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:

\[
Y_{ij} = \mu_{..} + \alpha_i + \beta_j + \left\{ \alpha\beta_{ij} + \epsilon_{ij} \right\}, \quad i = 1, \ldots, a, \quad j = 1, \ldots, b
\]

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 \( \mu_{ij} \) by the MVUE \( \bar{Y}_{i.} + \bar{Y}_{.j} - \bar{Y}_{..} \), rather than \( Y_{ij} \).
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 \(\alpha_i\) and \(\beta_j\) from the additive model.
Tukey’s test for additivity

\[
\hat{D} = \frac{\sum_{i=1}^{a} \sum_{j=1}^{b} (\bar{Y}_i - \bar{Y}) (\bar{Y}_j - \bar{Y}) Y_{ij}}{\sum_{i=1}^{a} (\bar{Y}_i - \bar{Y})^2 \sum_{j=1}^{b} (\bar{Y}_j - \bar{Y})^2}.
\]

\[
SSAB^* = \sum_{i=1}^{a} \sum_{j=1}^{b} (\hat{\alpha}_i \hat{\beta}_j)^2 = \hat{D}^2 \sum_{i=1}^{a} \sum_{j=1}^{b} \hat{\alpha}_i \hat{\beta}_j Y_{ij},
\]

and \( \text{SSTO} = \text{SSA} + \text{SSB} + \text{SSAB}^* + \text{SSE}^* \).

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

if \( H_0 : D = 0 \) is true.
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;
* 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;
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 $\sigma^2$.

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 \( n_T = n_br \).

We need to fit model IV to get \( \text{SSE} > 0 \)

\[
Y_{ij} = \mu_{..} + \rho_i + \tau_j + \epsilon_{ij}, \quad i = 1, \ldots, n_b, \quad j = 1, \ldots, r.
\]

Estimates are obtained via LS as usual,

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

minimized subject to \( \rho_{n_b} = \tau_r = 0 \).
### ANOVA table

<table>
<thead>
<tr>
<th>Source</th>
<th>SS</th>
<th>df</th>
<th>MS</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Block</td>
<td>$SSBL = r \sum_{i=1}^{nb} (\bar{Y}_i - \bar{Y}..)^2$</td>
<td>$nb - 1$</td>
<td>$\frac{SSBL}{n_b - 1}$</td>
<td>$\frac{MSBL}{MSBL.TR}$</td>
</tr>
<tr>
<td>Trt</td>
<td>$SSTR = n_b \sum_{j=1}^{r} (\bar{Y}_j - \bar{Y}..)^2$</td>
<td>$r - 1$</td>
<td>$\frac{SSTR}{r - 1}$</td>
<td>$\frac{MSB}{MSE}$</td>
</tr>
<tr>
<td>Error</td>
<td>$SSBL.TR = \sum_{i=1}^{nb} \sum_{j=1}^{r} (Y_{ij} - \bar{Y}_i - \bar{Y}_j + \bar{Y}..)^2$</td>
<td>$(nb - 1)(r - 1)$</td>
<td>$\frac{SSBL.TR}{(n_b - 1)(r - 1)}$</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>$SSTO = \sum_{i=1}^{nb} \sum_{j=1}^{r} (Y_{ij} - \bar{Y}..)^2$</td>
<td>$nb r - 1$</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Here, $F = \frac{MSBL}{MSBL.TR}$ tests $H_0: \rho_1 = \cdots = \rho_{nb} = 0$ (no blocking effect) and $F = \frac{MSTR}{MSBL.TR}$ tests $H_0: \tau_1 = \cdots = \tau_r = 0$ (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.
Blocking can be assessed post hoc to see whether it was efficient. You can compare the error term in a blocked design ($\sigma_b^2$, estimated by MSBL.TR) to $\sigma_r^2$, the error term in a completely randomized design. The estimator for $\sigma_r^2$ can be written a couple ways:

$$\hat{\sigma_r^2} = \frac{(n_b - 1) MSBL + n_b(r - 1) MSBL.TR}{n_b r - 1}$$

$$= \frac{df_{blocks} MS_{blocks} + (df_{Trt} + df_{error}) MSE}{df_{Blocks} + df_{Trt} + df_{error}}$$

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.
RCBD model extensions

- \( n_{ij} > 1 \)
- 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