Introduction

We describe how the Repeated Statement in PROC GLM in SAS transforms the data to provide tests of hypotheses of interest. A good reference for multivariate methods is Timm (1975). We use the SAS manual as a reference for the repeated statement. First, we briefly review notation and the context for multivariate data.

The Population, Sample, and Context

Consider a simple random sample of \( n \) subjects from a very large population. Assume that there are \( p \) measures of response made on each selected subject. The measures may correspond to measures of \( p \) different characteristics of the subjects (such as age, height, weight, systolic blood pressure, etc), or repeated measures of the same variable (total cholesterol) at different times or conditions. With these assumptions, we represent the vector of responses for the \( i^{th} \) selected subject as \( Y_i = \left( Y_{i1}, Y_{i2}, \ldots, Y_{ip} \right) \). We will assume that selections of subjects is independent, but that measures on a selected subject may be correlated, representing \( \text{var}(Y_i) = \Sigma_{pp} \).

In experimental settings, Factor level may be assigned to subjects (blocks) or to occasions within a subject (plots). Factors assigned to subjects are modeled with a design matrix such that

\[
Y = X\beta + E
\]

where \( Y_{np} = \begin{pmatrix} Y_1' \\ Y_2' \\ \vdots \\ Y_n' \end{pmatrix} \), \( X \) is a design matrix representing the levels of the factor assigned to selected subject, \( \beta = \begin{pmatrix} \beta_{11} & \beta_{12} & \cdots & \beta_{1p} \\ \beta_{21} & \beta_{22} & \cdots & \beta_{2p} \\ \vdots & \vdots & \ddots & \vdots \\ \beta_{k1} & \beta_{k2} & \cdots & \beta_{kp} \end{pmatrix} \) is a matrix of parameters, with rows corresponding to a level of factor A, and columns corresponding to the measures, or 'occasions'. With these assumptions, \( \text{var}(\text{vec}(Y)) = \Sigma_{pp} \otimes I_n \), or \( \text{var}(\text{vec}(Y)) = \Sigma_{pp} \otimes I_n \).

Estimation under a General Linear Multivariate Model

Estimates of the parameters corresponding to least squares estimates can be obtained similar to estimates in univariate models. The estimates are given by
\[
\hat{\beta} = (X'X)^{-1} X'Y.
\]
Since \(\text{vec}(ABC) = (C' \otimes A) \text{vec}(B)\), then expressing \(\hat{\beta} = \left( (X'X)^{-1} X' \right) \left[ Y \right] \left[ I_p \right] \), we find that \(\text{vec}\left( \hat{\beta} \right) = \left( I_p \otimes (X'X)^{-1} X' \right) \text{vec}(Y)\), and hence

\[
\text{var}\left( \text{vec}\left( \hat{\beta} \right) \right) = \left( I_p \otimes (X'X)^{-1} X' \right) \left( \Sigma \otimes I_n \right) \left( I_p \otimes X(X'X)^{-1} \right),
\]
which simplifies to \(\text{var}\left( \text{vec}\left( \hat{\beta} \right) \right) = \Sigma \otimes (X'X)^{-1}\). The variance matrix is estimated by

\[
\hat{\Sigma} = \frac{(Y - X\hat{\beta})' (Y - X\hat{\beta})}{n - k},
\]
so that \(\text{var}\left( \text{vec}\left( \hat{\beta} \right) \right) = \hat{\Sigma} \otimes (X'X)^{-1}\).

**Hypotheses under A General Linear Multivariate Normal Model**

Traditionally, hypotheses have been specified for a general linear multivariate model that are linear combinations of rows and columns of \(\beta = \begin{pmatrix}
\beta_{11} & \beta_{12} & \cdots & \beta_{1p} \\
\beta_{21} & \beta_{22} & \cdots & \beta_{2p} \\
\vdots  & \vdots  & \ddots & \vdots  \\
\beta_{k1} & \beta_{k2} & \cdots & \beta_{kp} 
\end{pmatrix}
\)
model. Such hypotheses are expressed as \(L \beta M = 0\), where \(L\) and \(M\) are matrices of constants. For example, the hypothesis of whether or not the average of the parameters in the first row equals the average of the parameters in the second row is specified by setting \(L = \begin{pmatrix} 1 & -1 & 0 & 0 & \cdots & 0 \end{pmatrix}\) and \(M = \frac{1}{p} I_p\). It should be clear that there are limitations in defining hypotheses in terms of \(L \beta M = 0\). With such a structure, it is not possible to define \(L\) and \(M\) to test the hypothesis that \(\beta_{11} + \beta_{12} = \beta_{1p} + \beta_{2p}\). Using mixed models, any linear hypothesis concerning the elements of \(\beta\) can be tested.

