Short Paper

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Abstract

This is the abstract.

It consists of two paragraphs.

Methods

All analysis were carried away with the R Statistical Software (R Core Team 2016), all meta-analyses were made on the metafor package (Viechtbauer 2010). Our estimations were based on the use of random/mixed-effects models form of meta-analyses, which provide an unconditional inference about a larger set of studies from which the k studies included in the meta-analysis are assumed to be a random sample (L. V. Hedges and Vevea 1998). This estimations do not assume that this larger set consists only of studies that have actually been conducted, but instead envision a hypothetical population of studies that comprises studies that have been conducted, that could have been conducted, or that may be conducted in the future (L. V. Hedges and Vevea 1998).

We used the *escalc* function of the metafor package to estimate the effect size estimates (Viechtbauer 2010), we used the *standardized mean difference with heteroscedastic population variances in the two groups* (SDMH) as our estimator for effect size (Bonett 2009), the metafor package also corrects the slight positive bias of the estimation following (Wasserman, Hedges, and Olkin 1988). To be extra conservative we used the unbiased estimates of the sampling variances. In all cases the residual heterogeneity estimator was Hedges.

Since we used mixed effect models we used the The Knapp and Hartung adjustment **(Knapp and Hartung, 2003)** to test the individual coefficients of the model.

Test for (Residual) Heterogeneity

For each model we tested for residual heterogeneity, if we used models without moderators, then the Cochran's Q-test (Cochran 1954) was used to test whether the variability in the observed effect sizes or outcomes is larger than would be expected based on sampling variability alone. *A significant test suggests that the true effects or outcomes are heterogeneous.* When moderators were included in the models the Q__E-test for residual heterogeneity was used, this tests whether the variability in the observed effect sizes or outcomes not accounted for by the moderators included in the model is larger than would be expected based on sampling variability alone. When using moderators to explain more variability a pseudo R squared was computed following (Raudenbush 2009).

Results

As we can see in figure 1, the most common type of performance measured in studies was abundance, with 101 estimations, followed by reproduction with 44 estimation, behavior with 23, and finally survival and condition with 16 each.

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Table 1: effect size of the Standardized mean difference for each type of estimation of performance, it's standard error and p-value

estimate	ci.ub	ci.lb	group	p	n	I2	pvalCT
-0.917	-0.423	-1.410	Abundance	0.000	101	90.594	0
-2.508	0.940	-5.957	Behavior	0.154	23	99.742	0
-5.319	-1.556	-9.083	Survival	0.006	16	98.756	0
-3.366	13.710	-20.441	Reproduction	0.699	44	99.995	0
-1.078	-0.128	-2.027	Condition	0.026	16	98.597	0

Overall effect size

As we can see in table 1 and figure 2, all estimations of the effects are negative. However, only abundance, survival and condition have significative negative effects. Survival has the highest effect size, with a mean difference estimation of -5.32

Estimations using moderators:

Abundance

Abundance and functional group

Using functional group as a moderator yields the following results

Table 2: effect size of the Standardized mean difference of abundance for each functional group and it's standard error

estimate	ci.ub	ci.lb	group	p	n
-0.917	-0.423	-1.410	Null	0.000	101
-0.456	0.538	-1.450	detritivore	0.368	24
-0.905	-0.052	-1.758	mixed	0.038	33
-4.069	-1.608	-6.531	omnivore	0.001	4
-1.654	0.626	-3.934	pollinator	0.155	4
-0.787	0.011	-1.585	predator	0.053	36

the the psuedo R squared for this model was 0.06, that is despite the mixed and omnivore funtional groups being statistically significant, functional group on its own does not explain the variability of the results very well.

Abundance and nesting area

Table 3: effect size of the Standardized mean difference of abundance controling for nesting area and it's standard error

estimate	ci.ub	ci.lb	group	p	n
-0.917	-0.423	-1.410	Null	0.000	101
-0.840	-0.101	-1.579	aboveground	0.026	0
-1.070	-0.386	-1.755	both	0.002	0
0.523	3.305	-2.259	ground	0.713	0

the the psuedo R squared for using nesting area as the only moderator was 0, this model does not explain much.

Abundance and concentration (ppb)

When we use concentration as parts per billion, the number of effect sizes diminishes from 101 to only nine.

Despite that, the r squared of this model is 0.45, that is over 40 percent of cariability explained by this factor alone. The relationship between concentration and Abundance can be seen in figure 4.

