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Meta-Analysis on grain yield effects of cereals-legume intercropping

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Introduction

Going abroad is a good opportunity to improve his foreign tongue practice, but it is also a rich human experience we can hardly forget.

An internship in Denmark was much better because I could not imagine I was going to learn very many things in such a very short time : Besides an adaptation to a different culture and different daily habits, it was my first experience in a National Laboratory, and among biologists.

Although not clear for me and considered as a bit difficult, the subject dealt with a meta analysis on cultures of intercropping of food and feed crops. The part of my job was then to contribute to show the benefit of farming practices thanks to statistics, whereas biologists I worked with had been in charge to show advantages by experiments.

My last internship was also about Agriculture and crop study, so I was more or less prepared to these kind of data, and elements which can contribute to get good yields. I enjoyed this last experience, that is why I wanted to do it again, but this time, in a more environmentally friendly approach.

This project was indeed about farming and biodiversity, but this time, the topic was more about practices, mainly the intercropping I did not know at all, and my first job was to understand perfectly this principle [1], [2]. In parallel, I had to understand the meta analysis principles thanks to tutorials [3], and anything I could find.

The second step, and a new task, was to collect data by my own, my first panic ! How could I do that ? Fortunately, people were here to help me.

After many discussions about the article selection, the measure to use and different features, we took the decision to do several analysis, because we had several perspectives and leads; it was very enjoyable because it meant I was free to try many different technics, and to learn a lot.

Risø National Laboratory
DTU

Their missions

Located in Roskilde, the second biggest city of the Zealand Island, after Copenhagen, the laboratory is attached to the Technical University of Denmark, and is focused on research for sustainable energy.

Composed of 7 departments, the research areas are sustainable energy supply, climate change mitigation and nuclear technologies in order to find sustainable solutions for Danish daily life. Using natural resources like wind or sun, they also lead research on plant characteristics to try to understand and use the Environment for the future.



One of these divisions is the biosystems division, which speciality is to study how can be used biomass for the energy production. This section consists of several divisions with specific tasks, and my project was affiliated of the biomass and bioenergy programme(NRG).

The NRG Programme

The experiments led in the biosystem division mainly concerned the analysis and treatment of plant biomass, its conversion into bioenergy and biomaterials. From practice to theory, the main task is to find practical idea_ and see if it is possible_ to encourage farms to reduce their CO_2 production, and show them it could represent real financial and time-saving advantages.

At the same time, scientists study how crops can be grown in an environment-friendly way, their properties, and which of these properties have an impact on how efficiently the plants are converted into energy and materials.



This programme is composed of approximately 30 people, consisted of technicians who lead experiments, researchers who, based on results of technicians' experiments, work on theoretical issues, try to solve and bring new ideas. The team is also composed of PhD student, post-PhD, researcher assistants, but also temporary trainees and summer students.

Most of the programme has a biological or/and chemical background. My project was mainly supervised my Risø supervisor, Hanne Østergård, a biometrician and a PhD student, Lars Pødenphant, working on meta analysis. In addition, 2 supervisors from Copenhagen University, Faculty of Life Science were involved : an agronomist, Bjarne Jørnsgård, and a statistician, Ib Michael Skovgaard.

The work strategy for me was to understand perfectly what was expected, to find some documentations and papers related to the problems, and to understand by my own how to deal with the subject. Of course, people around this project guided me to the right directions, made me suggestions, and replied to my biological-statistical questioning.

Meta analysis for Agriculture

Chapter 1

Project introduction

1.1 Agricultural design

In order to reduce costs and increase profits, while at the same time sustaining our land resource base, sustainable agriculture seeks to use Nature as the model for designing agricultural systems. One of these concepts is the intercropping, a simultaneous cultivation of more than one crop species on the same piece of land, which the main feature is to promote interaction between species.

Looking for a production optimization, this practice is based on principles we have to understand well to handle the following study.

1.1.1 Principles and strategies

When two or more species are growing together, each must have adequate space and architecture to produce an optimum yield.

To accomplish this, spatial arrangement has to be considered firstly. There are at least three basic spatial arrangement used in intercropping, one of the most common being the row intercropping, which consists in growing two or more crops at the same time with at least one crop planted in rows. Other arrangements exist, like the strip (crops are growing in strips) or mixed intercropping (no distinct row designs), and all these have to take into account the plant density.

Indeed, the seeding rates do not have to overload the field, unless to slow the yield down because of intense overcrowding.

The idea is to find the optimum proportion of seed density to be used in intercropping, which could be difficult because a lower rate of one of the crop can produce the same yield at the end than a higher rate of an other species. Therefore, in order to compare the monocropping with the intercropping, a seed proportion of one crop from monocropping is considered in intercropping, usually 50% of monocrop seed rate is used in a cereal-legume intercropping. Nonetheless, these proportions can be different, according to the species used and the study's goal.

The plot design is another important concept, used to observe the treatment effects on crops. The design choice has an impact on the analysis of variance led, and has a large importance for a meta analysis.

For these reasons, I will develop the 2 two most used in agricultural design, and I will try to stress up their differences in the statistical analysis.

1.1.2 Plot designs

In agricultural research, experimental designs are selected according to the number of factors, and the importance one can have compared with an other. According to the design used, analysis differ from degrees of freedom and dependance, drawing to different conclusions if these last are badly used.

However, the common point is that the replication (i.e. the repetition of the experiment) is considered as a factor, but its effect does not matter.

We will focus on the two most used plot design : The randomized complete block design, and the split plot design.

The randomized complete blocks design is one of the most widely used, especially suited for field experiments when the number of treatments is not large. The main specificity of this design is the presence of equal size blocks, containing all the treatments. The process is applied separately and independently to each of the blocks.

It is a classical case of ANOVA in analysis of variance.

The split plot design is suited for a two-factor experiment, with the feature that one of the factors is assigned to the *main-plot factor*, whereas the other is the *subplot factor*. In this situation, the precision of the effects of the main-plot factor is sacrificed to improve that of the subplot factor. The effect measurement of the interactions is also more precise than in a randomized complete block design.

Then, if a study wants to put more importance to a factor to one other, a split plot design is considered.

The understanding of these designs is very important for the information's extraction used in a meta analysis, but also for the whole project arose now.

1.2 Project framework

To show the multiple benefits of intercropping, one of these strategies has been carried out through an field experiment with specific conditions : During 3 years and in 2 different locations_ in a sandy loam soil, and a sandy soil_ in Denmark, scientists have observed the effects of mixing cereals and legumes in a 2-species organic intercropping. The cereals culture was spring barley, observed with pea, faba bean and lupin respectively, in randomized complete blocks. For each of the three crop combination, for each condition, the yield and the protein content have been studied in pure crop and intercrop.

Because one experiment is not enough to lead a statistical analysis, it gets usual that Agronomy has recourse to the meta analysis in order to collect more data, despite the loss of quality of information due to the fact that only treated data are available.

The aim of this process is to extract data from publications treating intercropping of cereals and legume to determine the effects of dual intercropping of either legume or cereals on yield performance.

After this first step, an effect measure is selected to reply to the problematic : Has intercropping got a positive effect on grain yield and protein grain contents ?

At last, according to the variance chosen and extracted from articles, technics will be set up to lead an analysis and answer to the questions, regarding the effect measure(s) chosen.

Chapter 2

Preliminaries

2.1 Data collection

Database retrieval

The criteria for retrieval of studies for the meta-analysis were publication in a peer-reviewed journal included in the DTU Article Database, from year 1900 and onwards.

Papers reporting on grain yield of sole crops and mixtures of cereals with legumes were searched for. The search [*wheat or oat or barley or triticale or cereal*] and [*legume or lupin or faba or pea*] and [*yield or protein or nitrogen*] and [*intercrop* or species mixture*] provided 204 papers. Titles and abstracts of these papers were studied by Bjarne Jørnsgård, and only papers where grain yield of the crops were recorded were selected for further investigation and full text retrieval. It implies that both pure and intercrop yields for both species (focus on 2-species intercropping) had to be provided.

From these 204 papers, only 10 has been retrieved but one study has usually more than one mixture (the several effect measures), so the dataset is reasonably large to carry out an analysis. The references are [4], [5], [6], [7], [8], [9], [10], [11], [12] & [13].

Data extraction

The database gathers information on growing conditions, such as fertilizer use, seed densities or type of soil, but also grain yields, variance and seed proportions were collected for analysis. From this set, grain yields will be used to get an effect measure, whereas the choice of the weight (to get an estimation of the overall mean effect) will depend on provided information in publications.

The measure effect has to be easily interpretable and it has to compare the pure and the intercrop yield using both to answer to our problematic.

2.2 The choice of the measure effect

For this meta-analysis, 2 measures are suggested : The Land Equivalent Ratio (LER) and the overall gain of intercropping proposed by Loreau and Hector [14] en 2001 .

