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Optimum allocation of plots to years, seasons, locations, and replications, and its application to once-over-harvest cucumber trials

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Summary

Large experiments and breeding trials are often conducted over years, seasons (or planting dates), and locations, and with replication (blocks). This is costly and time-consuming, but it is usually deemed necessary to sample a range of environments. In this paper, we describe a general approach to optimum allocation of sampling effort, and apply it to once-over-harvest cucumber trials. Two criteria for optimality are considered: minimizing the variance of a genotype (or treatment) mean, and minimizing cost per unit information. Costs could include penalties for delaying a breeding program. Thus, costs may depend on the goal, as well as the size, of the experiment or breeding trial.

We found that efficient allocation of resources favors using more years and/or seasons, with fewer locations and/or replications. Using more years with fewer locations and/or replications is suggested when genotypes are to be evaluated by yield alone. When both yield and quality variables are of interest, as is likely, using more seasons with fewer locations and/or replications is recommended.

Introduction

Plant breeders test large numbers of family lines, inbreds, hybrids and/or clones before discarding most and releasing a few as cultivars. Genotypes that perform well over a wide range of environmental conditions are most useful to growers and seed companies, because such genotypes have greater probability of performing well in future years and in diverse production areas. Therefore, breeding trials are usually conducted over years, seasons (or planting dates), and locations to pro- vide a number of test environments, and with repli- cation. This is costly and time-consuming, so that the question naturally arises 'How can resources be allocated over years, seasons, locations, and repli- cation to furnish as much information as possible, as cost-effectively as possible?' The related issue of estimation of appropriate sample sizes (e.g., Trout & Marini, 1984) is not pursued in this paper. Our focus here is on efficient allocation of the plots which ultimately provide the sample sizes for esti- mating genotype means.

It is generally agreed that data from only one

location, year, or season is insufficient if interaction of genotype with that environmental factor is known or suspected. Therefore, researchers commonly test such genotype × environment interactions to decide whether data need be collected over more than one location, year, or season (e.g., Jones et al., 1960; Miller et al., 1959). A few have explored the matter of whether one should prefer more years and/or locations, or more replication. The usual approach has been to see which allocation of sampling effort would minimize the variance of a genotype mean. This has been done for crops including cereals (Kaltsikes, 1970; Mycroft, 1983; Patterson et al., 1977; Rasmusson & Lambert, 1961), peanuts (Shorter & Norman, 1983), and potatoes (Sekioka & Lauer, 1970). A smaller number have introduced cost considerations as well. They include Lindgren (1985) for forest trees, and Sprague & Federer (1951) for maize. In general, these studies have concluded that adding more locations and/or years will be much more advantageous than adding replications.

Which allocation of resources is judged optimal may well depend on the criterion for optimality. We considered two optimality criteria. First, we compared designs or allocations by their variance of a genotype mean, ignoring costs. In comparing two designs, the one with the smaller variance of a genotype mean is preferred under this criterion. Second, we compared designs by their cost per unit information. After all, adding locations or seasons may be expensive, and adding years can seriously delay a breeding program. Preferences for one design over another may shift when costs are taken into account. We used two sets of costs to illustrate how costs may depend on the purpose as well as the size of a trial, and to explore the sensitivity of the conclusions to the cost inputs.

Materials and methods

Test environments. Cucumbers (*Cucumis sativus* L.) were grown in each of 24 test environments, being all combinations of 2 years (1984, 1985) by 3 seasons (spring, summer, fall), by 4 locations. Three North Carolina locations were used: the

Horticultural Crops Research Station near Clinton, the Central Crops Research Station near Clayton, and the Horticultural Crops Research Station near Castle Hayne. Fertilizer application and weed, disease, and insect control at these three locations were in accordance with recommended cultural practices (Hughes et al., 1983). An additional stress 'location' was created at the Clinton station using a field with poor soil conditions, and reduced fertilizer, irrigation, and pesticide inputs.

Each year, 3 plantings were made to sample the spring, summer, and fall growing seasons. In 1984, plantings at the 4 locations were on 25 April through 1 May, 10 and 11 July, and 7 and 8 August for the spring, summer, and fall seasons, respectively. In 1985, plantings were on 23 April through 10 May, 12 through 18 July, and 16 July through 8 August.

