

1. a) We have a  $2^3$  factorial treatment structure. Since recipe is difficult to change, it might make sense to do a split plot experiment with batch as whole plot and recipe as whole plot treatment, and the four mold/cooling combinations as split plot treatments. All effects are fixed and crossed; whole plots design is completely randomized.
- b) The units are the 9 groups of 400 voters, the treatments are the three bits of information (fixed). We can do a completely randomized assignment of the treatments to the units.
- c) Rose bush is unit; volunteer and moisture are extraneous sources of variation to block. We could do a replicated 4 by 4 Latin square, where moisture (row) and volunteer (column) are the blocking variables and we have 4 fungicide treatments. All treatments are fixed.
- d) We have a  $2^4$  factorial treatment structure (16 combinations, factors fixed and crossed) but can only afford 8 units. Thus a fractional factorial is appropriate. Use I=ABCD as a generator.
- e) Feet are units and subject is block. Since people only have two feet and we have four treatments (the four powders, fixed), we have incomplete blocks. There are 6 pairs of treatments, and since we have 60 boys, we can use each pair 10 times for a BIBD design. Another possible alternative would be a crossover design, though you might have to balance for residual effects.
- f) We have a  $2^4$  factorial treatment structure with all factors fixed and crossed. The cooler must serve as block, however, and it is of size 8. Thus we need incomplete blocks, and confounding is suggested. We could partially confound, using ABCD in replicate 1 and BCD in replicate 2.

2. a) This is a completely randomized design with children as unit and five fixed treatments. Cavities on nonmolars is a covariate. The treatment structure is a little funky, being a 2 by 2 factorial plus an additional control.

Source	df
cov	1
trt	4
error	34

- b) This is a fully nested design, with brand (fixed) on top, day (random) nested in brand, and carton (random) nested in day.

Source	df
brand	1
day (brand)	4
carton (day)	24
error	30

- c) This is a split plot, with branch as whole plot (blocked into high and low sales blocks), hardware as whole plot treatment, week as split plot, and software as split plot treatment. Factors are fixed and crossed.

Source	df
block	1
hardware	1
wp error	17
software	2
hard.soft	2
sp error	36

d) This is a randomized complete block design with batch as block. The treatments have a 2 by 3 factorial structure and are crossed and fixed.

Source	df
block	3
glue	2
curing	1
glue.curing	2
error	15

e) This is a partially balanced incomplete block. For example, A occurs 4 times with D, but only twice with B, C, E, and F. Treatments are fixed.

Source	df
block	5
variety	5
error	13

f) This is a replicated Latin square. Treatments are the three recorded calls (fixed), and the two blocking factors are phase of the breeding season and morning hour. The two clearings are the two replicates.

Source	df
clearing	1
hour	2
phase	2
trt	2
error	10

3. Start with a full factorial in A, B, C, D and add on E and F.

	-ACD		ABC							
	A	B	C	D	=E	=F	I	-ACDE	ABCF	-BDEF
e	-	-	-	-	+	-	A	-CDE	BCF	-ABDEF
af	+	-	-	-	-	+	B	-ABCDE	ACF	-DEF
bef	-	+	-	-	+	+	AB	-BCDE	CF	-ADEF
ab	+	+	-	-	-	-	C	-ADE	ABF	-BCDEF
cf	-	-	+	-	-	+	AC	-DE	BF	-ABCDEF
ace	+	-	+	-	+	-	BC	-ABDE	AF	-CDEF
bc	-	+	+	-	-	-	ABC	-BDE	F	-ACDEF
abcef	+	+	+	-	+	+	D	-ACE	ABCDF	-BEF
d	-	-	-	+	-	-	AD	-CE	BCDF	-ABEF
adef	+	-	-	+	+	+	BD	-ABCE	ACDF	-EF
bdf	-	+	-	+	-	+	ABD	-BCE	CDF	-AEF
abde	+	+	-	+	+	-	CD	-AE	ABDF	-BCEF
cdef	-	-	+	+	+	+	ACD	-E	BDF	-ABCEF
acd	+	-	+	+	-	-	BCD	-ABE	ADF	-CEF
bcde	-	+	+	+	+	-	ABCD	-BE	DF	-ACEF
abcdf	+	+	+	+	-	+				