When \(u = p\) and \(M\) is of full rank, then \(M\) is a square matrix that can be viewed as a transformation matrix. The standard multivariate model can be written as a model on a set of transformed random variables. This is the idea behind the Repeated Statement in PROC GLM.

**A Model for A Transformed Set of Random Variables**

We transform the random variables in a multivariate model by post-multiplying by
the non-singular matrix $M_{p \times p}$. The model is given by

$$YM = X\beta M + EM$$

which we express as

$$Y^* = X\beta^* + E^*$$

where $Y^* = YM$, $\beta^* = \beta M$, and $E^* = EM$. Note that

$$\text{vec}(Y^*) = \text{vec}(YM) = (M' \otimes I_n) \text{vec}(Y)$$

while

$$\text{vec}(Y'^*) = \text{vec}(M'Y') = (I_n \otimes M') \text{vec}(Y')$$

and

$$\text{vec}(\beta^*) = \text{vec}(\beta M) = (M' \otimes I_n) \text{vec}(\beta).$$

Then in the transformed model, $E(Y^*) = X\beta^*$ and

$$\text{var}(\text{vec}(Y'^*)) = (I_n \otimes M')(I_n \otimes \Sigma)(I_n \otimes M)$$

$$= I_n \otimes M' \Sigma M'$$

$$= I_n \otimes \Sigma^*_{p \times p}$$

where $\Sigma^*_{p \times p} = M' \Sigma M'$. Thus, all the analysis tools used for the usual multivariate model can be applied to the transformed multivariate model.

**Example: Special Case For A Simple Response Error Model**

Suppose that $p$ independent measures are made on each selected subject in a simple random sample of $n$ subjects from a large population. Let the model for the $k^{th}$ measure on the $i^{th}$ selected subject be given by

$$Y_{ik} = \mu + E_{ik}$$

where $\text{var}(Y_i) = \sigma^2_e I_p + \sigma^2 J_p = \Sigma$, with $
\sigma^2_e = \frac{1}{N} \sum_{s=1}^{N} \sigma^2_s$ representing the average response error in the population, and $\sigma^2 = \frac{1}{N-1} \sum_{s=1}^{N} (\mu_s - \mu)^2$ representing the variance between subjects.

Consider a transformation matrix $M = \begin{pmatrix} I_p & M' \end{pmatrix}$ where we assume that

$I_p M' = 0$. Thus, the column space spanned by the remaining $p-1$ columns is orthogonal to the column space of a 'one' vector. Using this transformation matrix,

$$Y^* = X\beta^* + E^*$$

and $E(Y^*) = X\beta^*$, and $\text{var}(\text{vec}(Y'^*)) = I_n \otimes \Sigma^*_{p \times p}$ where $\Sigma^*_{p \times p} = M' \Sigma M'$. Using
the definitions of these terms,
\[
\Sigma^* = \sum_{p} \Sigma_p M' \sum_{p} M'
\]
\[
= \left( \begin{array}{cc}
\sum_{p} p & \sum_{p(p-1)} M' \\
\sum_{p} p(p-1) & \sum_{p} (p-1) p
\end{array} \right) 
\left( \sigma^2 I_p + \sigma^2 J_p \right) \left( \begin{array}{c}
1_p \\
p(p(p-1))
\end{array} \right)
\]
\[
= \left( \begin{array}{cc}
1_p' \left( \sigma^2 I_p + \sigma^2 J_p \right) 1_p & 1_p' \left( \sigma^2 I_p + \sigma^2 J_p \right) M' \\
M'^* \left( \sigma^2 I_p + \sigma^2 J_p \right) 1_p & M'^* \left( \sigma^2 I_p + \sigma^2 J_p \right) M'
\end{array} \right).
\]
\[
= \left( \begin{array}{c}
p \left( \sigma^2 + p\sigma^2 \right) \\
0
\end{array} \right)
\left( \begin{array}{c}
0 \\
\sigma^2 M'^* M'
\end{array} \right)
\]

Frequently, we will require the columns of the second part of the transformation matrix to be orthogonal, and 'normal' (such that the inner product of the column vectors is 1).

