Global Effect Index: A New Approach to Analyzing Allelopathy Survey Data

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Global Effect Index: A New Approach to Analyzing Allelopathy Survey Data

Jose Pedro N. Ribeiro*

The analysis of allelopathic bioassay data commonly encounters two problems: one is the small number of biological replicates and the other is that the parameters used to infer allelopathic effects such as percentage and average time of seed germination are analyzed individually, and consequently, information on the global effects resulting from the cumulative effects of the tested agent (e.g., leaves extract) may be missed. Therefore, we propose an index to analyze several parameters altogether so as to have a better view of the global influence of a donor plant on a receptor, whose interference is more likely to be detected. The global effect index can help to detect allelopathic interferences of one plant on another, allowing for a more accurate interpretation of the data in the actual biological setting.
Nomenclature: Data analysis, *n* value, methodology, statistic, weed control.

Experimental designs used to test allelopathic effects of plant extracts commonly have two inherent problems. The first is the small number of biological replicates *n*, usually five or less (Gatti et al. 2008; Kato-Noguchi et al. 2009; Ribeiro et al. 2009; Yang et al. 2007), that substantially decreases the degrees of freedom and therefore the power of the statistical tests. The second is that the parameters used to infer allelopathic effects (PIAEs), such as percentage and average time of seed germination, size, or biomass of the plant/seedling and so forth, are analyzed individually. Thus, the global effects resulting from the cumulative effect of each PIAE may be underestimated or completely ignored.

Small differences in several PIAEs, such as a decrease in seed germination and an increase in average germination time, and a decrease in seedling size, may pass undetected when analyzed separately (in many cases because of small *n*). Nevertheless, the PIAEs reflect only the visible effects of the allelochemical on the plant metabolism (Chiapusio et al. 1999), and the cumulative effect of small differences in several PIAEs might result in great global effects.

One possible alternative is to increase the number of biological replicates (*n*). However, that may not be feasible if a great number of treatments is required (e.g., several extract concentrations) or little biological material is available (e.g., final stages of extract fractioning). On the other hand, analyzing PIAEs altogether may allow the evaluation of the global effect of one plant on another. Combining descriptors (i.e., PIAEs) is often used in the analysis of biological data (Legendre and Legendre 1998). This coding technique is a useful data-reduction tool, as it combines scores arising from different variables in one single value (Babbie 1973). Furthermore, it is unrealistic to expect that isolated PIAEs could be used to explain allelopathy, and this is one of the reasons why in many cases laboratory bioassays fail to predict responses in the field (Inderjit and Weston 2000). However, analyzing all PIAEs together as they occur in nature (i.e., one given allelochemical or a mixture in one extract may affect different processes and these alterations may have an additive impact resulting in reduced growth or survival of the receiving plant) could lead to a more accurate analysis of what happens in the actual biological. Hence, the objective of this work was to develop an index to analyze several PIAEs together, and so determine the global influence of a donor plant on a receptor.

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Determination of the Mann-Whitney Test Efficiency for Allelopathy Survey Data

There is an extensive debate on which statistical approach would be best to analyze data from allelopathic assays. Different authors use different procedures that include data manipulation, and parametric and nonparametric tests (Djurdjecvic et al. 2007; Santana and Ranal 2004). Despite all the discussion on the best approach, the index described herein was developed and analyzed by the nonparametric Mann-Whitney test. This test does not make assumptions about the distribution (e.g., normality) and sample size (Zar 1999). Thus, it is certainly not inaccurate.

To test the efficacy of the Mann-Whitney test in detecting differences among groups, a group of five numbers ($n = 5$) that ranged from 50 to 100 (intended to represent the control group germination percentages in an allelopathic assay) was randomly selected and called "control." Then another group of five numbers, ranging from 0.9 to 1, was randomly selected, and called "multipliers." After that, to generate groups with clear differences among them, a new group was generated by multiplying the control values by the different multipliers (Table 1). As the multiplier group average is 0.95, the treatment group is about 5% smaller than the control group.