The first one is a simple way to compare the pure yield with the intercropping yield by a sum of ratio, whereas the other is a measure based on the separation of a "selection effect" and a "complementary effect".

Land Equivalent Ratio

The Land Equivalent Ratio (LER) is a measure introduced by Mead and Willey in 1980 to compare the yields obtained by polyculture with yields obtained by monoculture of the same crops.

In our situation (i.e 2 species are intercropped), the expression is :

$$LER = \frac{Y_{I_1}}{y_1} + \frac{Y_{I_2}}{y_2}$$

when

- y_i is the yield of the pure crop i ($i=1,2$)
- Y_{I_i} is the yield of the intercropped culture i ($i=1,2$)

A LER greater than 1 shows that intercropping is advantageous, whereas less than 1 shows a disadvantage.

However, we often notice, by application, that the LER can be above 1, and yet the pure crop of one species is better than the mixture yield, or one of the 2 species loses productivity in intercropping. In this situation, the intercropping benefit remains unknown, because a more complex procedure occurs.

To remedy to this problem, Loreau and Hector [14] introduced an other measure, the covariance function firstly defined for the yield, but also used to measure other kinds of production (e.g. biomass).

The selection and complementary effects

These two effects are the decomposition of the overall gain and will determine the benefit (and the reasons of such a benefit) of intercropping :

$$\Delta Y = \sum_{i=1}^2 Y_{I_i} - \sum_{i=1}^2 Y_{p_i} = \underbrace{2 \cdot \text{cov}(R_Y, Y_p)}_{\text{selection effect}} + \underbrace{2 \cdot \bar{R}_Y \cdot \bar{Y}_p}_{\text{complementary effect}}$$

When

$$2 \cdot \text{cov}(R_Y, Y_p) = \sum_{i=1}^2 (R_{Y_i} - \bar{R}_Y)(Y_{p_i} - \bar{Y}_p)$$

and

$$Y_{p_i} = p_i \times y_i$$

$$R_{Y_i} = \frac{Y_{I_i}}{Y_{p_i}} - 1$$

$$\bar{R}_Y = \frac{1}{2} \sum_{i=1}^2 R_{Y_i}$$

$$\bar{Y}_p = \frac{1}{2} \sum_{i=1}^2 Y_{p_i}$$

- Y_{p_i} is the crop monoculture yield of the i^{th} species in the seed proportion p_i , corresponding to the seed proportion used in the intercropping for this species ;
- Y_{I_i} is the crop yield obtained for the i^{th} species when 2 species are cultivated as a mixture;
- y_i represents the crop yield per unit area.

The covariance function, up to a constant, is also called the selection effect because, comparable to 0, a high value (positive or negative) means the intercropping is favorable for one of the 2 culture, but not for the other : it predicts a dominance of one of the species on the other in the mixture, as if the selection of a specific species had influenced the intercrop yield.

Because the mean of two yields is always positive, the complementary effect sign depends on \bar{R}_Y , so the interpretation of this quantity is linked to the ratio $\frac{\text{intercrop yield}}{\text{pure yield}}$, considering the proportion used in the intercropping : If this quantity is widely positive, the intercropping is a general benefit, as if cultures stimulate each other, whereas a widely negative value means a real disadvantage of such a combination.

If the effects are both positive, intercropping has benefit on production, and it could be due to dominance (resp. competition) if the selection effect (resp. the complementary effect) is higher than the complementary effect (resp. the selection effect).

If the effects are both negative, both cultures are more efficient in monocrop, and there is no dominance species to make increase the yield.

If the effects have opposite signs, we can conclude to either a large dominance (resp. an good complementarity) if the selection effect (resp. the complementary effect) is widely positive or a non-benefit of intercropping if the selection effect is slightly positive and the complementary one widely negative.

We will choose to study the 3 recounted effects (considering 2 are linked) and give the appropriate interpretation in the following.

Chapter 3

Data description

3.1 The data

The data currently consists of 10 papers composed of 2 to 32 mixtures. Each mixture is composed of 4 yields, necessary to calculate the effect measures. In a word, it means that a effect measure does not correspond to a single study, as it is usually the case, but in a single study, several measures are carried out.

For each mixture, we want to study 3 effect measures, the LER index, the selection effect and the complementary effect. These 2 last measures will be analyzed together, because their general tendency will be compared for the interpretation.

The source of variation within studies can be due to the difference of seed densities used in mixtures, the experiment years, the location (sandy loam soil or sandy soil) or the difference of nitrogen amount used, mentioned in the database.

Details are shown in the table 3.1. The study numbers mentioned in the following analysis will always correspond to the identifiers of this table.

A quick statistical description allows to see the main data characteristics and this also brings us some ideas for the following work.

3.2 Descriptive Statistics

The most usual is to represent the grain yield of each species for monocropping and intercropping for each mixture and each study. Through these plots, we can easily compare the species yields in monoculture, then the yields in monoculture and intercropping.

The following representation concerns the first and the second papers, where the nitrogen amount and the seed density (resp.) are the sources of variation. The other representations are a part of the paper 4, composed of 32 mixtures, which source of variation is year (2002 and 2003) and the seed proportion used for intercropping, and a part of paper 7, which variation comes from the soil type and legume species.

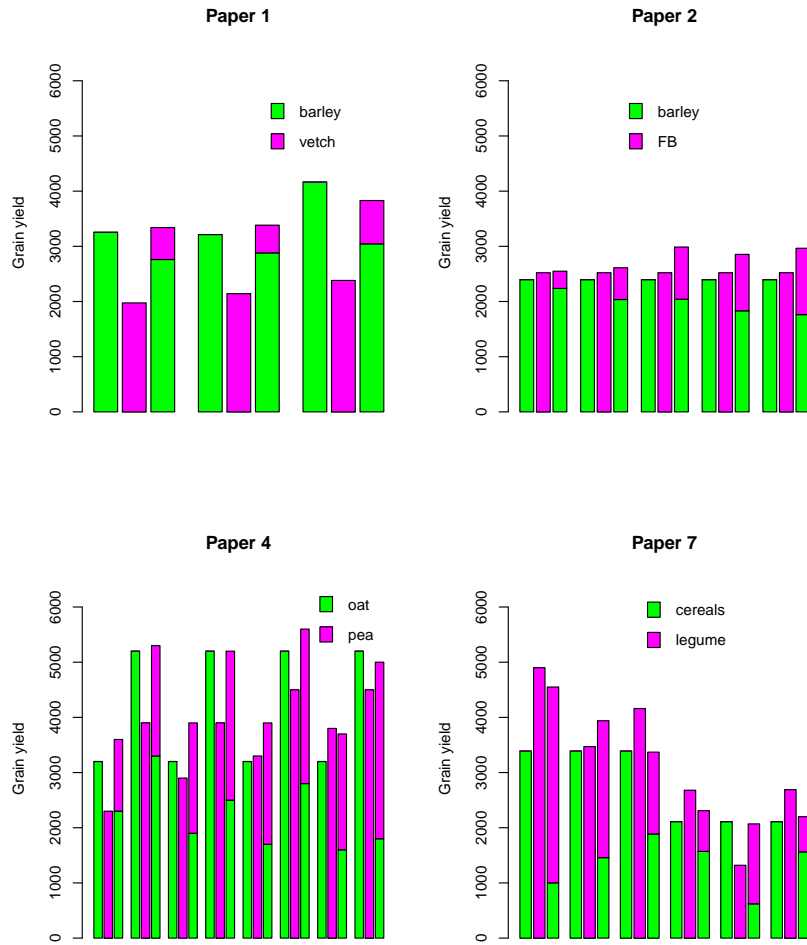


Figure 3.1: Barplot representation of grain yields per species & mixtures in 4 papers

For the first paper, we observe a difference between the production of barley and vetch, whereas the intercrop yield is barely higher than in monocrop situation. In the paper 2, the intercrop yield is higher in each situation than for the monoculture.

In paper 4, we can see a difference between years (alternately 2002 and 2003 have been represented), but also the important difference between pea and oat. Also, we can assume a dominance in the intercropping in most of the mixtures, because of the larger oat yield.

However, these patterns do not represent the seed proportion used in the intercropping (compared with the one used in the monoculture), so we have to be careful about conclusions drawn on them. It simply gives an idea on differences between species, and if a major gap exists between intercropping and monocropping.