When this is true, then \( M'^* M' = I_{(p-1)} \), and hence \( \Sigma^* = \left( \begin{array}{cc}
p \left( \sigma^2 + p\sigma^2 \right) & 0 \\
0 & \sigma^2 I_{(p-1)}
\end{array} \right) \). Notice that with this choice of a transformation, the columns of the transformed random variables are independent. Thus, univariate methods can be used to test hypotheses concerning the transformed random variables.

**Using the Repeated Statement in PROC GLM in SAS**

In repeated measures studies, the same variable is measured under different conditions. Often, there are simple functions of the measures that are of interest. For example, if there are 2 measures on each selected subject corresponding to a pretest and posttest measure, then the difference between the two measures is of interest. This difference is specified in terms of an \( M \) matrix. If there is a factorial structure on the repeated measures, the main effects, and interactions can be specified in terms of linear combinations.

We consider two examples as illustrations. First, suppose that \( p = 6 \) measures were made on each subject under each of the factor levels in a two factor study where Factor A had 2 levels, and Factor B had 3 levels. Let the responses be organized as follows:

<table>
<thead>
<tr>
<th>Level of Factor A</th>
<th>A1</th>
<th>A1</th>
<th>A2</th>
<th>A2</th>
<th>A2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Level of Factor B</td>
<td>B1</td>
<td>B2</td>
<td>B3</td>
<td>B1</td>
<td>B2</td>
</tr>
</tbody>
</table>

\( Y_i' = Y_{i11} Y_{i12} Y_{i13} Y_{i21} Y_{i22} Y_{i23} \)

Suppose an appropriate model for the \( m \)th measure on subject \( s \) under level \( j \) of Factor A and level \( k \) of Factor B is given by

\( Y_{sjkm} = \mu_{ijk} + E_{sjkm} \)
where $E(Y_{ijk}) = \mu_{ijk}$, and $\text{var}(Y_{ijk}) = \sigma^2_{ijk}$. Let us define parameters corresponding to the average expected response under level $j$ of Factor A and level $k$ of Factor B by

$$\mu_{jk} = \frac{1}{N_j} \sum_{s=1}^{N_j} \mu_{sjk},$$

and re-parameterize these averages such that

$$
\begin{pmatrix}
1 & 1 & 1 & 1 & 0 & 1 & 0 & 1 \\
1 & 1 & 0 & 1 & 0 & 1 \\
1 & 1 & -1 & -1 & -1 & -1 \\
1 & -1 & 1 & 1 & 0 & -1 & 0 \\
1 & -1 & 0 & 1 & 0 & -1 \\
1 & -1 & -1 & -1 & 1 & 1 & 1
\end{pmatrix}
\begin{pmatrix}
\mu \\
\alpha \\
\beta_1 \\
\beta_2 \\
\alpha \beta_{11} \\
\alpha \beta_{12}
\end{pmatrix}
= 
\begin{pmatrix}
\mu_{11} \\
\mu_{12} \\
\mu_{13} \\
\mu_{21} \\
\mu_{22} \\
\mu_{23}
\end{pmatrix}.
$$

With this parameterization, we can express

$$
\begin{pmatrix}
1 & 1 & 2 & -1 & 2 & -1 \\
1 & 1 & 1 & -1 & 2 & -1 \\
1 & 1 & -1 & 1 & 1 & -1 \\
1 & 1 & -1 & 1 & 2 & -1 \\
1 & 1 & -1 & 1 & 2 & -1 \\
1 & 1 & -1 & 1 & 1 & 1
\end{pmatrix}
\begin{pmatrix}
\mu \\
\alpha \\
\beta_1 \\
\beta_2 \\
\alpha \beta_{11} \\
\alpha \beta_{12}
\end{pmatrix}
= 
\begin{pmatrix}
\mu_{11} \\
\mu_{12} \\
\mu_{13} \\
\mu_{21} \\
\mu_{22} \\
\mu_{23}
\end{pmatrix}.
$$

(see bem03p12.sas). We summarize this by expressing

$$\mu_{ijk} = \mu + \alpha + \beta_1 + \beta_2 + \alpha \beta_{11} + \alpha \beta_{12}. $$