Genotypes evaluated. Twenty-two genotypes of each of 2 crops (pickling and fresh-market) were grown in the 24 test environments. The genotypes used represented a diverse sample of available cultivars and breeding lines with respect to sex expression (monoecious, gynoecious), heterozygosity (inbred, hybrid), vine length, growth habit, anthracnose resistance, yield, and fruit quality (Table 1).

Planting and data collection. Seeds were planted in plots 3 m long and 1.5 m wide. Plots were separated from each other by 1.5 m alleys at each end for easy identification of harvest areas. Each plot was planted with 40 seeds, and thinned to 30 plants at the first leaf stage. Two replications (complete blocks) were laid out for each of the 24 test environments.

All plots were harvested once-over when the check plots of 'Calypso' and 'Poinsett 76' for pickling and slicing cucumbers, respectively, had 10% oversized fruit (diameter >51 mm for pickling cucumbers and diameter >60 mm for slicing cucumbers). Miller & Hughes (1969) found that fraction of oversized fruit to be optimum for once-over harvest of pickling cucumbers; we used the same criterion for slicing cucumbers to standardize management practices. In 1984, harvests were on 15 June through 6 July, 28 August through 10 Septem-

Table 1. Description of the 44 cucumber genotypes tested, and mean yields and quality ratings over 24 North Carolina environments

Genotype	Seed[y] source	Sex expression	Hetero-zygosity	Anthracnose resistance	Yield[z] (Fruits per 3 m plot)	Quality[z] (Scored 1–9, 9 being best)
Pickling						
Addis	PS	Monoecious	Inbred	Resistant	28	7.2
Calypso	NK	Gynoecious	Hybrid	Resistant	40	6.4
Carolina	NK	Gynoecious	Hybrid	Resistant	34	6.2
Castlepik	SS	Gynoecious	Hybrid	Susceptible	43	6.2
Chipper	PS	Monoecious	Inbred	Resistant	24	6.6
Commander	PS	Gynoecious	Hybrid	Resistant	40	5.6
Earlipik 14	NK	Gynoecious	Hybrid	Susceptible	38	4.8
Gy 14A	NC	Gynoecious	Inbred	Resistant	40	4.9
Gynomite	AS	Gynoccious	Hybrid	Resistant	44	5.3
Lucky Strike	PS	Gynoecious	Hybrid	Resistant	38	6.1
M 21	NC	Monoecious	Inbred	Resistant	28	6.0
Nat. Pickling	NK	Monoecious	Inbred	Susceptible	16	3.5
Panorama	FM	Gynoecious	Hybrid	Resistant	28	5.9
Pennant	HM	Gynoecious	Hybrid	Resistant	35	5.5
Pikmaster	NK	Gynoecious	Hybrid	Resistant	34	6.2
Regal	NC	Gynoecious	Hybrid	Resistant	46	5.8
Score	AS	Gynoecious	Hybrid	Resistant	40	7.0
SMR 58	AS	Monoecious	Inbred	Susceptible	16	4.0
Spear It	FM	Gynoecious	Hybrid	Resistant	42	6.2
Sumter	AS	Monoecious	Inbred	Resistant	26	7.1
Tamor	AS	Gynoecious	Hybrid	Resistant	42	5.9
Tempo	HM	Gynoecious	Hybrid	Resistant	36	6.6
Slicing						
Aodai-Nazare	AS	Monoecious	Inbred	Susceptible	6	4.8
Ashley	NK	Monoecious	Inbred	Susceptible	22	5.2
Castlehy 2506	CS	Gynoecious	Hybrid	Susceptible	33	6.8
Coolgreen	AS	Gynoecious	Hybrid	Susceptible	30	5.1
Cypress	FM	Gynoecious	Hybrid	Susceptible	30	6.1
Dasher II	PS	Gynoecious	Hybrid	Resistant	41	6.9
Gemini 7	SS	Gynoecious	Hybrid	Resistant	40	5.6
Guardian	NK	Gynoecious	Hybrid	Resistant	31	6.8
Gy 57u	CU	Gynoecious	Inbred	Resistant	42	5.7
High Mark II	AS	Monoecious	Hybrid	Susceptible	24	6.1
Marketer	FM	Monoecious	Inbred	Susceptible	14	5.0
Marketmore 76	AS	Monoecious	Inbred	Susceptible	16	6.8
Marketmore 80F	CU	Gynoecious	Inbred	Susceptible	26	6.6
Monarch	AS	Monoecious	Hybrid	Resistant	37	6.7
Pacer	HM	Monoecious	Inbred	Susceptible	22	6.8
Palomar	FM	Monoecious	Inbred	Susceptible	20	5.5
Poinsett 76	AS	Monoecious	Inbred	Resistant	34	6.8
Slice Mor	HM	Gynoecious	Hybrid	Resistant	37	6.1
Sprint 440 S	AS	Gynoecious	Hybrid	Resistant	40	6.6
Sprint 440 II	AS	Gynoecious	Hybrid	Resistant	40	6.6
Straight 8	NK	Monoecious	Inbred	Susceptible	25	4.4
Verino	SG	Gynoecious	Hybrid	Susceptible	40	6.6

