5) The following statistical model can be used for heart rate data set:

$$Y_{ij} = \mu + \tau_i + \varepsilon_{ij}, \quad \begin{matrix} i = 1, 2, 3 & : \text{treatment} \\ j = 1, \ldots 8 & : \text{replicate} \end{matrix}$$

Y_{ij} is a 4×1 vector and $\varepsilon_{ij} \sim N(0, \Sigma_{4\times4})$ independent.

Regression model: $Y_{24\times4} = X_{24\times4} B_{4\times4} + \varepsilon_{24\times4}$

$\varepsilon \sim N(0$

where:

$$Y = \begin{bmatrix} y_{11}' \\ y_{18}' \\ y_{31}' \\ y_{38}' \end{bmatrix}$$

$$y_{ij}' = (y_{ij}^{(1)}, y_{ij}^{(2)}, y_{ij}^{(3)}, y_{ij}^{(4)}).$$

$$X_{24\times4} = \begin{bmatrix} 1_8 & 1_8 & 0_8 & 0_8 \\ 1_8 & 0 & 1_8 & 0 \\ 1_8 & 0 & 0 & 1_8 \end{bmatrix}_{24\times4}$$

where $\begin{matrix} 1_8 \\ 0_8 \end{matrix}$ is a 8×1 vector of $\begin{matrix} 1 \\ 0 \end{matrix}$.

and

$$B = \begin{matrix} \mu \\ AX23 \\ BWWG \\ Control \end{matrix} \begin{bmatrix} \mu^{(1)} & \mu^{(2)} & \mu^{(3)} & \mu^{(4)} \\ \tau_1^{(1)} & \tau_1^{(2)} & \tau_1^{(3)} & \tau_1^{(4)} \\ \tau_2^{(1)} & \tau_2^{(2)} & \tau_2^{(3)} & \tau_2^{(4)} \\ \tau_3^{(1)} & \tau_3^{(2)} & \tau_3^{(3)} & \tau_3^{(4)} \end{bmatrix}$$

First, we are interested in testing if there are any treatment effect:

$$H_0: \tau_1 = \tau_2 = \tau_3$$

SAS output show that Wilk's Lambda statistic is:

$$\Lambda = 0.079 \quad \text{and} \quad F\text{-value} = 11.51$$
$$\rightarrow p\text{ value} < 0.001$$

→ At significant level $\alpha = 0.05$ we are able to reject H_0 and conclude that there is treatment effect.

Parallel profile aims to test if the change of effect between the two consecutive time point is the same for each treatment:

$$H_0: \begin{bmatrix} 0 & 1 & -1 & 0 \\ 0 & 0 & 1 & -1 \end{bmatrix} \begin{bmatrix} \mu_1 \\ \tau_1 \\ \tau_2 \\ \tau_3 \end{bmatrix} \begin{bmatrix} 1 & 1 & 1 \\ -1 & 0 & 0 \\ 0 & -1 & 0 \\ 0 & 0 & -1 \end{bmatrix} = 0$$

↓

there is no need to input this column to SAS.

SAS output provides Wilk's Lambda test statistic is:

$\Lambda = 0.11$ and $F\text{-value} = 12.738$, $p\text{-value} = 0.0001$

→ At significant level $\alpha = 0.05$, we are able to reject the null hypothesis of parallel profile.

Note that, in fact if the null hypothesis is not rejected, we should also test of they are identical, but it is not the case for this Heart rate dataset.

