3.9 SAS Power Analysis for RCBD

SAS Code for determining power for a 4 treatment, 10 block RCBD for three α levels (.01,.05.10) and various σ values

```
ODS LISTING;
DM 'LOG;CLEAR;OUT;CLEAR;';
OPTIONS LS=72 PS=54 NONUMBER NODATE;

DATA rcbd;
b=10;                              ** enter number of blocks;
DO Trt = 'A', 'B', 'C', 'D';
DO Blocks = 1 to b;
   IF Trt = 'A' THEN tau = 3;     ** enter pattern for;
   IF Trt = 'B' THEN tau = 0;     ** the tau_i or mu_i;
   IF Trt = 'C' THEN tau = 0;
   IF Trt = 'D' THEN tau = 0;
OUTPUT;
END;
END;
;

DATA rcbd2; SET rcbd; BY Trt;
     IF last.Trt THEN OUTPUT;
DROP b taudiff;
PROC PRINT DATA=rcbd2;

PROC GLMPOWER DATA = rcbd;
      CLASS Trt Blocks;
      MODEL tau = Trt Blocks;
      POWER
         STDDEV = 1.5 2.0 2.5 3.0
         ALPHA  = 0.01 0.05 0.10
         NTOTAL = 40
         POWER  = .;
TITLE 'Determine power for an RCBD with 4 treatment and 10 blocks';
TITLE2 'for three alpha levels and various sigma values';
RUN;
```

SAS Output

```
Determine power for an RCBD with 4 treatment and 10 blocks
            for three alpha levels and sigma=2

               Obs    Trt    Blocks    tau

                1      A       10       3
                2      B       10       0
                3      C       10       0
                4      D       10       0
```

The GLMPOWER Procedure

Fixed Scenario Elements

Dependent Variable	tau
Total Sample Size	40
Error Degrees of Freedom	27

Computed Power

Index	Source	Alpha	Std Dev	Test DF	Power
1	Trt	0.01	1.5	3	0.963
2	Trt	0.01	2.0	3	0.730
3	Trt	0.01	2.5	3	0.465
4	Trt	0.01	3.0	3	0.292
5	Trt	0.05	1.5	3	0.995
6	Trt	0.05	2.0	3	0.909
7	Trt	0.05	2.5	3	0.729
8	Trt	0.05	3.0	3	0.554
9	Trt	0.10	1.5	3	0.998
10	Trt	0.10	2.0	3	0.955
11	Trt	0.10	2.5	3	0.833
12	Trt	0.10	3.0	3	0.688
13	Blocks	0.01	1.5	9	0.010
14	Blocks	0.01	2.0	9	0.010
15	Blocks	0.01	2.5	9	0.010
16	Blocks	0.01	3.0	9	0.010
17	Blocks	0.05	1.5	9	0.050
18	Blocks	0.05	2.0	9	0.050
19	Blocks	0.05	2.5	9	0.050
20	Blocks	0.05	3.0	9	0.050
21	Blocks	0.10	1.5	9	0.100
22	Blocks	0.10	2.0	9	0.100
23	Blocks	0.10	2.5	9	0.100
24	Blocks	0.10	3.0	9	0.100

3.10 Simple Repeated Measures Designs

The following comments are based on *Statistical Principles in Experimental Design* by B. Winer and from your text.

- In experimental work in biomedical, pharmaceutical, social, behavioral sciences, and occasionally in physical sciences and engineering, the experimental units are people (or animals).
- Because subjects vary (e.g., with respect to physical characteristics, health history, life experiences, training, etc.), the responses of subjects who receive the same treatment can vary greatly. If it is not controlled or accounted for in the analysis, it will can greatly inflate the experimental error making it difficult to detect real differences between treatments (i.e., a large Type II error).
- This is analogous to the case when blocking is ignored in a RCBD when there is large variability among the blocks.
- If the subject-to-subject source of variability can be separated from the treatment effects and the random experimental error, then the sensitivity of the experiment to detect real differences between treatments is increased (i.e., it will lower the Type II error).
- It may be possible to control for the subject-to-subject variability by running a design in which each subject receives all a treatments. Such a design is called a **repeated measures design (RMD)**.
- We will look at the simplest RMD in which each subject receives all a treatments in a random order.
- One potential problem is the **carry-over effect** in which the effect of receiving one treatment may influence the effect of (or carry-over to) the next treatment received by the subject.
- The goal is to prevent (or, at least minimize) any carry-over effects when designing the study. For example, in drug studies, this involves waiting a sufficient amount of time until the drug is out of the subject's system before administering the next drug.
- In our analysis, we will be assuming that there are no carry-over effects associated with a treatment. In essence, we are assuming that the subjects unique characteristics remain constant (uniform) at those times when the treatments are administered.