Finally, let us define

$$\mu_s = \mu + \delta_s = \frac{1}{ab} \sum_{j=1}^{a} \sum_{k=1}^{b} \mu_{sjk},$$

where $\mu = \frac{1}{Nab} \sum_{j=1}^{a} \sum_{k=1}^{b} \mu_{sjk}$. Then

$$\mu_{ijk} = \left( \mu_{sjk} - \mu_{jk} \right) + \mu_{jk}$$

$$= \left[ (\mu_{sjk} - \mu_{jk}) - (\mu_k - \mu) \right] + (\mu_s - \mu) + \mu_{jk}.$$ 

The first term is the subject by treatment interaction. This term is a difference in the subject effect under a specific treatment from the average subject effect. If a treatment affects subjects differently, this term will be non-zero.

If the subject by treatment interaction is zero, the model simplifies. The mean structure is given by

$$\mu_{ijk} = \left( \mu_{sjk} - \mu_{jk} \right) + \mu_{jk}$$

$$= \left( \mu_s - \mu \right) + \mu_{jk}$$

$$= \mu + \alpha + \beta_1 + \beta_2 + \alpha \beta_{11} + \alpha \beta_{12} + \delta_s$$

$$= \mu + \alpha + \beta_1 + \beta_2 + \alpha \beta_{11} + \alpha \beta_{12} + \delta_s,$$
Post-multiplying $Y_i'$ by $M$ given by $M = \begin{pmatrix} 1 & 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 1 & 0 & 1 \\ 1 & 1 & -1 & -1 & -1 & -1 \\ 1 & -1 & 1 & 0 & -1 & 0 \\ 1 & -1 & 0 & 1 & 0 & -1 \\ 1 & -1 & -1 & -1 & 1 & 1 \end{pmatrix}$ will result in $Z_i' = Y_i'M$

$$Z_i' = Y_i'M = \begin{pmatrix} \sum_{j=1}^{a} \sum_{k=1}^{b} Y_{jk} \\ \sum_{k=1}^{b} Y_{i1k} - \sum_{k=1}^{b} Y_{i2k} \\ \sum_{i=1}^{a} Y_{g1} - \sum_{i=1}^{a} Y_{g3} \\ \sum_{i=1}^{a} Y_{g2} - \sum_{i=1}^{a} Y_{g3} \\ (Y_{i11} - Y_{i13}) \\ (Y_{i12} - Y_{i13}) \\ -(Y_{i21} - Y_{i23}) \\ -(Y_{i22} - Y_{i23}) \end{pmatrix}.$$  

The columns of this vector correspond to functions that represent main effects and interactions of the two factors. For example, simply by testing the hypothesis that $E(Z_{i2}) = 0$ will test for a main effect for Factor A. In such settings, some of the univariate tests on the transformed data will be interpretable.
Polynomial Regression

Polynomial regression poses no special problems for analysis of data. Polynomial functions of \( x_i \) (i.e. \( x_i^2, x_i^3 \), etc) can be treated simply as different regression variables. There are two peculiarities in analysis, however, that deserves special discussion with respect to polynomial regression, or polynomial trends. The first relates to a computing problem. The second relates to testing contrasts in ANOVA applications that represent polynomial trends. We discuss these two issues here.

Example: Cubic Polynomial model

Suppose heart rate is measured at P=6 walking speeds, corresponding to \( x_i = 1, 2, 3, 4, 5 \) and 6 mph, for \( i=1,\ldots,6=P \). Let

\[
y_{ij} = \text{heart rate at walking speed } "i" \text{ on } j^{th} \text{ measure}.
\]

If we assume that heart rate is a cubic function of walking speed, then

\[
y_{ij} = \beta_0 + \beta_1 x_i + \beta_2 x_i^2 + \beta_3 x_i^3 + e_{ij}
\]

is a cubic polynomial model. When considering polynomial models, it is customary to include all lower order polynomial terms along with the highest polynomial term in the model. We will always follow this convention. We can estimate regression coefficients in the usual manner with a design matrix corresponding to

\[
X = \begin{pmatrix}
1 & x_1 & x_1^2 & x_1^3 \\
1 & x_2 & x_2^2 & x_2^3 \\
1 & x_3 & x_3^2 & x_3^3 \\
\vdots & \vdots & \vdots & \vdots \\
1 & x_P & x_P^2 & x_P^3
\end{pmatrix}
\]

Polynomial Models as Simple Transformation of Cell Mean Model.