However, if we failed to reject the null hypotheses of parallel, coincidental test should be considered:

$$H_0 : \begin{bmatrix} 0 & 1 & 0 & -1 \\ 0 & 0 & 1 & -1 \end{bmatrix} \begin{bmatrix} \mu_1' \\ \tau_1 \\ \tau_2' \\ \tau_3' \end{bmatrix} = 0$$

Wilk's lamba test statistic is 0.63954 and F-value = 5.92, p-value = 0.0092. → reject H_0

Suppose we failed to reject the null hypotheses of coincidental, then we will want to see if the common mean vector has all component equal:

$$H_0 : [1, 0, 0 0] \begin{bmatrix} \mu_1' \\ \tau_1 \\ \tau_2' \\ \tau_3' \end{bmatrix} \begin{bmatrix} 1 & 1 & 1 \\ -1 & 0 & 0 \\ 0 & -1 & 0 \\ 0 & 0 & -1 \end{bmatrix} = 0$$

Wilk's Lamba value is $\Lambda = 0.004$, $F = 5049.21$ and p-value < 0.001 → reject H_0.

Obviously, since hypothesis of parallel was rejected, hypothesis of coincidental and horizontal would be rejected.

Also, plot of profile mean show that:

AX23 is very different from BWWG and Control and it is also falls between profile of BWWG and Control. Then another hypothesis should be consider to gain insight of data:

$$H_0: \begin{bmatrix} 0 & 1 & -1 & 0 \end{bmatrix} \begin{bmatrix} \mu' \\ \tau_1' \\ \tau_2' \\ \tau_3' \end{bmatrix} \begin{bmatrix} 1 & 1 & 1 \\ -1 & 0 & 0 \\ 0 & -1 & 0 \\ 0 & 0 & -1 \end{bmatrix} = 0$$

↳ test for profile of BWWG and Control.

$\Lambda = 0.744$, $F = 2.18$, p-value $= 0.1233$

→ failed to reject H_0 and conclude that BWWG behaves similarly to Control over time.

$$H_0: \begin{bmatrix} 0 & 2 & -1 & -1 \end{bmatrix} \begin{bmatrix} \mu' \\ \tau_1' \\ \tau_2' \\ \tau_3' \end{bmatrix} \begin{bmatrix} 1 & 1 & 1 \\ -1 & 0 & 0 \\ 0 & -1 & 0 \\ 0 & 0 & -1 \end{bmatrix} = 0$$

↳ test of AX23 is the average of the other 2.

$\Lambda = 0.145$, $F = 37.45$, p-value < 0.0001

→ reject H_0

→ AX23 behaves very different from average of the other 2.

→ This result is consistent with the result that we rejected the parallism.

Heart Rate dataset

Obs	drug	y1	y2	y3	y4
1	ax23	72	86	81	77
2	ax23	78	83	88	82
3	ax23	71	82	81	75
4	ax23	72	83	83	69
5	ax23	66	79	77	66
6	ax23	74	83	84	77
7	ax23	62	73	78	70
8	ax23	69	75	76	70
9	bww9	85	86	83	80
10	bww9	82	86	80	84
11	bww9	71	78	70	75
12	bww9	83	88	79	81
13	bww9	86	85	76	76
14	bww9	85	82	83	80
15	bww9	79	83	80	81
16	bww9	83	84	78	81
17	control	69	73	72	74
18	control	66	62	67	73
19	control	84	90	88	87
20	control	80	81	77	72
21	control	72	72	69	70
22	control	65	62	65	61
23	control	75	69	69	68
24	control	71	70	65	65

Comparison of Drugs: Profile Analysis
H0: Any difference between ax23, bww9 and Control

The GLM Procedure

Class Level Information		
Class	Levels	Values
drug	3	ax23 bww9 control

Number of Observations Read	24
Number of Observations Used	24

Comparison of Drugs: Profile Analysis
H0: Any difference between ax23, bww9 and Control

The GLM Procedure
Multivariate Analysis of Variance

E = Error SSCP Matrix				
	y1	y2	y3	y4
y1	641	601.75	535.25	426
y2	601.75	823.875	615.5	534.25
y3	535.25	615.5	655.875	555.25