Study ID	Nber effect sizes	Species	Design	Source of variation	Informed variance index	Nber replications	PK($kg \cdot ha^{-1}$) ^a
1	3	Vetch barley	Split plot	Nitrogen amounts (0,45,90)	MSE	4	0
2	5	Barley Fababean	RCB ^b	Seed proportion	LSD	4	20
3 ^c	1	Wheat chickpea	Split plot	NA	NA	4	150
4	32	Oat Pea	Split plot	Years (2) Seed density(16)	LSD	4	0
5	4	Wheat Maize Fababean	RCB	2 years	SE	3	40
6	3	Wheat Pea	Split plot	Nitrogen amount (0,40)	SE	3	0
7	6	BarleyO, BarleyL Pea, FB Lupin	RCB	Soil (2)	SE	4	0
8	8	Barley Pea	Split plot	4 years Nitrogen amounts (0,50)	LSD	3	80
9	10	Oat Bean	RCB	Seed density	SE	4	118
10 ^d	4	Oat PeaMessire,PeaProfi	RCB	2 years	NA	4	0

Table 3.1: Main characteristics of data collect

^aAverage of PK fertilizer employed in the experiments

^bRCB = Randomized Complete Blocks

^cOmitted in the analysis due to no information on variances

^dOmitted in the analysis due to no information on variances

Chapter 4

Meta analysis : First approach

For this first part, we will assume mixtures as if they were independent. Moreover, the variance attributed to each mixture (and by consequence the weight) is extracted from the ANOVA tables supplied by the articles.

4.1 Modeling

For a meta estimation, two parametric models are suggested, the fixed-effects and the mixed/random-effects model. The difference between both is that the random-effects model takes in account the heterogeneity of studies whereas the other model assumes the between-study variation can be neglected.

The fixed-effects model is quite unrealistic in practice, although simple. A test of homogeneity allows us to test whether or not the heterogeneity can be considered as null.

Therefore the general form of the model is, if Y_i is the i^{th} effect measure :

$$Y_i = A_i + \varepsilon_i , \quad \begin{array}{l} \varepsilon_i \sim N(0, s_i^2) \\ A_i \sim N(\mu, \sigma^2) \end{array}$$

i.e.

$Y_i = \mu + \zeta_i + \varepsilon_i , \quad \begin{array}{l} \zeta_i \sim N(0, \sigma^2) \\ \varepsilon_i \sim N(0, s_i^2) \end{array}$
--

when

- μ is the mean effect measure to estimate;
- s_i^2 is the variance of the i^{th} mixture to deduce from papers;
- σ^2 is the between-mixture variation to estimate, $\sigma^2 = 0$ if it is a fixed-effects model.

In our situation, Y_i is the different measures we mentioned previously : the LER, the selection effect and the complementary effect.

For all these measures, we have 8 from 10 papers available and 80 effect measures. Thanks to the variance extracted from 8 papers, we will be able to estimate $s_i^2, \forall i$ (the procedure is not obvious and is explained in Annexe page 37), and use the *metafor* package in **R** to give an estimation of mean effect and its variance.

In addition, some graphics will allow us to observe general and detailed tendencies for interpretation.

For all the analysis, we will use the REML method developed by A. Harville [15] and briefly explained in Annexe page 40.

4.2 The LER effect measure

4.2.1 Estimation

The *rma* function of **R** gives these estimations :

```
sigma^2 (estimate of total amount of heterogeneity): 0.0016 (SE = 0.0017)
sigma (sqrt of the estimate of total heterogeneity): 0.0398
I^2 (% of total variability due to heterogeneity): 13.7%
```

Model Results:

estimate	se	test	p-value	Confidence Interval
1.1198	0.0123	90.8362	0.0000	1.0957 1.1440 ***

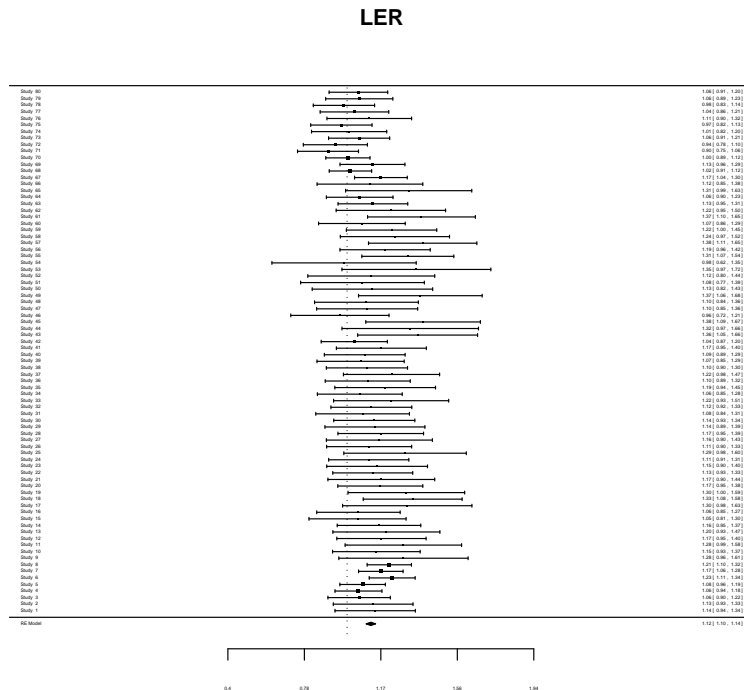


Figure 4.1: Forest plot of the 80 LER

The test for heterogeneity (explained in Annexe page 40) gives :

$Q(df = 79) = 80.855$, $p\text{-val} = 0.421$

4.2.2 Interpretation

The test of heterogeneity considers the model as fixed-effects model, i.e. σ^2 is significantly null. The estimation of the mean effect gives 1.12, number above 1, resulting that the intercropping is a benefit through all papers analyzed. Indeed, if we refer to the 80 LER figured out, a very important part is above 1.

However, the goal of the papers were to show the advantage of intercropping by the LER index, so we can have doubts about what it has been published. Therefore, we will study the publication bias and we will try to correct.

4.2.3 Publication bias

We can refer to the funnel plot and the Kendall's rank test :

T = 2241, p-value = 1.384e-08

alternative hypothesis: asymmetry in funnel plot

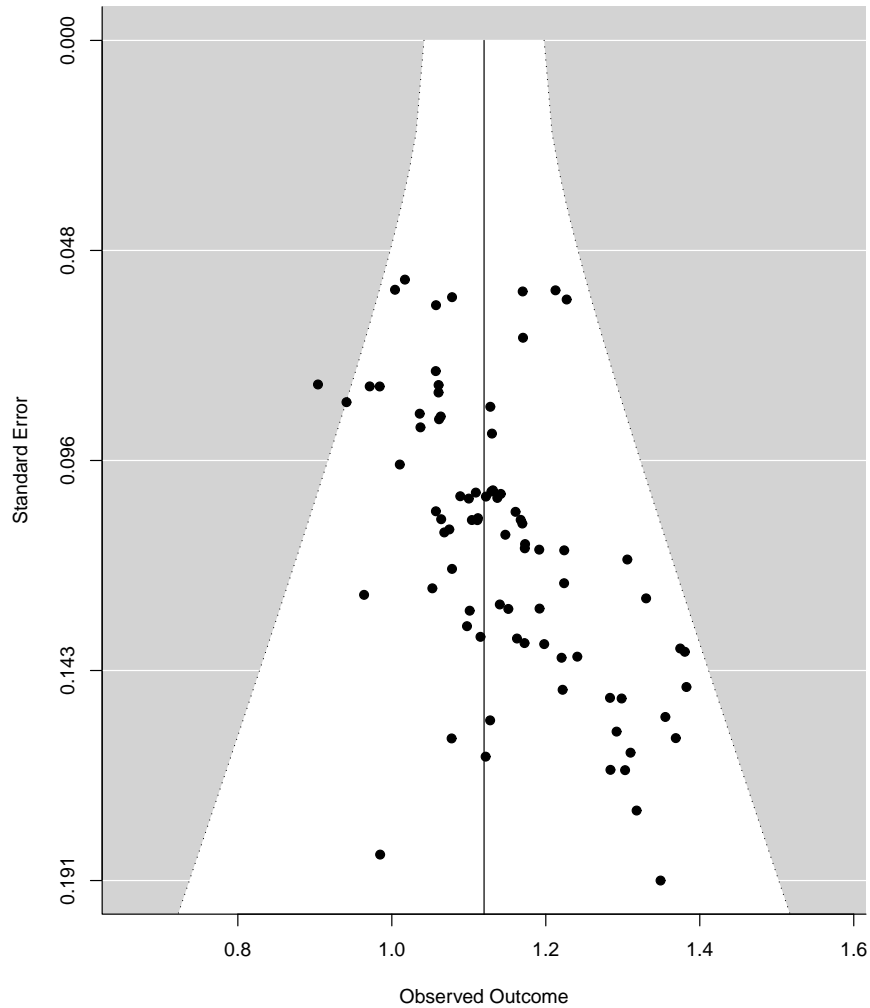


Figure 4.2: Funnel plot of the LER

By the test, we can observe that the symmetry hypothesis is rejected, probably due to very high measures, whereas the standard deviation is small.

Nevertheless, this empirical method can be challenged because they sometimes omit a publication bias yet existing.

