuals
	2004	Germany	Auchenorrhyncha (arthropods)	Bt maize	1.5	1.7	29	No. of individuals
	2005	Germany	Auchenorrhyncha (arthropods)	Bt maize	2	2.9	45	No. of individuals
	2006	Germany	Auchenorrhyncha (arthropods)	Bt maize	2.3	2.1	42	No. of individuals
	2007	Germany	Auchenorrhyncha (arthropods)	Bt maize	0.1	0	2	No. of individuals
Rauschen et al. (2009)	2005	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	16.63	17.75	8	No. of individuals
	2005	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	3.25	1.38	8	No. of individuals
	2006	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	31.13	20.88	8	No. of individuals
	2006	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	7.38	1.5	8	No. of individuals
	2006	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	1.13	1	8	No. of individuals
	2007	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	7.38	6.63	8	No. of individuals
	2007	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	1.5	0.63	8	No. of individuals
	2007	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	0.38	0.5	8	No. of individuals
	2006	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	0.13	0.25	8	No. of individuals
	2006	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	3.38	10.75	8	No. of individuals
	2006	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	4.75	3.75	8	No. of individuals
Rauschen et al. (2009)	2007	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	0.38	0.5	8	No. of individuals
	2007	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	5.63	3.25	8	No. of individuals
	2007	Germany	Trygonotylus caelestialium (arthropods)	Bt maize	0.38	1.25	8	No. of individuals
Deward et al. (2003)	1999	UK	Carabids+staogtkubuds+spiders (arthropods)	HT sugar beet	2536	2459	4	No. of individuals
	1999	UK	Carabids+staogtkubuds+spiders (arthropods)	HT sugar beet	2525	2493	4	No. of individuals
	2000	UK	Carabids+staogtkubuds+spiders (arthropods)	HT sugar beet	3690	3403	4	No. of individuals

Scientific Reference	Year	Country	Non- Target Species	Trait/ Crop	Mean GM	Mean Conv.	No. observations	Units
Deward et al. (2003)	2000	UK	Carabids+staogtkubuds+spiders (arthropods)	HT sugar beet	796	894	4	No. of individuals
Bai et al. (2012)	2007	China	Arthropods	Bt rice	1028.6	972.3	2	No. of individuals
	2008	China	Arthropods	Bt rice	4503	4883.7	2	No. of individuals
	2007	China	Arthropods	Bt rice	1169.7	972.3	2	No. of individuals
	2008	China	Arthropods	Bt rice	5084	4883.7	2	No. of individuals
Haughton et al. (2003)	2002	UK	Heteroptera (arthropods)	HT beet	2.8	5.18	48	No. of individuals
	2002	UK	Heteroptera (arthropods)	HT maize	3.14	3.53	42	No. of individuals
	2002	UK	Heteroptera (arthropods)	HT oilseed	3.82	5.05	41	No. of individuals
	2002	UK	Collembola (arthropods)	HT beet	66.75	59	64	No. of individuals
	2002	UK	Collembola (arthropods)	HT maize	119.01	75.81	57	No. of individuals
	2002	UK	Collembola (arthropods)	HT oilseed	125.36	118.3	64	No. of individuals
	2002	UK	Araneae (arthropods)	HT beet	8.73	8.68	64	No. of individuals
	2002	UK	Araneae (arthropods)	HT maize	6.11	6.5	55	No. of individuals
Haughton et al. (2003)	2002	UK	Araneae (arthropods)	HT oilseed	6.93	8.5	64	No. of individuals
	2002	UK	Bees (arthropods)	HT beet	1.55	3.62	20	No. of individuals
	2002	UK	Bees (arthropods)	HT maize	2.09	1.14	15	No. of individuals
	2002	UK	Bees (arthropods)	HT oilseed	36.52	44.28	62	No. of individuals
	2002	UK	Butterflies (arthropods)	HT beet	3.88	5.65	58	No. of individuals
	2002	UK	Butterflies (arthropods)	HT maize	3.74	3.28	35	No. of individuals
	2002	UK	Butterflies (arthropods)	HT oilseed	12.41	16.17	65	No. of individuals
	2002	UK	Carabidae (arthropods)	HT beet	3.84	4.26	57	No. of individuals
	2002	UK	Carabidae (arthropods)	HT maize	4.13	3.28	43	No. of individuals
	2002	UK	Carabidae (arthropods)	HT oilseed	3.55	3.5	54	No. of individuals
Balog et al. (2010)	2001	Hungary	Rove beetles (arthropods)	Bt maize	2	2	12	No. of individuals
	2001	Hungary	Rove beetles (arthropods)	Bt maize	6	4	12	No. of individuals
	2001	Hungary	Rove beetles (arthropods)	Bt maize	1	1	12	No. of individuals
	2001	Hungary	Rove beetles (arthropods)	Bt maize	24	12	12	No. of individuals