Abundance concentration and functional group

Again, when we have concentration, the number of studies is reduced form 101 to nine.

Adding functional group to the model increases R squared to 0.85

Abundance concentration and nesting area

Full model

Comparison of models

Table 4: Comparison of models taking into account p value, Pseudo R squared and AICc

model	p_value	R_squared	AICc	deltaAICc
y ~ Concentration	0.008	0.45	60.476	0.000
y ~ Concentration + Functional group	0.000	0.85	66.225	5.749
y ~ Concentration + Nesting area + Functional group	0.000	0.85	66.225	5.749
y ~ Concentration + Nesting area	0.032	0.40	67.454	6.978
y ~ Functional group	0.106	0.06	464.017	403.541
y ~ Nesting Area	0.532	0.00	466.648	406.173

Behaviour

Abundance

Abundance and functional group

Using functional group as a moderator yields the following results

Table 5: effect size of the Standardized mean difference of abundance for each functional group and it's standard error

estimate	ci.ub	ci.lb	group	p	n
-2.508	0.940	-5.957	Null	0.154	23
-5.932	4.630	-16.494	commercial	0.271	3
-3.763	9.232	-16.759	granular	0.570	2
-0.501	12.395	-13.396	not specified	0.939	2
-2.767	10.141	-15.675	seed treatment	0.674	2
-2.291	3.053	-7.634	solution	0.401	12
0.456	13.386	-12.474	technical grade	0.945	2

the the psuedo R squared for this model was 0, that is despite the mixed and omnivore funtional groups being statistically significant, functional group on its own does not explain the variability of the results very well.

Behavior/Reproduction and neonic AI (e.g., IMI, CLO) and ppb

Abundance

Seed treatment only and functional group and nesting area

AI type and functional group

Effects on:

Performance measures

Performance measures and functional group

Functional group

Performance measures and nesting area

Behavior

AI type and functional group

Reproduction and order and functional group

Abundance and order and functional group

Behavior and study type

Reproduction and nesting area

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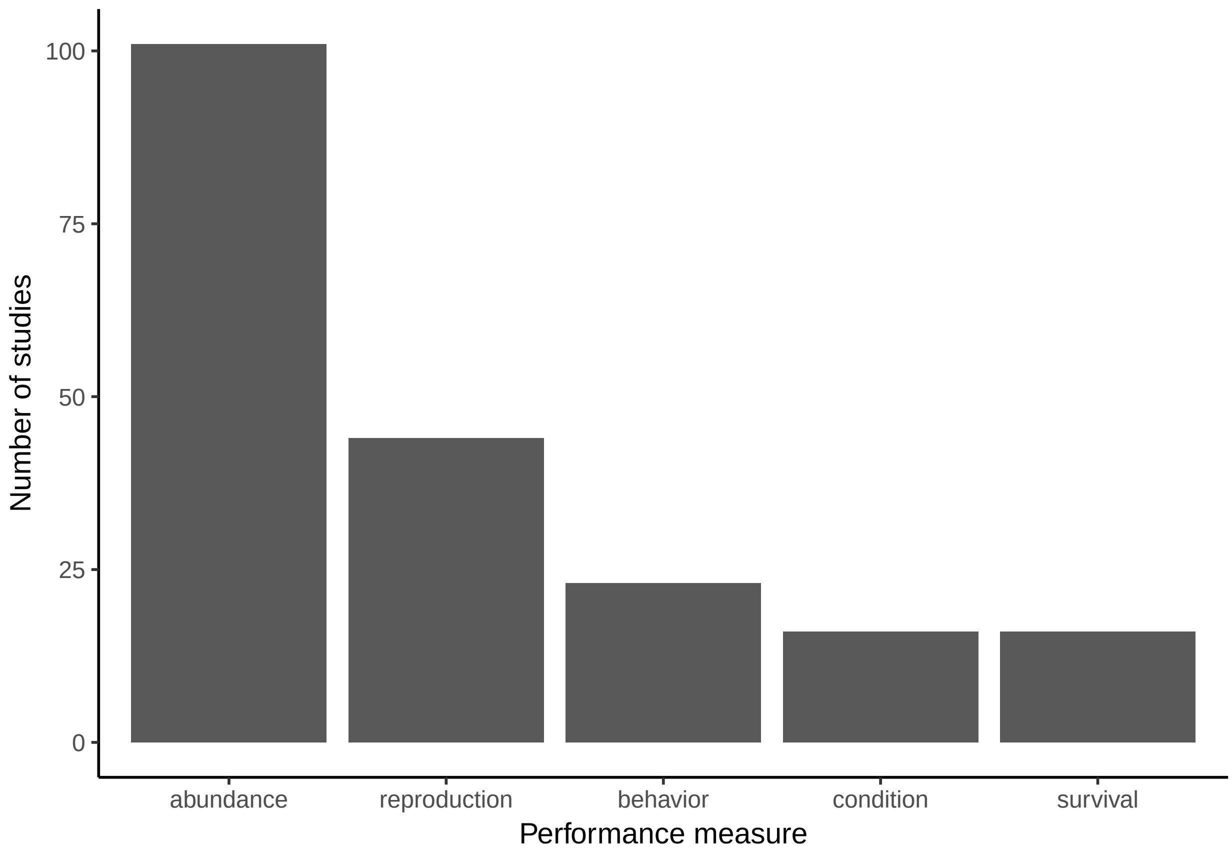

