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Westcott method for controlling heterogeneity on the field

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Why?

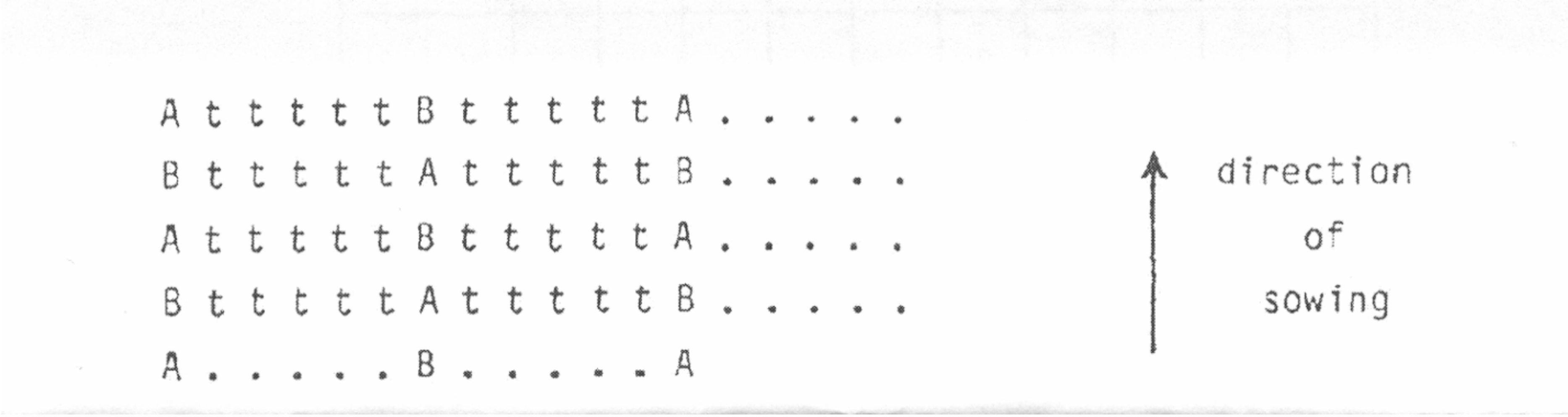
- In the early breeding stages a high number of genotypes are evaluated.
- This means large fields that typically exhibits great variability due to field conditions.
- How to control the heterogeneity on the field?
- Use a grid of checks to map heterogeneity on the field.
- A grid of checks also helps not to get lost on the field.

Westcott method

Implementation of a method proposed by Westcott (1981).

On a rectangular field plant one column of alternating checks (A and B) each *n* columns of testing materials (t).

Checks alternate in rows and columns.



```
A t t t t t B t t t t t A . . . . .
B t t t t t A t t t t t B . . . . .
A t t t t t B t t t t t A . . . . .
B t t t t t A t t t t t B . . . . .
A . . . . . B . . . . . A
```

Westcott, B. (1981). Two methods for early generation yield assessment in winter wheat. In: Proc. of the 4th meeting of the Biometrics in Plant Breeding Section of Eucarpia. INRA Poitier, France, pp 91-95.

Create Fieldbook and Fieldplan

Available in HIDAP and in the st4gi R package (function cd.w).