The procedure was repeated by using groups of multipliers ranging from 0.8 to 0.9, 0.7 to 0.8, 0.6 to 0.7, 0.5 to 0.6, 0.4 to 0.5, 0.3 to 0.4, 0.2 to 0.3, 0.1 to 0.2, and 0 to 0.1, so that the differences between the control group (that always ranged from 50 to 100) and the treatment group became respectively 15, 25, 35, 45, 55, 65, 75, 85, and 95%.

Following that, the control and all the treatment groups were compared by using the Mann-Whitney test, and for each analysis, the numbers were resorted and the test was reapplied 4,000 times. The procedure using groups of 6 ($n = 6$), 7 ($n = 7$), and 10 ($n = 10$) numbers (Figure 1) was repeated. From the obtained results, it is possible to point out the incapability of the test to detect statistical differences when the differences between the control and the treatment group are 15% or less, even when using $n = 10$, which is an unusually large n number for an allelopathy assay. Besides, when using the Mann-Whitney test, the adoption of the $n = 6$ can bring accuracy to the statistical analyses without increasing expressively the costs or efforts of the surveys.

Table 1. Example of generated values for both the "Control" and "Multiplier" groups and the resultant "Treatment" group. The values in bold represent the average.

Control	Multipliers	Treatment
62.95	0.953	59.99
74.31	0.942	70.00
83.25	0.951	79.18
76.52	0.931	71.22
77.71	0.971	75.46
74.95	**0.950**	**71.17**

Premise

When a given test plant presents a germination percentage of 100%, of every 100 seeds 100 will become seedlings. If each seedling weighs 100 g, these 100 seedlings will present a final weight of 10,000 g. If this plant has three growing cycles in 1 yr, the total biomass produced after this period will be 30,000 g (100 seedlings by 100 g each by 3 cycles a year). As an example, if these values are reduced in 35% by the application of an allelochemical, of 100 seeds 65 will become seedlings. These seedlings weigh now 65 g each, and they have only 1.95 cycles in 1 yr, producing after this period 8,235 g (65 seedlings by 65 g each by 1.95 a year), which would turn out to be a reduction of about 72%. As isolated reductions of 35% are likely to be detected by the Mann-Whitney test ($n = 5$, $P < 0.05$) only 36.2% of the times, global effect of 72% is unlikely to be detected. Therefore, looking on PIAEs separately might lead to a misinterpretation of the meaning of the global biological results. The development of the index takes this principle into account: to combine the isolated effects on PIAEs into one single value that reflects more accurately the global effects of a donor plant on a receptor plant.

Global Effect Index

The data sets mentioned in this section are hypothetical. To generate trial control data, the germination percentage values of all the control *n* replicates were divided by the average value of germination percentage of the control. This division aimed at transforming those values into dimensionless values. For biomass/size of the seedlings, the same transformation was applied to generate a data set. For the average time of germination, the average value of the control data was divided by each *n* replicate value (the smaller the germination percentage or seedling biomass/size, the higher the inhibition, and the longer the germination average time, the higher the inhibition) (Equation 1):

$$\text{Index for control} = (\%rC/\%aC) \times (BrC/BaC) \times (ATaC/ATrC) \quad [1]$$

where % is germination percentage, *B* is biomass/size, *AT* is average time of germination, *r* is replicate, *C* is control, and *a* is average of.

To generate trial treatment data, the germination percentage values of all the treatment *n* replicates were divided by the average value of germination percentage of the control. For biomass/size of the seedlings the same thing was done. For the average time of germination, the average value of the control was divided by each treatment *n* replicate value (as for average time a small value means stimulation, not inhibition). It is important to notice that the reference is always the average value of the control (Equation 2):

$$\text{Index for treatment} = (\%rT/\%aC) \times (BrT/BaC) \times (ATaC/ATrT) \quad [2]$$

where % is germination percentage, *B* is biomass/size, *AT* is average time of germination, *r* is replicate, *C* is control, *T* is treatment, and *a* is average of.