E = Error SSCP Matrix				
	y1	y2	y3	y4
y4	426	534.25	555.25	674.5

Partial Correlation Coefficients from the Error SSCP Matrix / Prob > |r|				
DF = 21	y1	y2	y3	y4
y1	1.000000	0.828050 <.0001	0.825500 <.0001	0.647873 0.0011
y2	0.828050 <.0001	1.000000	0.837311 <.0001	0.716676 0.0002
y3	0.825500 <.0001	0.837311 <.0001	1.000000	0.834809 <.0001
y4	0.647873 0.0011	0.716676 0.0002	0.834809 <.0001	1.000000

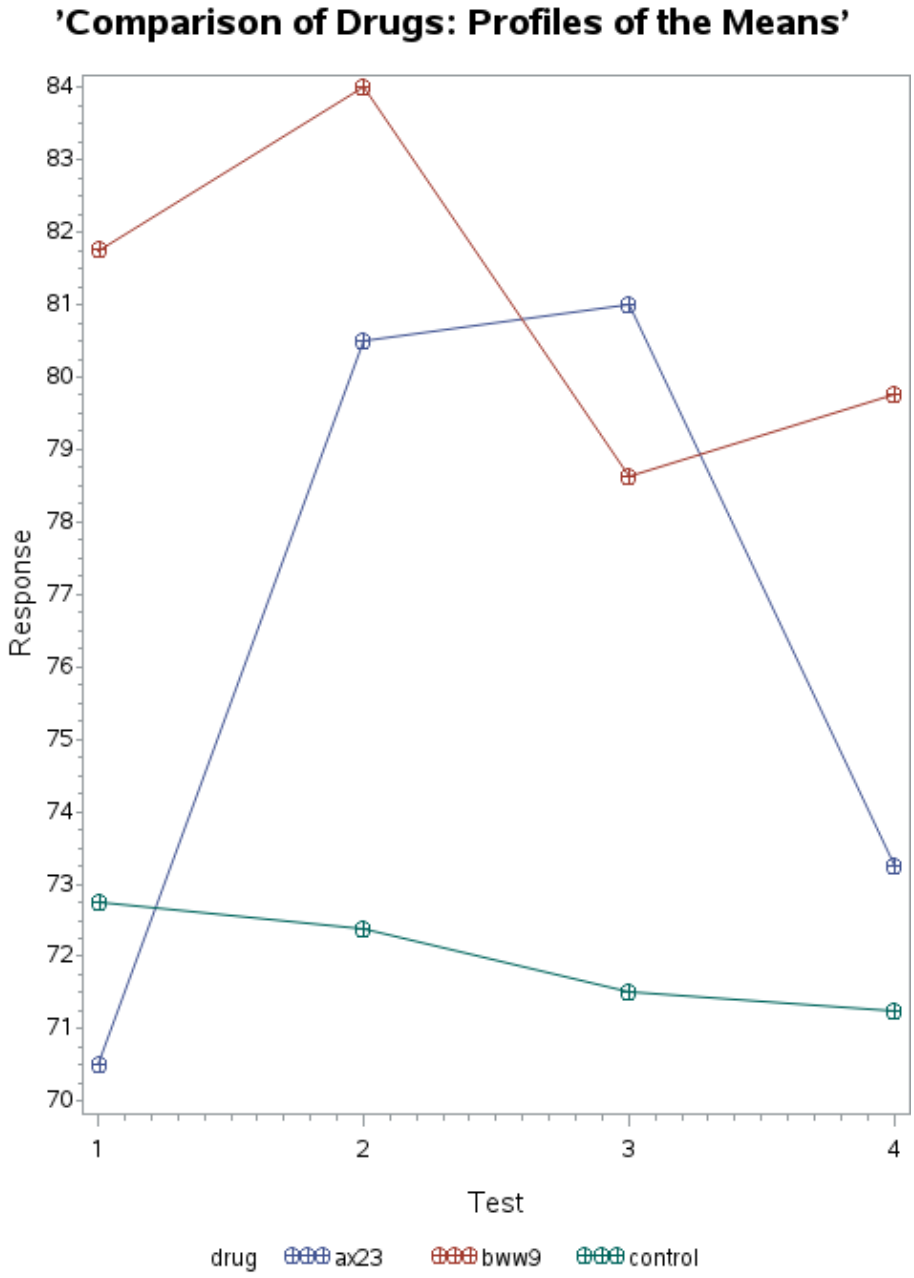
Comparison of Drugs: Profile Analysis
H0: Any difference between ax23, bww9 and Control