[z] Data are means over 2 years, 3 seasons, 4 locations, and 2 replications.
[y] AS = Asgrow Seed, CS = Castle Seed, CU = Cornell Univ., FM = Ferry-Morse, HM = Harris-Moran, NC = North Carolina State Univ., NK = Northrup King, PS = PetoSeed, SG = Sluis & Groot, SS = SunSeeds.

ber, and 3 through 17 October for the spring, summer, and fall seasons, respectively. In 1985, harvests were on 12 June through 3 July, 28 August through 11 September, and 19 September through 3 October.

Data collected on each plot included yield, measured as the total number of fruits, and average fruit quality (scored 1 to 9, where 1 = poor, 5 = average, 9 = excellent). The data were balanced (none missing), with 1056 observations per crop, 48 per genotype.

Variance of a genotype man. The experimental design for each crop (treated separately) involved four crossed factors (year, season, location, genotype), all viewed as random. For such a design, the variance of a genotype mean can be expressed in general as

$$V_{\bar{x}} = \frac{\sigma_{GY}^2}{y} + \frac{\sigma_{GS}^2}{s} + \frac{\sigma_{GL}^2}{l} + \frac{\sigma_{GYS}^2}{ys} + \frac{\sigma_{GYL}^2}{yl} +$$

$$\frac{\sigma_{GSL}^2}{sl} + \frac{\sigma_{GYSL}^2}{ysl} + \frac{\sigma_e^2}{rysl} \qquad (1)$$

for data collected over y years, s seasons, l locations, and r replications. The numerators in the terms in equation 1 are variance components associated with genotype × environment interactions, plus the error variance component from the replication. $V_{\bar{x}}$ is thus a weighted sum of the variance components, the weights being reciprocals of y, s, l, and r, and their products. An individual term to be summed in equation 1 will be more or less important according to (i) the relative size of its particular variance component (numerator), and (ii) the weight (divisor) for that component. Prevailing environmental conditions and their effects on the genotypes used determine the values of the variance components, but the experimenter has control over the divisors through choosing y, s, l, and r. That is central to any discussion of allocation of resources over years, seasons, locations, and replication.

The variance components in equation 1 are unknown parameters to be estimated from the available data. When estimates are used in place of the parameters in equation 1, the estimated variance of

a genotype mean, $\hat{V}_{\bar{x}}$, is obtained. We used the Type I estimates of the variance components from the Statistical Analysis System's (SAS, 1985) PROC VARCOMP, calculated from the (balanced) data described above. Type I estimators are often called analysis of variance (ANOVA) estimators, being obtained by equating observed and expected mean squares from an analysis of variance and solving the resulting equations. They are unbiased and, provided the data are balanced (having equal numbers of observations in corresponding subclasses), have some appealing properties: they are easy to compute, and have minimum variance among all unbiased estimators that are quadratic functions of the observations. Under normality, they have minimum variance among all unbiased estimators. Type I estimators, like all unbiased estimators, must permit negative estimates of the (nonnegative) variance components. Should negative estimates arise in practice, they should be used in equation 1, not set to zero as they sometimes are when one is interested only in reporting estimates of the individual variance components.