Figure 1: Number of estimation of effect size within the meta-analyses

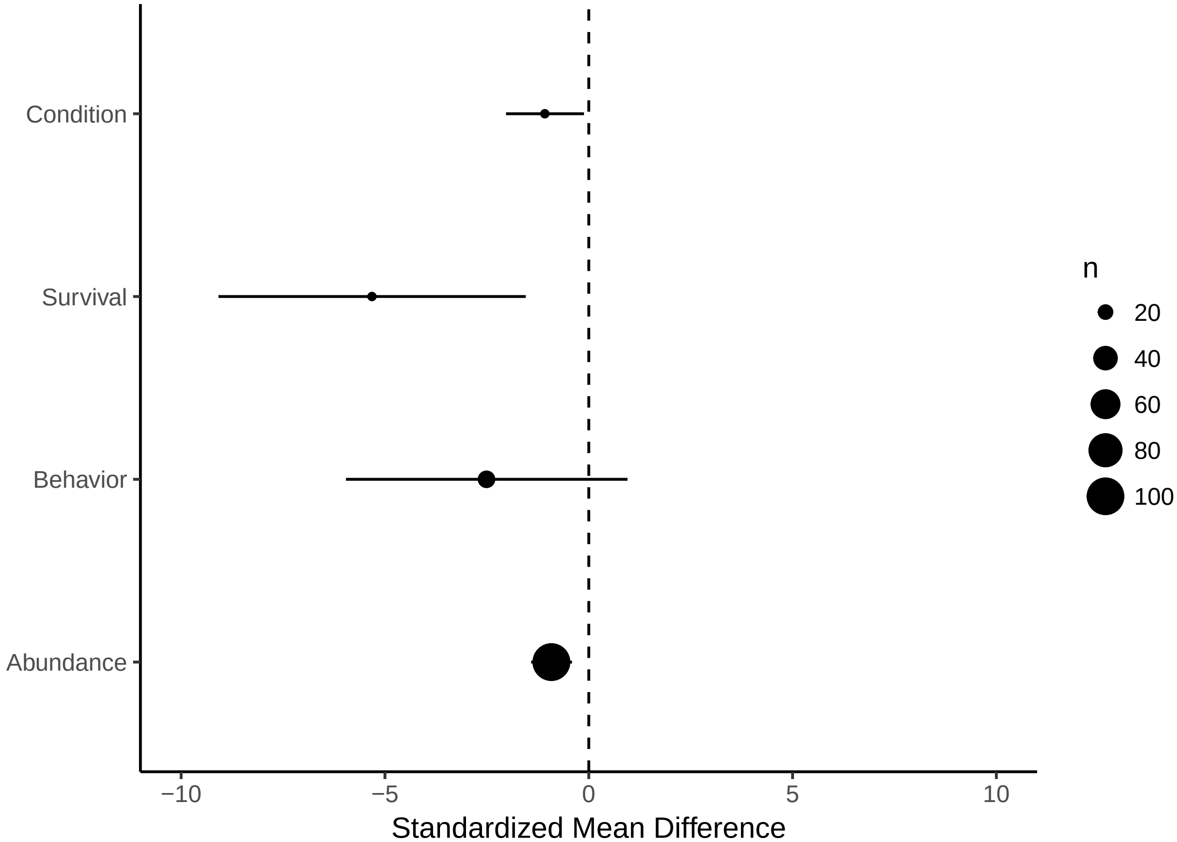

Figure 2: effect size of the Standardized mean difference for each type of estimation of performance and it's standard error