The GLM Procedure
Multivariate Analysis of Variance

H = Type III SSCP Matrix for drug				
	y1	y2	y3	y4
y1	567	335.25	42.75	387
y2	335.25	569.08333333	404.54166667	367.5
y3	42.75	404.54166667	391.08333333	171
y4	387	367.5	171	316

Characteristic Roots and Vectors of: E Inverse * H, where H = Type III SSCP Matrix for drug E = Error SSCP Matrix					
		Characteristic Vector V'EV=1			
Characteristic Root	Percent	y1	y2	y3	y4
6.34650854	89.77	-0.06623963	0.01459723	0.08399509	-0.04345948
0.72287558	10.23	-0.00802359	0.04371440	-0.01301412	0.00901360
0.00000000	0.00	-0.03240406	-0.00783026	-0.01269589	0.05566137
0.00000000	0.00	0.02815632	-0.05440373	0.05319811	0.00000000

MANOVA Test Criteria and F Approximations for the Hypothesis of No Overall drug Effect H = Type III SSCP Matrix for drug E = Error SSCP Matrix S=2 M=0.5 N=8					
Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.07900691	11.51	8	36	<.0001
Pillai's Trace	1.28345595	8.51	8	38	<.0001
Hotelling-Lawley Trace	7.06938412	15.45	8	23.508	<.0001
Roy's Greatest Root	6.34650854	30.15	4	19	<.0001
NOTE: F Statistic for Roy's Greatest Root is an upper bound.					
NOTE: F Statistic for Wilks' Lambda is exact.					



'Comparison of Drugs: Profiles of the Means'

The GLM Procedure

Class Level Information		
Class	**Levels**	**Values**
drug	3	ax23 bww9 control

Number of Observations Read	24
Number of Observations Used	24

'Comparison of Drugs: Profiles of the Means'

The GLM Procedure
Multivariate Analysis of Variance

M Matrix Describing Transformed Variables				
	y1	y2	y3	y4
MVAR1	1	-1	0	0
MVAR2	1	0	-1	0
MVAR3	1	0	0	-1

E = Error SSCP Matrix			
	MVAR1	MVAR2	MVAR3
MVAR1	261.375	119.5	147.5
MVAR2	119.5	226.375	235
MVAR3	147.5	235	463.5

Partial Correlation Coefficients from the Error SSCP Matrix of the Variables Defined by the Specified Transformation / Prob > |r|			
DF = 21	MVAR1	MVAR2	MVAR3
MVAR1	1.000000	0.491272 0.0202	0.423775 0.0494
MVAR2	0.491272 0.0202	1.000000	0.725486 0.0001
MVAR3	0.423775 0.0494	0.725486 0.0001	1.000000

'Comparison of Drugs: Profiles of the Means'

The GLM Procedure
Multivariate Analysis of Variance

H = Type III SSCP Matrix for drug			
	MVAR1	MVAR2	MVAR3
MVAR1	465.58333333	593.54166667	212.25
MVAR2	593.54166667	872.58333333	308.25
MVAR3	212.25	308.25	109

Characteristic Roots and Vectors of: E Inverse * H, where H = Type III SSCP Matrix for drug E = Error SSCP Matrix Variables have been transformed by the M Matrix				
		Characteristic Vector V'EV=1		
Characteristic Root	Percent	MVAR1	MVAR2	MVAR3
5.95508874	95.15	0.01461289	0.08646881	-0.03926112
0.30369649	4.85	-0.06991922	0.04912790	-0.00222979
0.00000000	0.00	-0.00230526	-0.01799476	0.05537774

MANOVA Test Criteria and F Approximations for the Hypothesis of No Overall drug Effect on the Variables Defined by the M Matrix Transformation H = Type III SSCP Matrix for drug E = Error SSCP Matrix S=2 M=0 N=8.5					
Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.11028611	12.74	6	38	<.0001
Pillai's Trace	1.08917068	7.97	6	40	<.0001
Hotelling-Lawley Trace	6.25878523	19.37	6	23.636	<.0001

NOTE: F Statistic for Roy's Greatest Root is an upper bound.