Type I estimates of variance components lose their appealing properties when they must be obtained from unbalanced data. Especially when using badly unbalanced data, one should consider using instead maximum likelihood (ML) or restricted maximum likelihood (REML) estimators. For a more detailed discussion and comparison of these variance components estimators, see, for example, Swallow & Monahan (1984).

Once the variance components in equation 1 have been estimated, the estimates and various combinations of y, s, l, and r can be substituted into that equation to study the behavior of the estimated variance of a genotype mean as a function of y, s, l, and r – that is, of the allocation of resources to years, seasons, locations, and replication. Of course, an implicit assumption is that the variance components estimates employed are reasonable estimates for the future trial being designed.

Cost per unit information. In experimental design, 'information' is often defined to be the reciprocal of variance. Then for a genotype mean,

cost per unit information $= \text{cost} / (1/\text{variance})$
$$= \text{cost} \times \text{variance}.$$
$$= \text{cost} \times V_{\hat{x}}. \qquad (2)$$

When $\hat{V}_x$ is substituted for V_x, equation 2 gives the estimated cost per unit information.

Costs will differ from one kind of experiment or trial to another. They may include not only capital outlays for supplies and equipment, and costs related to time spent (worker-hours), but also, for example, costs (penalties) for delaying a breeding program. Two experimenters may reckon costs somewhat differently. But that notwithstanding, costs are such a serious concern in experimentation, attempting to take them into account in designing experiments seems only sensible.

Results and discussion

Allocation based on minimizing the variance of a genotype mean. Table 2 gives the variance components estimates obtained from our data. These estimates were used in equation 1, along with various combinations of values of y, s, *l*, and r, to obtain Table 3. Table 3 displays the estimated variances of a genotype mean for 13 alternative allocations of 16 plots (per genotype) into y years, s seasons, l locations, and r replications, holding $(y \times s \times l \times r) = 16$. The basic allocation takes $y = s = l = r = 2$. Other allocations increase one component to 4 while reducing another to 1, exploring the merits of possible exchanges while keeping the number of plots fixed. Results are shown for both yield and quality response variables for each cucumber crop (pickling, fresh-market).

If one's goal (optimality criterion) is to minimize the estimated variance of a genotype mean, Table 3 shows that allocation of resources to sampling over more years with less replication (for yield), or to using more seasons with fewer locations (for quality), will be most helpful. This applies to either crop. The differences between the best and worst allocations is considerable, even in this small illustrative example. Comparing values within each column of Table 3 shows that even within this limited set of alternative allocations, approximately a 2-fold difference in variance of a genotype mean between the best and worst allocations is predicted. Clearly, the bigger the difference between alternative allocations, the more important the choice of allocations becomes. With balanced data, the 2-fold difference seen in this example implies the following: Compared to the best allocation, the worst allocation is expected to yield (1) an LSD which is $2 \times$ larger, (2) confidence intervals for differences between genotype means which are $2 \times$ wider, (3) confidence intervals for individual genotype means which are $\sqrt{2} \times$ wider, and (4) an analysis of variance F test having substantially less power to detect genotype differences. The advantage in using a superior allocation is clearly enough to be important.

For each crop and response, Table 3 shows that

Table 2. Estimates of variance components for error and the interactions of genotype and environmental effects (year, season, location) in cucumber trials

Crop and variable	Overall means	Variance component							
		σ^2_{GY}	σ^2_{GS}	σ^2_{GL}	σ^2_{GYS}	σ^2_{GYL}	σ^2_{GSL}	σ^2_{GYSL}	σ^2_{e}
Pickling									
Yield[1]	34.45	17.13	0.25	− 2.60	11.92	3.07	8.20	15.58	67.64
Quality[2]	5.86	0.020	0.035	− 0.015	− 0.013	− 0.045	0.061	0.033	0.821
Slicing									
Yield	29.55	11.65	7.79	2.83	6.67	3.71	6.89	6.58	64.20
Quality	6.07	0.009	0.099	− 0.017	− 0.007	− 0.011	0.013	0.141	0.741

