

```
manova healthATT by Gender (1,2) AgeGroup (1,2)
/design gender, agegroup, gender*agegroup
/design gender, agegroup w gender(1) agegroup w gender(2)
/design agegroup, gender w agegroup(1) gender w agegroup(2).
```

Manova

Notes

Output Created	14-OCT-2008 12:21:30	
Comments		
Input	Data	C:\Users\william marelich\Desktop\CGU-prep\2X2ANO~1.SAV
	Active Dataset	DataSet15
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	12
Missing Value Handling	Definition of Missing Cases Used	
Weight Handling		
Syntax	manova healthATT by Gender (1,2) AgeGroup (1,2) /design gender, agegroup, gender*agegroup /design gender, agegroup w gender(1) agegroup w gender(2) /design agegroup, gender w agegroup(1) gender w agegroup(2).	
Resources	Elapsed Time	0:00:00.02
	Processor Time	0:00:00.05

[DataSet15] C:\Users\william marelich\Desktop\CGU-prep\2X2ANO~1.SAV

The default error term in MANOVA has been changed from WITHIN CELLS to WITHIN+RESIDUAL. Note that these are the same for all full factorial designs.

* * * * * A n a l y s i s o f V a r i a n c e * * * * *

12 cases accepted.
0 cases rejected because of out-of-range factor values.
0 cases rejected because of missing data.
4 non-empty cells.

3 designs will be processed.

* * * * * A n a l y s i s o f V a r i a n c e -- design 1 * * * * *

Tests of Significance for HealthATT using UNIQUE sums of squares

Source of Variation	SS	DF	MS	F	Sig of F
WITHIN+RESIDUAL	6.00	8	.75		
GENDER	18.75	1	18.75	25.00	.001
AGEGROUP	14.08	1	14.08	18.78	.003
GENDER * AGEGROUP	10.08	1	10.08	13.44	.006
(Model)	42.92	3	14.31	19.07	.001
(Total)	48.92	11	4.45		

R-Squared = .877
Adjusted R-Squared = .831

* * * * * A n a l y s i s o f V a r i a n c e -- design 2 * * * * *

Tests of Significance for HealthATT using UNIQUE sums of squares

Source of Variation	SS	DF	MS	F	Sig of F
WITHIN+RESIDUAL	6.00	8	.75		

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GENDER                18.75      1    18.75    25.00    .001
AGEGROUP W GENDER(1)   .17      1     .17     .22     .650
AGEGROUP W GENDER(2)  24.00     1    24.00    32.00    .000

(Model)                42.92     3    14.31    19.07    .001
(Total)                48.92    11     4.45
R-Squared =            .877
Adjusted R-Squared =   .831

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* * * * * A n a l y s i s o f V a r i a n c e -- design 3 * * * * *

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Tests of Significance for HealthATT using UNIQUE sums of squares
Source of Variation      SS      DF      MS      F      Sig of F

WITHIN+RESIDUAL          6.00      8      .75
AGEGROUP                 14.08      1    14.08    18.78    .003
GENDER W AGEGROUP(1)    28.17      1    28.17    37.56    .000
GENDER W AGEGROUP(2)     .67      1     .67     .89     .373

(Model)                  42.92     3    14.31    19.07    .001
(Total)                  48.92    11     4.45
R-Squared =              .877
Adjusted R-Squared =     .831

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manova Aspir_DV by Norms (1,2) Standing (1,3)
  /design
  /design standing, norms w standing(1) norms w standing(2) norms w standing(3)
  /design norms, standing w norms(1) standing w norms(2).

```

Manova

Notes

Output Created	14-OCT-2008 12:26:04	
Comments		
Input	Data	C:\Users\william marelich\Desktop\CGU-prep\HAYS-2X3.sav
	Active Dataset	DataSet13
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	60
Missing Value Handling	Definition of Missing Cases Used	
Weight Handling		
Syntax	manova Aspir_DV by Norms (1,2) Standing (1,3) /design /design standing, norms w standing(1) norms w standing(2) norms w standing(3) /design norms, standing w norms(1) standing w norms(2).	
Resources	Elapsed Time	0:00:00.02
	Processor Time	0:00:00.03

[DataSet13] C:\Users\william marelich\Desktop\CGU-prep\HAYS-2X3.sav

The default error term in MANOVA has been changed from WITHIN CELLS to WITHIN+RESIDUAL. Note that these are the same for all full factorial designs.

* * * * * A n a l y s i s o f V a r i a n c e * * * * *

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60 cases accepted.
0 cases rejected because of out-of-range factor values.
0 cases rejected because of missing data.

```

6 non-empty cells.

3 designs will be processed.

* * * * * A n a l y s i s o f V a r i a n c e -- design 1 * * * * *

Tests of Significance for Aspir_DV using UNIQUE sums of squares

Source of Variation	SS	DF	MS	F	Sig of F
WITHIN CELLS	643.20	54	11.91		
Norms	4.27	1	4.27	.36	.552
Standing	4994.13	2	2497.07	209.64	.000
Norms BY Standing	810.13	2	405.07	34.01	.000
(Model)	5808.53	5	1161.71	97.53	.000
(Total)	6451.73	59	109.35		

R-Squared = .900
Adjusted R-Squared = .891

* * * * * A n a l y s i s o f V a r i a n c e -- design 2 * * * * *

Tests of Significance for Aspir_DV using UNIQUE sums of squares

Source of Variation	SS	DF	MS	F	Sig of F
WITHIN+RESIDUAL	643.20	54	11.91		
STANDING	4994.13	2	2497.07	209.64	.000
NORMS W STANDING(1)	460.80	1	460.80	38.69	.000
NORMS W STANDING(2)	288.80	1	288.80	24.25	.000
NORMS W STANDING(3)	64.80	1	64.80	5.44	.023
(Model)	5808.53	5	1161.71	97.53	.000
(Total)	6451.73	59	109.35		

R-Squared = .900
Adjusted R-Squared = .891

* * * * * A n a l y s i s o f V a r i a n c e -- design 3 * * * * *

Tests of Significance for Aspir_DV using UNIQUE sums of squares

Source of Variation	SS	DF	MS	F	Sig of F
WITHIN+RESIDUAL	643.20	54	11.91		
NORMS	4.27	1	4.27	.36	.552
STANDING W NORMS(1)	4113.87	2	2056.93	172.69	.000
STANDING W NORMS(2)	1690.40	2	845.20	70.96	.000
(Model)	5808.53	5	1161.71	97.53	.000
(Total)	6451.73	59	109.35		

R-Squared = .900
Adjusted R-Squared = .891