NOTE: F Statistic for Wilks' Lambda is exact.

MANOVA Test Criteria and F Approximations for the Hypothesis of No Overall drug Effect on the Variables Defined by the M Matrix Transformation
H = Type III SSCP Matrix for drug
E = Error SSCP Matrix

S=2 M=0 N=8.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Roy's Greatest Root	5.95508874	39.70	3	20	<.0001

NOTE: F Statistic for Roy's Greatest Root is an upper bound.

NOTE: F Statistic for Wilks' Lambda is exact.

H = Contrast SSCP Matrix for bww9 vs. control

	MVAR1	MVAR2	MVAR3
MVAR1	27.5625	-19.6875	-5.25
MVAR2	-19.6875	14.0625	3.75
MVAR3	-5.25	3.75	1

Characteristic Roots and Vectors of: E Inverse * H, where
H = Contrast SSCP Matrix for bww9 vs. control
E = Error SSCP Matrix

Variables have been transformed by the M Matrix

Characteristic Root	Percent	Characteristic Vector V'EV=1		
		MVAR1	MVAR2	MVAR3
0.34486444	100.00	0.06019122	-0.07660192	0.01600949
0.00000000	0.00	-0.02286312	-0.04960997	0.06600604
0.00000000	0.00	0.03101360	0.04341905	0.00000000

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall bww9 vs. control Effect on the Variables Defined by the M Matrix Transformation
H = Contrast SSCP Matrix for bww9 vs. control
E = Error SSCP Matrix

S=1 M=0.5 N=8.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.74356937	2.18	3	19	0.1233
Pillai's Trace	0.25643063	2.18	3	19	0.1233
Hotelling-Lawley Trace	0.34486444	2.18	3	19	0.1233
Roy's Greatest Root	0.34486444	2.18	3	19	0.1233

H = Contrast SSCP Matrix for ax23 vs. the rest

	MVAR1	MVAR2	MVAR3
MVAR1	438.02083333	613.22916667	217.5
MVAR2	613.22916667	858.52083333	304.5
MVAR3	217.5	304.5	108

Characteristic Roots and Vectors of: E Inverse * H, where
H = Contrast SSCP Matrix for ax23 vs. the rest
E = Error SSCP Matrix

Variables have been transformed by the M Matrix

Characteristic Root	Percent	Characteristic Vector V'EV=1		
		MVAR1	MVAR2	MVAR3
5.91392079	100.00	0.01596248	0.08550244	-0.03921064
0.00000000	0.00	0.00145020	-0.02070581	0.05545833
0.00000000	0.00	-0.06964657	0.04974755	0.00000000

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall ax23 vs. the rest Effect on the Variables Defined by the M Matrix Transformation
H = Contrast SSCP Matrix for ax23 vs. the rest
E = Error SSCP Matrix

S=1 M=0.5 N=8.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.14463573	37.45	3	19	<.0001
Pillai's Trace	0.85536427	37.45	3	19	<.0001
Hotelling-Lawley Trace	5.91392079	37.45	3	19	<.0001
Roy's Greatest Root	5.91392079	37.45	3	19	<.0001

H = Contrast SSCP Matrix for parallel?