After the index is applied to an assay with *n* replicates, all the *n*-sized group values of PIAEs will become one *n*-sized group of values for control and one for treatment, as demonstrated next.

In this hypothetical example, the following values for percentage and average time of seed germination and for biomass of the seedlings were used (Table 2).

Analyzing all PIAEs separately with the Mann-Whitney test ($P < 0.05$), no significant differences for any of them were found. Subsequently, the following index was applied: control percentage of germination (Demonstration Table 1); control biomass (Demonstration Table 2); control average time (Demonstration Table 3); hence, the final index value for control is in Demonstration Table 4.

For treatment, the same method was used, as demonstrated next: treatment percentage of germination (Demonstration Table 5); treatment biomass (Demonstration Table 6); treatment average time (Demonstration Table 7); hence, the final index value for treatment is in Demonstration Table 8.

Table 2. Hypothetical allelopathy survey data. Values in bold represent the average. The arrow indicates the direction of the allelopathy effect (down means inhibition and up means stimulation). The ns indicates that these effects were statistically insignificant (Mann-Whitney $P < 0.05$).

Control			Treatment		
%	AT[a]	B	%	AT	B
97	32	0.0100	80	30	0.0079
94	25	0.0090	96	27	0.0088
95	28	0.0076	75	43	0.0130
88	29	0.0103	91	33	0.0082
92	24	0.0093	86	37	0.0072
93.2	**27.6**	**0.00924**	↓ **85.6** ns	↓ **34.0** ns	↓ **0.00902** ns

[a] Abbreviations: AT, average time of germination; B, biomass.

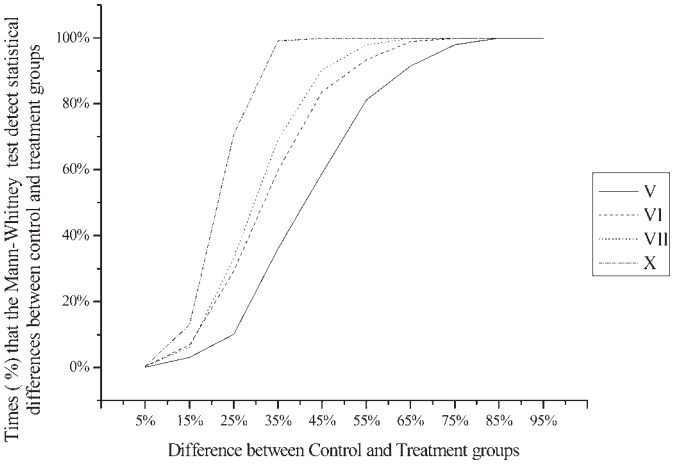

Figure 1. Efficiency of the Mann-Whitney tests in allelopathy survey data. V, VI, VII, and X mean *n* values equal to 5, 6, 7, and 10, respectively.

Demonstration Table 1. Index application on values of the control percentage of germination. Values in bold represent the averages. Underlined values highlight the used control values.

Control		Index for %
%		
97	= 97/**93.2**	1.040
94	= 90/**93.2**	1.008
95	= 95/**93.2**	1.019
88	= 88/**93.2**	0.944
92	= 92/**93.2**	0.987
93.2		

Demonstration Table 2. Index application on values of the control biomass (B), and control percentage of germination. Values in bold represent the averages. Underlined values highlight the used control values.

Control		Index for B
B		
0.0100	= 0.0100/**0.00924**	1.082
0.0090	= 0.0090/**0.00924**	0.974
0.0076	= 0.0076/**0.00924**	0.822
0.0103	= 0.0103/**0.00924**	1.110
0.0093	= 0.0093/**0.00924**	1.006
0.00924		

Demonstration Table 3. Index application on values of the control average time (AT), and control percentage of germination. Values in bold represent the averages. Underlined values highlight the used control values.

