

## Evidence for resilient agriculture for Land Equivalent Ratio Outcomes

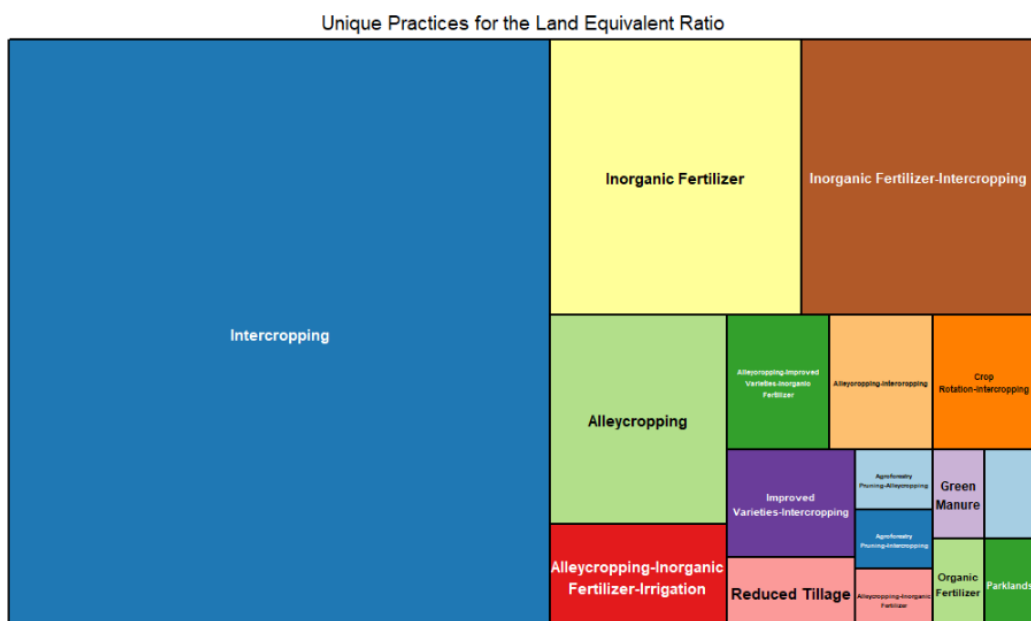
The data we are interested in, is the one the one only with **Land Equivalent Ratio**. After subsetting our data in this regard, we will be using **ERA\_LER** having **808** observations and **142** variables.

### Let's look at the effect on ERA practices on LER

First of all, we have in total **17 practices** for this specific LER outcome

- 1) "Agroforestry Pruning-Alleycropping"
- 2) "Alleycropping"
- 3) "Alleycropping-Improved Varieties-Inorganic Fertilizer"
- 4) "Alleycropping-Inorganic Fertilizer-Irrigation"
- 5) "Alleycropping-Inorganic Fertilizer"
- 6) "Intercropping"
- 7) "Inorganic Fertilizer-Intercropping"
- 8) "Inorganic Fertilizer"
- 9) "Improved Varieties-Intercropping"
- 10) "Reduced Tillage"
- 11) "Parklands"
- 12) "Green Manure"
- 13) "Crop Rotation-Intercropping"
- 14) "Agroforestry Pruning-Intercropping"
- 15) "Alleycropping-Intercropping"
- 16) "Organic Fertilizer"
- 17) "Inorganic Fertilizer-Organic Fertilizer"

Let's visualize this on the treemap to see their number before looking at the effects



