PRACTICAL XIII
SOLUTIONS

XIII.1 The following is an unrandomized plan for a partially balanced incomplete block design.

Block Plot	1	2	3	4	5	6	7	8	9	10
1	1	2	3	4	5	6	7	8	9	10
2	4	5	6	7	8	9	10	1	2	3
3	3	4	5	6	7	8	9	10	1	2

Use S-Plus with a seed of 1012 to obtain a randomized layout for the experiment.

The S-Plus output containing the randomized layout is:

```
> library(DAE, lib.loc = "f:")
> set.seed(1012)
> b <- 10
> k <- 3
> t <- 10
> n <- b * k
> Standard.Order <- factor(1:n)
> Random.Order <- order(rep(runif(b), each = k), runif(n))
> PBIBD.Design <- fac.divide(Random.Order, factor.names = list(Blocks = b,
Plots = k))
> Treats <- factor(c(1, 4, 3, 2, 5, 4, 3, 6, 5, 4, 7, 6, 5, 8, 7, 6, 9, 8, 7,
10, 9, 8, 1, 10, 9, 2, 1, 10, 3, 2))
> PBIBD.Design <- design(Standard.Order, Random.Order, PBIBD.Design, Treats)
> PBIBD.Design <- sort.col(PBIBD.Design, "@ALL", "Random.Order")
> PBIBD.Design
   Standard.Order Random.Order Blocks Plots Treats
 4              4            1      1     1      2
 5              5            2      1     2      5
 6              6            3      1     3      4
27             27            4      2     1      1
25             25            5      2     2      9
26             26            6      2     3      2
13             13            7      3     1      5
15             15            8      3     2      7
14             14            9      3     3      8
10             10           10      4     1      4
11             11           11      4     2      7
12             12           12      4     3      6
 9              9           13      5     1      5
 7              7           14      5     2      3
 8              8           15      5     3      6
18             18           16      6     1      8
17             17           17      6     2      9
16             16           18      6     3      6
24             24           19      7     1     10
22             22           20      7     2      8
23             23           21      7     3      1
21             21           22      8     1      9
19             19           23      8     2      7
20             20           24      8     3     10
28             28           25      9     1     10
30             30           26      9     2      2
29             29           27      9     3      3
 3              3           28     10     1      3
 2              2           29     10     2      4
 1              1           30     10     3      1
```

Consequently the randomized layout is:

Block Plot	1	2	3	4	5	6	7	8	9	10
1	2	1	5	4	5	8	10	8	10	3
2	5	9	7	7	3	9	8	7	2	4
3	4	2	8	6	6	6	1	10	3	1

XIII.2 An experiment was designed to compare five brands of perfume. People were to rate the perfume on a ten-point scale but it was decided that each person should only evaluate three perfumes at a time. This resulted in the use of a BIBD with the judge acting as a block. The design is given in the following table and is resolvable, although this was ignored in assigning the treatment combinations to judges.

	Judge (Person)									
Test	I	II	III	IV	V	VI	VII	VIII	IX	X
1	1	1	1	1	1	1	2	2	2	3
2	2	2	2	3	3	4	3	3	4	4
3	3	4	5	4	5	5	4	5	5	5

What are the components of the study?

1. Observational unit - a test

   Variables (incl. factors) are?
   Ans. Rating, Judges, Tests, Perfumes

2. Response variable - Rating
3. Unrandomized factors - Judges, Tests
4. Randomized factors - Perfumes
5. Type of study - BIBD