[1] Yield in fruits per 3 m plot.
[2] Quality scored 1 to 9, 9 being best.

there are other allocations which are nearly as good as the best one. Realizing this is important for at least two reasons. First, when allocations differ little in their estimated variance of a genotype mean, one may want to take account of other factors such as convenience or practicality in choosing one allocation over another. This is treated more explicitly in the next section, when costs are considered. Second, in practice one usually faces the impossible task of choosing an allocation which will be simultaneously optimal for all responses (traits) of interest. As noted for the example of Table 3, for comparing genotypes by yield we would like more years, but for comparing them by quality, more seasons. Compromises must be made. In this case, increasing the number of seasons while decreasing replication seems to be the most acceptable compromise allocation for both variables of both crops. It is not the best allocation for any of them, but is second-best in all cases. As a second choice, one might consider increasing the number of seasons and decreasing the number of locations. This allocation was optimal for quality and reasonably favorable for yield.

The above example illustrates how one can compare allocations, but 'best' and 'worst' are within the set of allocations considered. One is usually interested in finding an optimum only within some set of reasonable alternatives. In our examples, comparing all allocations which satisfied the requirement that $(y \times s \times l \times r) = 16$ would be of little interest. For example, the allocation that uses $y = 16$ with $s = l = r = 1$ would not be considered by anyone interested in rapid breeding progress. In practice, however, one might compare a wider range of alternative allocations than we did in our small example.

Allocation based on minimizing cost per unit information. To illustrate the use of cost per unit information as a criterion for comparing resource allocations, we considered two cases: (1) an experiment with 25 genotypes, and (2) a breeding trial with 250 genotypes. We had in mind that the goal of an experiment is to make definitive distinctions between advanced genotypes, whereas the goal of

Table 3. Comparisons of estimated variances of a genotype mean in cucumber trials for some alternative allocations of equal numbers of plots over y years, s seasons, *l* locations, with r replications ($y \times s \times l \times r = 16$)

Allocation				Crop and variable			
y	s	*l*	r	Pickling		Slicing	
				Yield	Quality	Yield	Quality
2	2	2	2	19.4	0.076	20.3	0.108
4	1	2	2	16.9	0.110	22.5	0.160
4	2	1	2	14.3	0.081	19.7	0.102
4	2	2	1	12.2[1]	0.076	15.7[1]	0.099
1	4	2	2	27.6	0.059	24.2	0.084
2	4	1	2	17.3	0.050[1]	19.8	0.073[1]
2	4	2	1	15.8	0.059	16.2	0.074
1	2	4	2	30.5	0.079	26.2	0.114
2	1	4	2	22.7	0.100	24.7	0.162
2	2	4	1	17.6	0.076	17.8	0.103
1	2	2	4	33.6[2]	0.076	29.5[2]	0.126
2	1	2	4	26.5	0.110[2]	28.4	0.177[2]
2	2	1	4	22.8	0.077	25.2	0.118

[1] Smallest estimated variance of a genotype mean within column (best allocation).
[2] Largest estimated variance of a genotype mean within column (worst allocation).

a large breeding (screening) trial is to identify promising genotypes for further study. This difference in goals influenced our reckoning of costs, giving us two sets of cost figures (Table 4). Using two sets of cost estimates also allowed us to explore the sensitivity of the methodology to cost inputs. Because costs are usually estimated inexactly, we prefer that the conclusions not be greatly affected by modest changes in the cost inputs. Recognizing that other experimenters will count their costs differently in any case, we offer below only a brief explanation and justification of our cost reckoning. One of our objectives was to illustrate in general how costs might be considered; using different values for the various costs will alter the arithmetic and possibly the conclusions reached, but not the approach.