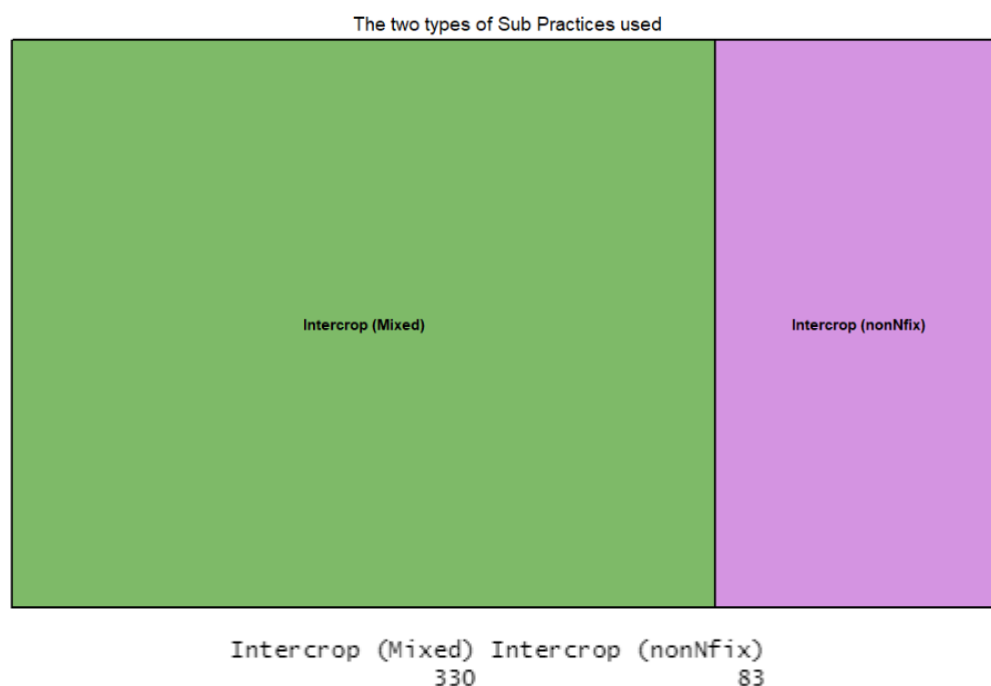
Agroforestry Pruning-Alleycropping	36	Agroforestry Pruning-Intercropping	16
Alleycropping	49	Alleycropping-Improved Varieties-Inorganic Fertilizer	8
Alleycropping-Inorganic Fertilizer	2	Alleycropping-Inorganic Fertilizer-Irrigation	10
Alleycropping-Intercropping	8	Crop Rotation-Intercropping	27
Green Manure	6	Improved Varieties-Intercropping	23
Inorganic Fertilizer	87	Inorganic Fertilizer-Intercropping	92
Inorganic Fertilizer-Organic Fertilizer	8	Intercropping	413
Organic Fertilizer	16	Parklands	3
Reduced Tillage	4		

So we can see many intercropping practices **413** compare to others.

Let's subset again on the intercropping practices.

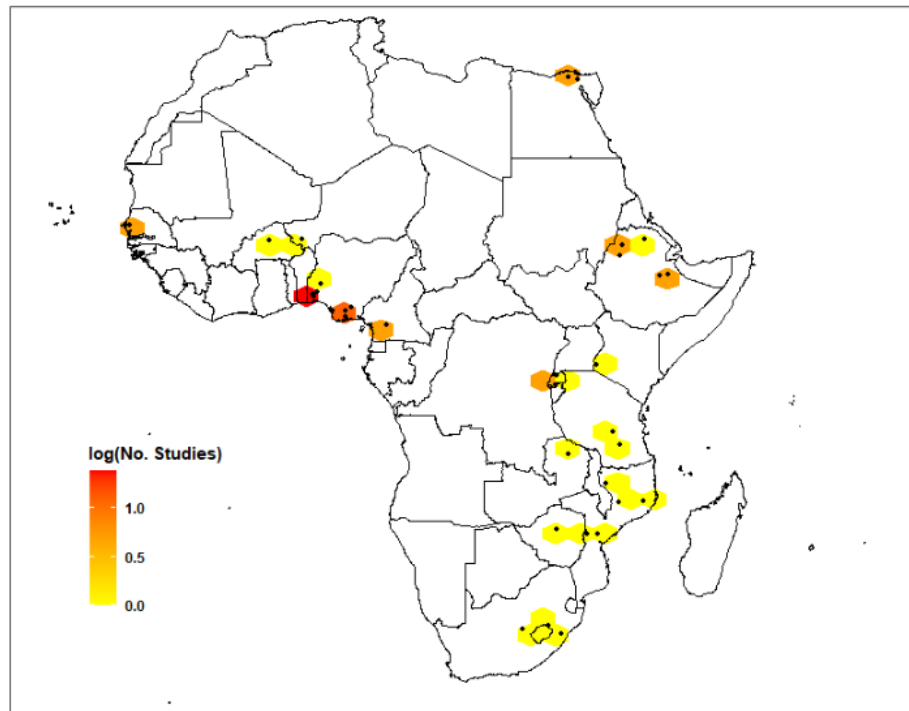
```
Data_LER_inter <- Data_LER[Data_LER$PrName == "Intercropping", ]
```