Notation:

- Assume there are a treatments and n subjects.
- If we have one observation per treatment level for each subject, and the order in which the treatments are run within each subject is determined randomly, then we have a **simple repeated measures design (SRMD)**.
- In a SRMD, treatment effects for subject j are measured relative to the average response of subject j across a treatments.
- In this sense, a subjects serves as its own control: responses of a subject to the treatments are measured in terms of deviations about a point which measures the subject's average response.
- Thus, variability due to differences in the average response of the subjects to treatments is removed from the experimental error (assuming the SRMD model is appropriate).
- Like the RCBD, because randomization occurs within each subject, this represents an example of restricted randomization.
- The SRMD data can be summarized as:

	Treatment (i)				
Subject (j)	1	2	$\cdots$	a	Totals
1	y_{11}	y_{21}	$\cdots$	y_{a1}	$y_{\cdot 1}$
2	y_{12}	y_{22}	$\cdots$	y_{a2}	$y_{\cdot 2}$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
n	y_{1n}	y_{2n}	$\cdots$	y_{an}	$y_{\cdot n}$
Totals	$y_{1\cdot}$	$y_{2\cdot}$	$\cdots$	$y_{a\cdot}$	$y_{\cdot\cdot}$

- Like all designs, we have for total variation ($df \ = \ N-1 \ = \ an-1$):

$$SS_{total} \ = \ \sum_{i=1}^{a}\sum_{j=1}^{n}$$

- The part of total variation attributable to differences among the means of the subjects is

$$SS_{between\,subj} \ = \ a\sum_{j=1}^{n} \qquad (11)$$

- The variation within subject j having $df = a-1$ is

$$SS_{within\,subj\,j} \ = \ \sum_{i=1}^{a} \qquad (12)$$

- The within-subject variation in (12) pooled over the n subjects having $df = n(a-1)$ is

$$SS_{within\,subj} \ = \ \sum_{j=1}^{n}\sum_{i=1}^{a} \qquad (13)$$

- It can be shown that SS_{total} partitions as

$$SS_{total} \ = \ SS_{between\,subj} \ + \ SS_{within\,subj} \qquad (14)$$

- Note that the variation of responses within a subject has two sources: one part depends on differences due to the treatment received and the other is random error variation. The part which depends on differences due to the treatments (like the RCBD) is defined as

$$SS_{trt} \ = \ n\sum_{i=1}^{a} \qquad (15)$$

  and the part that is residual error variation is

$$SS_E \ = \ \sum_{i=1}^{a}\sum_{j=1}^{b}\left(y_{ij} - \overline{y}_{i\cdot} - \overline{y}_{\cdot j} + \overline{y}_{\cdot\cdot}\right)^2 \qquad (16)$$

- It can be shown that $SS_{within\,subj}$ partitions as

$$SS_{within\,subj} \ = \ SS_{trt} \ + \ SS_E \qquad (17)$$

- Combining (14) and (17) we have

$$SS_{total} \ = \ SS_{between\,subj} \ + \ SS_{trt} \ + \ SS_E$$

- Numerically, these are exactly the same sums of squares for the RCBD with $SS_{between\ subjects}$ for the SRMD replacing the SS_{blocks} for the RCBD notationally.
- If μ is the baseline mean, τ_i is the i^{th} treatment effect, β_j is the j^{th} subject effect, and ϵ_{ij} is the random error of the observation, then the statistical model for a SRMD is:

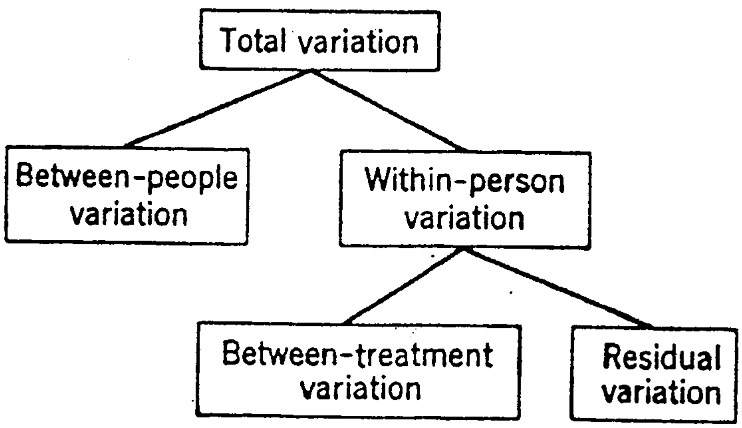
$$y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}$$

  with random error $\epsilon \sim N(0, \sigma^2)$ and random subject effects $\beta_j \sim N(0, \sigma_\beta^2)$.

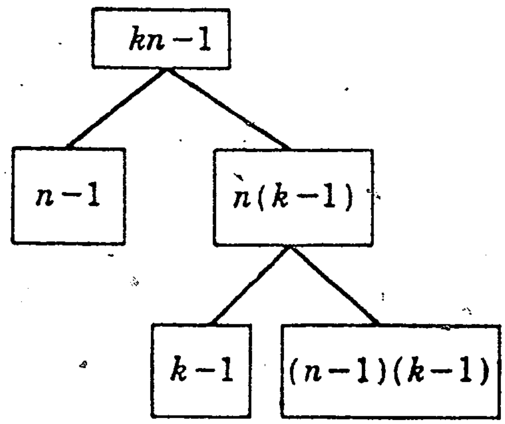
- Like the RBCD, we use $F = \dfrac{MS_{trt}}{MS_e}$ to test

$$\text{H}_0 : \tau_1 = \tau_2 = \cdots = \tau_a \qquad \text{vs} \qquad \text{H}_1 : \tau_i \neq \tau_j \ \text{ for some } \ i \neq j$$

Partition of the total variation



Partition of the degrees of freedom



EXAMPLE (from Winer): The purpose of this experiment was to study the effects of 4 drugs upon reaction time to a series of standardized tasks. The 5 subjects were randomly selected and had been given extensive training on these tasks prior to the experiment. Each of the subjects was observed under each of the 4 drugs and the order of administering the drug was randomized. A sufficient amount of time was allowed between administration of the drugs to avoid a carryover effect of one drug upon the effects of subsequent drugs (known as a drug interaction). The following table summarizes the reaction times.

	Drug Treatment			
Subject	1	2	3	4
1	30	28	16	34
2	14	18	10	22
3	24	20	18	30
4	38	34	20	44
5	26	28	14	30

SAS Code for Simple Repeated Measures Design

```
DM 'LOG; CLEAR; OUT; CLEAR;';

ODS GRAPHICS ON;
ODS PRINTER PDF file='C:\COURSES\ST541\REPMEAS.PDF';
OPTIONS NODATE NONUMBER;

DATA IN;
   DO drug =1 TO 4;
   DO subject = 1 TO 5;
      INPUT reaction @@; OUTPUT;
   END; END;
CARDS;
30 14 24 38 26    28 18 20 34 28
16 10 18 20 14    34 22 30 44 30
;
PROC GLM DATA=IN PLOTS=(ALL);
     CLASS subject drug;
     MODEL reaction = drug subject / SS3;
     MEANS drug / TUKEY;
     MEANS subject;
TITLE 'SINGLE FACTOR REPEATED MEASURES DESIGN';
RUN;
```