Scientific Reference	Year	Country	Non- Target Species	Trait/ Crop	Mean GM	Mean Conv.	No. observations	Units
Balog et al. (2010)	2001	Hungary	Rove beetles (arthropods)	Bt maize	1	11	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	21	12	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	7	14	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	4	5	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	7	7	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	7	4	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	3	2	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	1	6	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	1	4	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	2	7	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	1	4	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	17	29	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	14	6	12	No. of individuals
	2002	Hungary	Rove beetles (arthropods)	Bt maize	2	1	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	25	3	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	13	11	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	1	1	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	12	8	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	7	7	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	1	7	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	6	3	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	1	3	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	456	646	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	5	5	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	13	18	12	No. of individuals
	2003	Hungary	Rove beetles (arthropods)	Bt maize	6	4	12	No. of individuals
Chamberlain et al. (2007)	2001	UK	Red-legged partridge (Birds)	HT beet	30	12.52	8	No. of individuals
	2001	UK	Skylark (Birds)	HT beet	49.995	47.52	11	No. of individuals

Scientific Reference	Year	Country	Non- Target Species	Trait/ Crop	Mean GM	Mean Conv.	No. observations	Units
Chamberlain et al. (2007)	2001	UK	Blackbird (Birds)	HT beet	24.99	22.5	6	No. of individuals
	2001	UK	Thrushes (Birds)	HT beet	27.51	22.5	6	No. of individuals
	2001	UK	Granivores (Birds)	HT beet	64.2	52.5	15	No. of individuals
	2001	UK	Red-legged partridge (Birds)	HT beet	61.11	27.23	14	No. of individuals
	2001	UK	Skylark (Birds)	HT beet	42.49	53.76	14	No. of individuals
	2001	UK	Dunnock (Birds)	HT beet	5	11.25	5	No. of individuals
	2001	UK	Blackbird (Birds)	HT beet	33.825	30.91	11	No. of individuals
	2001	UK	Yellowhammer (Birds)	HT beet	2.925	12.675	5	No. of individuals
	2001	UK	Trushes (Birds)	HT beet	35.475	35.09	11	No. of individuals
	2001	UK	Granivores (Birds)	HT beet	47.88	81.45	18	No. of individuals
	2001	UK	Granivores (Birds)	HT maize	5.82	31.68	6	No. of individuals
	2001	UK	Granivores (Birds)	HT oilseed	43.68	31.83	6	No. of individuals
Li et al. (2011)	2007	China	Hemiptera (arthropods)	Bt cotton	3.2	3.1	3	No. indiv /100 plants
	2007	China	Hemiptera (arthropods)	Bt cotton	3.3	3.4	3	No. indiv /100 plants
	2008	China	Hemiptera (arthropods)	Bt cotton	9.6	9.8	3	No. indiv /100 plants
	2008	China	Hemiptera (arthropods)	Bt cotton	8.5	7.1	3	No. indiv /100 plants
	2009	China	Hemiptera (arthropods)	Bt cotton	3.4	2.6	3	No. indiv /100 plants
	2009	China	Hemiptera (arthropods)	Bt cotton	2.1	2.8	3	No. indiv /100 plants
	2010	China	Hemiptera (arthropods)	Bt cotton	2.5	2.3	3	No. indiv /100 plants
	2010	China	Hemiptera (arthropods)	Bt cotton	2.5	2.5	3	No. indiv /100 plants
Lu et al. (2012)	2001	China	Ladybirds+lacewings+spiders (arthropods)	Bt cotton	19.63	18.5	360	No. indiv /100 plants
	2002	China	Ladybirds+lacewings+spiders (arthropods)	Bt cotton	16.04	17.06	360	No. indiv /100 plants
	2003	China	Ladybirds+lacewings+spiders (arthropods)	Bt cotton	61.13	63.93	360	No. indiv /100 plants
	2004	China	Ladybirds+lacewings+spiders (arthropods)	Bt cotton	27.93	28.41	360	No. indiv /100 plants
	2005	China	Ladybirds+lacewings+spiders (arthropods)	Bt cotton	16.07	16.65	360	No. indiv /100 plants
	2006	China	Ladybirds+lacewings+spiders (arthropods)	Bt cotton	24.91	24.93	360	No. indiv /100 plants
	2007	China	Ladybirds+lacewings+spiders (arthropods)	Bt cotton	23.67	22.35	360	No. indiv /100 plants