We have a new subset of data with the for LER outcome for intercropping practice. This data has **413 observations** and **142 variables**



### Intercrop (Mixed) & Intercrop nonNfix

Let's first check where these practices are



We can also see the distribution in percentage

Burkina Faso	Cameroon	Egypt	Ethiopia	Kenya	Mozambique	Niger	Nigeria	Rwanda
7.7	2.4	4.4	6.3	15.5	11.6	2.2	32.4	2.9
Senegal	South Africa	Tanzania	Zambia	Zimbabwe				
2.9	5.6	1.7	3.9	0.5				

### Number of practices Studies reporting LER

Since we have many observations with the same Codes (same Authors), a single study corresponds to the unique same name within a column.

### Intercropping

For intercropping reporting LER, we have a total of **413** observations. The corresponding number of Studies is **30**

```
> unique(Data_LER_inter$Code)
[1] "NN0058" "NN0130.3" "NN0142" "NN0250" "LM0141" "HK0043" "HK0093" "HK0135" "HK0181" "HK0233" "HK0249"
[12] "HK0300" "JS0223" "AN0005" "AN0062" "AN0076" "AG0025" "AG0078" "AG0091" "AG0104" "AG0120" "AG0137"
[23] "DK0016" "DK0117" "DK0148" "E00019" "E00024" "E00094" "NJ0075" "NJ0148"
```

### Inorganic Fertilizer-Intercropping

Here we have a total of **92** observations and the number of Studies is **5**

```
> unique(Data_LER_Inor_fert_inter$Code)
[1] "NN0058" "NN0142" "HK0093" "HK0233" "JS0064"
```

### Inorganic Fertilizer

Here we have a total of **87** observations and the number of Studies is **5**

```
> unique(Data_LER_Inor_fert$Code)
[1] "NN0142" "LM0066" "HK0093" "HK0233" "AG0078"
```

### **Alleycropping**

Here we have a total of **49** observations and the number of Studies is **4**

```
> unique(Data_LER_Alleycro$Code)
[1] "LM0279" "JS0152" "JS0204" "DK0117"
```

### **Agroforestry Pruning-Alleycropping**

Here we have a total of **36** observations and the number of Studies is **1**

```
> unique(Data_LER_Agro_prun_Alle$Code)
[1] "LM0173"
```

### **Crop Rotation-Intercropping**

Here we have a total of **27** observations and the number of Studies is **1**

```
> unique(Data_LER_crop_rot_inter$Code)
[1] "JS0078"
```

### **Improved Varieties-Intercropping**

Here we have a total of **23** observations and the number of Studies is **2**

```
> unique(Data_LER_impr_var_inter$Code)
[1] "NN0250" "JS0064"
```

### **Agroforestry Pruning-Intercropping**

Here we have a total of **16** observations and the number of Studies is **1**

```
> unique(Data_LER_Agro_prun_inter$Code)
[1] "JS0164"
```

### **Organic Fertilizer**

Here we have a total of **16** observations and the number of Studies is **1**

```
> unique(Data_LER_Org_fert$Code)
[1] "AG0078"
```

### **Alleycropping-Inorganic Fertilizer-Irrigation**

Here we have a total of **10** observations and the number of Studies is **1**

```
> unique(Data_LER_Ally_Inor_fert_irri$Code)
[1] "JS0116"
```

### **Alleycropping-Intercropping**

Here we have a total of **8** observations and the number of Studies is **1**

```
> unique(Data_LER_Agro_Alle_inter$Code)
[1] "JS0204"
```

### **Alleycropping-Improved Varieties-Inorganic Fertilizer**

Here we have a total of **8** observations and the number of Studies is **1**

```
> unique(Data_LER_Agro_Alle_impro_var_inor_fer$Code)
[1] "JS0116"
```

