Options for Analyzing a One-Way Within-Subject Design with Replications

Assume 5 levels of factor A, 3 participants who complete 4 replications of each of the 5 levels of factor A (20 observations per participant; 60 observations in the whole experiment).

A. Average each participant=s responses within treatment condition. Now we have 5 observations per person, one for each level of factor A. It is now analyzed as a regular one-way within-subject design.
Subjects is random; A is fixed.

Source	df	E(MS)
Mean	1	$\sigma_e^2 + a\sigma_S^2 + an\mu^2$
Subjects	n - 1 = 2	$\sigma_e^2 + a\sigma_S^2$
A	a - 1 = 4	$\sigma_e^2 + \sigma_{SxA}^2 + n\theta_A^2$
A x S	8	$\sigma_e^2 + \sigma_{SxA}^2$

Linear model:

$$Y_{ij} = \mu + \alpha_j + \pi_i + \alpha\pi_{ij} + \varepsilon_{ij}$$

ε_{ij} can't be separated from $\alpha\pi_{ij}$

B. Consider replications to be random and nested in Subject x A combinations. Subjects is also random.

Source	df	E(MS)
Mean	1	$\sigma_e^2 + ar\sigma_S^2 + anr\mu^2$
Subjects	n - 1 = 2	$\sigma_e^2 + ar\sigma_S^2$
A	a - 1 = 4	$\sigma_e^2 + r\sigma_{AxS}^2 + rn\theta_A^2$
A x S	(a-1)(n-1) = 8	$\sigma_e^2 + r\sigma_{AxS}^2$
Reps/AS	an(r - 1) = 45	σ_e^2

B′. Replications is random and nested in S x A combinations, but subjects is fixed.

Source	df	E(MS)
Mean	1	$\sigma_e^2 + anr\mu^2$
Subjects	n - 1	$\sigma_e^2 + ar\theta_S^2$
A	a - 1	$\sigma_e^2 + nr\theta_A^2$
A x S	(a-1)(n-1)	$\sigma_e^2 + r\theta_{AxS}^2$
R/AS	an(r - 1)	σ_e^2

C. Consider replications to be a fixed factor crossed with other factors. Subjects is random. This analysis allows Reps to be tested.

Source	df	E(MS)
Mean	1	$\sigma_e^2 + ar\sigma_S^2 + anr\mu^2$
Subjects	n - 1	$\sigma_e^2 + ar\sigma_S^2$
A	a - 1	$\sigma_e^2 + r\sigma_{AxS}^2 + ar\theta_A^2$
A x S	(a-1)(n-1)	$\sigma_e^2 + r\sigma_{AxS}^2$
Reps	r - 1	$\sigma_e^2 + a\sigma_{RxS}^2 + an\theta_R^2$
R x S	(r-1)(n-1)	$\sigma_e^2 + a\sigma_{RxS}^2$
A x R	(a-1)(r-1)	$\sigma_e^2 + \sigma_{AxRxS}^2 + n\theta_{AxR}^2$
A x R x S	(a-1)(r-1)(n-1)	$\sigma_e^2 + \sigma_{AxRxS}^2$

D. Analyze the data of each subject in a separate ANOVA. Replications is a random factor in each analysis, nested in treatment. This allows the effect of factor A to be tested for each individual.

Source	df	E(MS)
Mean	1	$\sigma_e^2 + ar\mu^2$
A	a - 1	$\sigma_e^2 + r\theta_A^2$
Reps/A	a(r - 1)	σ_e^2

D′. Individual subject ANOVAs; Replications is random and crossed with factor A (factor A is fixed).

Source	df	E(MS)
Mean	1	$\sigma_e^2 + a\sigma_R^2 + ar\mu^2$
Reps	r - 1	$\sigma_e^2 + a\sigma_R^2$
A	a - 1	$\sigma_e^2 + \sigma_{AxR}^2 + r\theta_A^2$
A x R	(a-1)(r-1)	$\sigma_e^2 + \sigma_{AxR}^2$

Comments:

A. In this approach, reps are not of interest. By averaging reps together for each subject, the scores to be analyzed will have more stability. Variance due to replications is averaged away.

B. & B′. In these approaches, reps is also not of interest, but it becomes the error term for at least one test. The interaction of treatment (A) with Subjects can be tested. Subjects can also be tested. A question for BN is when it might be legitimate to consider subjects to be a fixed factor.

C. In this approach, reps is a factor that the investigator is interested in testing, along with its interaction with the treatment effect.

D. & D′. In these approaches the focus is on individual differences in the effect of factor A. Do some subjects show a treatment effect whereas others do not? There is a design issue in considering reps to be nested vs. crossed. Nested would be implied by a totally random order of the ar trials of the experiment. Crossed seems to be implied by a design in which all of the a trials of the first replication are completed before the second replication, etc. What are the implications of crossed versus nested for statistical power?

Four Alternatives for Analyzing Massaro and Anderson design (*American Journal of Psychology*, 1970)

Data averaged over reps.

Source	df
Mean	1
Subjects	15
Orientations	1
SxO	15
Length	1
SxL	15
Angle	4
SxA	60
OxL	1
SxOxL	15
OxA	4
SxOxA	60
LxA	4
SxLxA	60
OxLxA	4
SxOxLxA	60
	320

Cells for systematic sources = 2 orientations x 2 lengths x 5 angles = 20

20 scores per S x 16 S = 320 obs.

Reps. nested within SOLA

Source	df
Mean	1
Subjects	15
Orientations	1
SxO	15
Length	1
SxL	15
Angle	4
SxA	60
OxL	1
SxOxL	15
OxA	4
SxOxA	60
LxA	4
SxLxA	60
OxLxA	4
SxOxLxA	60
Reps/SOLA	1280
	1600

Cells for systematic sources = 20
20 cells x 5 trials = 100 per S
100 scores per S x 16 S = 1600 obs.

Reps is random
S is random

Reps. treated as factor

Source	df
Mean	1
Subjects	15
Orientations	1
SxO	15
Length	1
SxL	15
Angle	4
SxA	60
OxL	1
SxOxL	15
OxA	4
SxOxA	60
OxT	4
SxOxT	60
LxA	4
SxLxA	60
LxT	4
SxLxT	60
AxT	16
SxAxT	240
OxLxA	4
SxOxLxA	60
OxLxT	4
SxOxLxT	60
OxAxT	16
SxOxAxT	240
LxAxT	16
SxLxAxT	240
OxLxAxT	16
SxOxLxAxT	240
	1400

Cells for systematic sources = 20 x 5 trials = 100
100 scores per S x 16 S = 1600 obs.

Single subject analysis

Source	df
Mean	1
Orientation	1
Length	1
Angle	4
OxL	1
OxA	4
LxA	4
OxLxA	4
Reps/OLA	80
	100

Cells for systematic sources = 20

5 reps per cell = 100 obs.