Control		Index for AT
AT		
32	= **27.6**/30	0.863
25	= **27.6**/25	1.104
28	= **27.6**/28	0.986
29	= **27.6**/29	0.952
24	= **27.6**/24	1.150
27.6		

Demonstration Table 4. Final index values for the control data, and control percentage of germination. Values in bold represent averages. Underlined values highlight the used control values.

%	Biomass	AT[a]	Final index value
1.040	1.082	0.863	0.972
1.008	0.974	1.104	1.085
1.019	0.822	0.986	0.826
0.944	1.110	0.952	1.002
0.987	1.006	1.150	1.143
1	**1**	**1.010**	**1.005**

[a] Abbreviation: AT, average time.

Demonstration Table 5. Index application on values of the treatment percentage of germination, and control percentage of germination. Values in bold represent the averages. Underlined values highlight the used control values.

Treatment		Index for %
%		
80	= 80/**93.2**	0.858
96	= 96/**93.2**	1.030
75	= 75/**93.2**	0.804
91	= 91/**93.2**	0.976
86	= 86/**93.2**	0.922
85.6		

Demonstration Table 6. Index application on values of the treatment biomass (B), and control percentage of germination. Values in bold represent the averages. Underlined values highlight the used control values.

Treatment		Index for B
B		
0.0079	= 0.0079/**0.00924**	0.854
0.0088	= 0.0088/**0.00924**	0.952
0.0130	= 0.0130/**0.00924**	1.406
0.0082	= 0.0082/**0.00924**	0.887
0.0072	= 0.0072/**0.00924**	0.779
0.00902		

Demonstration Table 7. Index application on values of the treatment average time (AT), and control percentage of germination. Values in bold represent the averages. Underlined values highlight the used control values.

Treatment		Index for AT
AT		
32	= **27.6**/32	0.920
27	= **27.6**/27	1.022
43	= **27.6**/43	0.642
33	= **27.6**/33	0.836
37	= **27.6**/37	0.746
34.4		

Demonstration Table 8. Final index values for the treatment data, and control percentage of germination. Values in bold represent the averages. Underlined values highlight the used control values.

%	B[a]	AT	Final index value
0.858	0.854	0.920	0.675
1.030	0.952	1.022	1.003
0.804	1.406	0.642	0.727
0.976	0.887	0.836	0.725
0.922	0.779	0.746	0.536
0.918	**0.976**	**0.833**	**0.733**

[a] Abbreviations: B, biomass; AT, average time.

Demonstration Table 9. Final index values. Values in bold represent the averages. The arrows indicate the direction of the allelopathy effect (down means inhibition and up means stimulation). The s indicates that these effects were statistically significant (Mann-Whitney $P < 0.05$).

Control	Treatment
0.972	0.675
1.085	1.003
0.826	0.727
1.002	0.725
1.143	0.536
1.005	↓ **0.733** s

After applying the proposed transformations, two $n = 5$ sized groups, which are made of dimensionless values, were obtained. These represent the control and treatment values. Using these new groups, a new Mann-Whitney test analysis was run and significant differences were found between control and treatment, detecting potential biological allelopathic effects that may have otherwise passed undetected when data were analyzed separately (Demonstration Table 9).

The global effect index (GEI) was developed by using percentage and average time of seed germination and biomass/size of seedlings, as they are the most common PIAEs used in

Table 3. Randomly generated values representing control percentage (%) and control average time of germination (AT) and control biomass (B), and their respective multiplier values and the resulting treatment groups. Values in bold represent the averages.