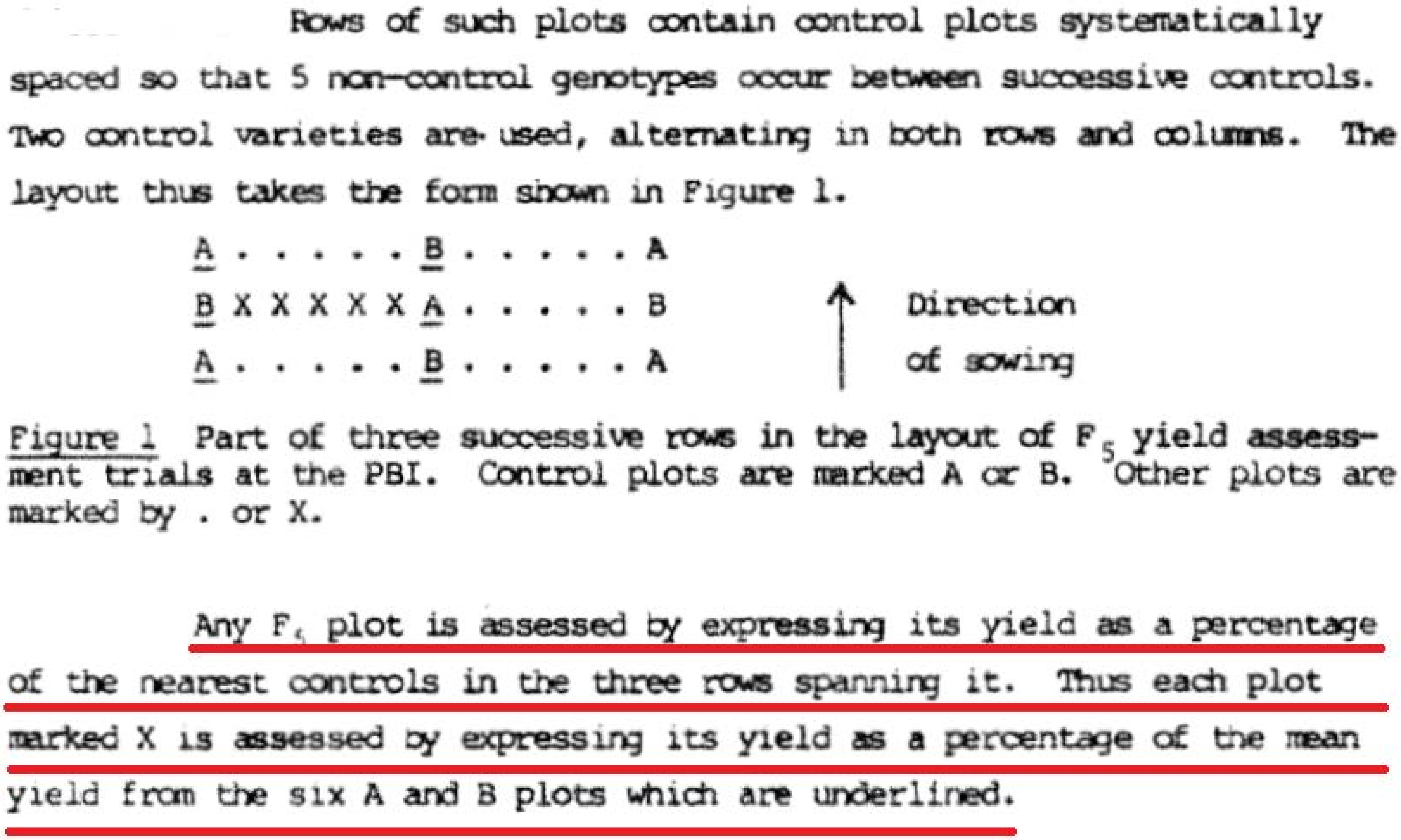
```
> library(st4gi)
> cd.w(geno, "A", "B", 13, 5)
$`plan`
      col 1 col 2  col 3  col 4  col 5  col 6  col 7 col 8  col 9  col 10 col 11 col 12 col 13
row 1 "A"   "t.35" "t.32" "t.4"  "t.19" "t.38" "B"   "t.15" "t.33" "t.37" "t.8"  "t.14" "A"
row 2 "B"   "t.21" "t.40" "t.13" "t.26" "t.16" "A"   "t.3"  "t.17" "t.5"  "t.27" "t.20" "B"
row 3 "A"   "t.2"  "t.12" "t.7"  "t.18" "t.11" "B"   "t.36" "t.34" "t.25" "t.30" "t.29" "A"
row 4 "B"   "t.24" "t.1"  "t.39" "t.6"  "t.10" "A"   "t.23" "t.9"  "t.28" "t.31" "t.22" "B"

$book
   plot row col geno
1     1   1   1    A
2     2   1   2 t.35
3     3   1   3 t.32
4     4   1   4  t.4
5     5   1   5 t.19
6     6   1   6 t.38
7     7   1   7    B
8     8   1   8 t.15
9     9   1   9 t.33
10   10   1  10 t.37
```

Example

High Fe and Zn hybrid population planted in Cañete:

- 272 families, 3292 clones, one replication.
- Each parent and grandparent replicated 8 times.
- 2 checks: Dagga and Cemsa.

Adjusted values



Rows of such plots contain control plots systematically spaced so that 5 non-control genotypes occur between successive controls. Two control varieties are used, alternating in both rows and columns. The layout thus takes the form shown in Figure 1.

```
A . . . . . B . . . . . A
B X X X X X A . . . . . B        ↑    Direction
A . . . . . B . . . . . A        |    of sowing
```

Figure 1 Part of three successive rows in the layout of F_5 yield assessment trials at the PBI. Control plots are marked A or B. Other plots are marked by . or X.

Any F_5 plot is assessed by expressing its yield as a percentage of the nearest controls in the three rows spanning it. Thus each plot marked X is assessed by expressing its yield as a percentage of the mean yield from the six A and B plots which are underlined.

Adjusted values – example

Mean of all checks: 100

Mean of 6 checks for the adjustment: 110

Then the region where the plot is located has a 10% higher yield.