If a polynomial model is of degree (P-1) for \( i=1,\ldots,P \) times, then there will be as many polynomial parameters as time points. For example, with \( P=6 \) walking speeds, a 5th degree polynomial model will have 6 parameters. In such cases, the polynomial parameters are simply a re-parameterization of the cell mean response at each time.

The ideas can be illustrated with a simple example with \( P=4 \). Suppose that mean response at four doses are recorded, where the doses are 1, 2, 3, and 4. The four means can be represented as their individual means. Alternatively, the four means
can be represented by four regression parameters corresponding to a constant, linear, quadratic, and cubic parameter. The cell mean parameters can be transformed to form the regression parameters. The transformation is a re-parameterization. The connection between the parameters can be seen by considering the relationship

$$\mu_i = \beta_0 + \beta_1 x_i + \beta_2 x_i^2 + \beta_3 x_i^3$$

Using matrix notation,

$$\mu = X\beta = \begin{pmatrix} 1 & 1 & 1 & 1 \\ 1 & 2 & 4 & 8 \\ 1 & 3 & 9 & 27 \\ 1 & 4 & 16 & 64 \end{pmatrix} \begin{pmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \\ \beta_3 \end{pmatrix}$$

or

$$\beta = X^{-1}\mu.$$  

This is a simple transformation of the means. If we had n measures at each dose, we could first estimate the population mean response based on the sample mean. We could then transform these mean responses to regression coefficients. Estimate of regression coefficients in a model with n measures per dose can be fit directly using a design matrix, where the design matrix can be expressed as a set of individual design matrices (like the one given above).

$$X_0' = X \parallel X \ldots$$

Then $X_0'X_0 = n (XX)$. As a result, when the same number of measures are made at each dose level (or time point), the $XX$ matrix is a function of the polynomial matrix for a single set of measures.

**Problems With Polynomial Design Matrices: Example With 10 Times:**

Suppose a child is measured at P=10 times. Let the times be given by 1,2,3,4,5,6,7,8,9,10, where the measures correspond to the weight of at each of 10 ages. Suppose a 8th order ($x^8$) regression model is to be fit to these data. To fit this, we need to invert the design matrix, $XX$. This turns out to be a difficult computing problem. For example, in PROC REG, the program will not form the regression coefficients. In PROC IML, a check of $(XX)^{-1} (XX)$ results in a matrix that is not an identify matrix.

Orthogonal polynomials enable tests to be constructed for regression coefficients
in this problem by reparameterizing the regression parameters, and thereby avoiding inverting a an ill conditionned matrix. The test results avoid the inaccuracies that may be introduced by matrix inversion. Although tests can be constructed based on orthogonal polynomials (as well as predicted values), the matrix inversion is necessary to estimate regression parameters on the original metric. For this reason, this re-parameterization is often not done.

Choleski Decomposition of Symmetric Full Rank Matrix and its Relationship to Orthogonal Polynomials

Orthogonal polynomials were introduced as a way of making tests more precise and not dependent on the inversion of $X'X$. While their use improves accuracy of the tests, it transforms parameters into quantities that are not easily interpretable. We illustrate orthogonal polynomials in the context of a polynomial regression with P time points, where a polynomial of degree (P-1) (having P parameters) is fit. We assume that the matrix $X$ is a P x P square square polynomial matrix.

When $X$ represents a matrix of polynomials, the matrix $X'X$ will be positive definite (of full rank) and symmetrical. In such cases, it is possible to factor the matrix using a Cholesky decomposition (see Timm, (1975), p73-75). Cholesky factoring of a matrix $A$ results in an upper triangular matrix $T'$ such that

$$A = T T'$$

In PROC IML, the Cholesky decompositon is specified via the ROOT function, and results in the matrix

$$T'=\text{ROOT}(A).$$

Of course, the question is how does this factorization help in estimating sums of squares for regression problems. To answer this question, we consider a transformation of the original $X$ matrix that will result in a $T$ matrix. First, note that

$$X'X = TT'$$

Both the matrices $X$ and $T$ are P x P matrices. Let us indictate the relationship between $X$ and $T$ via a matrix $P$ such that

$$X=PT' , \text{ or } P=X T'^{-1}$$

Then since
\[ \mathbf{X}' \mathbf{X} = \mathbf{T} \mathbf{T}' = \mathbf{T} \mathbf{P}' \mathbf{P}' \mathbf{T}' , \]

which implies that

\[ \mathbf{P}' \mathbf{P} = \mathbf{I} \]