Scientific Reference	Year	Country	Non- Target Species	Trait/ Crop	Mean GM	Mean Conv.	No. observations	Units
Lu et al. (2012)	2008	China	Ladybirds+lacewings+spiders (arthropods)	Bt cotton	35.13	36.44	360	No. indiv /100 plants
	2009	China	Ladybirds+lacewings+spiders (arthropods)	Bt cotton	20.37	19.03	360	No. indiv /100 plants
	2010	China	Ladybirds+lacewings+spiders (arthropods)	Bt cotton	39.89	42.7	360	No. indiv /100 plants
	2011	China	Ladybirds+lacewings+spiders (arthropods)	Bt cotton	14.57	15.3	360	No. indiv /100 plants
	2001	China	Aphids (arthropods)	Bt cotton	152.81	90.67	240	No. indiv /100 plants
	2002	China	Aphids (arthropods)	Bt cotton	1961.49	821.41	240	No. indiv /100 plants
	2003	China	Aphids (arthropods)	Bt cotton	1675.47	812.32	240	No. indiv /100 plants
	2004	China	Aphids (arthropods)	Bt cotton	852	780.85	240	No. indiv /100 plants
	2005	China	Aphids (arthropods)	Bt cotton	1344.12	1292.85	240	No. indiv /100 plants
	2006	China	Aphids (arthropods)	Bt cotton	1804.89	1665.39	240	No. indiv /100 plants
	2007	China	Aphids (arthropods)	Bt cotton	443.38	386.11	240	No. indiv /100 plants
	2008	China	Aphids (arthropods)	Bt cotton	810.39	732.76	240	No. indiv /100 plants
	2009	China	Aphids (arthropods)	Bt cotton	3214.58	3291.07	240	No. of individuals /100
	2010	China	Aphids (arthropods)	Bt cotton	1550.33	1427.44	240	No. of individuals /100
	2011	China	Aphids (arthropods)	Bt cotton	3041.88	3067.78	240	No. of individuals /100
Zeilinger et al. (2010)	2005	USA	Earthworms	Bt maize	0.51	0	24	mg/m^2
	2005	USA	Earthworms	Bt maize	1.09	1.08	24	mg/m^2
	2005	USA	Earthworms	Bt maize	0	0.5	24	mg/m^2
	2005	USA	Earthworms	Bt maize	1.75	1.08	24	mg/m^2
	2005	USA	Earthworms	Bt maize	0.5	0	24	mg/m^2
	2005	USA	Earthworms	Bt maize	0.5	0.5	24	mg/m^2
	2005	USA	Earthworms	Bt maize	38.1	27.1	24	mg/m^2
	2005	USA	Earthworms	Bt maize	21.9	45.9	24	mg/m^2
	2005	USA	Earthworms	Bt maize	24.6	90.4	24	mg/m^2
	2005	USA	Earthworms	Bt maize	112	31.9	24	mg/m^2
	2005	USA	Earthworms	Bt maize	107	71.1	24	mg/m^2
	2005	USA	Earthworms	Bt maize	124	97.8	24	mg/m^2
	2005	USA	Earthworms	Bt maize	0	1.1	24	mg/m^2

Scientific Reference	Year	Country	Non- Target Species	Trait/ Crop	Mean GM	Mean Conv.	No. observations	Units
Zeilinger et al. (2010)	2005	USA	Earthworms	Bt maize	0	0.51	24	mg/m^2
	2005	USA	Earthworms	Bt maize	0	1.77	24	mg/m^2
	2005	USA	Earthworms	Bt maize	3.48	1.1	24	mg/m^2
	2005	USA	Earthworms	Bt maize	1.09	0.51	24	mg/m^2
	2005	USA	Earthworms	Bt maize	0.51	1.77	24	mg/m^2
	2005	USA	Earthworms	Bt maize	1.42	1.42	24	mg/m^2
	2005	USA	Earthworms	Bt maize	0.25	0.65	24	mg/m^2
	2005	USA	Earthworms	Bt maize	1.1	1.25	24	mg/m^2
	2005	USA	Earthworms	Bt maize	40.6	22.7	24	mg/m^2
	2005	USA	Earthworms	Bt maize	11	19.9	24	mg/m^2
	2005	USA	Earthworms	Bt maize	7.05	15.2	24	mg/m^2
	2006	USA	Earthworms	Bt maize	38.1	34.6	24	mg/m^2
	2006	USA	Earthworms	Bt maize	22.6	26.3	24	mg/m^2
	2006	USA	Earthworms	Bt maize	47.2	74.1	24	mg/m^2
	2006	USA	Earthworms	Bt maize	70.2	73.3	24	mg/m^2
	2006	USA	Earthworms	Bt maize	32.6	29.9	24	mg/m^2
	2006	USA	Earthworms	Bt maize	87.2	41.9	24	mg/m^2

