

Chapter 20 : Two factor studies—one case per
treatment
Chapter 21: Randomized complete block designs

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Stat 705: Data Analysis II

Additive design when $n_{ij} \equiv 1$

When $n_{ij} \equiv 1$, the subscript k is suppressed, and we must assume that interaction is negligible compared to experimental error:

$$Y_{ij} = \mu_{..} + \alpha_i + \beta_j + \underbrace{\{\alpha\beta_{ij} + \epsilon_{ij}\}}_{\text{Error}}, \quad i = 1, \dots, a, \quad j = 1, \dots, b$$

The additive effects A and B are tested against the error term, which has $(a - 1) \times (b - 1)$ degrees of freedom. The book notes we may choose to estimate μ_{ij} by the MVUE $\bar{Y}_{i.} + \bar{Y}_{.j} - \bar{Y}_{..}$, rather than Y_{ij} .

Tukey's test for additivity

Tukey's test for additivity provides a 1 df test for interaction, rather than a $(a - 1) \times (b - 1)$ df test, which would be impractical for $n_{ij} \equiv 1$. 0.5

The reduced model is additive: $Y_{ij} = \mu_{..} + \alpha_i + \beta_j + \epsilon_{ij}$. The full model is

$$Y_{ij} = \mu_{..} + \alpha_i + \beta_j + D\alpha_i\beta_j + \epsilon_{ij}.$$

This is more restrictive than using a general interaction $(\alpha\beta)_{ij}$, leaving $(a - 1) \times (b - 1) - 1 = ab - a - b$ df to estimate error. The full LS estimator would be nonlinear in our parameters. Instead, we solve for D separately, and then plug in LS estimates of α_i and β_j from the additive model.

Tukey's test for additivity

$$\hat{D} = \frac{\sum_{i=1}^a \sum_{j=1}^b (\bar{Y}_{i\cdot} - \bar{Y}_{\cdot\cdot})(\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot}) Y_{ij}}{\sum_{i=1}^a (\bar{Y}_{i\cdot} - \bar{Y}_{\cdot\cdot})^2 \sum_{j=1}^b (\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot})^2}.$$

$$SSAB^* = \sum_{i=1}^a \sum_{j=1}^b (\hat{\alpha}\hat{\beta})_{ij}^2 =$$

$$\sum_{i=1}^a \sum_{j=1}^b \hat{D}^2 \hat{\alpha}_i^2 \hat{\beta}_j^2 = \hat{D} \sum_{i=1}^a \sum_{j=1}^b \hat{\alpha}_i \hat{\beta}_j Y_{ij},$$

and $SSTO = SSA + SSB + SSAB^* + SSE^*$.

$$F^* = \frac{SSAB^*}{SSE^*/(ab - a - b)} \sim F(1, ab - a - b),$$

if $H_0 : D = 0$ is true.

Trick for additivity test

Let \hat{Y}_{ij} be fitted values from the additive model. Make a second pass through PROC GLM to fit the ANCOVA model

$$Y_{ij} = \mu + \alpha_i + \beta_j + \gamma \hat{Y}_{ij}^2 + \epsilon_{ij}.$$

The test of $H_0 : \gamma = 0$ is the same as the test of $H_0 : D = 0$, the F-statistics are the same and the p-values are the same!

Example (p. 895): Executives are exposed to one of three methods (treatment, $i = 1$ utility method, $i = 2$ worry method, $i = 3$ comparison method) of quantifying the maximum risk premium they would be willing to pay to avoid uncertainty in a business decision. The response variable is “degree of confidence” in the method on a scale from 0 (no confidence) to 20 (complete confidence). It is thought that confidence is related to age, so the subjects are blocked according to age ($j = 1, 2, 3, 4, 5$ from oldest to youngest). $n_T = 15$ subjects are recruited, with three subjects in each of the 5 age categories. Within each age category, the three subjects are randomly given one of the three treatments.

```
data conf;
  input rating age method @@;
datalines;
  1 1 1 5 1 2 8 1 3
  2 2 1 8 2 2 14 2 3
  7 3 1 9 3 2 16 3 3
  6 4 1 13 4 2 18 4 3
  12 5 1 14 5 2 17 5 3
;

proc format;
value ac 1='oldest' 2='age grp II' 3='age grp III' 4='age grp IV' 5='youngest';
value mc 1='utility' 2='worry' 3='compare';

* first obtain interaction plot by fitting model V;
* trajectories look reasonably parallel;
proc glm data=conf plots=all;
  class age method;
  model rating=age|method;
run;
```

Confidence ratings

```
* fit additive model;
proc glm data=conf plots=all;
  class age method;
  format age $ac. method $mc.;
  model rating=age method / solution;
  output out=tukeytest p=p; * p=yhat values for Tukey's test;
run;

* Tukey test for additivity;
* p-value=0.79 so model IV is okay;
proc glm data=tukeytest;
  title 'Test for additivity is Type III p*p p-value';
  class age method;
  model rating=age method p*p;
run;
```


21.1 Randomized complete block designs

Subjects are placed into homogeneous groups, called *blocks*, which are selected based on either characteristics of experimental units or the experimental setting. All treatment combinations assigned randomly to subjects within blocks.