**Simple Example with P=3. (x=1,2,3):**

<table>
<thead>
<tr>
<th>x</th>
<th>x'x</th>
<th>(x'x)(^{-1})</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>1 6 14</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>6 14 36</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>14 36 98</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>19 -21 5</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>-21 24.5 -6</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>5 -6 1.5</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>\mathbf{T}</th>
<th>\mathbf{T}'</th>
<th>(\mathbf{T}\mathbf{T}')(^{-1})</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.7320508</td>
<td>0 0 1.7320508 3.4641016 8.0829038</td>
<td>19 -21 5</td>
</tr>
<tr>
<td>3.4641016</td>
<td>1.4142136 0 0 1.4142136 5.6568542</td>
<td>-21 24.5 -6</td>
</tr>
<tr>
<td>8.0829038</td>
<td>5.6568542 0.8164966 0 0 0.8164966</td>
<td>5 -6 1.5</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>\mathbf{P}</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.5773503 -0.707107 0.4082483</td>
</tr>
<tr>
<td>0.5773503 0 -0.816497</td>
</tr>
<tr>
<td>0.5773503 0.7071068 0.4082483</td>
</tr>
</tbody>
</table>

Column Scale Factors:

3 2 6

The coefficients in the matrix \( \mathbf{P} \) are orthogonal polynomial coefficients.

Aside: Note that the solution we have given for \( \mathbf{P} \) requires inversion of the matrix \( \mathbf{T} \). If the design matrix is ill conditioned, then the matrix \( \mathbf{T} \) will also be ill conditioned. Hence, it may be questionable as to how much the problem of inverting the matrix has been resolved. Another function, ORPOL, in SAS will generate orthogonal polynomials without inverting \( \mathbf{T} \). This function using a slightly different algorithm, but does not appear to be better than simple use of the Choleski decomposition.

**Summary of Transformations of Regression Coefficients with Orthogonal Polynomials**

To summarize, if the model is

\[ \mathbf{Y} = \mathbf{X} \mathbf{\beta} + \mathbf{e} \]

where \( \mathbf{X} = \mathbf{P} \mathbf{T}' \), we can transform the model such that

\[ \mathbf{Y} = \mathbf{P} \mathbf{T}' \mathbf{\beta} + \mathbf{e} \]
where $\hat{\beta}^* = T'\beta$. The model with transformed parameters will fit identical to
the original model. It is easy to fit this model, since the design matrix is orthogonal, ($P'P=I$) and hence,

$$\hat{\beta}^* = P'y$$

Also,

$$\text{var}(\hat{\beta}^*) = I_p \sigma^2$$

where $\sigma^2$ is estimated via the MSE. [Aside: It is this transformation that is used in the
SAS Procedure PROC GLM with a REPEATED POLYNOMIAL option.]
Note that the diagonal form of the variance of the transformed parameters indicates the
independence of the parameters.
A similar analysis can be made when measures are made over time. Suppose three measures of pulse rate are made on each selected subject immediately following exercise, 1 minute following exercise, and 2 minutes following exercise. We may consider a transformation matrix similar to a polynomial matrix given by

\[
\begin{bmatrix}
1 & 0 & 0 \\
1 & 1 & 1 \\
1 & 2 & 4
\end{bmatrix}
\]

where columns correspond to a mean, a linear, and a quadratic trend. The transformation used in SAS is a normalized orthogonal polynomial matrix, not the polynomial matrix given above. A normalized matrix means that the sum of the squared values of the coefficients in any column add up to 1. Orthogonal means that the inner product of any two columns of the matrix is zero.

The orthonormal polynomial matrix is formed by taking the Choleski decomposition of the polynomial matrix (see Timm, (1975) p73-75). The decomposition results in \( M = TT' \), where \( T' \) is an upper triangular matrix. All elements of \( T' \) below the diagonal are zero. In PROC IML, this can be obtained by the command \( T' = \text{ROOT}(A); \). With this transformation,

**References**