For an experiment, we use a basic overhead cost of 11.0 worker-hours for the first year-season-location combination. This includes contributions for such factors as seed packeting, plot stake preparation, field plans, travel, instruction of field workers, and data analysis. We then figure other costs as follows: Adding another season (same year and location) costs only 70% as much. Adding another location (same year and season) costs 80% of the basic cost, more than adding a season because additional personnel must be trained. And adding a year (same location and season) costs 85% of the basic cost, as even more additional personnel training is needed. In addition, there is a fixed cost per plot of 0.13 worker-hours for planting, thinning, data collection, etc. Discriminating between 'fixed' and 'variable' costs in this way is reminiscent of the work of Smith (1938). Only the relative costs in these categories actually matter; all costs can be

multiplied by a common factor without altering the conclusions summarized below.

For a breeding trial, we increased the basic cost to 20.4 worker-hours, reflecting additional preparation related to the increased size of the undertaking. Again, we figure that adding a location (same year and season) costs 80% of the basic cost. But the costs associated with adding seasons and years are now taken to be 130% and 300% of the basic cost, respectively. This reflects our belief that a significant cost or penalty must accrue to any allocation which delays the progress of a breeding program – the greater the delay, the greater the penalty. If plant breeders could easily quantify their subjective feelings toward allocations which delay a breeding program, many breeders would probably attach much larger penalties to using additional seasons or, especially, additional years than we have. The 0.13 worker-hour cost per plot still applies. Costs may now include both actual costs (worker-hours) and penalties for delays.

The cost per genotype for an experiment with 25 genotypes is then

$$[11.0 + 8.8\,(l-1) + 7.7\,(s-1) + 9.4\,(y-1) + 0.13\,(25 \times r/sy)]/25, \quad (3)$$

and the cost per genotype for a breeding trial with 250 genotypes is

$$[20.4 + 16.3\,(l-1) + 26.5\,(s-1) + 61.2\,(y-1) + 0.13\,(250 \times r/sy)]/250, \quad (4)$$

using the costs from Table 4. The final divisor is, in each equation, the number of genotypes tested. The numerator in square brackets is the total cost

Table 4. Costs associated with planning and running an experiment (25 genotypes) or breeding trial (250 genotypes) with cucumbers[1]

Cost source	Experiment	Breeding trial
Planning for the first year-season-location combination	11.0	20.4
Adding a location (same year & season)	0.8 × 11.0 = 8.8	0.8 × 20.4 = 16.3
Adding a season (same year & location)	0.7 × 11.0 = 7.7	1.3 × 20.4 = 26.5
Adding a year (same location & season)	0.85 × 11.0 = 9.4	3.0 × 20.4 = 61.2
Cost per plot	0.13	0.13

[1] Costs are in relative units, and include actual costs in worker-hours and penalty costs for delaying a breeding program.

of running the experiment or breeding trial, this total to be shared equally by the genotypes tested (hence the divisor).

Through Table 5 we compare cost per unit information for 13 possible allocations over y years, s seasons, and l locations, all having $(y \times s \times l \times r) = 16$. Figures are shown for total yield and average quality rating for both pickling and slicing cucumbers, grown in either an experiment or a breeding trial. Each entry in Table 5 was obtained according to equation 2 by multiplying the cost of obtaining a genotype mean, calculated using equation 3 or 4, by the estimated variance of that genotype mean, calculated using equation 1. As comparing the values within each column of Table 5 shows, allocations do differ substantially in cost per unit information; on average, there is approximately a 2-fold difference between the best and worst allocations considered.

The conclusions to be drawn from Table 5 are very similar for the experiment and for the breeding trial, and for both crops. For comparing genotypes by yield alone, allocations expected to give the lowest cost per unit information use more years with fewer replications. However, these would be poor allocations for comparing genotypes by the quality rating, and are allocations that many breeders would fault for requiring too much time. The best allocations for comparison by quality use more seasons and fewer locations. These are good allocations for yield too, and the best compromise allocations when both yield and quality variables are of interest, as would usually be the case. The second best compromise allocations for both yield and quality use more seasons and fewer replications. These are good allocations for both variables of both crops.