Control			Multiplier			Treatment		
%	AT	B				%	AT	B
55.92	88.53	77.19	0.937	0.954	0.914	52.39	84.45	70.55
74.26	73.41	76.58	0.977	0.942	0.964	72.55	69.15	73.82
65.71	59.42	65.26	0.923	0.940	0.903	60.65	55.85	58.92
91.15	84.62	77.47	0.925	0.965	0.998	84.31	81.65	77.31
77.35	80.20	75.73	0.956	0.923	0.927	73.94	74.02	70.20
72.88	**77.24**	**74.45**	**0.943**	**0.945**	**0.941**	**68.77**	**73.05**	**70.16**

allelopathic surveys (Chiapusio et al. 1999; Inderjit and Dakshini 1995). Nevertheless, it is possible to replace these PIAEs by other ones. It is of crucial importance not to use related PIAEs, such as germination speed and germination average time or seedling biomass and seedling size in the same analysis, so as not to overestimate the effect of one given factor on the overall index. It is also possible to use the GEI using only two PIAEs, by simply excluding from the equation the values that refer to the nonanalyzed PIAEs.

The nonparametric Mann-Whitney tests for the development of the GEI were used. Nevertheless, after the index is calculated, the data can be analyzed with other tests and each author might use the ones they find more suitable for their own data. The data can also be transformed by a second index (An et al. 2005) and then analyzed.

Using the GEI with Simulated Data

Data were generated to test the index the same way it was done when assessing the efficacy of the Mann-Whitney test. The only difference is that this time two or three groups of numbers (that intend to represent different PIAEs) were used (Table 3).

The GEI was applied to the generated data by using two or three PIAEs. As done previously, The Mann-Whitney test efficiency was tested in allelopathy survey data by using multiplier groups that ranged from 1–0.9 to 0.1–0 and groups of 5, 6, 7, and 10 elements (n). For all situations, the numbers were resorted and the GEI reapplied and the analysis reperformed 4,000 times (Figure 2).

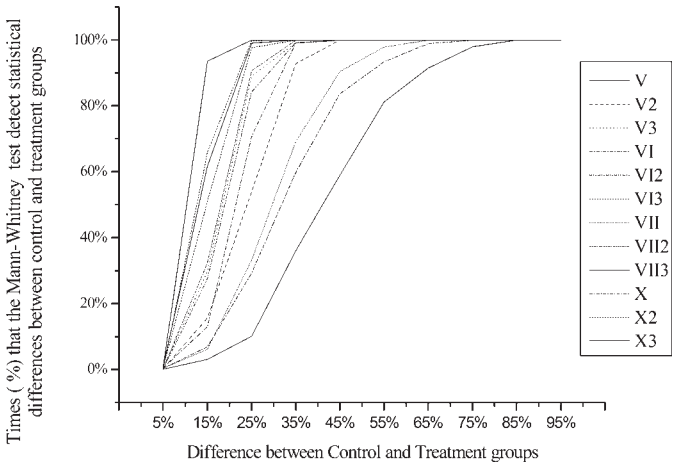

Figure 2. Efficacy of the Mann-Whitney tests in allelopathy survey data after the global effect index is applied. Roman numbers represent the n values and the Arabic numbers represent the numbers of PIAEs used.

Table 4a. Example of bioassay data for which statistical analysis of separate parameters used to infer allelopathic effects (PIAEs) found no differences between control and treatment percentage of germination (%) and average time of germination (AT, in hours). After the global effect index (GEI) is applied, the statistical test reveals the differences. Values in bold represent the averages. The arrows indicates the direction of the allelopathic effect (down means inhibition and up means stimulation). The s and the ns indicate whether these effects were statistically significant or not, respectively (Mann-Whitney $P < 0.05$).

Control			Treatment		
%	AT	GEI	%	AT	GEI
96.67	43.20	1.043	83.33	40.55	0.958
76.67	46.95	0.761	86.67	54.92	0.735
76.67	43.50	0.821	70.00	46.86	0.696
93.33	32.57	1.316	83.33	54.72	0.710
86.67	34.15	1.183	83.33	54.24	0.716
86.00	**40.07**	**1.029**	↓ **81.33** ns	↓ **50.25** ns	**0.763** s

The results indicate that the use of the index significantly increases the capacity of the tests to detect differences. For example, in $n = 5$, when differences were of the magnitude of 35%, the Mann-Whitney tests find differences in about 36% of the tests. When applying the index to two PIAEs, this value goes up to 92.9% and with three, the Mann-Whitney test finds significant differences in 99.2% of the cases.