Table A2- Dataset of pesticide use for GM and conventional crops

Scientific Reference	Year	Country	Trait/ Crop	Mean GM	Mean Conv.	No. observations	Units
Sisterson et al. (2007)	2004	USA	Bt cotton	0.23	1.63	8	No. of sprays
	2004	USA	Bt cotton	1.08	2.63	8	No. of sprays
Qaim and de Janvry (2005)	2000	Argentina	Bt maize	2.14	3.74	29	No. of sprays
	2001	Argentina	Bt maize	2.84	3.7	73	No. of sprays
Cattaneo et al. (2006)	2002	USA	Bt cotton	3.4	6.6	21	No. of sprays
	2003	USA	Bt cotton	5.1	6.8	21	No. of sprays
	2002	USA	Stacked cotton	2.8	6.6	20	No. of sprays
	2003	USA	Stacked cotton	4.7	6.8	20	No. of sprays
Huang et al. (2005)	2003	China	GM rice	0.5	3.7	123	No. of sprays
Qaim and Traxler (2005)	2001	Argentina	HT soybean	2.3	1.97	59	No. of sprays
Qaim and Zilberman (2003)	2001	India	Bt cotton	4.19	7.19	157	No. of sprays
Huang et al. (2002)	1999	China	Bt cotton	6.6	19.8	45	No. of sprays
Hofs et al. (2006)	2003	South Africa	Bt cotton	2.3	2.9	10	No. of sprays
	2004	South Africa	Bt cotton	3.5	6.7	10	No. of sprays
Qaim et al. (2006)	2003	India	Bt cotton	4.18	6.79	133	No. of sprays
Champion et al. (2003)	2001	UK	HT sugar beet	1.65	3.65	20	No. of sprays
	2001	UK	HT maize	1.18	1.32	29	No. of sprays
	2001	UK	HT oilseed rape	1.69	1.91	33	No. of sprays
Zhao et al. (2011)	2005	China	Bt cotton	23	17	69	No. of sprays
	2006	China	Bt cotton	22	13	63	No. of sprays
	2007	China	Bt cotton	17	12	90	No. of sprays
	2008	China	Bt cotton	16	11	97	No. of sprays
Bambawale et al. (2004)	2003	India	Bt cotton	3	9	7	No. of sprays
Bennet et al. (2004b)	2002	South Africa	Bt cotton	3.8	11.2	8	No. of sprays
Pray et al. (2002)	2000	China	Bt cotton	20.5	48.5	122	No. of sprays
	2001	China	Bt cotton	32.9	87.5	176	No. of sprays

Scientific Reference	Year	Country	Trait/ Crop	Mean GM	Mean Conv.	No. observations	Units
Traxler et al. (2003)	1997	Mexico	Bt cotton	2.98	5.24	59	No. of sprays
	1998	Mexico	Bt cotton	1.55	4.6	87	No. of sprays
Fitt (2003)	1997	Australia	Bt cotton	5	10.3	210	No. of sprays
	1998	Australia	Bt cotton	6	10.2	179	No. of sprays
	1999	Australia	Bt cotton	8.7	14	110	No. of sprays
	2000	Australia	Bt cotton	6.2	10.3	149	No. of sprays
	2001	Australia	Bt cotton	4.6	9.9	142	No. of sprays
	2002	Australia	Bt cotton	3.1	8.6	229	No. of sprays
Gomez-barbero et al. (2008)	2004	Spain	Bt maize	1.9	6.4	42	No. of sprays
	2004	Spain	Bt maize	0.68	1.97	52	No. of sprays
	2004	Spain	Bt maize	4.16	9.61	71	No. of sprays
Pemsl et al. (2004)	2003	India	Bt cotton	2	3.7	11	No. of sprays
	2004	India	Bt cotton	2.3	2.8	66	No. of sprays
Krishna and Qaim (2012)	2002-2004	India	Bt cotton	4.41	7	298	No. of sprays
	2006-2008	India	Bt cotton	3.47	3.47	62	No. of sprays
Stone (2011)	2003-2007	India	Bt cotton	5.1	11.9	59	No. of sprays
	2003-2007	India	Bt cotton	4	6.9	16	No. of sprays
	2003-2007	India	Bt cotton	3.9	7.3	30	No. of sprays
	2003-2007	India	Bt cotton	5.5	10.7	26	No. of sprays
Luttrell and Jackson (2012)	2000-07	USA	Bt cotton	3.85	4.97	41	No. of sprays
Kouser and Qaim (2013)	2005-2008	Pakistan	Bt cotton	1.52	2.22	385	No. of sprays
Qaim and de Janvry (2005)	2000	Argentina	Bt maize	0.64	1.15	29	Kg of active ingredient/ ha
	2001	Argentina	Bt maize	0.78	1.08	73	Kg of active ingredient/ ha
Morse et al. (2006)	1999	South Africa	Bt cotton	0.49	1.05	87	Kg of active ingredient/ ha
	2000	South Africa	Bt cotton	0.95	1.58	112	Kg of active ingredient/ ha
	2001	South Africa	Bt cotton	0.75	1.99	245	Kg of active ingredient/ ha
Qaim and Zilberman (2003)	2001	India	Bt cotton	0.48	1.55	157	Kg of active ingredient/ ha
Krishna and Qaim (2012)	2002-2004	India	Bt cotton	1.55	2.46	298	Kg of active ingredient/ ha
	2006-2008	India	Bt cotton	1.24	1.19	62	Kg of active ingredient/ ha
Huang et al. (2005)	2003	China	GM rice	2	21.2	123	Kg of pesticide/ ha