To spot it and to estimate a new model taking into account some possible unpublished bias, some techniques are suggested : We will focus on two of them, the trim and fill method, a non parametric and quite empirical way, and the Copas selection model, based on normality assumptions, but much more elaborated than the trim and fill technique.

The Trim and fill method

The trim and fill method, developed by Duval & Tweedie [16], is a non parametric method which consists in trimming the studies of the asymmetric part, then do a new estimation without these studies, and replace them with their missing symmetric counterparts.

The *trimfill* function of *meta* package in **R** gives the following correction, and its numerical modification is in Annexe page 42.

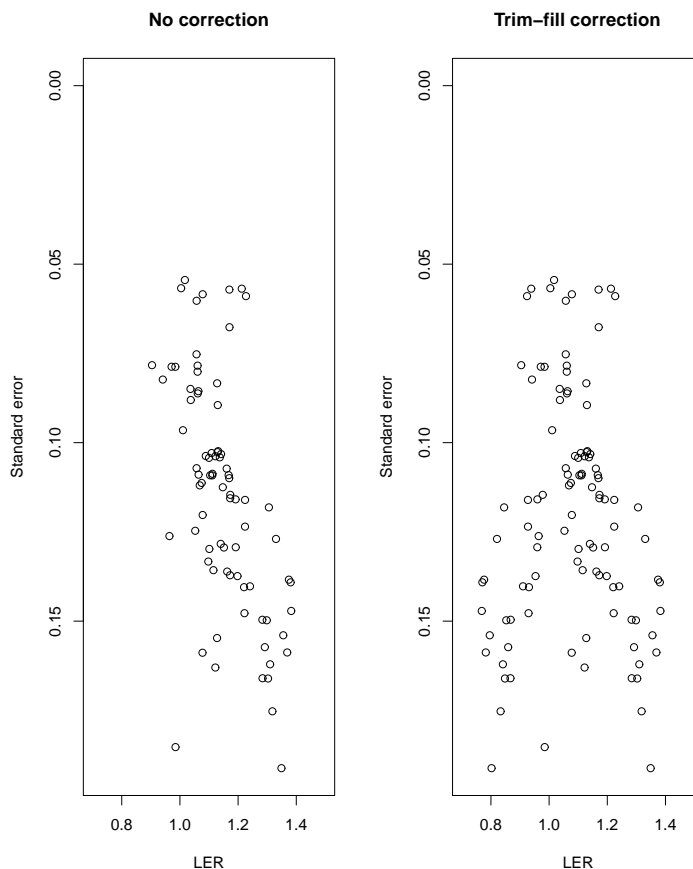


Figure 4.3: Funnel plot of the LER corrected by trim-fill technique

The heterogeneity is much higher this time but still can be neglected, whereas the mean effect is estimated to 1.08, higher than 1. This correction slightly changes the tendency, considering that 26 (i.e 32.5%) effect measures are missing to correct the bias.

The Copas function

An other approach, less empirical, has been developed by Copas and Shi [17], and consists in treating a generalized Tobit model, with a new introduction of a variable z , linked to the probability for a study to be selected : If a study is selected, then the outcome is observed. The details of the approach is given in annexe page 42. In that way, thanks to the *copas* package available in **R**, the Copas function supplies a result for the LER, as shown below.

Summary of Copas selection model analysis:

	publprob	Outcomes	95%-CI	pval.treat	pval.rsb	N.unpubl
	1.00	1.1196	[1.0949; 1.1442]	< 0.0001	< 0.0001	0
	0.79	1.1001	[1.0752; 1.1250]	< 0.0001	0.0016	13
	0.64	1.0801	[1.0550; 1.1052]	< 0.0001	0.0149	28
	0.54	1.0597	[1.0339; 1.0855]	< 0.0001	0.083	45
	0.45	1.0395	[1.0118; 1.0671]	< 0.0001	0.3006	65
	0.38	1.0203	[0.9891; 1.0514]	< 0.0001	0.7213	88
Copas model (adj)	1.0395		[1.0118; 1.0671]	< 0.0001	0.3006	65
Random effects model	1.1168		[1.0946; 1.1390]	< 0.0001		

Legend:

publprob - Probability of publishing the study with the largest standard error
pval.treat - P-value for hypothesis that the treatment effect is equal in both groups
pval.rsb - P-value for hypothesis that no further selection remains unexplained
N.unpubl - Approximate number of studies the model suggests remain unpublished

This function would estimate $\hat{\mu} = 1.04$, a very small error of this mean (confidence interval very tight) and 65 effect measures would not be published.

The two methods give different results, but they agree to admit there is a publication bias, and that an important number of lower outcomes are not published.

Conclusion

With an estimated LER of 1.12 and a very neglecting variance, this analysis predicts a publication bias, assuming that at least 30% of effect sizes are not published, getting a mean effect lower, barely bur nonetheless above 1.

The 2 others effect sizes allow a more in-depth analysis, giving an explanation of the benefit (or not) of intercropping, as shown below.

4.3 The selection and complementary effects

4.3.1 Estimation

The analysis under **R** gives the following output :

```

Selection effect
sigma (sqrt of the estimate of total heterogeneity): 327.8766
I^2 (% of total variability due to heterogeneity): 96.1%
Test for Heterogeneity:
Q(df = 79) = 856.6181, p-val = 0
Model Results:
estimate      se    test      p-value  Confidence Interval
100.4873  38.9194  2.5819  0.0098  24.2067 176.7678      **

Complementary effect
sigma (sqrt of the estimate of total heterogeneity): 2143.999
I^2 (% of total variability due to heterogeneity): 96.9%
Test for Heterogeneity:
Q(df = 79) = 1459.202, p-val = 0

```

Model Results:

estimate	se	test	p-value	Confidence Interval	
-922.5773	246.5199	-3.7424	0.0002	-1405.7474 -439.4072	***

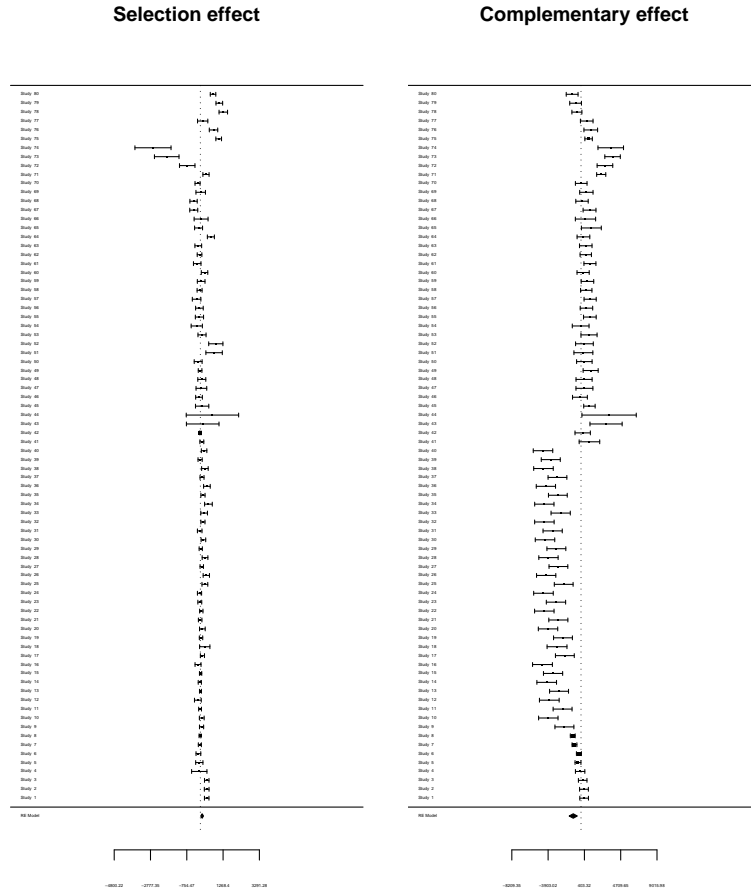


Figure 4.4: Forest plot of the selection and complementary effects

4.3.2 Interpretation

At first, the Q-test confirms the heterogeneity of the model for both effects, testing $H_0 : \mu = A_1 = \dots = A_{80}$, widely rejected.

Secondly, we can see, using the REML method to estimate the mean effect, that the selection is positive, $\hat{\mu} = 100.5$, whereas the complementary effect is widely negative, with $\hat{\mu} = -922.6$.

This means that the benefit of intercropping, as a general tendency, is due to the dominance of one species, and not due to the fact that cereals and legumes stimulate each other when they grow together.

However, we note that a big series of measures of the complementary effect is widely negative, and this series corresponds to an only paper. We also note that it represents an important number of the total number of effect measures, so it probably has a strong influence of the general effect. To verify our believes, a "leave-one-out" method can be employed to show the possible influence on some papers.

