Test of simple main effects can be requested as well. To test factor A within the B BY C treatment combinations the following DESIGN subcommand is used:

```
DESIGN=B, C, B BY C, A WITHIN B(1) BY C(1),
          A WITHIN B(1) BY C(2), A WITHIN B(2) BY C(1),
          A WITHIN B(2) BY C(2)/
```

It may also be desirable to compare two or more means at particular levels of another factor or treatment combinations. For example, it may be interesting to compare the effectiveness of drug 1 with drug 2 within each patient category. Such comparisons can be performed by extending the methods used for ordinary simple effects. The procedure is as follows:

1 Define a contrast incorporating the comparisons of interest such as

```
CONTRAST(DRUG)=SPECIAL(1 1 1 1 -1 0 2 -1 -1)/
```

2 Partition the factor into the desired components by specifying

```
PARTITION(DRUG)/
```

In subsequent designs, DRUG(1) will refer to the drug 1 versus drug 2 comparison. DRUG(2) will refer to the drug 1 versus drugs 2 and 3 combined comparison.

3 Request regression-approach sums of squares by using

```
METHOD=SSTYPE(UNIQUE)/
```

This is mandatory even for orthogonal designs, because DRUG(1) and DRUG(2) are not independent.

4 Specify the designs as for ordinary simple effects, but expand the simple effects terms according to the CONTRAST/PARTITION specification:

```
DESIGN=CAT, DRUG(1) WITHIN CAT(1),
            DRUG(1) WITHIN CAT(2),
            DRUG(2) WITHIN CAT(1),
            DRUG(2) WITHIN CAT(2)/
```

Figure 1.30b presents the output for this design.

Figure 1.30b

```
TESTS OF SIGNIFICANCE FOR Y USING UNIQUE SUMS OF SQUARES

SOURCE OF VARIATION              SUM OF SQUARES      DF   MEAN SQUARE           F    SIG. OF F

WITHIN CELLS                          106.00000      12       8.83333
CONSTANT                              882.00000       1     882.00000    99.84906          0.0
CAT                                    18.00000       1      18.00000     2.03774         .179
DRUG(1) WITHIN CAT(1)                  24.00000       1      24.00000     2.71698         .125
DRUG(2) WITHIN CAT(2)                  18.00000       1      18.00000     2.03774         .179
DRUG(1) WITHIN CAT(2)                  96.00000       1      96.00000    10.86792         .006
DRUG(2) WITHIN CAT(1)                  18.00000       1      18.00000     2.03774         .179
```

1.31 MULTIVARIATE TESTS OF SIGNIFICANCE

1.32 Standard MANOVA Output

In the univariate *F* test, the *F* value is a function of the ratio (SSH)/(SSE), where SSH is the sum of squares due to the hypothesis and SSE the sum of squares due to error. Significance tests in multivariate analysis of variance models are based on functions of the eigenvalues of the matrix $S_hS_e^{-1}$, where S_h is the matrix of the sums of squares and cross products (SSCP) for the hypothesis and S_e is the SSCP matrix for the error. The MANOVA procedure computes four statistics used for significance tests: Roy's largest root, Wilks' lambda, Hotelling's trace, and Pillai's criterion. (All of these are functions of the eigenvalues.)

The MANOVA commands for the multivariate analysis are exactly the same as in the univariate case, except that two or more response variables are specified instead of one. Figure 1.32a, given below, illustrates the use of MANOVA to analyze the dental calculus reduction data in Finn (1974). The response variables in this example are RCAN, RLI, and RCI.