Scientific Reference	Year	Country	Trait/ Crop	Mean GM	Mean Conv.	No. observations	Units
Wossink and Denaux (2006)	2000	USA	HT cotton	12.35	15.69	44	Kg of pesticide/ ha
	2001	USA	Stacked cotton	9.79	15.69	44	Kg of pesticide/ ha
Nelson and Bullock (2003)	1997	USA	HT soybean	3.91	17.49	500	Kg of pesticide/ ha
Qaim and Zilberman (2003)	2001	India	Bt cotton	1.74	5.56	157	Kg of pesticide/ ha
Huang et al. (2005)	1999	China	Bt cotton	11.8	60.7	45	Kg of pesticide/ ha
Qaim et al. (2006)	2003	India	Bt cotton	5.12	10.30	133	Kg of pesticide/ ha
Kouser and Qaim (2013)	2005-2008	Pakistan	Bt cotton	3.16	8.74	385	Kg of pesticide/ ha
Hofs et al. (2006)	2003	South Africa	Bt cotton	2.14	1.41	10	Litre/ ha
	2004	South Africa	Bt cotton	2.99	3.47	10	Litre/ ha
Shankar et al. (2008)	2000	South Africa	Bt cotton	1.6	2.4	33	Litre/ ha
Qaim and Traxler (2005)	2001	Argentina	HT soybean	0.07	0.42	59	Litre/ ha
	2002	Argentina	HT soybean	0	0.68	59	Litre/ ha
	2003	Argentina	HT soybean	5.5	1.58	59	Litre/ ha

Figure A-1a. Density plots for individual environmental impact indicators using min-max normalising method for GM and conventional crops

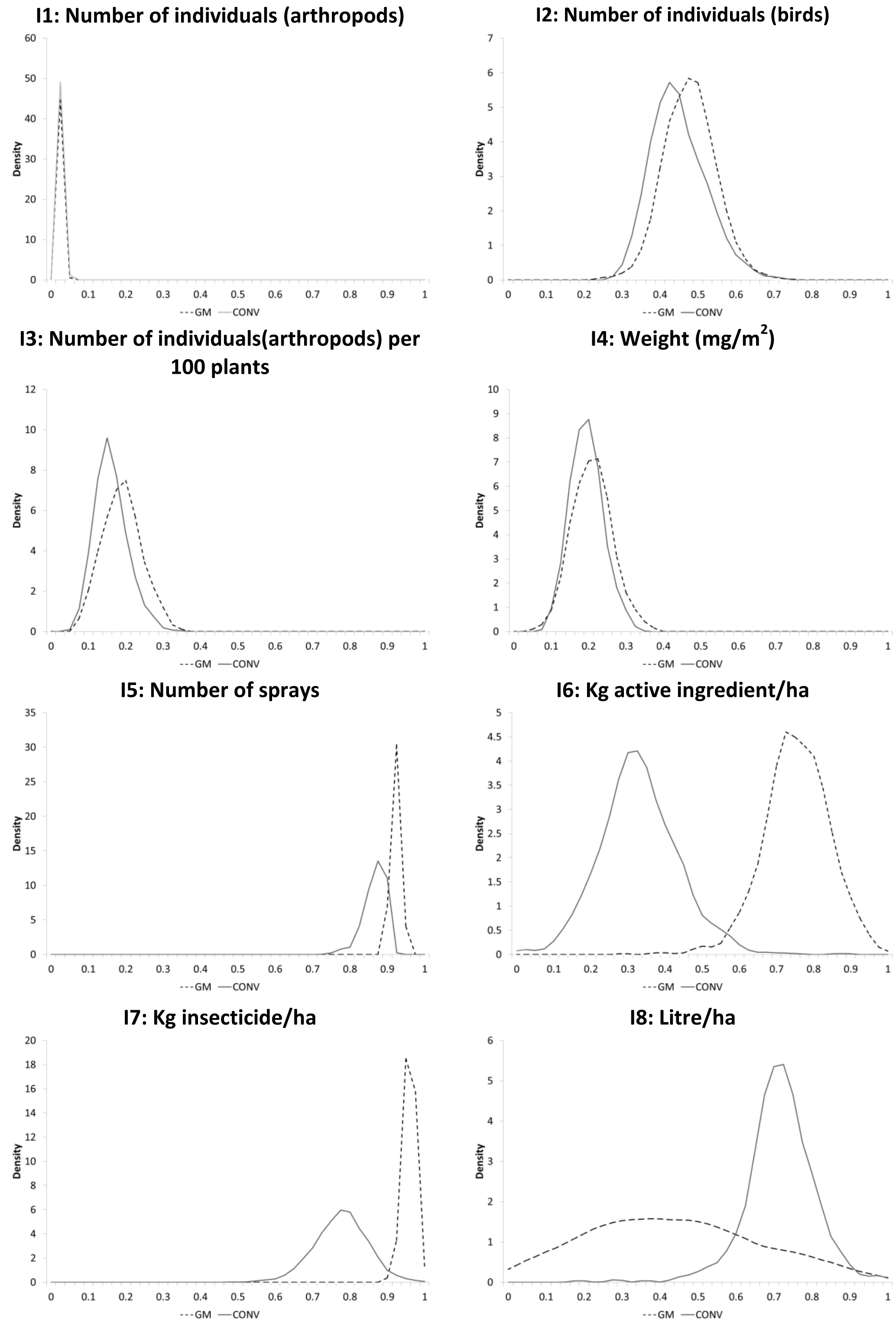


Figure A-1b. Density plots for environmental impact indicators using distance normalising method for GM and conventional crops