4.3.3 The "leave-one-out" analysis

If we decide to carry out an analysis **without the paper 4**, we get :

Selection effect :

sigma² (estimate of total amount of heterogeneity): 225808.9 (SE = 50958.75)
 sigma (sqrt of the estimate of total heterogeneity): 475.1936
 I² (% of total variability due to heterogeneity): 97.3%

estimate	se	test	p-value	Confidence Interval
85.1024	72.1543	1.1795	0.2382	-56.3173 226.5222

Complementary effect :

sigma² (estimate of total amount of heterogeneity): 769944.4 (SE = 194108)
 sigma (sqrt of the estimate of total heterogeneity): 877.4647
 I² (% of total variability due to heterogeneity): 88%

estimate	se	test	p-value	Confidence Interval
602.9886	140.8970	4.2796	0.0000	326.8356 879.1417 ***

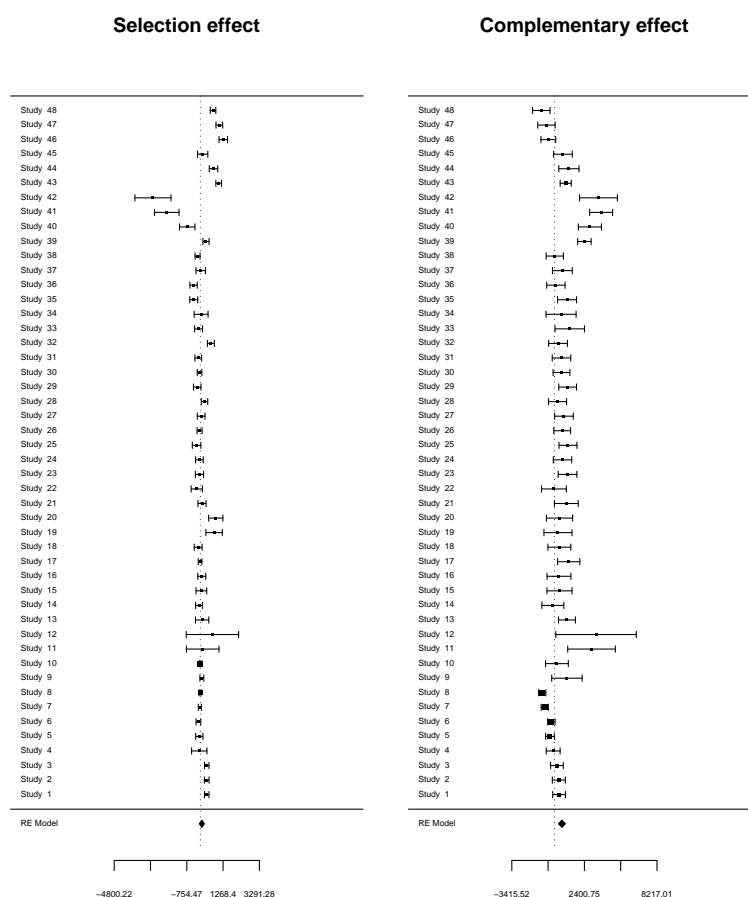


Figure 4.5: Graphical Representation of the selection & complementary effect without paper 4

The selection effect is still positive but very small and not significant, whereas the complementary effect is very significant and largely positive.

The eliminated study has an important impact on results, but also show that it is at the origin of a negative complementary effect.

By looking at its features in the paper, we notice this is the only mixture oat+pea treated and that all experiments from other articles received a N (and/or P and/or K) fertilizer except the studies 4 and 7. However, we did not notice a particular tendency for the study 7.

If we look further, we also notice that the study 4, which experiments (with different seed proportions tested) have been led in 2002 and 2003, had a precipitation of 338 mm the first year, but only 185 mm the other year. We note that both effects are higher in 2002 than in 2003. Moreover, the annual rainfall in the paper 7 is much higher with 600 mm or 700 mm of precipitation according to the location.

As a consequence, we could think that a lack of commercial fertilization and rainfall has an impact on the effects, resulting a negative complementary effect, and a low positive selection effect, i.e. an inefficiency of intercropping in this context.

An other study has also an influence : Composed of 10 effect measures (study 9), the effects are much lower if we remove it alone, like their respective variabilities. The results are shown in Annexe page 43.

Oat and bean intercropping, the 10 effects result of the seed proportion variability. A focus on it reveals an interesting fact. We represented the forest plot of effects of this study only:

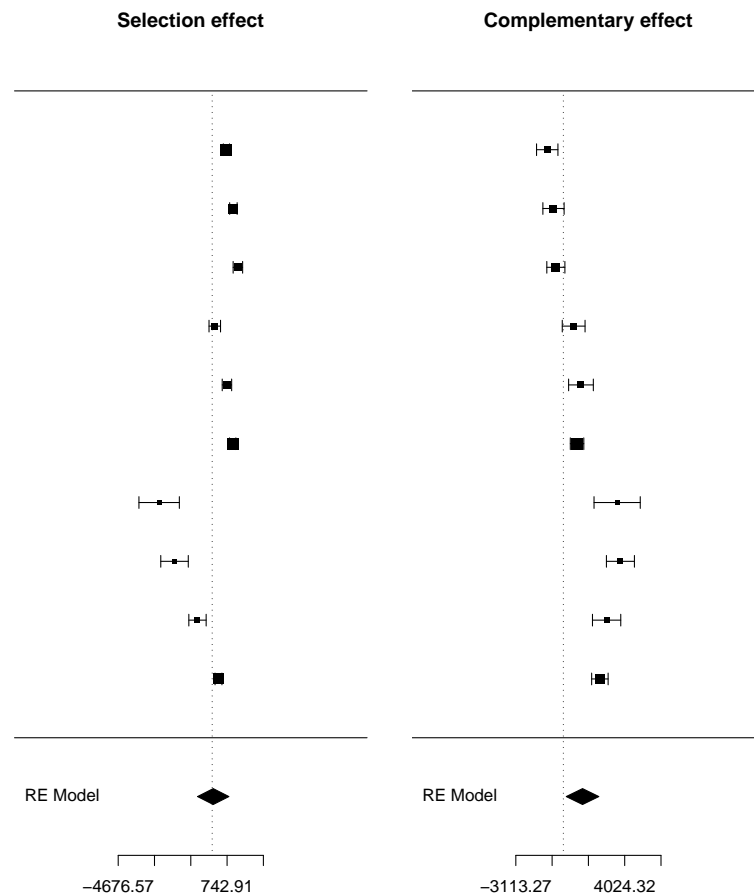


Figure 4.6: Graphical Representation of the selection & complementary effects of paper 9

We note 3 different tendencies, corresponding in fact to 3 different seed proportion of oat (the lowest correspond to the first represented effects). With a low seed density, the complementary effect is obvious, species stimulate each other.

At the highest densities, there is an inverse phenomenon : oat dominates bean.

The sensitivity analysis showed influences of 2 studies, in which the lack of commercial fertilizer and/or water, and a too important seed density provokes a lack of competition, in favour of a dominance of one of the species. The use of specific cultures in intercropping may also play a role on this phenomenon.

A publication bias is explained by the fact that some studies do not show what they have, but what they *want* to have. In this analysis, studies wanted to prove the benefit of intercropping through the LER index and not through these double effects. For these reasons, we will not develop a publication bias study for the 2 effects.

Conclusion

We notice this time a strong influence of 2 studies, the first being large, with an inefficacy of intercropping because of a large negative complementary effect and a small positive selection effect, and the second with an important variability according to the proportion used to grow the dominant culture (oat). However, the other effects reveal a competition between species, then a real benefit of the intercropping practice.

So far, we did not consider effect measures were in studies, but we noticed however some study effects. Therefore, a variation within study and between study can be taken into account to improve the model and our statement.

Chapter 5

Meta analysis : Second approach

This time, mixtures are not considered as independent, but included in studies. Therefore, between-mixture and between-study variation are taken into account.