	MVAR1	MVAR2	MVAR3
MVAR1	465.58333333	593.54166667	212.25
MVAR2	593.54166667	872.58333333	308.25
MVAR3	212.25	308.25	109

Characteristic Roots and Vectors of: E Inverse * H, where
H = Contrast SSCP Matrix for parallel?
E = Error SSCP Matrix

Variables have been transformed by the M Matrix

Characteristic Root	Percent	Characteristic Vector V'EV=1		
		MVAR1	MVAR2	MVAR3
5.95508874	95.15	0.01461289	0.08646881	-0.03926112
0.30369649	4.85	-0.06991922	0.04912790	-0.00222979
0.00000000	0.00	-0.00230526	-0.01799476	0.05537774

MANOVA Test Criteria and F Approximations for the Hypothesis of No Overall parallel? Effect on the Variables Defined by the M Matrix Transformation
H = Contrast SSCP Matrix for parallel?
E = Error SSCP Matrix

S=2 M=0 N=8.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.11028611	12.74	6	38	<.0001
Pillai's Trace	1.08917068	7.97	6	40	<.0001
Hotelling-Lawley Trace	6.25878523	19.37	6	23.636	<.0001
Roy's Greatest Root	5.95508874	39.70	3	20	<.0001

NOTE: F Statistic for Roy's Greatest Root is an upper bound.

NOTE: F Statistic for Wilks' Lambda is exact.

H = Contrast SSCP Matrix for horizontal?

	MVAR1	MVAR2	MVAR3
MVAR1	376.04166667	193.95833333	-23.75
MVAR2	193.95833333	100.04166667	-12.25
MVAR3	-23.75	-12.25	1.5

Characteristic Roots and Vectors of: E Inverse * H, where
H = Contrast SSCP Matrix for horizontal?
E = Error SSCP Matrix

Variables have been transformed by the M Matrix

Characteristic Root	Percent	Characteristic Vector V'EV=1

Characteristic Roots and Vectors of: E Inverse * H, where MVAR1 MVAR2 MVAR3 H = Contrast SSCP Matrix for horizontal? E = Error SSCP Matrix Variables have been transformed by the M Matrix				
Characteristic Root	Percent	Characteristic Vector V'EV=1		
		MVAR1	MVAR2	MVAR3
2.25935995	100.00	0.05216409	0.04415659	-0.04074607
0.00000000	0.00	0.03751150	-0.06626004	0.05280847
0.00000000	0.00	-0.03129445	0.06224163	0.01281109

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall horizontal? Effect on the Variables Defined by the M Matrix Transformation H = Contrast SSCP Matrix for horizontal? E = Error SSCP Matrix S=1 M=0.5 N=8.5					
Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.30680870	14.31	3	19	<.0001
Pillai's Trace	0.69319130	14.31	3	19	<.0001
Hotelling-Lawley Trace	2.25935995	14.31	3	19	<.0001
Roy's Greatest Root	2.25935995	14.31	3	19	<.0001

'Comparison of Drugs: Profiles of the Means'

The GLM Procedure
Multivariate Analysis of Variance

M Matrix Describing Transformed Variables				
	y1	y2	y3	y4
MVAR1	1	1	1	1

E = Error SSCP Matrix	
	MVAR1
MVAR1	9331.25

'Comparison of Drugs: Profiles of the Means'

The GLM Procedure
Multivariate Analysis of Variance

H = Type III SSCP Matrix for drug	
	MVAR1
MVAR1	5259.25

Characteristic Roots and Vectors of: E Inverse * H, where H = Type III SSCP Matrix for drug E = Error SSCP Matrix Variables have been transformed by the M Matrix		
Characteristic Root	Percent	Characteristic Vector V'EV=1
		MVAR1
0.56361688	100.00	0.01035214

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall drug Effect on the Variables Defined by the M Matrix Transformation
H = Type III SSCP Matrix for drug
E = Error SSCP Matrix

S=1 M=0 N=9.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.63954285	5.92	2	21	0.0092
Pillai's Trace	0.36045715	5.92	2	21	0.0092
Hotelling-Lawley Trace	0.56361688	5.92	2	21	0.0092
Roy's Greatest Root	0.56361688	5.92	2	21	0.0092