### **Inorganic Fertilizer-Organic Fertilizer**

Here we have a total of **8** observations and the number of Studies is **1**

```
> unique(Data_LER_inor_fer_org_fer$Code)
[1] "AG0078"
```

### **Reduced Tillage**

Here we have a total of **4** observations and the number of Studies is **1**

```
> unique(Data_LER_redu_tillage$Code)
[1] "HK0041"
```

### **Parklands**

Here we have a total of **3** observations and the number of Studies is **1**

```
> unique(Data_LER_parklands$Code)
[1] "JS0042"
```

### **Alleycropping-Inorganic Fertilizer**

Here we have a total of **2** observations and the number of Studies is **1**. This is the same practice we had on *Alleycropping-Inorganic Fertilizer-Irrigation*.

```
> unique(Data_LER_All_Inorg_fert$Code)
[1] "JS0116"
```

This is the diversity we have for our **Data\_LER\_inter**, 48 of them

[1] "Pearl millet-Cowpea"	"Yam-Maize"	"Yam-Maize-Mucuna"
[4] "Yam-Maize-Lima Bean"	"Yam-Maize-African Yam Bean"	"Yam-Maize-Cassava"
[7] "Yam-Maize-Cassava-Mucuna"	"Yam-Maize-Cassava-Lima Bean"	"Yam-Maize-Cassava-African Yam Bean"
[10] "Cassava-Maize"	"Cassava-Maize-Mucuna"	"Cassava-Maize-Lima Bean"
[13] "Cassava-Maize-African Yam Bean"	"Maize-Pigeon pea"	"Maize-Cowpea"
[16] "Maize-Bean"	"Cassava-Maize-Melon"	"Cassava-Maize-Groundnut"
[19] "Cassava-Maize-Cowpea"	"Melon-Maize"	"Melon-Cassava"
[22] "Sorghum-Bean"	"Sorghum-Soybean"	"Cowpea-Cotton"
[25] "Cotton-Wheat"	"Cowpea-Finger Millet"	"Finger Millet-Mung Bean"
[28] "Common Bean-Okra"	"Maize-Okra"	"Common Bean-Maize-Okra"
[31] "Butter Bean-Maize"	"Cowpea-Pearl Millet"	"Groundnut-Rice"
[34] "Cassava-Cowpea"	"Maize-Soybean"	"Common Bean-Maize"
[37] "Cowpea-Maize"	"Maize-Mung Bean"	"Groundnut-Maize"
[40] "Maize-Pigeon Pea"	"Cassava-Okra"	"Cassava-Pepper"
[43] "Cassava-Pumpkin"	"Lablab-Maize"	"Lablab-Lablab"
[46] "Barley-Fava Bean"	"Calabash-Sorghum"	"Cowpea-Sorghum"

Overall, let's see what we have for **every outcome** with **intercropping** practice in term of **diversity** in our **whole dataset**,

```
[1] "The diversity is 130 for Crop Yield"
[1] "The diversity is 60 for Biomass Yield"
[1] "The diversity is 26 for Soil Nitrogen"
[1] "The diversity is 21 for Soil Organic Carbon"
[1] "The diversity is 0 for Weight Gain"
[1] "The diversity is 0 for Meat Yield"
[1] "The diversity is 6 for Water Use"
[1] "The diversity is 8 for Water Use Efficiency"
[1] "The diversity is 30 for Soil Moisture"
[1] "The diversity is 1 for Pest & Pathogen (Losses)"
[1] "The diversity is 1 for Pest & Pathogen (Numbers)"
[1] "The diversity is 0 for Feed Conversion Ratio (Out In)"
[1] "The diversity is 32 for Gross Return"
[1] "The diversity is 17 for Variable Cost"
[1] "The diversity is 15 for Gross Margin"
[1] "The diversity is 3 for Soil Organic Matter"
[1] "The diversity is 8 for Cation Exchange Capacity"
[1] "The diversity is 0 for Milk Yield"
[1] "The diversity is 0 for Nitrogen Use Efficiency (ARE AGB)"
[1] "The diversity is 0 for Phosphorus Use Efficiency (ARE AGB)"

[1] "The diversity is 0 for Effective Cation Exchange Capacity"
[1] "The diversity is 0 for Phosphorus Agronomic Efficiency"
[1] "The diversity is 0 for Nitrogen Use Efficiency (Isotopic AGB)"
[1] "The diversity is 0 for Protein Conversion Ratio (In Out)"
[1] "The diversity is 0 for Methane Emissions"
[1] "The diversity is 0 for CO2 Equivalent Emissions"
[1] "The diversity is 48 for Land Equivalent Ratio"
[1] "The diversity is 0 for Benefit Cost Ratio (NRVC)"
[1] "The diversity is 7 for Net Present Value"
[1] "The diversity is 3 for Phosphorus Use Efficiency (ARE Product)"
```