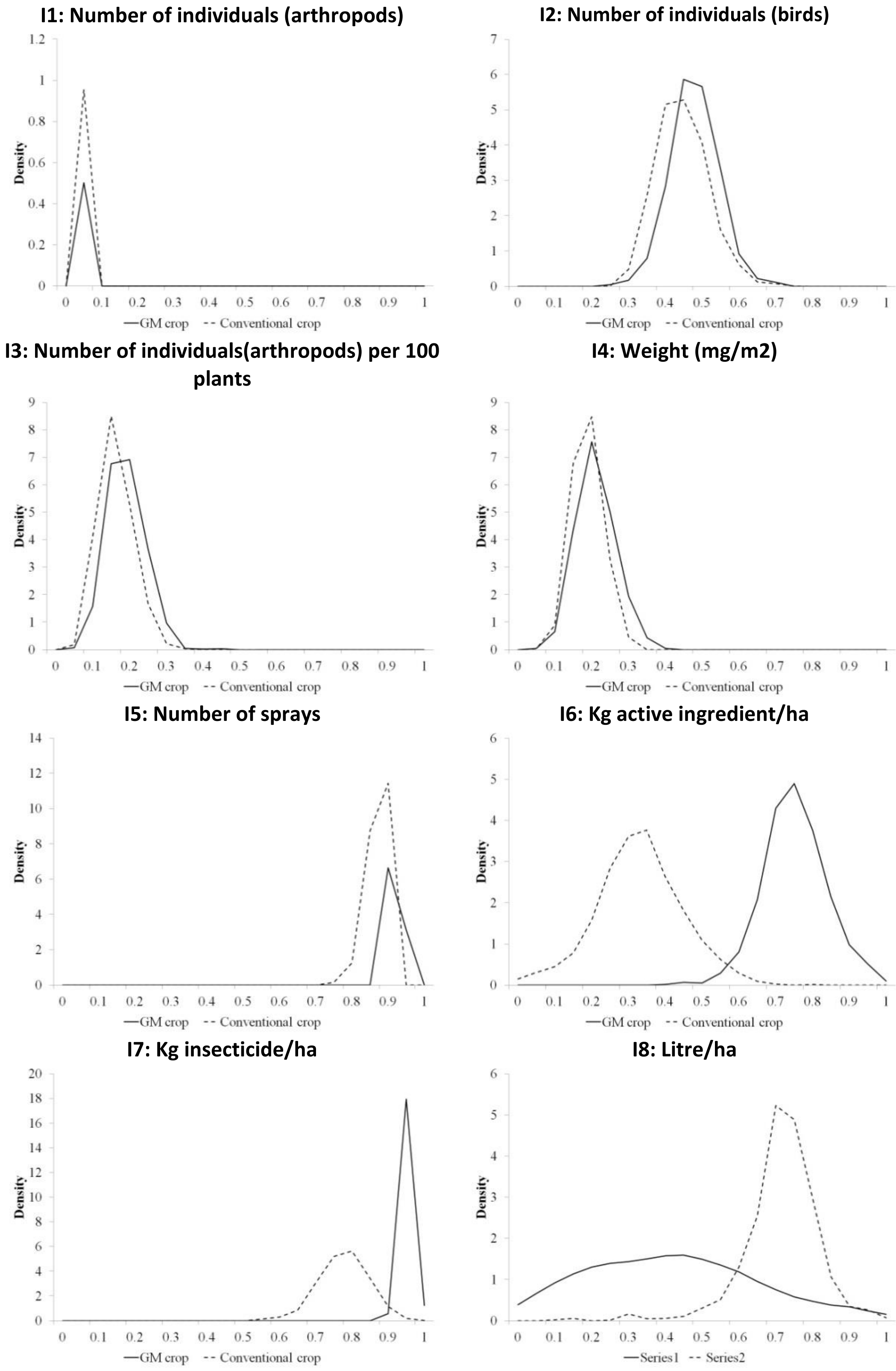


Table A-3. Indicator results for GM and conventional crops (distance method)

	GM		**Conventional**		**Pr (GM>Conv)**
	Mean	*Std. Dev*	*Mean*	*Std. Dev*	
I1. Number of individuals (arthropods)	0.024	0.008	0.024	0.008	0.504
I2. Number of individuals (birds)	0.495	0.062	0.466	0.067	0.622
I3. Number of individuals (arthropods) per 100 plants	0.191	0.051	0.162	0.045	0.663
I4. Earthworm weight (mg/m^2)	0.209	0.053	0.193	0.045	0.589
I5. Number of sprays	0.922	0.014	0.863	0.031	0.986
I6. Kg active ingredient per ha	0.609	0.075	0.266	0.089	0.996
I7. Kg insecticide per ha	0.933	0.017	0.757	0.069	0.991
I8. Litre per ha	0.337	0.190	0.541	0.072	0.148

Figure A-2. Density plots for the average composite indicators using the min-max normalising method and additive and multiplicative aggregation methods for GM and conventional crops