H = Contrast SSCP Matrix for bww9 vs. control

	MVAR1
MVAR1	5256.25

Characteristic Roots and Vectors of: E Inverse * H, where
H = Contrast SSCP Matrix for bww9 vs. control
E = Error SSCP Matrix

Variables have been transformed by the M Matrix

		Characteristic Vector V'EV=1
Characteristic Root	Percent	MVAR1
0.56329538	100.00	0.01035214

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall bww9 vs. control Effect on the Variables Defined by the M Matrix Transformation
H = Contrast SSCP Matrix for bww9 vs. control
E = Error SSCP Matrix

S=1 M=-0.5 N=9.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.63967438	11.83	1	21	0.0025
Pillai's Trace	0.36032562	11.83	1	21	0.0025
Hotelling-Lawley Trace	0.56329538	11.83	1	21	0.0025
Roy's Greatest Root	0.56329538	11.83	1	21	0.0025

H = Contrast SSCP Matrix for ax23 vs. the rest

	MVAR1
MVAR1	3

Characteristic Roots and Vectors of: E Inverse * H, where
H = Contrast SSCP Matrix for ax23 vs. the rest
E = Error SSCP Matrix

Variables have been transformed by the M Matrix

		Characteristic Vector V'EV=1
Characteristic Root	Percent	MVAR1
0.00032150	100.00	0.01035214

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall ax23 vs. the rest Effect on the Variables Defined by the M Matrix Transformation
H = Contrast SSCP Matrix for ax23 vs. the rest
E = Error SSCP Matrix

S=1 M=-0.5 N=9.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall ax23 vs. the rest Effect on the Variables Defined by the M Matrix Transformation
H = Contrast SSCP Matrix for ax23 vs. the rest
E = Error SSCP Matrix

S=1 M=-0.5 N=9.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.99967860	0.01	1	21	0.9353
Pillai's Trace	0.00032140	0.01	1	21	0.9353
Hotelling-Lawley Trace	0.00032150	0.01	1	21	0.9353
Roy's Greatest Root	0.00032150	0.01	1	21	0.9353

H = Contrast SSCP Matrix for parallel?

	MVAR1
MVAR1	5259.25

Characteristic Roots and Vectors of: E Inverse * H, where
H = Contrast SSCP Matrix for parallel?
E = Error SSCP Matrix

Variables have been transformed by the M Matrix

Characteristic Root	Percent	Characteristic Vector V'EV=1
		MVAR1
0.56361688	100.00	0.01035214

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall parallel? Effect on the Variables Defined by the M Matrix Transformation
H = Contrast SSCP Matrix for parallel?
E = Error SSCP Matrix

S=1 M=0 N=9.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.63954285	5.92	2	21	0.0092
Pillai's Trace	0.36045715	5.92	2	21	0.0092
Hotelling-Lawley Trace	0.56361688	5.92	2	21	0.0092
Roy's Greatest Root	0.56361688	5.92	2	21	0.0092

H = Contrast SSCP Matrix for horizontal?

	MVAR1
MVAR1	2243593.5

Characteristic Roots and Vectors of: E Inverse * H, where
H = Contrast SSCP Matrix for horizontal?
E = Error SSCP Matrix

Variables have been transformed by the M Matrix

Characteristic Root	Percent	Characteristic Vector V'EV=1
		MVAR1
240.438687	100.00	0.01035214

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall horizontal? Effect on the Variables Defined by the M Matrix Transformation
H = Contrast SSCP Matrix for horizontal?
E = Error SSCP Matrix

S=1 M=-0.5 N=9.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.00414184	5049.21	1	21	<.0001

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall horizontal? Effect on the Variables Defined by the M Matrix Transformation
H = Contrast SSCP Matrix for horizontal?
E = Error SSCP Matrix

S=1 M=-0.5 N=9.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Pillai's Trace	0.99585816	5049.21	1	21	<.0001
Hotelling-Lawley Trace	240.43868721	5049.21	1	21	<.0001
Roy's Greatest Root	240.43868721	5049.21	1	21	<.0001

H = Contrast SSCP Matrix for coincidental?