Plot value: 90

Plot adjusted value: 90 / 1.10 = 81.8

Adjusted values – real example – one variation

Trait: TRW

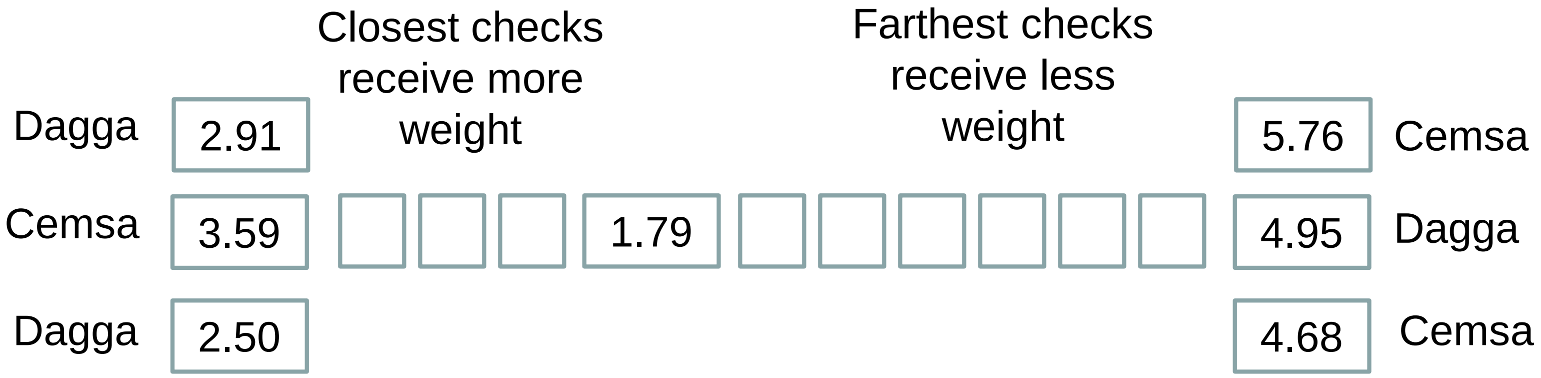
Dagga 2.91 5.76 Cemsa

Cemsa 3.59 1.79 4.95 Dagga

Dagga 2.50 4.68 Cemsa

Checks	Means on the full field	Means on the region	Relative difference %	Average difference	Arguments in the aj.wd function	Adjusted value
Both	4.32	4.07	5.86↓	- 5.86%	ind = FALSE	1.90
Cemsa	3.97	4.68	17.8 ↑	- 4.09%	ind = TRUE	1.87
Dagga	4.67	3.45	26.0 ↓			

Adjusted values – real example – another variation



Closest checks receive more weight

Farthest checks receive less weight

Method	Independent means	Arguments in the aj.wd function	Adjusted value
All checks same weight	Yes	method = 1, ind = TRUE	1.87
	No	method = 1, ind = FALSE	1.90
Closest checks more weight	Yes	method = 2, ind = TRUE	2.07
	No	method = 2, ind = FALSE	2.10

Adjusted values – real example – last variation

Empirically I have noted that with the full correction some additional noise is introduced. Let’s give a weight to the magnitude of the correction. Empirically, best results are gotten with weights between 0.2 and 0.6.

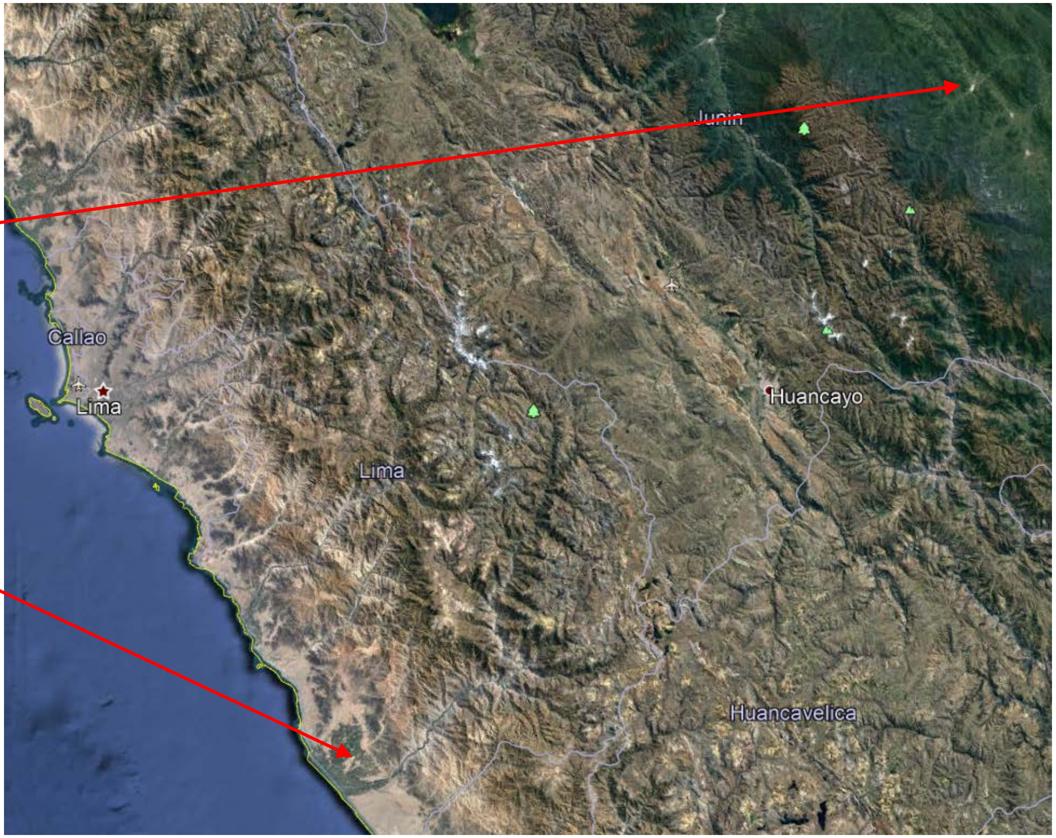
Method	Independent means	Arguments in the aj.wd function	Adjusted value
All checks same weight	Yes	method = 1, ind = TRUE, w = 0.4	1.87 => 1.82
	No	method = 1, ind = FALSE, w = 0.4	1.90 => 1.83
Closest checks more weight	Yes	method = 2, ind = TRUE, w = 0.4	2.07 => 1.89
	No	method = 2, ind = FALSE, w = 0.4	2.10 => 1.90

Available data sets – Populations in Peru

- High Fe and Zn population: 3292 clones, 56 progenitors.
- Low sugar population: 3742 clones, 53 progenitors.
- Wide adaptation population: 9881 clones, 82 progenitors.

Each population planted in two locations:

- Satipo
- Cañete



Each progenitor and each base line clone (80 grandparents) planted with 8 replications in each location.