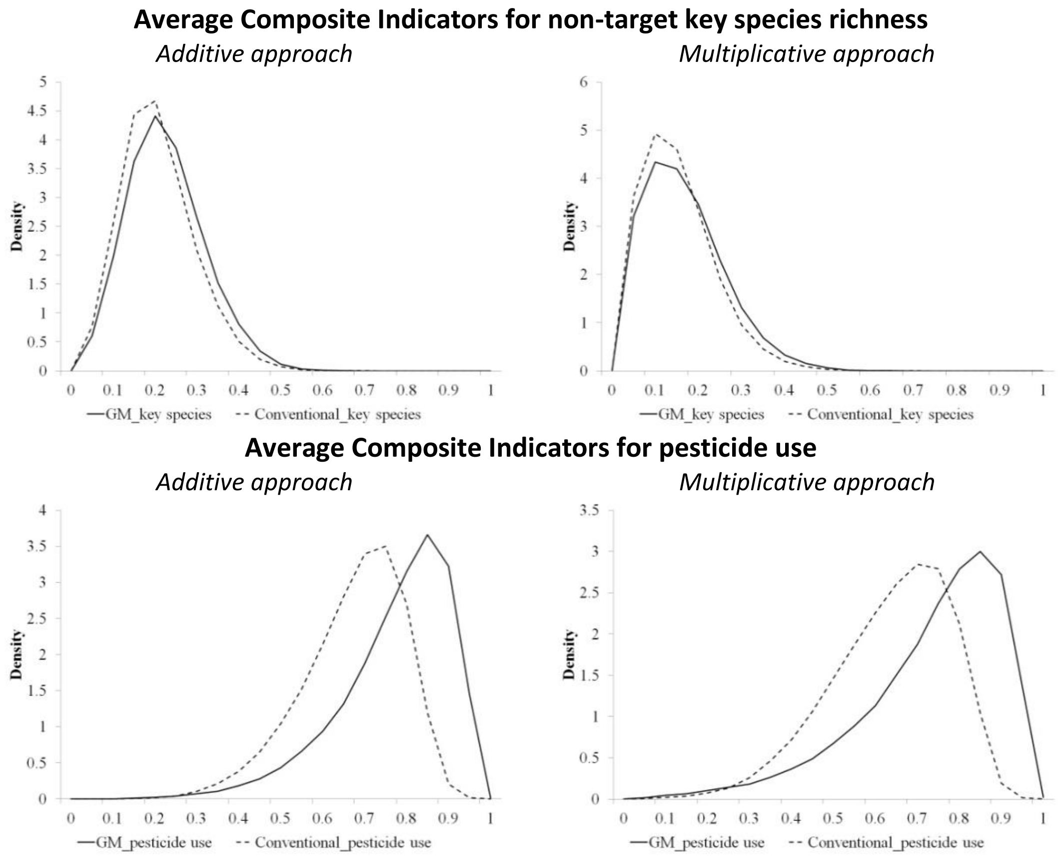
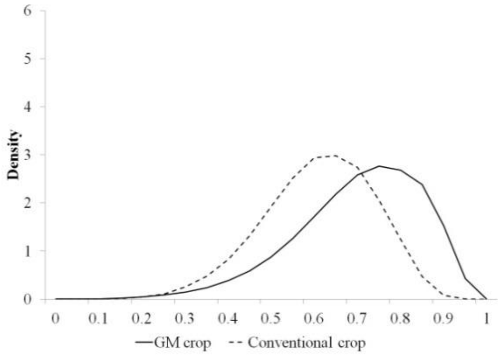


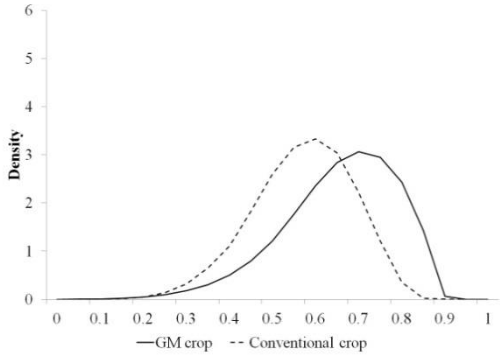
Table A-4. Non-target key species richness and pesticides composite indicators results for GM and conventional crops (using distance and the additive/multiplicative methods)

	GM		Conventional		Pr (GM>Conv)
	Mean	***Std. Dev***	***Mean***	***Std. Dev***	
Addition					
Non-target key species richness CI	0.23	0.10	0.21	0.09	0.66
Pesticide use CI	0.70	0.15	0.61	0.13	0.80
Multiplicative					
Non-target key species richness CI	0.17	0.09	0.16	0.09	0.63
Pesticide use CI	0.65	0.18	0.57	0.14	0.72

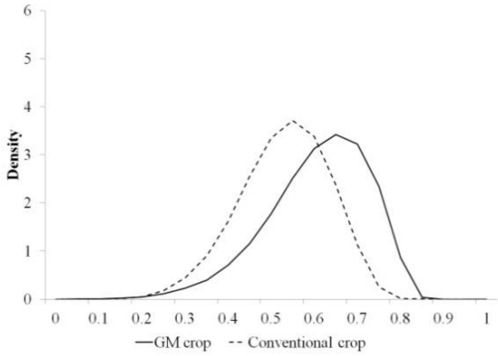
Figure A-3. Density plots for the overall environmental composite indicator using the min-max normalising method and the additive aggregation methods (I)