This shows us first that **intercropping practice** does not only gives us **LER outcome** indeed we also have **Crop Yield Outcome 0.31% (Diversity)**; **Biomass Yield outcome 0.37% (Diversity)**; **Land Equivalent Ratio outcome 5.94% (Diversity)**

$8/808*100=5.94\%$       413 in total

$130/41093*100 = 0.31\%$       1850 in total

$60/15956*100 = 0.37\%$       572 in total

From this study we can conclude that, **Intercropping Practice is applied to get various outcomes among the ones we are using but for the LER outcomes, we have more diversity than other outcomes.**

## ERAAAnalyse function

Here I will group some column (Variable) names and check their statistics

### Aggregate By Out.SubInd:

We already know all our outcome are **Land Equivalent Ratio** but we are aggregating by this in order to have more information. By setting **rmOut** = T four extreme outliers have been removed in the row numbers **97, 101, 165, 578**

### Aggregate By PrName:

R	[data.table]
Data	
bysub1	List of 2
byval	List of 1
groups	List of 1
SEnv	Environment
x	805 obs. of 145 variables
Values	
allbyvars	"PrName"
allcols	chr [1:145] "Index" "Code" "Author" "Date" "Journal" "DOI" "Elevation" "Country" "ISO.316
allow.cartesian	allbyvars (character, "datatable.allow.cartesian")
ansvals	112 bytes) 2 93 52 51 145 50
ansvars	chr [1:6] "Code" "ID" "MeanT" "MeanC" "Weight.Study" "Units"
av	chr [1:28] "list" ".N" "length" "unique" "Code" "ID" "round" "FunShap" "log" "/" "MeanT"
backslash_idx	integer (empty)
backtick_idx	1L
by	Aggregate.By
byindex	FALSE
byjoin	FALSE
bynames	"PrName"
bynull	FALSE
bysameorder	FALSE
bysub	list(PrName)
bysuborig	Aggregate.By
byvars	"PrName"
cols	NULL
drop	NULL
f__	int [1:17] 1 37 86 94 104 106 518 610 696 719 ...
firsttoeachgroup	int [1:17] 1 37 46 47 57 74 83 166 278 308 ...
firstopt	FALSE
funi	1L
GForce	FALSE
grpcols	1L
grporder	int [1:805] 1 2 3 4 5 6 7 8 9 10 ...
headopt	FALSE
i	NULL
icols	integer (empty)
icolsAns	integer (empty)
idotprefix	character (empty)
idx	1L
ii	3L
irows	NULL
j	list(Observations = .N, Studies = length(unique(Code)), Sites = length(unique(ID)), R
jiscols	NULL
jj	1L
jsub	list(.N, length(unique(Code)), length(unique(ID)), round(FunShap(log(MeanT/MeanC)),
jvnames	chr [1:16] "Observations" "Studies" "Sites" "RR.Shapiro.Sig" "RR" "RR.median" 1L se" "RR
keyby	FALSE
leftcols	integer (empty)
len__	int [1:17] 36 49 8 10 2 412 92 86 23 4 ...