5.1 Modeling

The effect measure for the j^{th} mixture in the i^{th} study could be modeled as it follows :

$$Y_{ij} = A_{ij} + \varepsilon_{ij} , \quad \begin{array}{l} \varepsilon_{ij} \sim N(0, s_{ij}^2) \\ A_{ij} \sim N(B_i, \tau_i^2) \end{array}$$

i.e

$$A_{ij} = B_i + \xi_{ij} , \quad \begin{array}{l} \xi_{ij} \sim N(0, \tau_i^2) \\ B_i \sim N(\mu, \sigma^2) \end{array}$$

It follows that :

$$Y_{ij} = \mu + \gamma_i + \xi_{ij} + \varepsilon_{ij} , \quad \begin{array}{l} \varepsilon_{ij} \sim N(0, s_{ij}^2) \\ \gamma_i \sim N(0, \sigma^2) \\ \xi_{ij} \sim N(0, \tau_i^2) \end{array}$$

As a consequence, the variance matrix of Y is a block matrix (if k is the number of studies, and n_i the number of experiments in study i) :

$$Var(Y) = \mathbf{V} = \begin{pmatrix} \mathbf{B}_1 & 0 & 0 & \dots & 0 \\ 0 & \mathbf{B}_2 & 0 & \dots & 0 \\ \dots & \dots & \dots & \dots & \dots \\ 0 & \dots & \dots & \dots & \mathbf{B}_k \end{pmatrix}$$

and

$$\mathbf{B}_i = \begin{pmatrix} s_{i1}^2 + \tau_i^2 + \sigma^2 & \sigma^2 & \dots \\ \sigma^2 & s_{i2}^2 + \tau_i^2 + \sigma^2 & \sigma^2 \\ \sigma^2 & \dots & s_{in_i}^2 + \tau_i^2 + \sigma^2 \end{pmatrix}$$

5.2 Method and results

We note a more complicated model because of the covariance of Y, σ^2 . The method would then, as studies are reasonably considered as independent, to lead a meta analysis in 2 steps : For each study, estimate the mean effect and its standard error; afterwards use these new results to estimate the overall mean effect and σ^2 . In some ways, we lead 8 meta analysis (for each study), then a last one with all mean study effects.

In the following, results will be compared with the one from the first approach (see page 24).

5.2.1 LER estimations

```

Tau^2
[1] 0.000000000 0.002456713 0.000000000 0.009257221 0.068864560 0.000000000
[7] 0.001333113 0.000000000

Mean effect per study
[1] 1.102187 1.150058 1.149962 1.178249 1.166468 1.202671 1.083167 1.008455
se(Mean effect per study)
[1] 0.05383532 0.03422608 0.02114593 0.07898863 0.20923206 0.03455759 0.03083643
[8] 0.02646416

sigma^2 (estimate of total amount of heterogeneity): 0.0036 (SE = 0.0029)
sigma (sqrt of the estimate of total heterogeneity): 0.0596
I^2 (% of total variability due to heterogeneity): 73.7%

Test for Heterogeneity:
Q(df = 7) = 28.2506, p-val = 2e-04

```

Model Results:

estimate	se	test	p-value	Confidence Interval
1.1207	0.0266	42.0579	0.0000	1.0685 1.1730 ***

The mean estimation remains the same, but a larger interval, in adequation with a large heterogeneity. The difference of heterogeneity compared with the first part is due to the fact that the within study variation is very small, then the between study variation is larger : As a consequence, this technic allows us to detect where the variability comes from. Here, it is clearly due to differences between studies.

5.2.2 The double effect estimations

SELECTION EFFECT

```

Mean effect per study
[1] 355.93309 -29.63122 86.99683 28.13834 -37.89256 37.54898 -60.47740
[8] 53.55361
se(Mean effect per study)
[1] 37.29896 21.93535 21.38700 43.59502 85.07029 53.88135 110.89567
[8] 398.05046

sigma^2 (estimate of total amount of heterogeneity): 18220.86 (SE = 12255.18)
sigma (sqrt of the estimate of total heterogeneity): 134.9847
I^2 (% of total variability due to heterogeneity): 92%

```

Model Results:

estimate	se	test	p-value	Confidence Interval
63.8059	54.8208	1.1639	0.2445	-43.6410 171.2527

COMPLEMENTARY EFFECT

```

Mean effect per study
[1] 305.4820 -523.0890 -3375.2383 1487.6033 472.3606 667.3891 473.5123
[8] 1261.5355

```

```

se(Mean effect per study)
[1] 151.3047 163.8788 155.8710 727.5789 561.6030 104.1883 145.6815 545.3527

sigma^2 (estimate of total amount of heterogeneity): 2288904 (SE = 1297869)
sigma (sqrt of the estimate of total heterogeneity): 1512.912
I^2 (% of total variability due to heterogeneity): 98.6%

Model Results:
estimate   se           test    p-value   Confidence Interval
42.3429   551.3303     0.0768   0.9388   -1038.2447  1122.9304

Tau^2 Selection effect
[1]      0.000      0.000  10159.856   2433.125      0.000  32438.854
[7]  84463.452 1536677.259

Tau^2 Complementary effect
[1]      0.0 101664.2 438907.1 1357499.4 472869.5      0.0      0.0
[8] 2797927.3

```

We note a difference of heterogeneity with the 1st approach for the selection effect because it was mainly due to the last study (see graphic 4.6), for which the within variation is high. The mean effect is lower ($\hat{\mu} = 73$ instead of $\hat{\mu} = 100$) with a larger confidence interval. Therefore, more variable studies (like the publication 9) giving high positive effect has less influence.

The mean complementary effect is now positive, but has a very large standard error, indicating this estimation is very sensitive. This might also mean that this 2-steps method attribute less weight to publication 4, responsible for a large negative mean effect in the first part, because this last counts for only one study. The part of heterogeneity is very high, indicating the origin of the variability is the difference between studies. this is not surprising if we look at the forest plot of the first part (graphic 25).

When removing this last, the complementary effect is much higher, with a smaller heterogeneity, and we find similar results than previously. See annexes page 45.

With all studies, we have a dominance and competition operating together whereas a clear competition advantages is shown when omitting the study 4.

Conclusion

From the classical method to a more elaborated model, the approaches dealt with 3 effect sizes to give different perspectives to a single question : Has intercropping got benefic effects on grain yields ?

Principal results are summed up in the following table :

		1 st approach all studies	1 st approach study 4 omitted	2 st approach all studies	2 st approach study 4 omitted
LER	Mean effect	1.12	NA	1.12	NA
	σ	0.04	NA	0.06	NA
	% heterogeneity	13.7%	NA	73.7%	NA
Selection effect	Mean effect	100.5	85.1	63.8	57.94
	σ	327.9	475.2	135	149.4
	% heterogeneity	96.1 %	97.3%	92%	90.4%
Complementary effect	Mean effect	-922.6	603	42.3	440.1
	σ	2144	877.5	1512.9	513.3
	% heterogeneity	96.9%	88%	98.6%	88%

Figure 5.1: Summary table of different technics used

The Land Equivalent Ratio (or LER), above 1 in all analysis proves the efficiency to intercrop cereals and legume, even it was more adapted to the classical model, as the mean effect test was very significant. Also, the measure was considered as homogeneous, proving there was very small variability between different experiments. The last analysis revealed the heterogeneity (even very small) was due to the difference between studies. However, an important publication bias has been predicted, suspecting many measures under 1 were not published.

The selection and complementary effects, analyzed together, suggested this benefit was due to one of the 2 species dominance, whereas the competition was inefficient, yet it is a fundamental principle of intercropping.

However, one study has a strong influence in the results and was responsible of a large negative complementary effect. When omitting it, we got an important complementary effect of species whereas the selection effect remained positive but lower.

An other paper presented an important within-variability, according the seed proportion cultivated in intercropping, and contributed to a large heterogeneity.

As for the last approach, because the influence of very variable studies was less important, it concluded a more or less balance between dominance and complementarity, even if it was more sensitive.

Finally, a benefit from this practice was observed through all analysis led, but it also reminded us that depends on the culture practices, such as use of fertilizers, provided water, type of crops or seed proportion.

Nevertheless, the different approaches did not consider the covariance existing between experiments of a same study, something it has to be developed in theory, but also for the software **R**.

Personal Outcome

I was hesitant to go there because the subject was quite hard, I had never met my supervisor, and it was not a English-speaking country. But I like challenges, so I decided to spent my summer there for a new adventure.

Danes speak very well English, so the language was not a problem, my supervisor is a very nice person and this experience brought me much more than expected in terms of relationships and culture.

As for the subject, it was obscure at first because my work consisted in doing a meta analysis, something I did not know, but the project was really interesting, exactly the kind of topic I wanted to deal with : By proving that farming practices can be an advantage for people and Environment protection, my work would contribute to bring concrete solutions for the sustainable development.

From meta analysis to biodiversity and Agriculture, I improved my knowledge and it gave me clearer ideas of my future career, and what I should expect when confronting data in real context.

Annexes

Preliminaries

Calculation of mixture variance

In each experiment, two species are intercropped, so we can write the yield Y as a vector of 4 components corresponding to the pure yield of each species and their respective intercrop yields :

$$\mathbf{Y} = \begin{pmatrix} Y_1 \\ Y_2 \\ Y_{I_1} \\ Y_{I_2} \end{pmatrix}$$

Our interest is to find an expression of the variance of 2 measures, the selection effect (SE) and the complementary effect (CE) which expressions are :

$$SE = 2 \cdot cov(R_Y, Y_p) = \sum_{i=1}^2 (R_{Y_i} - \bar{R}_Y)(Y_{p_i} - \bar{Y}_p)$$
$$CE = 2 \cdot \bar{R}_Y \cdot \bar{Y}_p$$

with

$$Y_{p_i} = sp_i \times Y_i$$

$$R_{Y_i} = \frac{Y_{I_i}}{Y_{p_i}} - 1$$

$$\bar{R}_Y = \frac{1}{2} \sum_{i=1}^2 R_{Y_i}$$

$$\bar{Y}_p = \frac{1}{2} \sum_{i=1}^2 Y_{p_i}$$

and

- Y_{p_i} is the crop monoculture yield of the i^{th} species in the seed proportion sp_i , corresponding to the seed proportion used in the intercropping for this species ;
- Y_{I_i} is the crop yield obtained for the i^{th} species ($i \in 1, 2$);
- Y_i represents the crop yield per unit area (the pure yield).