	MVAR1
MVAR1	5259.25

Characteristic Roots and Vectors of: E Inverse * H, where
H = Contrast SSCP Matrix for coincidental?
E = Error SSCP Matrix

Variables have been transformed by the M Matrix

		Characteristic Vector V'EV=1
Characteristic Root	Percent	MVAR1
0.56361688	100.00	0.01035214

MANOVA Test Criteria and Exact F Statistics for the Hypothesis of No Overall coincidental? Effect on the Variables Defined by the M Matrix Transformation
H = Contrast SSCP Matrix for coincidental?
E = Error SSCP Matrix

S=1 M=0 N=9.5

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilks' Lambda	0.63954285	5.92	2	21	0.0092
Pillai's Trace	0.36045715	5.92	2	21	0.0092
Hotelling-Lawley Trace	0.56361688	5.92	2	21	0.0092
Roy's Greatest Root	0.56361688	5.92	2	21	0.0092

```
data heart;
input drug $ y1 y2 y3 y4;
datalines;
ax23 72 86 81 77
ax23 78 83 88 82
ax23 71 82 81 75
ax23 72 83 83 69
ax23 66 79 77 66
ax23 74 83 84 77
ax23 62 73 78 70
ax23 69 75 76 70
bww9 85 86 83 80
bww9 82 86 80 84
bww9 71 78 70 75
bww9 83 88 79 81
bww9 86 85 76 76
bww9 85 82 83 80
bww9 79 83 80 81
bww9 83 84 78 81
control 69 73 72 74
control 66 62 67 73
control 84 90 88 87
control 80 81 77 72
control 72 72 69 70
control 65 62 65 61
control 75 69 69 68
control 71 70 65 65
;
proc print data= heart;
title1 "Heart Rate dataset";
run;

*sample profiles plot;
options ls=64 ps=45;

title1 "Comparison of Drugs: Profile Analysis";
title2 "H0: Any difference between ax23, bww9 and Control ";
proc glm data = heart;
class drug;
model y1 y2 y3 y4 = drug/nouni;
manova h = drug/printe printh ;
run;

filename gsasfile "prog58.graph";
goptions gaccess=gsasfile dev=pslmono;
goptions horigin=1in vorigin=2in;
goptions hsize=5in vsize=7in;
title1 h=1.5 'Comparison of Drugs: Profiles of the Means';
proc summary nway data=heart;
class drug;
var y1 y2 y3 y4;
output out=new mean=my1-my4;
data plot;
```

```
set new;
array my{4} my1-my4;
do test =1 to 4;
Response=my(test);
output;
end;
drop my1-my4;
    proc gplot data = plot;
plot response*test=drug /vaxis=axis1 haxis=axis2
vminor=3 legend=legend1 ;
axis1 label =(a=90 h=1.2 "Response");
axis2 offset=(2) label=(h=1.2 "Test");
symbol1 v=+ i = join;
symbol2 v=x i=join;
symbol3 v=* i=join;
legend1 across = 3;
run;

title2 ;
proc glm data = heart ;
class drug;
model y1 y2 y3 y4 =drug/nouni;
contrast 'bww9 vs. control' drug 0 1  -1;
contrast "ax23 vs. the rest"  drug 2 -1 -1;
contrast "parallel?" drug 1 0 -1, drug  0 1 -1;
contrast "horizontal?" intercept 1;
manova h=drug
m=(1 -1 0 0, 1 0 -1 0, 1 0 0 -1)/printe printh;
contrast "coincidental?" drug 1 0 -1, drug 0 1 -1;
manova h=drug m=(1 1 1 1) /printe printh;
run;
```