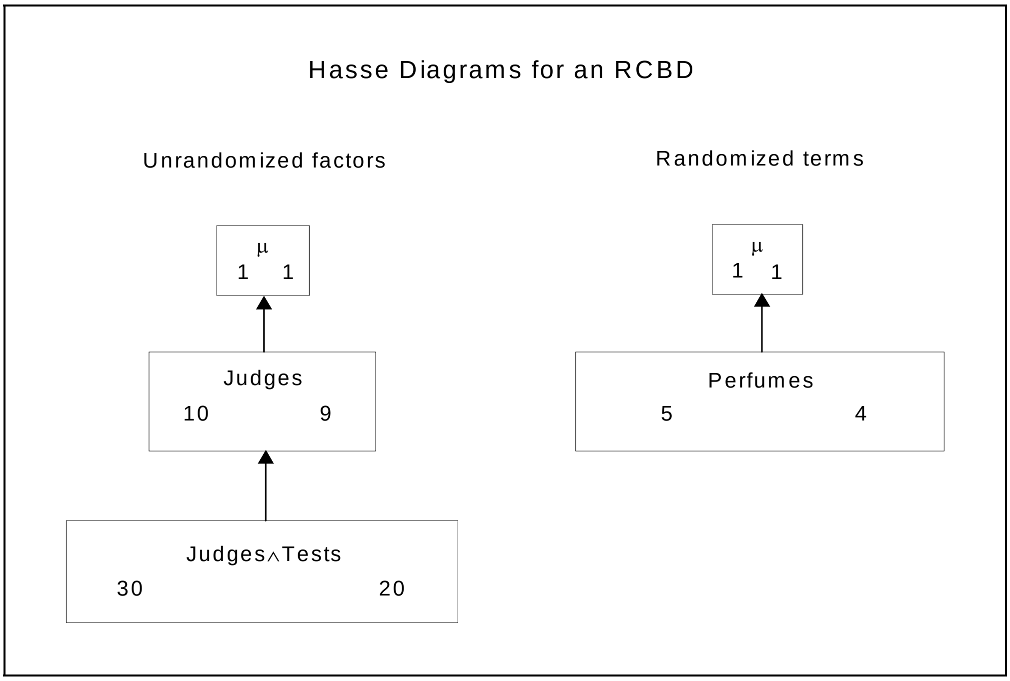
What is the experimental structure for this experiment?

Structure	Formula
unrandomized	*10* Judges/*3* Tests
randomized	*5* Perfumes

What are the terms derived from the experimental structure? Write out the Hasse diagram for each structure formula.

Judges/Tests = Judges+Tests[Judges]

Perfumes = Perfumes



What are the expected mean squares for the lines in the analysis of variance table based on all unrandomized factors being random and all randomized factors being fixed?

E[Y] = Perfumes and

Var[Y] = Judges + Tests[Judges]

Write down the analysis of variance table, including the expected mean squares for the lines in it.

Since $b = 3$, $t = 5$, $k = 3$, $r = 6$ *and* $\lambda = 3$, *the efficiency factors for the design are* $e_2 = (t\lambda)/(kr) = (5\times3)/(3\times6) = 5/6$ *and* $e_1 = 1 - e_2 = 1 - 5/6 = 1/6$.

Source	df	E[MSq]
Judges	9	
Perfumes	4	$\sigma^2_{\mathrm{JT}} + 3\sigma^2_{\mathrm{J}} + 0.167q_{\mathrm{P}}(\boldsymbol{\psi})$
Residual	5	$\sigma^2_{\mathrm{JT}} + 3\sigma^2_{\mathrm{J}}$
Tests[Judges]	20	
Perfumes	4	$\sigma^2_{\mathrm{JT}} + 0.833q_{\mathrm{P}}(\boldsymbol{\psi})$
Residual	16	σ^2_{JT}
Total	29	

Comment on the advisability of using just the intrablock information about Perfume differences given the design employed.

As the efficiency factor for Perfumes confounded with Tests[Judges] is 0.833, the majority of the information about Perfume differences will be available from just the intrablock information.

