

HW 9

3A.) As per page 158 of the notes

the random block effects are represented by block $j : b_j$

the effect due to treatments is represented by : α_i

and the model is represented by : $X_{ij} = \mu + \alpha_i + b_j + \epsilon_{ij}$

Where $I = 1-4$ and $j = 1-8$

3b.) the null hypothesis here would be $H_o = \alpha_1 + \alpha_2 + \alpha_3 + \alpha_4$ and the alternative would be that if any of the 4 effect due to treatment are different.

3C.) the R output below tells us that we can reject the null hypothesis given the fact that the p-values for both design and pilot are both well below the level of significance .01.

```
PROBLEMS 35 OUTPUT DEBUG CONSOLE TERMINAL

> anova(fitpilot)
Analysis of Variance Table

Response: times
      Df Sum Sq Mean Sq F value    Pr(>F)
design   3  8.3729   2.7910   9.1936 0.0004409 ***
pilot   7 29.1090   4.1584  13.6982 1.495e-06 ***
Residuals 21  6.3751   0.3036
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> █
```

4.) from the output of tukey's function the pairs of designs that end up being significantly different are D and A and D and C due to the fact that these are the only pairs of designs who interval doesn't include 0 and shown by the output below:

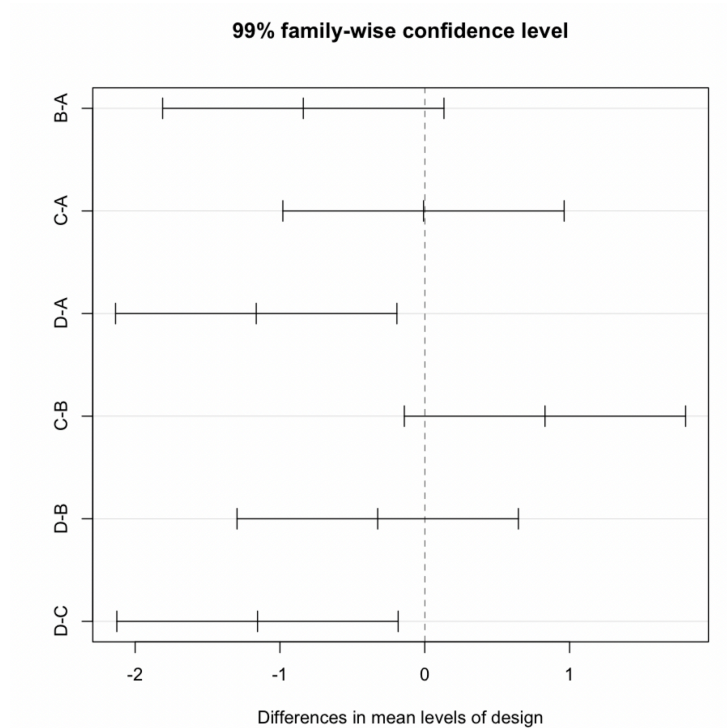
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PROBLEMS 39 OUTPUT DEBUG CONSOLE TERMINAL

> TukeyHSD(fitpilot,"design",conf.level=.99)
  Tukey multiple comparisons of means
    99% family-wise confidence level

Fit: aov(formula = times ~ design + pilot, data = pilotdata)

$design
      diff      lwr      upr    p adj
B-A -0.83875 -1.8099955  0.1324955 0.0290281
C-A -0.00875 -0.9799955  0.9624955 0.9999881
D-A -1.16375 -2.1349955 -0.1925045 0.0019931
C-B  0.83000  -0.1412455  1.8012455 0.0310802
D-B -0.32500 -1.2962455  0.6462455 0.6458100
D-C -1.15500 -2.1262455 -0.1837545 0.0021465
```

We can visualize this with a plot:



5.)

1.) because chemicals are being tested On the fabric samples , I would say the blocking factor is the type of fabric being used.

2.) Outright lets state the null hypothesis $H_0: \alpha_1 = \alpha_2 = \alpha_3 = \alpha_4$ where 1-4 represent the different chemicals . To do this completing the anova table below will give us the Statistic of interest.(work is on a image attached at the end of this doc)

Fabrics = 5 N = 20 Dof chem = 3
 chems = 4 Dof Fab = 4

| | DOF | Sum Sq | Mean Sq | F-Val | P-Val |
|-------|-----|--------|---------|--------|------------------------|
| chem | 3 | 2.4815 | .821 | 19.547 | 6.513×10^{-5} |
| Fab | 4 | 5.453 | 1.363 | 32.452 | 2.565×10^{-6} |
| resid | 12 | .511 | .042 | | |
| | | 8.4455 | | | |

$$8.4455 - .511 - 5.453 = SST_r \quad \frac{.821}{.042} = F_r = 6.513 \times 10^{-5}$$

$$MST_r = \frac{2.4815}{3} \dots \text{for } MSF \quad \frac{1.363}{.042} = F_B$$

$$MSB = \frac{5.453}{4}$$

For the p-values i used the 1-pt commands

H_0 is rejected when $F_{r/B} \geq F_{r/12-1, 12-1, \text{resid Dof } \alpha}$

From the image above we can see that the p-values are way under the level of significance we can reject H_o and conclude the effect due to treatments are different.