SINGLE FACTOR REPEATED MEASURES DESIGN

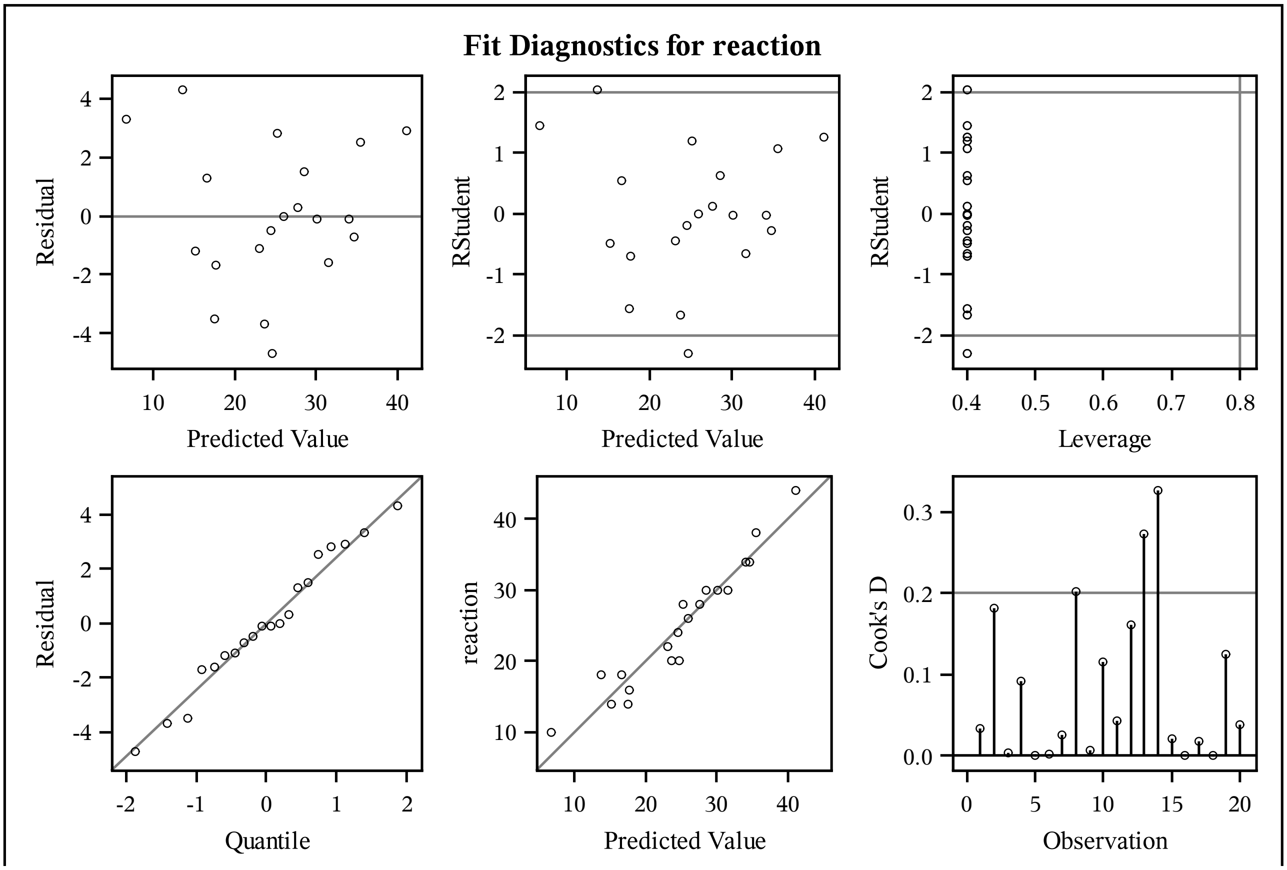
The GLM Procedure

Variable: reaction

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	7	1379.000000	197.000000	20.96	<.0001
Error	12	112.800000	9.400000		
Corrected Total	19	1491.800000			

R-Square	Coeff Var	Root MSE	reaction Mean
0.924387	12.31302	3.065942	24.90000

Source	DF	Type III SS	Mean Square	F Value	Pr > F
drug	3	698.2000000	232.7333333	24.76	<.0001
subject	4	680.8000000	170.2000000	18.11	<.0001



Tukey's Studentized Range (HSD) Test for reaction

Alpha	0.05
Error Degrees of Freedom	12
Error Mean Square	9.4
Critical Value of Studentized Range	4.19851
Minimum Significant Difference	5.7567

Means with the same letter are not significantly different.				
Tukey Grouping		**Mean**	**N**	**drug**
	A	32.000	5	4
	A			
B	A	26.400	5	1
B				
B		25.600	5	2
	C	15.600	5	3

Level of subject	**N**	**reaction**	
		Mean	**Std Dev**
1	4	27.0000000	7.7459667
2	4	16.0000000	5.1639778
3	4	23.0000000	5.2915026
4	4	34.0000000	10.1980390
5	4	24.5000000	7.1879529