We discussed the idea of adding a permutation matrix for assignments of treatments. In the document C05ed19.doc, an experiment is represented by a set of random variables that represent the units that could be potentially observed. An estimator of a treatment group mean is developed. Further analysis now will develop a predictor of a realized treatment by adding a permutation of treatments, and considering the treatment levels to be random effects.

Step 1:

Based on the previous analysis in C05ed19.doc, suppose we define an indicator random variable $V_{ja}, j = 1, \ldots, A$, that indexes the position of a treatment in a treatment permutation, where $a = 1, \ldots, A$ are labels of the treatments. The indicator random variables $V_{ja}$ takes on a value of one if the treatment $a$ is assigned to position $j$ in a permutation, or zero otherwise. We can develop the expected value and variance of $V_{ja}$.

When adding permutations of treatments, we can develop a matrix

$$Y^* = \left( Y_j^* \right) = U_{ij} V^*,$$

where $Y_j^*$ indicates the response of the unit assigned to position $i$ that receives the treatment level assigned to position $j$ in a permutation of treatment levels. Take the column expansion of $Y^* = V (y'U')$.

$$Y = vec \left( Y^* \right) = \left( (y'U') \otimes I_n \right) vec(V).$$

$$= \left( (Uy) \otimes I_n \right) vec(V)$$

First we try to find $E_{U'}(Y)$. Next, we try to figure out variance-covariance matrix, $\text{var}_{U'}(Y)$.

Evaluating the expected value should be straightforward. To evaluate the variance, we plan to use the expansion,

$$Var_{U'} \left( Y^* \right) = E_{U'} \left[ \text{Var}_{U'} \left( Y^* \right) \right] + \text{Var}_{U'} \left[ E_{U'} \left( Y^* \right) \right],$$

making use of the vec expansion given above. We can determine $\text{var} \left[ vec(V) \right]$ in the same way as we found $\text{var} \left[ vec(U) \right]$ (Refer to Highlights740-6.doc in notes for BIOSTAT&EPI 740).

Step 2:

Subsequent steps follow from other derivations. We will re-arrange and collapse the random variables into a set corresponding to the sample totals, $Y_j^*$, and a set
corresponding to the weighted remaining totals for each treatment, \( Y^*_{ji} \) such that
\[
\begin{pmatrix}
Y^*_{i1} \\
Y^*_{ii}
\end{pmatrix} = \begin{pmatrix}
K_j \\
Kii
\end{pmatrix} Y^*. 
\]
Then, we will define the random variable corresponding to the mean response for a treatment level assigned to position \( j \) as
\[
P_j = \frac{1}{N} I_n Y^* e_j',
\]
where \( e_j \) is an \( A \times 1 \) vector with element \( j \) equal to one, and all other elements equal to zero. We will then express
\[
P_j = g'_j Y^* + g'_{ii} Y^*_{ii},
\]
determine these quantities that predict \( g'_{ii} Y^*_{ii} \). We will develop a predictor that is a linear function of the sample, subject to an unconditional unbiased constraint.