4. Blocks ( $\alpha_i$ ) are random, and meters random and nested in block ( $\beta_{j(i)}$ ). Weeks are random ( $\gamma_k$ ). I would say that day ( $\delta_l$ ) is fixed and crossed with the other effects, because day of week effects are likely to be similar from week to week and block to block. Weeks, day, and meter are crossed. All interactions are random.

$$y_{ijkl} = \alpha_i + \beta_{j(i)} + \gamma_k + \alpha\gamma_{ik} + \beta\gamma_{jk(i)} + \delta_l + \alpha\delta_{il} + \beta\delta_{jl(i)} + \gamma\delta_{kl} + \alpha\gamma\delta_{ikl} + \beta\gamma\delta_{jkl(i)}$$

b) The skeleton ANOVA table also includes the expected mean squares and tests to use, though

that was not required in the problem.

Source	df	EMS	test
$\alpha_j$	7	$7\sigma_{\beta\gamma}^2 + 35\sigma_{\alpha\gamma}^2 + 42\sigma_{\beta}^2 + 210\sigma_{\alpha}^2$	$(A+BC(A))/(B(A)+AC)$
$\beta_{j(i)}$	32	$7\sigma_{\beta\gamma}^2 + 42\sigma_{\beta}^2$	$B(A)/BC(A)$
$\gamma_k$	5	$7\sigma_{\beta\gamma}^2 + 35\sigma_{\alpha\gamma}^2 + 280\sigma_{\gamma}^2$	$C/AC$
$\alpha\gamma_{ik}$	35	$7\sigma_{\beta\gamma}^2 + 35\sigma_{\alpha\gamma}^2$	$AC/BC(A)$
$\beta\gamma_{jk(i)}$	160	$7\sigma_{\beta\gamma}^2$	none
$\delta_l$	6	$\sigma_{\beta\gamma\delta}^2 + 5\sigma_{\alpha\gamma\delta}^2 + 40\sigma_{\gamma\delta}^2 + 6\sigma_{\beta\delta}^2 + 30\sigma_{\alpha\delta}^2 + 240 \sum \delta_l^2 / 7$	$(D+ACD)/(AD+CD)$
$\alpha\delta_{il}$	42	$\sigma_{\beta\gamma\delta}^2 + 5\sigma_{\alpha\gamma\delta}^2 + 6\sigma_{\beta\delta}^2 + 30\sigma_{\alpha\delta}^2$	$(AD+BCD(A))/(BD(A)+ACD)$
$\beta\delta_{jl(i)}$	192	$\sigma_{\beta\gamma\delta}^2 + 6\sigma_{\beta\delta}^2$	$BD/BCD(A)$
$\gamma\delta_{kl}$	30	$\sigma_{\beta\gamma\delta}^2 + 5\sigma_{\alpha\gamma\delta}^2 + 40\sigma_{\gamma\delta}^2$	$CD/ACD$
$\alpha\gamma\delta_{ikl}$	210	$\sigma_{\beta\gamma\delta}^2 + 5\sigma_{\alpha\gamma\delta}^2$	$ACD/BCD(A)$
$\beta\gamma\delta_{jkl(i)}$	960	$\sigma_{\beta\gamma\delta}^2$	none

	Source	df	SS	MS	F
5.	trt	4	104.69	26.17	
	error	15	60.18	4.012	

The F ratio is 6.52, with 4 and 15 df. This gives a p-value of 0.003, so we would reject the null hypothesis that all means are equal.

b) We could use the contrast with coefficients (-3, -3, 2, 2, 2). This contrast has estimated value 7.0852, with  $SE = (MSE \sum c_i^2 / n_i)^{1/2} = 5.485$ , giving a t ratio of  $7.0852 / 5.485 = 1.29$ . This t-ratio has a two sided p-value of about 0.2, so the null hypothesis is not rejected.