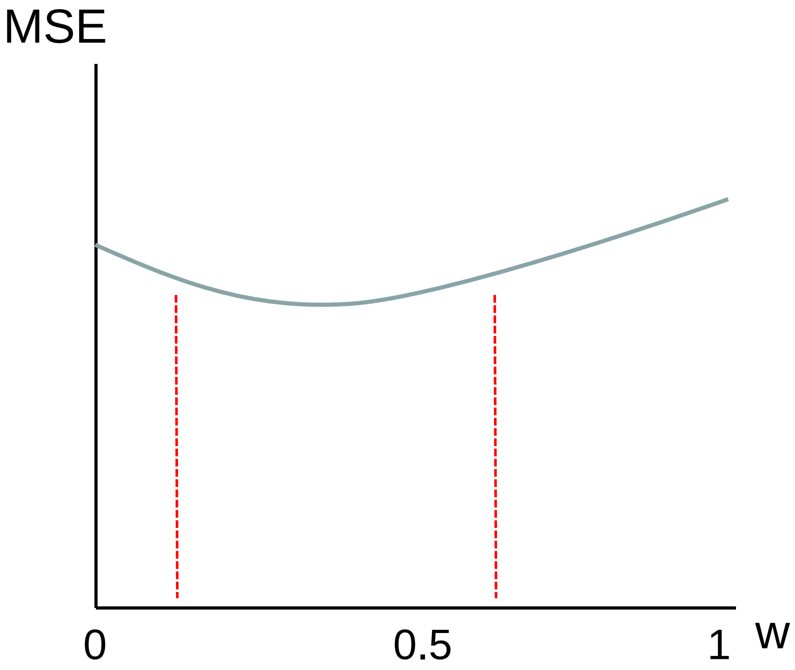
Reduction in the MSE for different weights

```
> aj.wd(trait, "geno", "Cem", "Dag", "row", "col", 10, method = 1, w, ind = FALSE, fb)
```

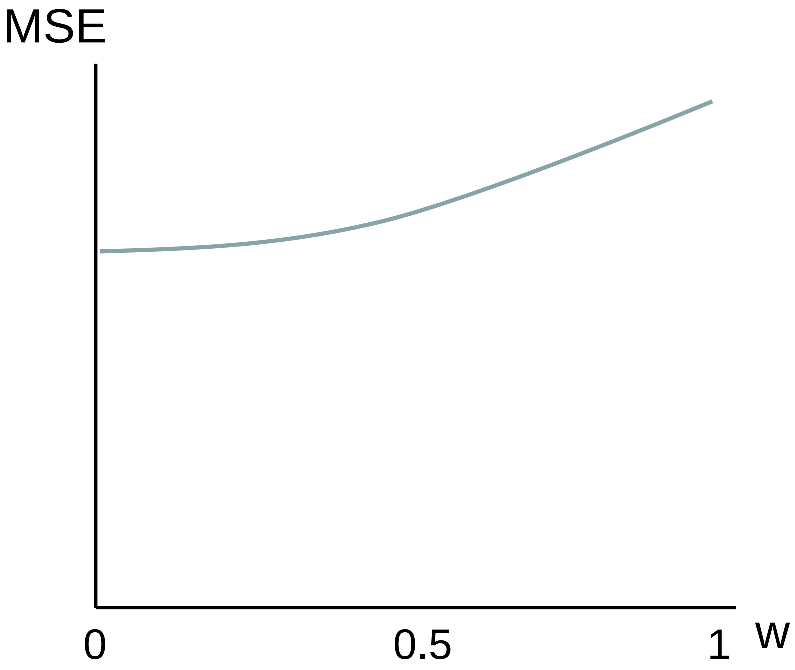
Population	Location	Trait	No Adj.	w = 0.2	w = 0.3	w = 0.4	w = 0.5	w = 0.6
Fe & Zn	Cañete	TRW	0.4828	0.4895	0.5015	0.5201	0.5461	0.5815
		VW	2.568	2.472	2.452	2.450	2.466	2.503
	Satipo	TRW	1.135	1.074	1.052	1.035	1.025	1.019
		VW	1.133	1.026	0.992	0.969	0.958	0.959
Low sugar	Cañete	TRW	0.7001	0.6889	0.6915	0.6998	0.7144	0.7359
		VW	1.716	1.645	1.623	1.609	1.605	1.609
	Satipo	TRW	1.063	0.993	0.988	1.000	1.029	1.078
		VW	9.963	9.798	9.792	9.838	9.937	10.093
Wide adapt	Cañete	TRW	0.3013	0.2804	0.2761	0.2755	0.2786	0.2857
		VW	0.7711	0.7186	0.7086	0.7069	0.7124	0.7248
	Satipo	TRW	2.981	3.002	3.042	3.101	3.180	3.283
		VW	11.95	11.62	11.67	11.85	12.14	12.55