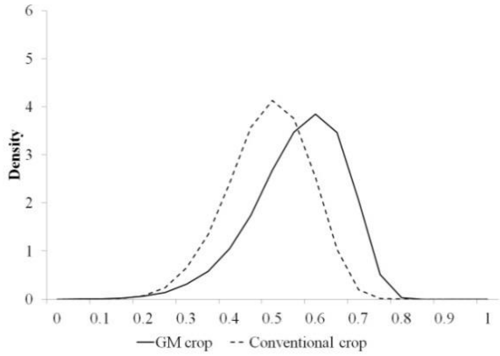
CI 1	**CI 2**
Weight to non-target species =0	Weight to non-target species =0.1
Weight to pesticide use =1	Weight to pesticide use =0.9



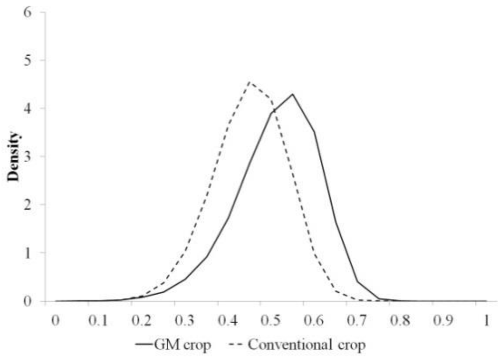


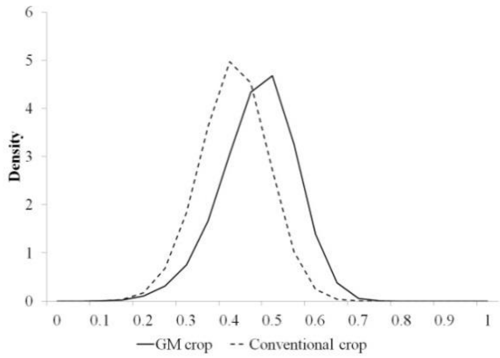
CI 3	**CI 4**
Weight to non-target species =0.2	Weight to non-target species =0.3
Weight to pesticide use =0.8	Weight to pesticide use =0.7





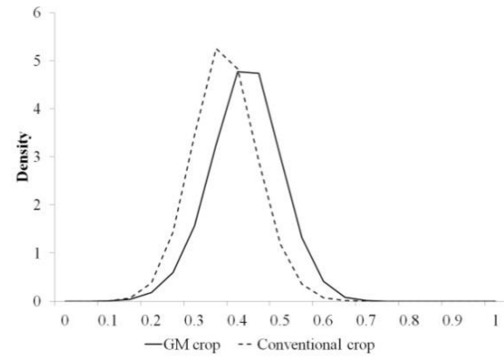
CI 5	**CI 6**
Weight to non-target species =0.4	Weight to non-target species =0.5
Weight to pesticide use =0.6	Weight to pesticide use =0.5

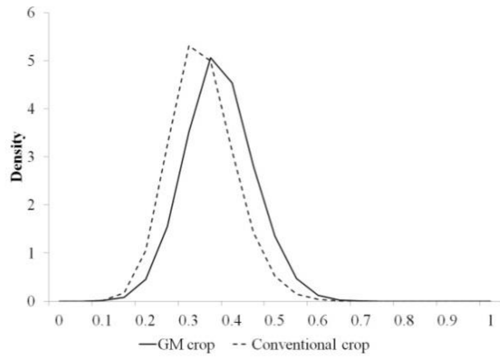




CI7	**CI 8**
Weight to non-target species =0.6	Weight to non-target species =0.7
Weight to pesticide use =0.4	Weight to pesticide use =0.3

Figure A-3. Density plots for the overall environmental composite indicator using the min-max normalising method and the additive aggregation methods (II)





CI 9

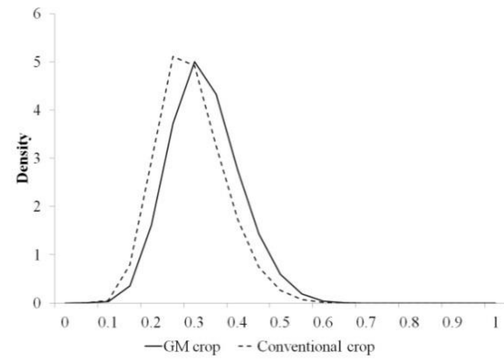
Weight to non-target species =0.8

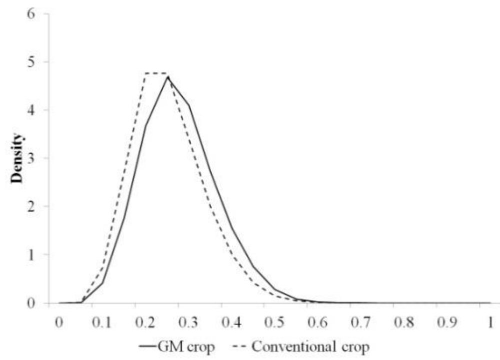
Weight to pesticide use =0.2

CI 10

Weight to non-target species =0.9

Weight to pesticide use =0.1





CI11

Weight to non-target species =1

Weight to pesticide use =0