Example: Stream habitat is being tested for biodiversity. In an observational study, three different types of habitat along streams are tested: farmland, high-density rural, forested. Four streams are selected for testing: Myers Creek, Cedar Creek, Dry Branch and Toms Creek. For each stream and habitat type, a randomly selected 100-meter stretch is seined and electrofished to measure fish and macroinvertebrates. A single measure of biodiversity (IBI-Index of Biotic Integrity) is computed for each stream reach. The observational treatment here is Habitat, while the block is Stream.

- With thoughtful blocking, a RCBD can provide more precise results than completely randomized design.
- There is only one replication for each pairing of treatment and block; we need to assume no interaction between treatments and blocks to obtain an estimate of σ^2 .
- Note, as in the example above, that some experiments lend themselves to a single replication by the nature of their response variable.
- If interaction were present, it has troubling implications for inference on the treatment.
- The blocking variable is observational, not experimental. We cannot infer a causal relationship. This is usually not a problem, since the experimenter cares more about the treatment. It's a source of endless debates among statisticians though!

One observation per block/treatment combination gives $n_T = n_b r$.
We need to fit model IV to get $SSE > 0$

$$Y_{ij} = \mu_{..} + \underbrace{\rho_i}_{Bl} + \underbrace{\tau_j}_{Trt} + \epsilon_{ij}, \quad i = 1, \dots, n_b, \quad j = 1, \dots, r.$$

Estimates are obtained via LS as usual,

$$Q(\boldsymbol{\rho}, \boldsymbol{\tau}) = \sum_{i=1}^{n_b} \sum_{j=1}^r (Y_{ij} - [\mu_{..} + \rho_i + \tau_j])^2$$

minimized subject to $\rho_{n_b} = \tau_r = 0$.

ANOVA table

Source	SS	df	MS	F
Block	$SSBL = r \sum_{i=1}^{n_b} (\bar{Y}_i - \bar{Y}_{..})^2$	$n_b - 1$	$\frac{SSBL}{n_b - 1}$	$\frac{MSBL}{MSBL.TR}$
Trt	$SSTR = n_b \sum_{j=1}^r (\bar{Y}_{.j} - \bar{Y}_{..})^2$	$r - 1$	$\frac{SSTR}{r - 1}$	$\frac{MSB}{MSE}$
Error	$SSBL.TR = \sum_{i=1}^{n_b} \sum_{j=1}^r (Y_{ij} - \bar{Y}_i - \bar{Y}_{.j} + \bar{Y}_{..})^2$	$(n_b - 1)(r - 1)$	$\frac{SSBL.TR}{(n_b - 1)(r - 1)}$	
Total	$SSTO = \sum_{i=1}^{n_b} \sum_{j=1}^r (Y_{ij} - \bar{Y}_{..})^2$	$n_b r - 1$		

Here, $F = \frac{MSBL}{MSBL.TR}$ tests $H_0 : \rho_1 = \dots = \rho_{n_b} = 0$ (no blocking effect) and $F = \frac{MSTR}{MSBL.TR}$ tests $H_0 : \tau_1 = \dots = \tau_r = 0$ (no treatment effect). These appear in SAS as Type III tests.

If we reject $H_0 : \tau_j = 0$, then we obtain inferences in treatment effects as usual, e.g. `lsmeans B / pdiff adjust=tukey cl;`

- 1 Profile (spaghetti) plots of the Y_{ij} vs. treatment j , connected by block i are useful. They should be somewhat parallel if the additive model is okay, but there is a lot of sampling variability here as $\hat{\mu}_{ij} = Y_{ij}$. For this reason, the book actually recommends using $\hat{\mu}_{ij} = \bar{Y}_{i.} + \bar{Y}_{.j} - \bar{Y}_{..}$ for inference.
- 2 Standard SAS diagnostic panel: e_{ij} vs. \hat{Y}_{ij} , normal probability plot of the $\{e_{ij}\}$, etc. Can also look at e_{ij} vs. either i or j , should show constant variance within blocks and treatments.
- 3 Friedman's test is a nonparametric test based on within-block ranks. Yes, it's named after Milton Friedman. This can be readily analyzed in *PROC FREQ*.
- 4 Tukey's test for additivity.

- 1 Blocking can be assessed post hoc to see whether it was efficient. You can compare the error term in a blocked design (σ_b^2 , estimated by $MSBL.TR$) to σ_r^2 , the error term in a completely randomized design. The estimator for σ_r^2 can be written a couple ways:

$$\begin{aligned}\hat{\sigma}_r^2 &= \frac{(n_b - 1)MSBL + n_b(r - 1)MSBL.TR}{(n_b r - 1)} \\ &= \frac{df_{blocks}MS_{blocks} + (df_{Trt} + df_{error})MSE}{df_{Blocks} + df_{Trt} + df_{error}}\end{aligned}$$

- 2 The relative efficiency of blocking $E = \hat{\sigma}_r^2 / MSBL.TR$ measures the increase in sample size needed for a CRD to match the RCBD in efficiency.

- $n_{ij} > 1$
- Factorial treatment structure (e.g., $\tau_{jk} = \beta_j + \gamma_k + (\beta\gamma)_{jk}$) is a straightforward extension of RCBD.
- Multiple blocking variables require a little more consideration
- A couple of these topics are explored further in STAT 706