MSE as a function of the weight

Most of the time we get a lower MSE with a weight between 0.2 and 0.6



In a few cases it is not possible to get a lower MSE



Reduction in the MSE for different methods

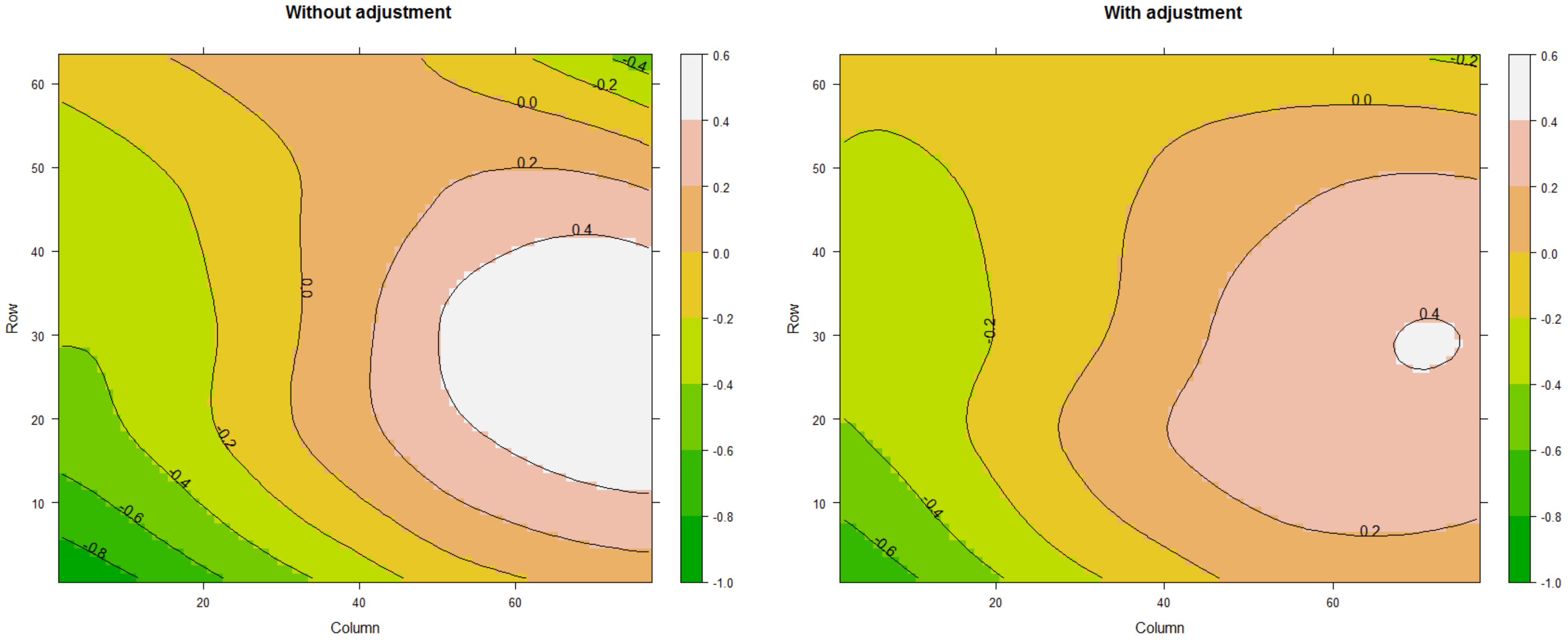
```
> aj.wd(trait, "geno", "Cem", "Dag", "row", "col", 10, method, w = 0.4, ind, fb)
```

Population	Location	Trait	No Adj.	met = 1 ind = T	met = 1 ind = F	met = 2 ind = T	met = 2 ind = F
Fe & Zn	Cañete	TRW	0.4828	0.5171	0.5201	0.5401	0.5457
		VW	2.568	2.460	2.450	2.522	2.510
	Satipo	TRW	1.135	1.039	1.035	1.035	1.031
		VW	1.133	0.961	0.969	0.956	0.964
Low sugar	Cañete	TRW	0.7001	0.7035	0.6998	0.7245	0.7208
		VW	1.716	1.609	1.609	1.627	1.626
	Satipo	TRW	1.063	1.002	1.000	1.039	1.038
		VW	9.963	9.880	9.838	10.063	9.989
Wide adapt	Cañete	TRW	0.3013	0.2725	0.2755	0.2691	0.2736
		VW	0.7711	0.7067	0.7069	0.7029	0.7030
	Satipo	TRW	2.981	3.108	3.101	3.166	3.160
		VW	11.95	11.85	11.85	11.93	11.92

Heat map of residuals on the field

High Fe and Zn population – Satipo – TRW

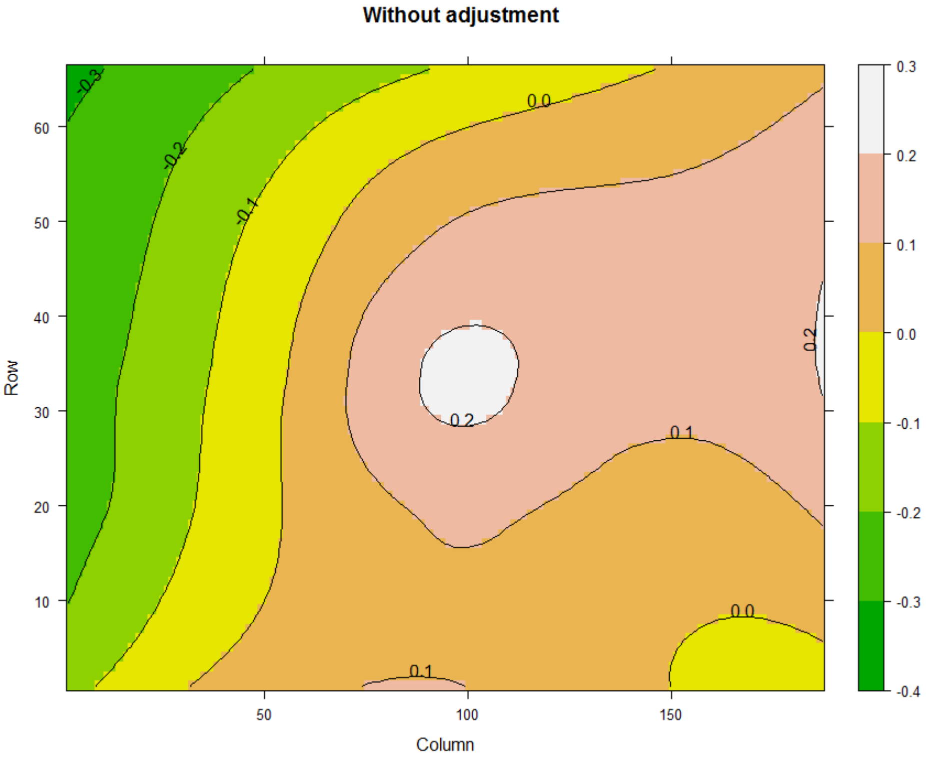
```
> aj.wd("trw", "geno", "Cem", "Dag", "row", "col", 10, method = 2, w = 0.4, ind = TRUE, fb)
```