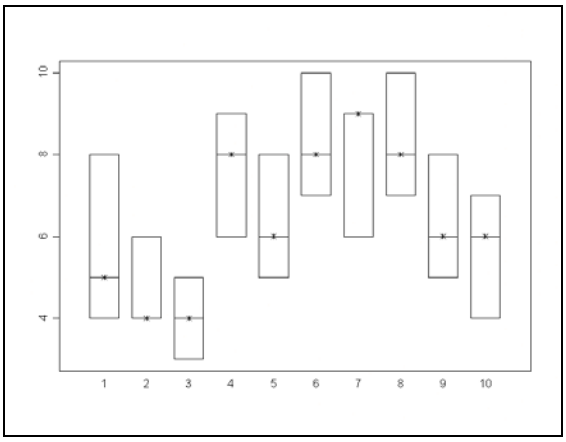
The results of the experiment are given in the following table, in the same order as the treatments are given in the first table. The data are available in *BIBDPerfume.sdd* in the *AdvDesign* directory of the data share \\cwpool0\briencj and from the web site.

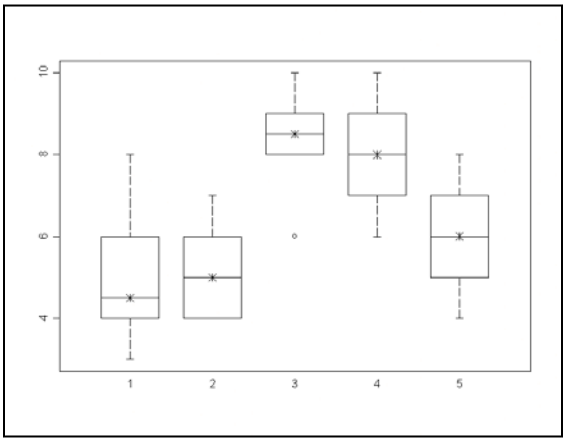
	Judge (Person)									
	I	II	III	IV	V	VI	VII	VIII	IX	X
Test										
1	4	4	3	6	5	8	6	7	5	6
2	5	4	4	9	8	10	9	10	8	7
3	8	6	5	8	6	7	9	8	6	4

Analyze the data using S-Plus, including diagnostic checking and the examination of treatment differences.

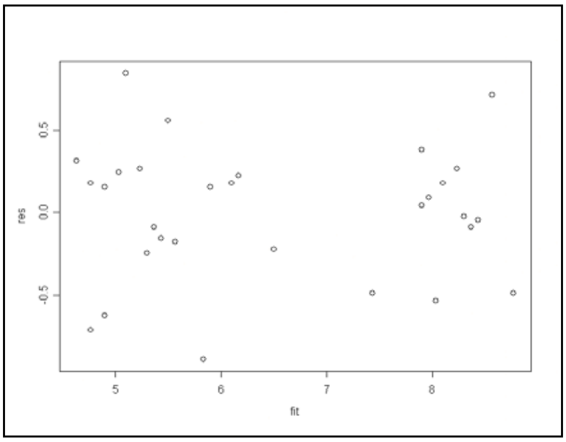
The S-Plus output file for computing the analysis of variance table is:

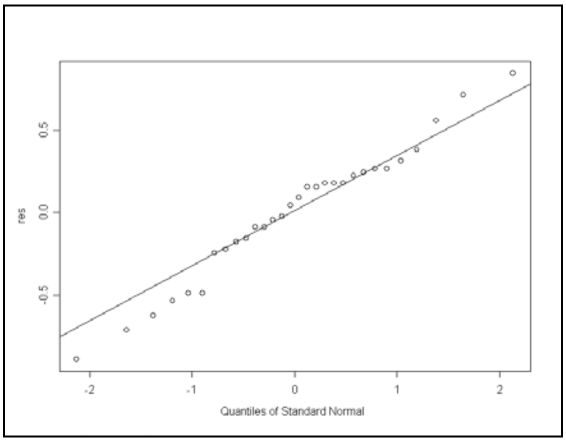
```
> attach(BIBDPerfume)
> library(DAE, lib.loc = "f:")
> boxplot(split(Rating, Judges), style.bxp = "old", medchar = T, medpch = 8)
> boxplot(split(Rating, Perfumes), style.bxp = "old", medchar = T, medpch = 8)
> BIBDPerfume.aov <- aov(Rating ~ Perfumes + Error(Judges/Tests), BIBDPerfume)
> summary(BIBDPerfume.aov)
Error: Judges
          Df Sum of Sq  Mean Sq   F Value     Pr(F)
 Perfumes  4  19.33333 4.833333 0.5390335 0.7154379
Residuals  5  44.83333 8.966667

Error: Tests %in% Judges
          Df Sum of Sq  Mean Sq  F Value         Pr(F)
 Perfumes  4  42.53333 10.63333 35.44444 9.158194e-008
Residuals 16   4.80000  0.30000

> #
# Diagnostic checking
#
> res <- resid.errors(BIBDPerfume.aov)
Refitting model to allow projection
> fit <- fitted.errors(BIBDPerfume.aov)
Refitting model to allow projection
> plot(fit, res)
> qqnorm(res)
> qqline(res)
> tukey.1df(BIBDPerfume.aov, BIBDPerfume, error.term = "Tests %in% Judges")
Refitting model to allow projection
Refitting model to allow projection
$SS.1df:
[1] 0.07345079

$SS.res.1:
[1] 4.726549

$F.1df:
[1] 0.2331007

$p.1df:
[1] 0.6362047
```





There appears to be differences between Judges and Perfumes.





Source	df	SSq	MSq	E[MSq]	F	Prob
Judges	9	64.17				
Perfumes	4	19.33	4.83	$\sigma^2_{\mathrm{JT}} + 3\sigma^2_{\mathrm{J}} + 0.167 q_{\mathrm{P}}(\boldsymbol{\psi})$	0.54	0.715
Residual	5	44.83	8.97	$\sigma^2_{\mathrm{JT}} + 3\sigma^2_{\mathrm{J}}$		
Tests[Judges]	20	47.33				
Perfumes	4	42.53	10.63	$\sigma^2_{\mathrm{JT}} + 0.833 q_{\mathrm{P}}(\boldsymbol{\psi})$	35.44	<0.001
Residual	16	4.80	0.30	σ^2_{JT}		
Nonadditivity	1	0.07	0.07		0.23	0.636
Deviation	15	4.73	0.32			
Total	29	112.00				

$e_2 = 5/6 = 0.833$,

$e_1 = 1 - 0.833 = 0.167$

$q_{\mathrm{T}}(\boldsymbol{\psi}) = 3\sum(\tau_k - \overline{\tau}_.)^2 / 4$

The residual-versus-fitted-values plots and the normal probability plot appear to be satisfactory. Tukey's test for nonadditivity is not significant. The assumptions appear to be met.

In this analysis, the Perfumes are significant different ($p < 0.001$) between Tests, but not significant ($p = 0.715$) between Judges. The latter result is explained by the larger Residual for Judges.

```
> #
# multiple comparisons
#
> BIBDPerfume.tab <- model.tables(BIBDPerfume.aov, type = "means")
Refitting model to allow projection
> BIBDPerfume.tab

Tables of means
Grand mean

 6.5

 Perfumes
      1   2      3      4   5
 5.1667 5.3 8.1667 7.9667 5.9
> sed <- as.vector(se.contrast(BIBDPerfume.aov, list(Perfumes == "1", Perfumes
==
     "2"), data = BIBDPerfume))
Refitting model to allow projection
> q <- qtukey(0.95, 5, 16)
> hsd <- q/sqrt(2) * sed
> data.frame(sed, q, hsd)
        sed     q      hsd
1 0.3464102 4.333 1.061364
> #
# plotting
#
> title("Fitted values for Rating")
> Perfume.Mean <- BIBDPerfume.tab$tables$Perfume
> BIBDPerfume.Means <- data.sheet(Perfume.Mean)
```

		Perfumes			
1	2	5	4	3	HSD(5%)
5.17	5.30	5.90	8.00	8.17	1.06

Perfumes 4 and 3 are rated higher than 1, 2 and 5. There are no differences within these two groups.