Using the Index with Obtained Data

After testing the index with the simulated data, it was tested with data from the São Carlos University Allelopathy Research Group with two or three PIAEs. They are always referred to as ''control'' and ''treatment'' to preserve the unpublished raw data from contributor authors. Several results were obtained, summarized as follows:

I. Isolated analysis that presents nonsignificant differences for either PIAE. When using the GEI, the differences were detected (Tables 4a and 4b).
II. Isolated analysis that presents nonsignificant differences for either PIAE. When using the GEI, I still found no significant differences (Table 5).
III. One PIAE that presents significant differences (usually the germination average time) and the other(s) do not. When using the index, the differences were detected (Tables 6a and 6b).
IV. PIAEs that point to opposite direction (such as percentage of germination and average time of germina-

Table 4b. Example of bioassay data in which statistical analysis of separate parameters used to infer allelopathic effects (PIAEs) found no significant differences between control and treatment percentage of germination (%), average time of germination (AT, in hours), and biomass (B, in grams). After the global effect index (GEI) is applied, the statistical test reveals the differences. Values in bold represent the average. The arrows indicates the direction of the allelopathy effect (down means inhibition and up means stimulation). The s and the ns indicate whether these effects were statistically significant or not, respectively (Mann-Whitney $P < 0.05$).

Control				Treatment			
%	AT	B	GEI	%	AT	B	GEI
97	32	0.0100	0.979	80	31	0.0079	0.659
90	25	0.0090	1.047	96	28	0.0088	0.975
95	28	0.0076	1.033	75	43	0.0130	0.732
88	29	0.0103	1.010	91	33	0.0082	0.730
92	24	0.0093	1.152	86	37	0.0072	0.540
92.4	**27.6**	**0.00924**	**1.005**	↓ **85.6** ns	↓ **34.4** ns	↓ **0.00902** ns	**0.727** s

Table 5. Example of bioassay data in which statistical analysis of separate parameters used to infer allelopathic effects (PIAEs) found no differences between control and treatment percentage of germination (%) and average time of germination (AT, in hours). After the global effect index (GEI) is applied the statistical test still found no differences. Values in bold represent the average. The arrows indicates the direction of the allelopathy effect (down means inhibition and up means stimulation). The ns indicates that these effects were statistically insignificant (Mann-Whitney $P < 0.05$).

Control			Treatment		
%	AT	GEI	%	AT	GEI
50.00	68.00	0.898	60.00	83.33	0.879
90.00	89.78	1.225	53.33	71.25	0.914
56.67	79.06	0.875	53.33	83.25	0.782
66.67	77.4	1.052	66.67	84.40	0.965
53.33	72.75	0.895	66.67	94.20	0.864
63.33	**77.398**	**0.989**	↓ **60** ns	↓ **83.28** ns	**0.881** ns

tion) are reduced by the same extract. In these cases the GEI tends to neutralize the differences and finds no global effects (Table 7).

Other Applications

As the GEI is dimensionless, it is possible to compare different donor plants with a single target plant, and determine, for example, which donor plants have greater inhibition effects. This can be particularly useful when trying to decide which donor plant to use when each donor plant causes different effects on one specific PIAE (Table 8).

Table 6a. Example of bioassay data in which statistical analysis of separate parameters used to infer allelopathic effects (PIAEs) (percentage of germination [%] and average time of germination [AT, in hours]) found differences between control and treatment in only one PIAE and after the global effect index (GEI) is applied, the statistical test found differences. Values in bold represent the average. The arrows indicates the direction of the allelopathic effect (down means inhibition and up means stimulation). The s and the ns indicate whether these effects were statistically significant or not, respectively (Mann-Whitney $P < 0.05$).