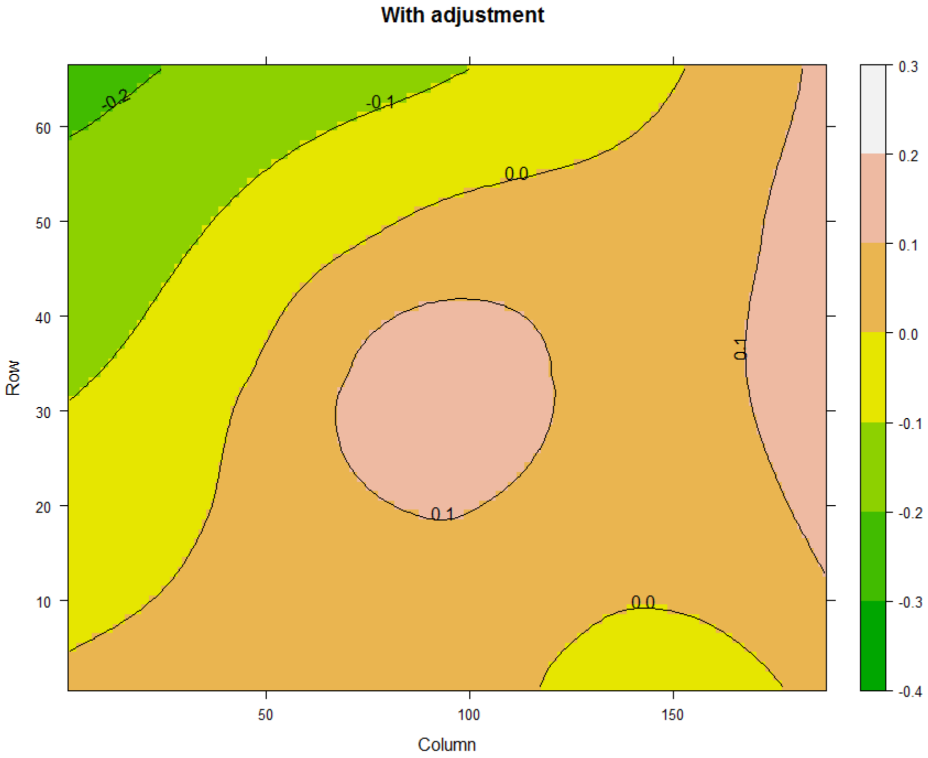
Heat map of residuals on the field

Wide adaptation population – Cañete – TRW

```
> aj.wd("trw", "geno", "Cem", "Dag", "row", "col", 10, method = 2, w = 0.4, ind = TRUE, data)
```



Without adjustment



With adjustment

Heterosis experiment – Fumesua, Ghana

- 2980 genotypes.
- 22 progenitors replicated 4 times (RCBD).
- Checks: Bohye (CIP199062.1) and Ligri (Cemsa 74-228).

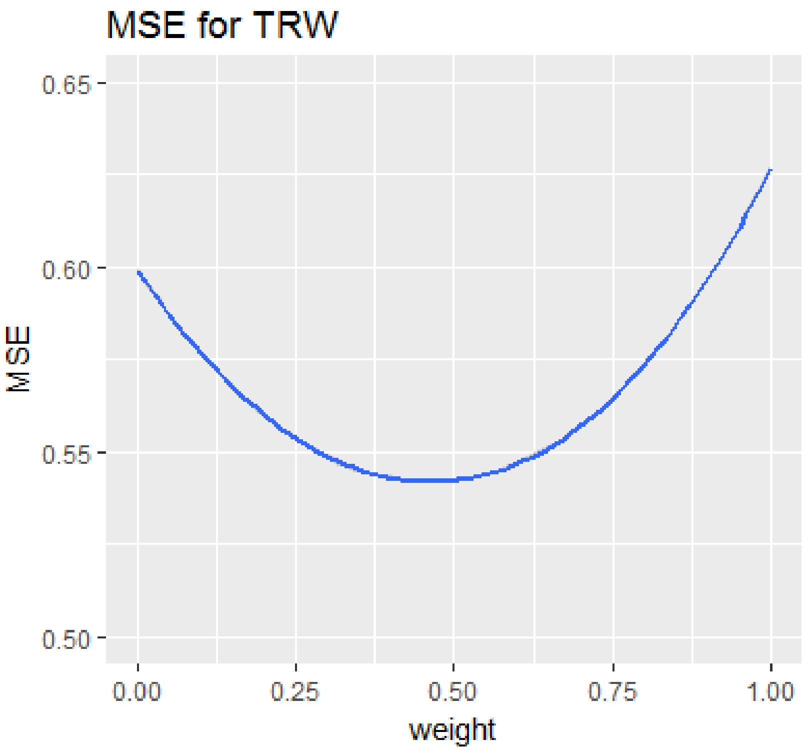
MSE under different adjustment methods:

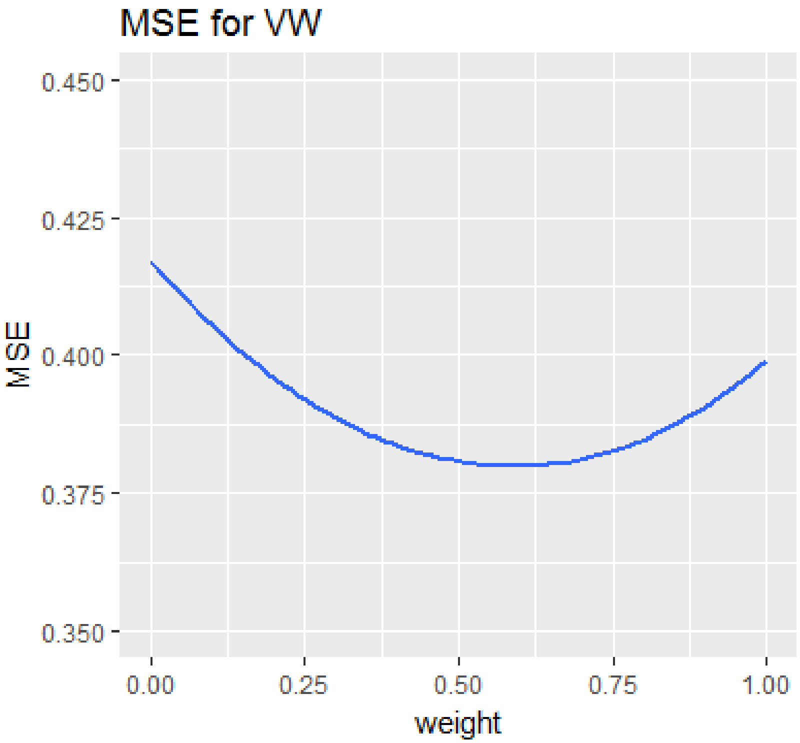
```
> aj.wd(trait, "geno", "Bohye", "Ligri", "row", "col", 10, method, w = 0.4, ind, fb)
```

Method	Independent means	TRW	VW	HI
		0.5993	0.4173	99.96
1	TRUE	0.5818	0.3885	93.41
1	FALSE	0.5937	0.3895	92.94
2	TRUE	0.5431	0.3837	90.33
2	FALSE	0.5674	0.3812	90.54

Heterosis experiment – Fumesua, Ghana

MSE as a function of weight:

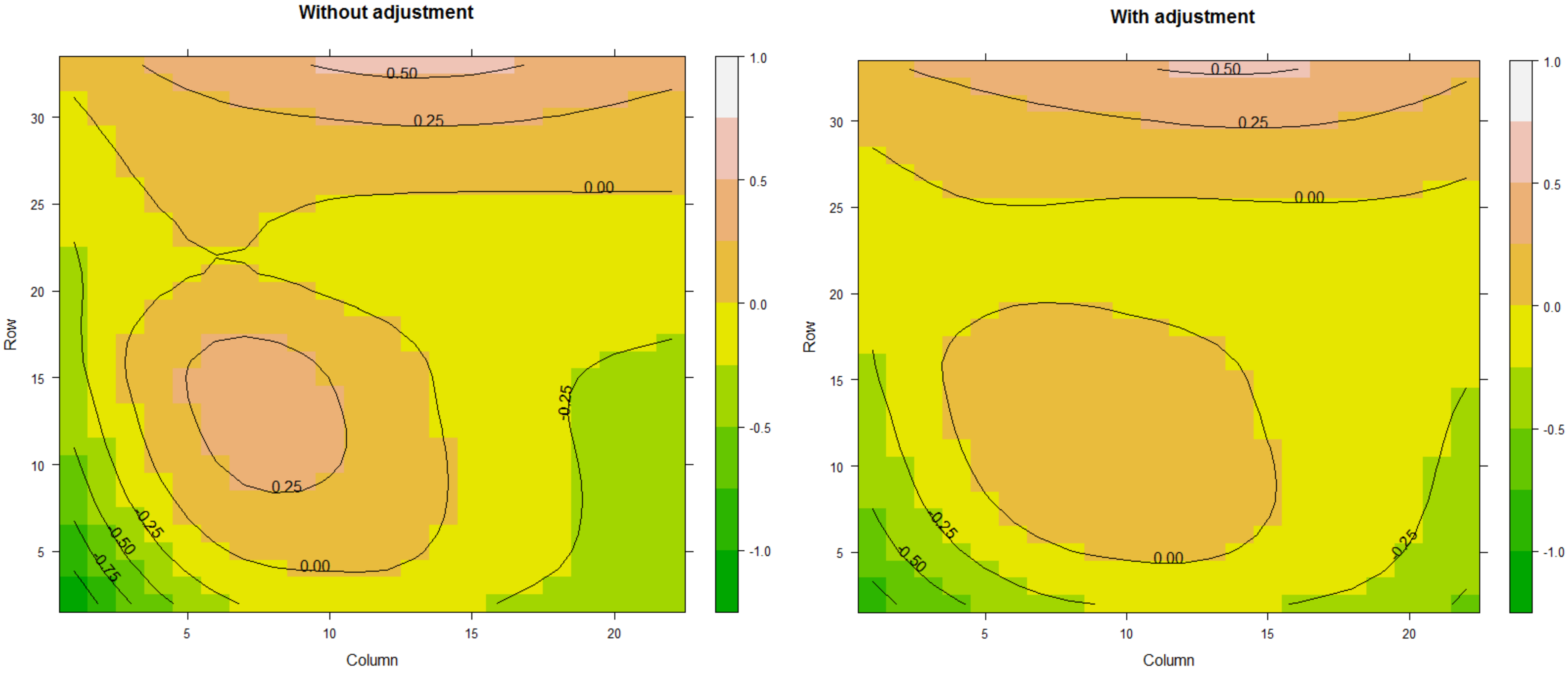




Heterosis experiment – Fumesua, Ghana

Heat maps for TRW

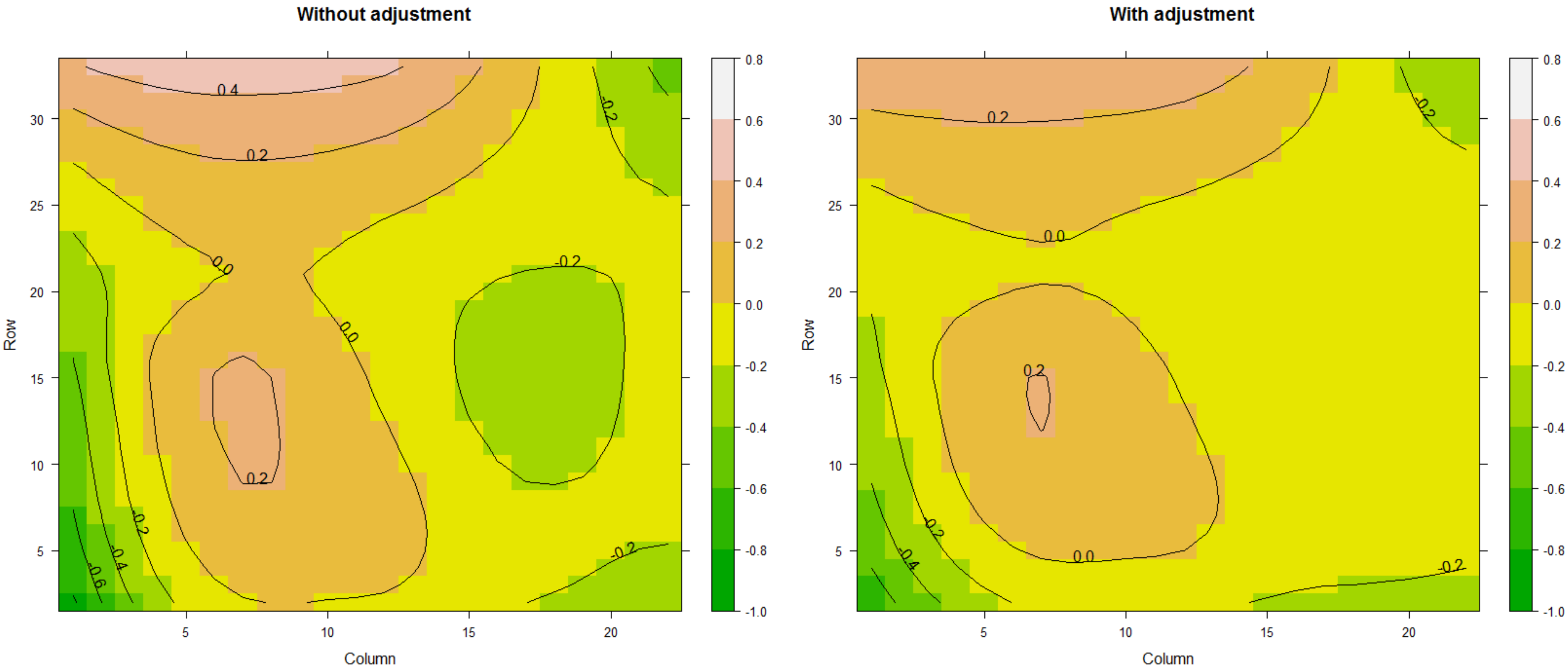
```
> aj.wd("trw", "geno", "Bohye", "Ligri", "row", "col", 10, method = 2, w = 0.4, ind = TRUE, fb)
```



Heterosis experiment – Fumesua, Ghana

Heat maps for VW

```
> aj.wd(“vw", "geno", "Bohye", "Ligri", "row", "col", 10, method = 2, w = 0.4, ind = TRUE, fb)
```



Conclusions

- The method proves to control for field heterogeneity.
- Doesn’t need complicated computational routines, so can be used with big experiments (thousands of clones).
- Using the full differences among checks can increase the error. It is recommended to weigh the adjustment between 20% and 60%. Default value 40%.
- This designs has proved to be valuable during planting for big experiments.
- To apply the method it is needed to have the row and column position of each plot. Use HIDAP or the cd.w command to create the fieldbook and fieldplan.

Thanks!