That only minor differences are found in Table 5 when comparing the experiment and the breeding trial has two important implications, both relating to the costs in Table 4. First, the extra costs (penalties) assigned in the breeding trial for adding seasons or years, and thereby delaying a breeding program, are too small to have much impact on cost per unit information. The reason for this is evident in equations 3 and 4. In both equations, the size of

Table 5. Comparison of cost per unit information in cucumber trials for some alternative allocations of plots over y years, s seasons, l locations, with r replications ($y \times s \times l \times r = 16$)

Allocation				Experiment (25 lines)				Breeding trial (250 lines)			
				Pickling		Slicing		Pickling		Slicing	
y	s	l	r	Yield	Quality	Yield	Quality	Yield	Quality	Yield	Quality
2	2	2	2	69.	0.27	72.	0.38	50.	0.20	52.	0.28
4	1	2	2	67.	0.44[2]	90.	0.64[2]	50.	0.32[2]	67.	0.47[2]
4	2	1	2	57.	0.32	78.	0.40	43.	0.24	59.	0.30
4	2	2	1	53.[1]	0.33	67.[1]	0.43	38.[1]	0.23	48.	0.30
1	4	2	2	105.	0.22	92.	0.32	70.	0.15	62.	0.21
2	4	1	2	66.	0.19[1]	76.	0.28[1]	47.	0.14[1]	54.	0.20[1]
2	4	2	1	66.	0.25	68.	0.31	44.	0.17	45.[1]	0.21
1	2	4	2	119.[2]	0.31	102.[2]	0.44	75.	0.19	65.	0.28
2	1	4	2	90.	0.39	98.	0.64[2]	59.	0.26	64.	0.42
2	2	4	1	75.	0.32	76.	0.44	48.	0.21	48.	0.28
1	2	2	4	107.	0.24	94.	0.40	78.[2]	0.18	69.	0.29
2	1	2	4	86.	0.36	92.	0.57	65.	0.27	70.[2]	0.44
2	2	1	4	73.	0.25	81.	0.38	57.	0.19	63.	0.30

[1] Smallest estimated cost per unit information within column (best allocation).
[2] Largest estimate cost per unit information within column (worst allocation).

the numerator is dominated by the final term in which the cost per plot (0.13) is multiplied by a very large number. Second, the conclusions reached in judging allocations by cost per unit information are not overly sensitive to the cost inputs. The two sets of costs specified in Table 4 led to very similar conclusions in Table 5.

Final comments and conclusions. We have compared alternative allocations of experimental resources over years, seasons, locations, and replication by doing calculations for an instructive set of examples (alternative allocations). Our focus has been on investigating possible trade-offs involving the sampling of fewer levels of one factor in favor of sampling more levels of another. In this way, we have tried to illustrate how one can in general explore the relative advantages of alternative sampling strategies. The required computations are quite straightforward, and easily adapted to other experimental designs where the expression for the variance of a mean may differ from equation 1, or where the total cost is computed by a formula different from equation 3 or 4.

An alternative approach to optimum allocation is to use the calculus to obtain formulae for optimum values of l, r, s, and y (Marcuse, 1949; Schultz, 1955; Sprague & Federer, 1951). In practice, this approach is less useful than the one illustrated here. Its principal deficiency is that it provides no information about other allocations which may be nearly as good as the optimal one for a given trait. As illustrated in this paper, when more than one trait is of interest, as is usually the case, compromises may be required. One will usually have to settle for an allocation of plots which is desirable for all traits of interest, though perhaps not the optimal allocation for any of them.

In summary, our results for cucumbers suggest that efficient allocation of plots to years, seasons, locations, and replication, favors more years and/ or seasons, with fewer locations and/or replications. Increasing the number of years is efficient when genotypes are to be evaluated by yield alone, but is inappropriate for evaluation by quality, and may impose unacceptable delays in a breeding program. If both yield and quality variables are of

interest, as is likely, allocations which use more seasons, and fewer locations and/or replications are appropriate. Similar results were observed for both pickling and slicing cucumbers.

Although we have shown results only for the variables total yield and average quality rating, our conclusions are more general. Conclusions stated for total yield apply also to marketable yield. Those for the average quality rating apply also to the rating for fruit shape, an important component of quality (desirability).

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