These two functions can be summed up as :

$$\begin{pmatrix} SE \\ CE \end{pmatrix} = \begin{pmatrix} f_1 \\ f_2 \end{pmatrix} (Y) = f(Y)$$

The idea is to find an approximation of $f(Y)$ as linear expression, $f(Y) \simeq AY + \text{constant}$, so that

$$\text{Var} \begin{pmatrix} SE \\ CE \end{pmatrix} = \text{var}(f(Y)) \simeq \text{var}(AY + \text{constant}) = A \cdot \text{var}(Y) \cdot {}^t A$$

By a Taylor Young development, we can write :

$$\begin{aligned} f(Y) &\simeq f(\mathbb{E}Y) + \Delta f(\mathbb{E}Y)(Y - \mathbb{E}Y) \\ &\simeq \Delta f(\mathbb{E}Y)Y + (f(\mathbb{E}Y) - \Delta f(\mathbb{E}Y)\mathbb{E}Y) \end{aligned} \quad (5.1)$$

when

- $\mathbb{E}Y$ is the expectancy of Y
- Δf is the gradient of f , a \mathbb{R}^2 -function defined on \mathbb{R}^4

As a result, we have :

$$f(Y) \simeq AY + c$$

and

$$\begin{aligned} A &= \Delta f(\mathbb{E}Y) \\ c &= f(\mathbb{E}Y) - \Delta f(\mathbb{E}Y)\mathbb{E}Y \end{aligned} \quad (5.2)$$

Calculation of A

Let's write the selection effect (SE) and the complementary effect (CE) as a function of Y :

$$\begin{aligned} SE &= \frac{1}{2} \left(Y_{I_1} + Y_{I_2} - \frac{Y_{I_1} sp_2 Y_2}{sp_1 Y_1} - \frac{Y_{I_2} sp_1 Y_1}{sp_2 Y_2} \right) \\ CE &= \frac{1}{2} \left(Y_{I_1} + Y_{I_2} + \frac{Y_{I_1} sp_2 Y_2}{sp_1 Y_1} + \frac{Y_{I_2} sp_1 Y_1}{sp_2 Y_2} - 2sp_1 Y_1 - 2sp_2 Y_2 \right) \end{aligned} \quad (5.3)$$

Moreover, we can estimate $\mathbb{E}Y$ by \bar{Y} , the mean grain yield observed, so the approximation of $\Delta f(\mathbb{E}Y)$ has the following form :

$$A = \Delta f(\mathbb{E}Y) \simeq \frac{1}{2} \begin{bmatrix} \frac{\bar{Y}_{I_1} sp_2 \bar{Y}_2}{sp_1 \bar{Y}_1^2} - \frac{\bar{Y}_{I_2} sp_1}{sp_2 \bar{Y}_2} & \frac{\bar{Y}_{I_2} sp_1 \bar{Y}_1}{sp_2 \bar{Y}_2^2} - \frac{\bar{Y}_{I_1} sp_2}{sp_1 \bar{Y}_1} & 1 - \frac{sp_2 \bar{Y}_2}{sp_1 \bar{Y}_1} & 1 - \frac{sp_1 \bar{Y}_1}{sp_2 \bar{Y}_2} \\ \frac{sp_1 \bar{Y}_{I_2}}{sp_2 \bar{Y}_2} - \frac{\bar{Y}_{I_1} sp_2 \bar{Y}_2}{sp_1 \bar{Y}_1^2} - 2sp_1 & \frac{sp_2 \bar{Y}_{I_1}}{sp_1 \bar{Y}_1} - \frac{\bar{Y}_{I_2} sp_1 \bar{Y}_1}{sp_2 \bar{Y}_2^2} - 2sp_2 & 1 + \frac{sp_2 \bar{Y}_2}{sp_1 \bar{Y}_1} & 1 + \frac{sp_1 \bar{Y}_1}{sp_2 \bar{Y}_2} \end{bmatrix}$$

The same can be done with the LER :

$$LER = \frac{Y_{I_1}}{Y_1} + \frac{Y_{I_2}}{Y_2}$$

and the expression for A is :

$$A = \Delta f(\mathbb{E}Y) \simeq \begin{bmatrix} -\frac{\bar{Y}_{I_1}}{\bar{Y}_1^2} & -\frac{\bar{Y}_{I_2}}{\bar{Y}_2^2} & \frac{1}{\bar{Y}_1} & \frac{1}{\bar{Y}_2} \end{bmatrix} \quad (5.4)$$

For each experiment, we can easily calculate A with \mathbf{R} and its transposed matrix.

Now, we have to express the variance-covariance matrix of Y with the variance measures supplied by the studies. Indeed, the analysis of variance carried out for each study allows us to make a reasonable approximation of $var(Y)$.

Use of analysis of variance

The publications provide several variance index enumerated below :

1. The Mean Square Error (MSE) of an experiment
Under conditions of normality and independency,

$$MSE = \hat{\sigma}^2$$

2. The coefficient of variation (CV) for each species
It is defined as the ratio of the standard deviation σ to the mean μ :

$$C_v = \frac{\sigma}{\mu}$$

3. The Standard Error (SE) of the mean
It is defined as the ratio of σ to the sample size square root :

$$SE = \frac{\sigma}{\sqrt{n}}$$

4. The Least Significant Difference (LSD)
The expression is :

$$LSD = \sigma \cdot t_{1-\frac{\alpha}{2}} \cdot \sqrt{\frac{2}{n}}$$

- The LSD is used to compare several groups, so n corresponds to the number of observations contained in each group (this number must be the same for each group);
- $t_{1-\frac{\alpha}{2}}$ is the quantile value with the degree of freedom of the error. It is reasonable to approximate it by 2;
- α is the test level (usually $\alpha = 5\%$).

Some assumptions can be deduced by studies, and others are assumed to figure out $Var(Y)$.

1. Due to lack of information, we assume $cov(Y_a, Y_b) = 0, \forall a \neq b$
2. $var(Y_1) = var(Y_{I_1})$ and $var(Y_2) = var(Y_{I_2})$
3. In case of mean yields provided for each level of a factor (e.g. 3 different nitrogen amounts used as fertilizer), $var(Y_{i,N_1}) = var(Y_{i,N_2}) = var(Y_{i,N_3}), \forall i \in \{1, 2\}$

As the yields obtained correspond to the mean yields (we don't have the original data) of yields from a number of combinations _ let's say m combinations _ we have, for example for \bar{Y}_1 :

$$\bar{Y}_1 = \frac{1}{m} \sum_{i=1}^m Y_{1(i)} \Rightarrow \text{var}(\bar{Y}_1) = \frac{\hat{\sigma}^2}{m}$$

This $\hat{\sigma}^2$ can be deduced from one of the variance index enumerated above. Thus, we can deduce $\text{Var}(Y)$, knowing the number of combinations there was required to get the mean yields and assuming the above hypothesis.

Once we get $\text{var}(Y)$, we can deduce the variance-covariance matrix of the effects, because, as you remind :

$$\text{Var} \begin{pmatrix} SE \\ CE \end{pmatrix} = \text{var}(f(Y)) \simeq \text{var}(AY + \text{constant}) = A \cdot \text{var}(Y) \cdot {}^t A$$

Restricted Maximum Likelihood

The method of the Restricted Maximum Likelihood, or REML, has been developed to correct a bias, and it is very used in meta analysis. Indeed, it allows a estimation of μ , σ^2 in the model :

$$Y_i = A_i + \varepsilon_i, \quad \begin{array}{l} \varepsilon_i \sim N(0, s_i^2) \\ A_i \sim N(\mu, \sigma^2) \end{array}$$

The REML expression is :

$$\log L(Y, \mu, \tau^2, \sigma^2) = -\frac{1}{2} \log|\det(V)| - \frac{1}{2} \log|\det({}^t \mathbf{1} V^{-1} \mathbf{1})| - \frac{1}{2} {}^t (Y - \mu \mathbf{1}) V^{-1} (Y - \mu \mathbf{1})$$

when

$$V = \text{Var}(Y) = \begin{pmatrix} s_1^2 & 0 & \dots & \dots \\ 0 & s_2^2 & 0 & \dots \\ \dots & \dots & \dots & \dots \\ \dots & \dots & \dots & s_n^2 \end{pmatrix} + \sigma^2 I_n$$

$$\mu = \frac{\sum_{i=1}^n w_i Y_i}{\sum_{i=1}^n w_i}$$

$$w_i = \frac{1}{s_i^2 + \sigma^2}, \quad \forall i \in \{1, \dots, n\}$$

The heterogeneity test

The test for heterogeneity tests the hypothesis(in our case, we have 80 effect measures) :

$$H_0 : \mu = A_1 = \dots = A_{80} \text{ against}$$

$$H_1 : \exists(i, j) A_i \neq A_j$$

$$\text{Under } H_0, Q = \sum_{i=1}^{80} w_i (Y_i - \hat{\mu})^2 \sim \chi_{79}^2$$

where

$$\hat{\mu} = \frac{\sum_{i=1}^{80} w_i Y_i}{\sum_{i=1}^{80} w_i}$$
$$w_i = \frac{1}{s_i^2}$$

If the p-value is under the significative level α (usually 0.05), the hypothesis H_0 is rejected, so we can not talk about homogeneity, i.e there is a significant difference between mixture effects, therefore a between-mixture variation has to be considered; thus σ^2 , the between-study variation is significantly different from 0.