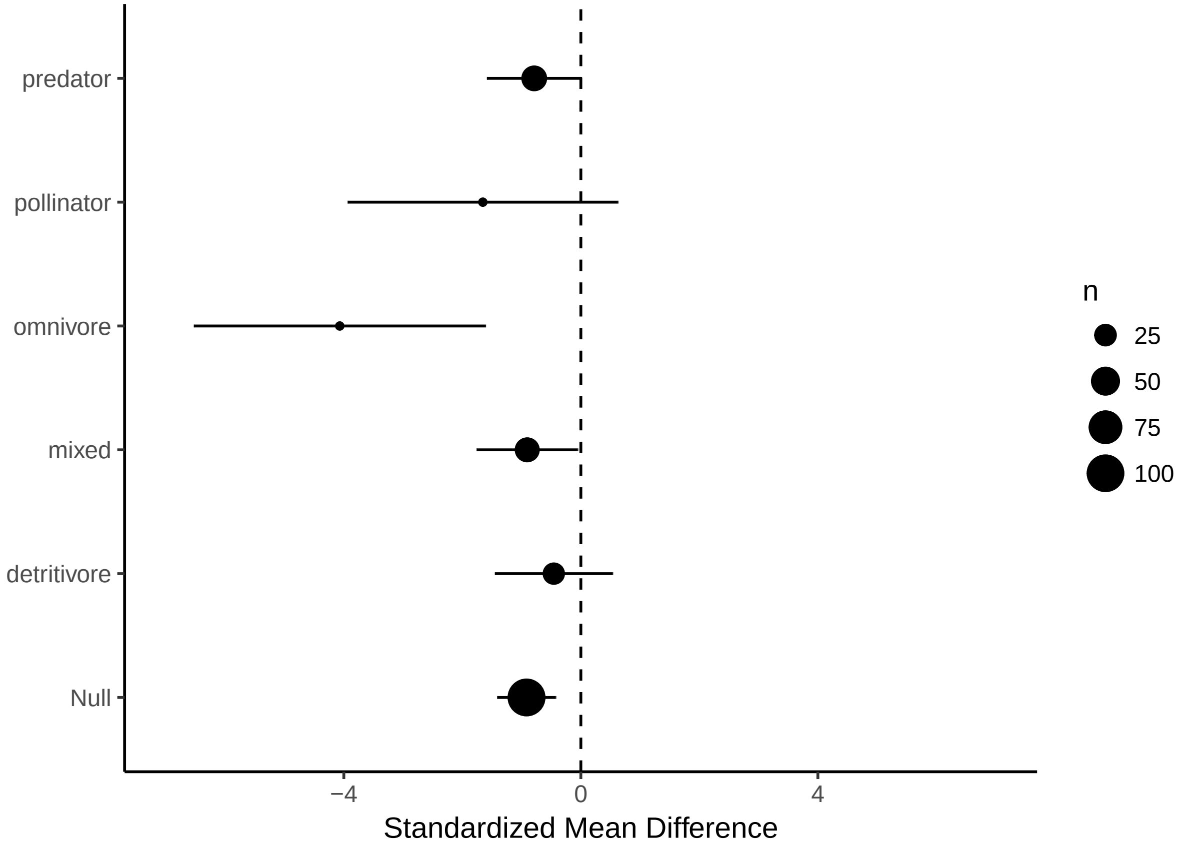

Figure 3: effect size of the Standardized mean difference of abundance for each functional group and it's standard error