Control			Treatment		
%	AT	GEI	%	AT	GEI
96.67	40.55	1.057	60	45.33	0.587
76.67	46.95	0.724	90	49.33	0.809
76.67	36.52	0.931	86.67	64.15	0.599
93.33	32.57	1.271	70	53.71	0.578
86.67	34.15	1.125	96.67	55.86	0.767
86.00	**38.148**	**1.021**	↓ **80.66** ns	↓ **53.676** s	**0.668** s

Table 6b. Example of bioassay data in which statistical analysis of separate parameters used to infer allelopathic effects (PIAEs) (percentage of germination [%] and average time of germination [AT, in hours]) found differences between control and treatment in only one PIAE, and after the global effect index (GEI) is applied, the statistical test found differences. Values in bold represent the average. The arrows indicates the direction of the allelopathy effect (down means inhibition and up means stimulation). The s and the ns indicate whether these effects were statistically significant or not, respectively (Mann-Whitney $P < 0.05$).

Control			Treatment		
%	AT	GEI	%	AT	GEI
50.00	68.00	0.898	50	101.6	0.601
90.00	89.78	1.225	63.33	85.26	0.908
56.67	79.06	0.875	60	92	0.797
66.67	77.40	1.052	46.67	86.57	0.659
53.33	72.75	0.895	63.33	114.32	0.677
63.33	**77.40**	**0.989**	↓ **56.66** ns	↓ **95.95** s	**0.728** s

Table 7. Example of bioassay data in which the parameter used to infer allelopathic effects (PIAE) points to the opposite direction (such as percentage of germination [%] and average time of germination [AT, in hours] are reduced by the same extract) and after the global effect index (GEI) is applied, the statistical test found no differences. Values in bold represent the average. The arrows indicates the direction of the allelopathic effect (down means inhibition and up means stimulation). The s and the ns indicate whether these effects were statistically significant or not, respectively (Mann-Whitney $P < 0.05$).

Control			Treatment		
%	AT	GEI	%	AT	GEI
50	68.00	0.881	76.67	81.39	1.129
90	82.4	1.309	70.00	81.14	1.034
56.67	79.06	0.859	56.67	86.11	0.788
66.67	77.4	1.032	53.33	86.25	0.741
53.33	72.75	0.878	73.33	84.54	1.039
63.33	**75.92**	**0.992**	↑ **66** ns	↓ **83.88** s	**0.946** ns

Table 8. Comparing two treatments (T1 and T2) on a single target species using the global effects index (GEI). The control is the same to both treatments, and the reference is still its average values, in this case 63.33 for percentage of germination (%) and 77.4 for germination average time (AT, in hours). Values in bold represent the average. The arrows indicate the direction of the allelopathic effect (down means inhibition and up means stimulation). The s and the ns indicate whether these effects were statistically significant or not, respectively (Mann-Whitney $P < 0.05$).

Control		T1			T2		
%	AT	%	AT	GEI	%	AT	GEI
50.00	68.00	46.67	90.27	0.632	70.00	132.57	0.644
90.00	89.78	56.67	104.70	0.661	43.33	123.69	0.427
56.67	79.06	56.67	102.40	0.676	60.00	147.33	0.497
66.67	77.4	56.67	94.59	0.732	53.33	105.00	0.620
53.33	72.75	50.00	86.29	0.708	66.67	121.30	0.671
63.33	**77.398**	**53.33**	**95.65**	**0.681**	↑ **58.669** ns	↓ **125.98** s	**0.572** s

Another application of the GEI is that it can be used as a criterion for including or not a plant in the allelopathic list (Ahn et al. 2008). As the index summarizes the allelopathic potential of a plant in one value, its use can be more practical and accurate than choosing one (or more) PIAE. This can be especially useful in surveys that scan large areas for allelopathic plants.

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