lhs	NULL
missingby	FALSE
missingnomatch	TRUE
missingroll	TRUE
mult	"all"
names_i	NULL
names_x	chr [1:145] "Index" "Code" "Author" "Date" "Journal" "DOI" "Elevation" "Country" "ISO.316...
naturaljoin	FALSE
newnames	NULL
nomatch	NA_integer_
nomeanopt	FALSE
non_sdvars	character (empty)
notjoin	FALSE
o__	int [1:805] 1 2 3 4 5 6 7 8 9 10 ...
oldjsub	list(.N, length(unique(Code)), length(unique(ID)), round(FunShap(log(MeanT/MeanC))),
on	NULL
optimizedSubset	FALSE
orderedrows	TRUE
origorder	integer (empty)
rightcols	integer (empty)
roll	0
rollends	logi [1:2] FALSE TRUE
root	"list"
sdvars	chr [1:6] "Code" "ID" "MeanT" "MeanC" "Weight.Study" "Units"
subopt	FALSE
subopt	FALSE
sym	NULL
syms	character (empty)
todo	logi [1:17] FALSE FALSE FALSE FALSE FALSE FALSE ...
tt	"PrName"
use.I	FALSE
verbose	FALSE
w	int [1:6] 2 93 52 51 145 50
which	FALSE
with	TRUE
wna	logi [1:6] FALSE FALSE FALSE FALSE FALSE FALSE
xcols	int [1:6] 2 93 52 51 145 50
xcolsAns	int [1:6] 1 2 3 4 5 6
xdotcols	FALSE
xdotprefix	character (empty)
xdotprefixvals	logi [1:6] FALSE FALSE FALSE FALSE FALSE FALSE
xjiscols	NULL
xnrow	805L
unctions	
do_j_names	function (q)
dotN	function (x)
drop_dot	function (x)
dupdiff	function (x, y)
suppPrint	function (x)

```
> ERA.Analyze(Data_LER, rmOut = T, Aggregate.By = "PrName", ROUND = 5, Fast = T)
Error in weighted_se(log(MeanT/MeanC), Weight.Study, na.rm = T) :
  could not find function "weighted_se"
Called from: [.data.table(Data[, `:=`(N.Obs.Study, .N), by = Weight.Group][,
  `:=`(Weight.Study, (Rep^2/(2 * Rep))/N.Obs.Study)],
  , list(Observations = .N, Studies = length(unique(Code)),
  Sites = length(unique(ID)), RR.Shapiro.Sig = round(FunShap(log(MeanT/MeanC)),
  ROUND), RR = weighted.mean(log(MeanT/MeanC), Weight.Study,
  na.rm = T), RR.median = weighted.median(log(MeanT/MeanC),
  Weight.Study, na.rm = T), RR.se = weighted_se(log(MeanT/MeanC),
  Weight.Study, na.rm = T), RR.var = suppressWarnings(abs(wtd.var(log(MeanT/MeanC),
  Weight.Study, na.rm = T))), RR.Quantiles0.5 = paste(round(weighted.quantile(log(MeanT/MeanC),
  Weight.Study, probs = seq(0, 1, 0.25), na.rm = T),
  ROUND), collapse = "|"), PC.Shapiro.Sig = round(FunShap(MeanT/MeanC),
  ROUND), PC = weighted.mean(MeanT/MeanC, Weight.Study,
  na.rm = T), PC.median = weighted.median(MeanT/MeanC,
  Weight.Study, na.rm = T), PC.se = weighted_se(MeanT/MeanC,
  Weight.Study, na.rm = T), PC.var = suppressWarnings(abs(wtd.var(MeanT/MeanC,
  Weight.Study, na.rm = T))), PC.Quantiles0.5 = paste(round(weighted.quantile(MeanT/MeanC,
  Weight.Study, probs = seq(0, 1, 0.25), na.rm = T),
  ROUND), collapse = "|"), Units = if (length(unique(Units)) ==
  1) {
  unique(Units)
  } else {
  "Multiple"
  }
  )), by = Aggregate.By)
```

#### Traceback

☐ Show internals

```
✚ eval(substitute(browse(skipCalls = pos), list(pos = (length(sys.frames()) -
  [.data.table(Data[, `:=`(N.Obs.Study, .N), by = Weight.Group][,
  Data[, `:=`(N.Obs.Study, .N), by = Weight.Group][, `:=`(Weight.Study,
  cbind(Data[, `:=`(N.Obs.Study, .N), by = Weight.Group][, `:=`(Weight.Study,
  ERA.Analyze(Data_LER, rmOut = T, Aggregate.By = "PrName", ROUND = 5,
```