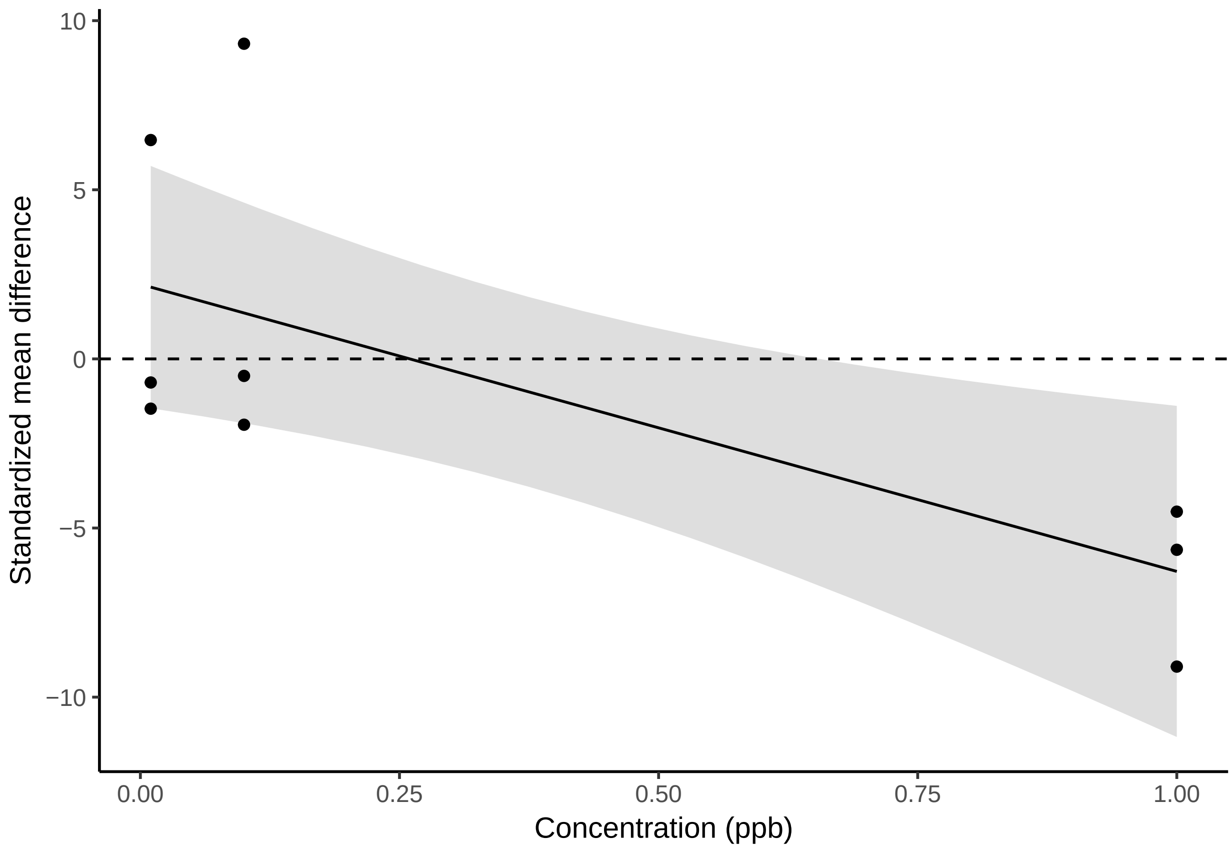

Figure 4: effect size of the Standardized mean difference of abundance and concentration (ppb)