Meta analysis : First approach

LER

The trim and fill method

The *trimfill* function of **R** gives the following results :

```
> Number of studies added  
[1] 26
```

		95%-CI	z	p.value
Fixed effect model	1.0756	[1.0559; 1.0953]	106.9780	< 0.0001
Random effects model	1.0782	[1.0525; 1.1040]	82.1514	< 0.0001

Quantifying heterogeneity:

tau² = 0.0057; H = 1.24 [1.1; 1.39]; I² = 34.5% [16.7%; 48.5%]

Test of heterogeneity:

Q	d.f.	p.value
160.32	105	0.0004

The Copas function

The approach is as followed :

$$X_i = Y_i \cdot \mathbf{1}[z_i > 0]$$

$$Y_i = \mu + \zeta_i + \varepsilon_i, \quad \begin{array}{l} \zeta_i \sim N(0, \sigma^2) \\ \varepsilon_i \sim N(0, s_i^2) \end{array}$$

$$z_i = a + \frac{b}{\eta_i} + \delta_i, \quad \delta_i \sim N(0, 1)$$

$$\text{corr}(Y_i, z_i) = \rho$$

when

- a and b are unknown parameters, $b > 0$;
- η_i is the reported standard deviation of the effect estimate Y_i .

The log-likelihood is now given by the conditional distribution of Y given $z > 0$, and depends on μ , a and b .

As it is impossible to estimate a and b because we do not know anything about unpublished studies, we use the following inequality and equality to deduce a grid of (a, b) pairs, with $b > 0$:

$$0.01 \leq P(\text{article selection}/\eta_i) \leq 0.99$$

$$P(\text{article selection}/\eta_i) = \Phi\left(a + \frac{b}{\eta_i}\right)$$

where Φ is the standard normal cumulative distribution function.

At each point of the grid, we can estimate μ thanks to the log-likelihood maximization.

In parallel, we want to test if the model in Y_i is adapted, we compare it to this model :

$$Y_i = A_i + \beta\eta_i + s_i\varepsilon_i, \quad \varepsilon_i \sim N(0, 1)$$

For each estimation of μ with above technique, we can figure out the corresponding P-values of the likelihood ratio test testing $H_0 : \beta = 0$. Then, we can accept any value of $\hat{\mu}$ associated with a P-value exceeding α (usually $\alpha = 0.05$), meaning that the initial model is valid.

Because the model takes into account the publication, the most reasonable value of $\hat{\mu}$ (with the corresponding between-study variation) is the one associated with a P-value exceeding α and with the highest probability to select the trial.

The selection and complementary effects

The leave-one-out method

Meta results when we remove the study 9 **alone** from analysis :

Selection effect

sigma (sqrt of the estimate of total heterogeneity): 158.8341

Model Results:

estimate	se	test	p-value	Confidence Interval	
64.8147	22.0088	2.9449	0.0032	21.6783 107.9511	**

Complementary effect

sigma (sqrt of the estimate of total heterogeneity): 2020.013

Model Results:

estimate	se	test	p-value	Confidence Interval	
-1242.1474	249.4785	-4.9790	0.0000	-1731.1163 -753.1785	***

Meta analysis : Third approach

The LER measure

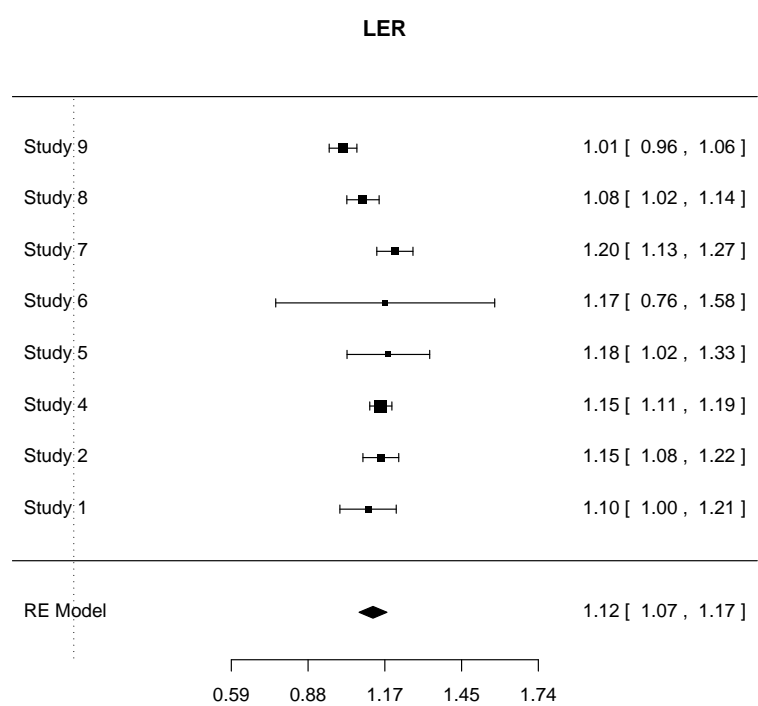


Figure 5.2: Forest plot of the LER

The double effects

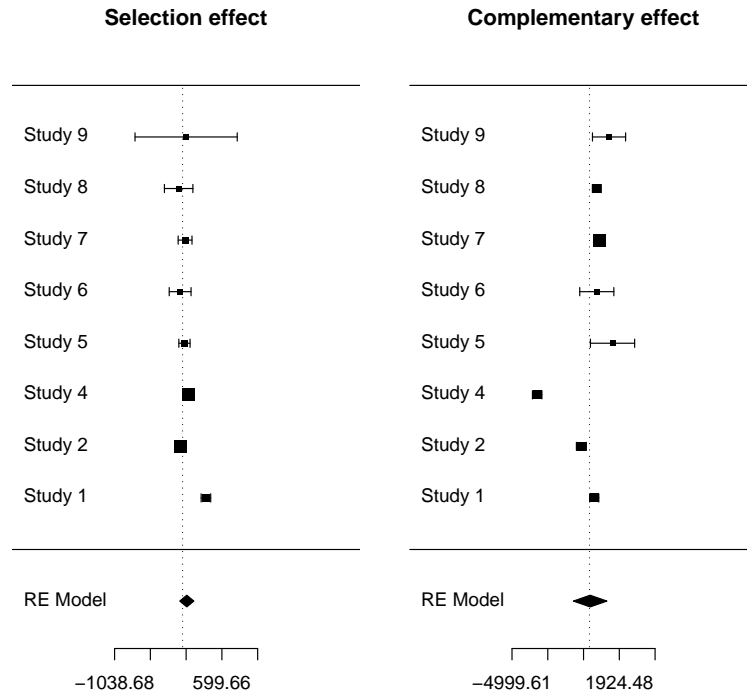


Figure 5.3: Forest plot of the double effects

Analysis on selection and complementary effects when study 4 has been removed:

SELECTION EFFECT

σ^2 (estimate of total amount of heterogeneity): 22328.34 (SE = 16412.64)

σ (sqrt of the estimate of total heterogeneity): 149.4267

I^2 (% of total variability due to heterogeneity): 90.4%

Model Results:

estimate	se	test	p-value	CI
57.9410	65.2131	0.8885	0.3743	-69.8743 185.7564

COMPLEMENTARY EFFECT

σ^2 (estimate of total amount of heterogeneity): 263462.9 (SE = 206781.5)

σ (sqrt of the estimate of total heterogeneity): 513.2864

I^2 (% of total variability due to heterogeneity): 88%

Model Results:

estimate	se	test	p-value	CI
440.0810	230.2263	1.9115	0.0559	-11.1542 891.3162

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