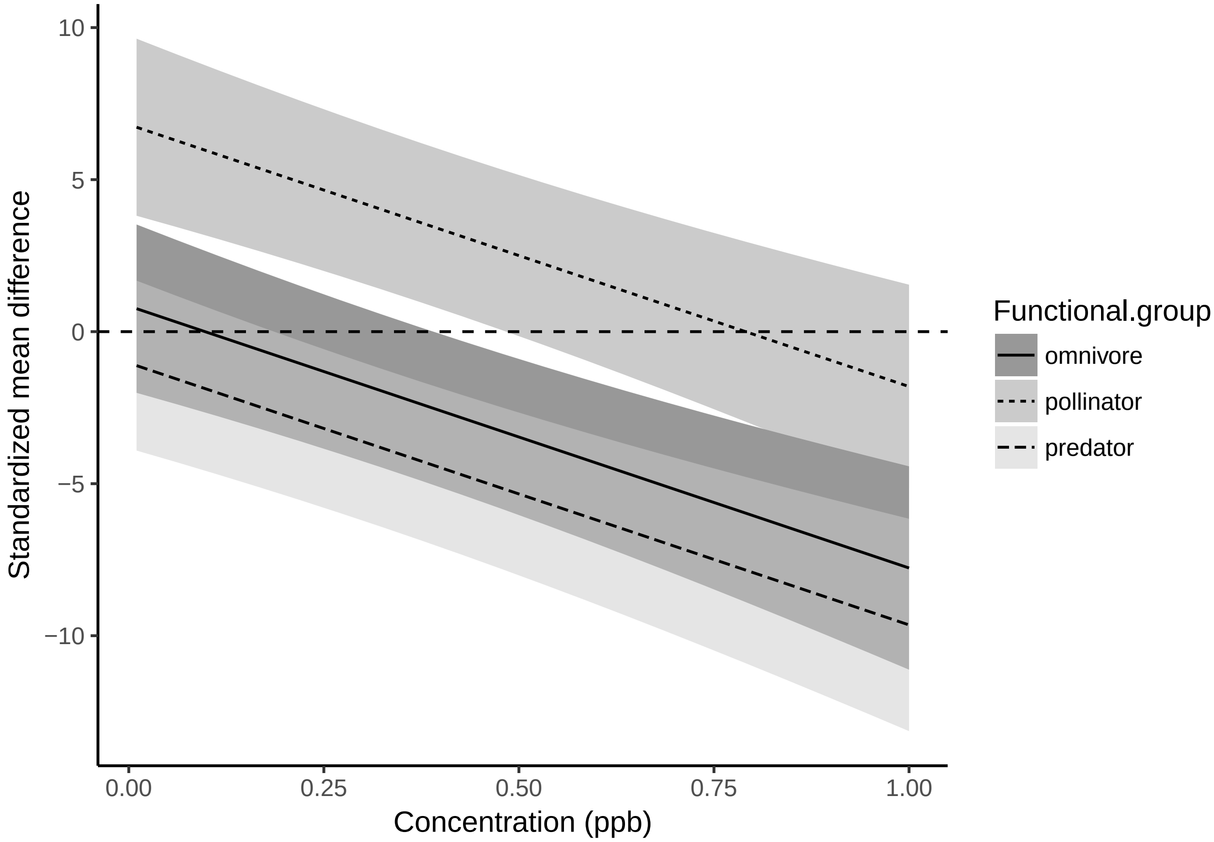

Figure 5: effect size of the concentration and functional group on the Standardized mean difference of abundance

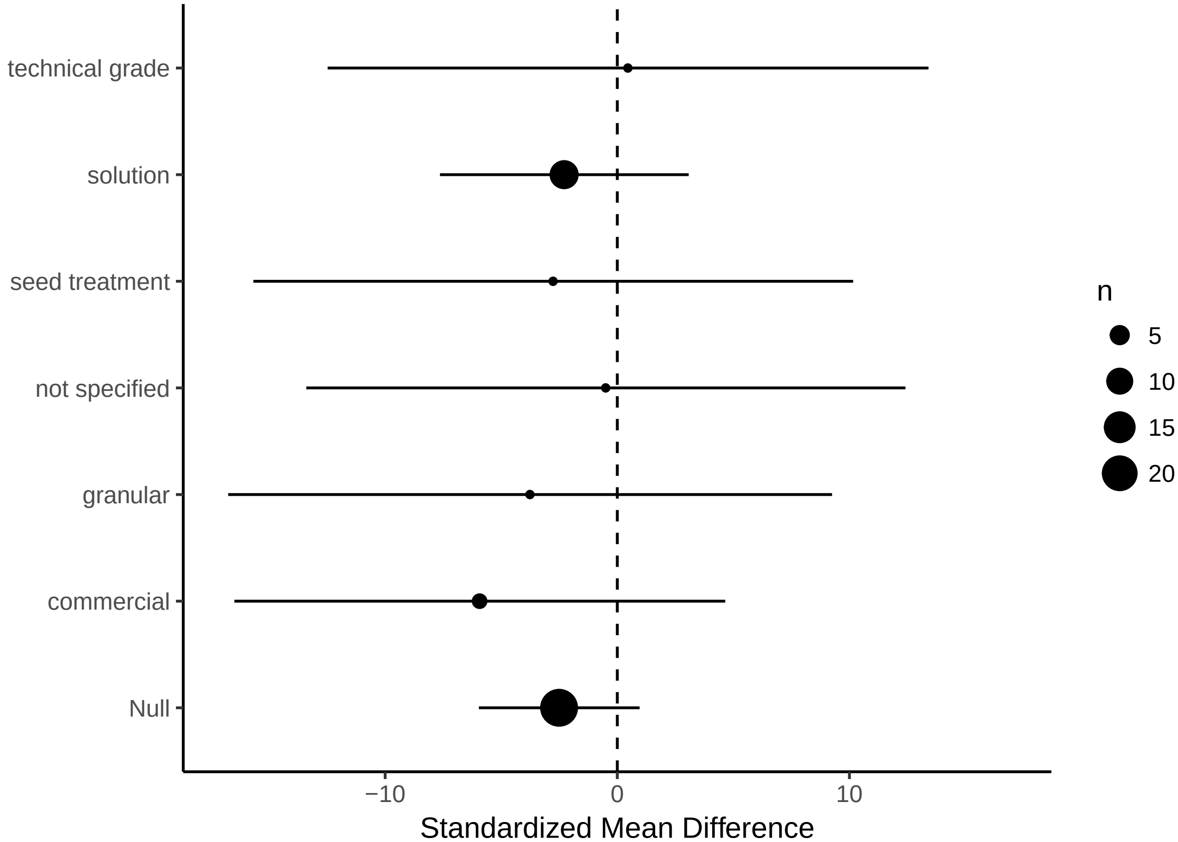

Figure 6: effect size of the Standardized mean difference of behavior for each AI type and it's standard error

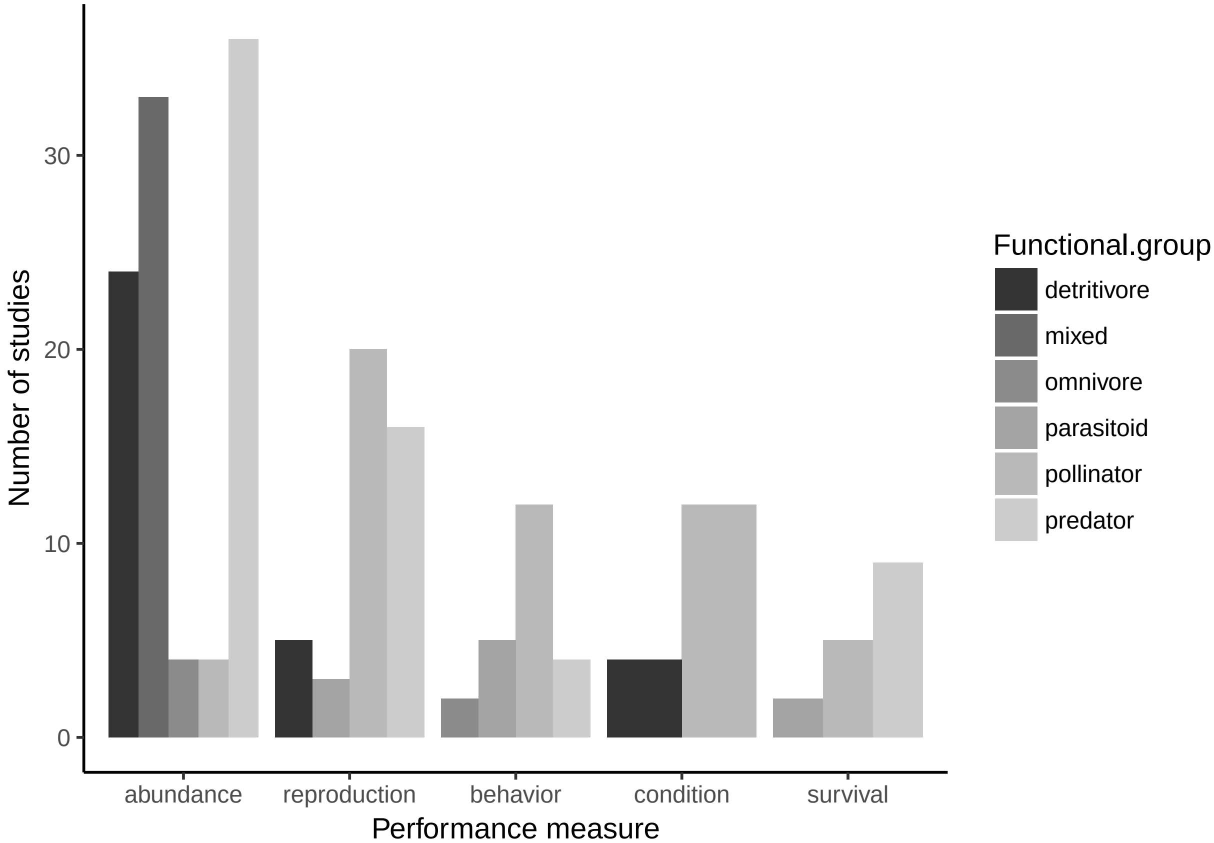

Figure 7: test