ranova

Class: RepeatedMeasuresModel

Repeated measures analysis of variance

Syntax

```
ranovatbl = ranova(rm)
ranovatbl = ranova(rm,'WithinModel',WM)
[ranovatbl,A,C,D] = ranova( __ )
```

Description

`ranovatbl = ranova(rm)` returns the results of repeated measures analysis of variance for a repeated measures model `rm` in table `ranovatbl`. example

`ranovatbl = ranova(rm,'WithinModel',WM)` returns the results of repeated measures analysis of variance using the responses specified by the within-subject model `WM`. example

`[ranovatbl,A,C,D] = ranova( __ )` also returns arrays `A`, `C`, and `D` for the hypotheses tests of the form `A*B*C = D`, where `D` is zero. example

Input Arguments

collapse all

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

`WM` — Model specifying responses

`'separatemeans'` (default) | r-by-nc contrast matrix | character vector that defines a model specification

Model specifying the responses, specified as one of the following:

- `'separatemeans'` — Compute a separate mean for each group.
- `C` — r-by-nc contrast matrix specifying the nc contrasts among the r repeated measures. If Y represents a matrix of repeated measures, `ranova` tests the hypothesis that the means of $Y*C$ are zero.
- A character vector that defines a model specification in the within-subject factors. You can define the model based on the rules for the `terms` in the `modelspec` argument of `fitrm`. Also see Model Specification for Repeated Measures Models.

For example, if there are three within-subject factors `w1`, `w2`, and `w3`, then you can specify a model for the within-subject factors as follows.

Example: `'WithinModel','w1+w2+w2*w3'`

Data Types: `single` | `double`

Output Arguments

expand all

`ranovatbl` — Results of repeated measures anova

table

Results of repeated measures anova, returned as a `table`.

`ranovatbl` includes a term representing all differences across the within-subjects factors. This term has either the name of the within-subjects factor if specified while fitting the model, or the name `Time` if the name of the within-subjects factor is not specified while fitting the model or there are more than one within-subjects factors. `ranovatbl` also includes all interactions between the terms in the within-subject model and all between-subject model terms. It contains the following columns.

Column Name	Definition
`SumSq`	Sum of squares.
`DF`	Degrees of freedom.
`MeanSq`	Mean squared error.
`F`	F-statistic.
`pValue`	p-value for the corresponding F-statistic. A small p-value indicates significant term effect.
`pValueGG`	p-value with Greenhouse-Geisser adjustment.
`pValueHF`	p-value with Huynh-Feldt adjustment.
`pValueLB`	p-value with Lower bound adjustment.

Column Name	Definition

The last three p-values are the adjusted p-values for use when the compound symmetry assumption is not satisfied. For details, see Compound Symmetry Assumption and Epsilon Corrections. The `mauchy` method tests for sphericity (hence, compound symmetry) and `epsilon` method returns the epsilon adjustment values.

A — Specification based on between-subjects model
matrix | cell array

C — Specification based on within-subjects model
matrix | cell array

D — Hypothesis value
0

Examples

collapse all

Repeated Measures Analysis of Variance

Load the sample data.

Try it in MATLAB

```
load fisheriris
```

The column vector `species` consists of iris flowers of three different species: setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = table([1 2 3 4]','VariableNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Perform repeated measures analysis of variance.

```
ranovatbl = ranova(rm)
```

```
ranovatbl =

  3x8 table

                              SumSq     DF      MeanSq       F         pValue        pValueGG      pValueHF       pValueLB
                              ______    ___    ________    ______    __________    __________    __________    __________

    (Intercept):Measurements    1656.3     3      552.09    6873.3             0    9.4491e-279    2.9213e-283    2.5871e-125
    species:Measurements        282.47     6      47.078     586.1    1.4271e-206    4.9313e-156    1.5406e-158     9.0151e-71
    Error(Measurements)         35.423   441    0.080324
```

There are four measurements, three types of species, and 150 observations. So, degrees of freedom for measurements is (4–1) = 3, for species-measurements interaction it is (4–1)*(3–1) = 6, and for error it is (150–4)*(3–1) = 441. `ranova` computes the last three p-values using Greenhouse-Geisser, Huynh-Feldt, and Lower bound corrections, respectively. You can check the compound symmetry (sphericity) assumption using the `mauchly` method, and display the epsilon corrections using the `epsilon` method.

Longitudinal Data

Load the sample data.

Try it in MATLAB

```
load(fullfile(matlabroot,'examples','stats','longitudinalData.mat'));
```

The matrix Y contains response data for 16 individuals. The response is the blood level of a drug measured at five time points (time = 0, 2, 4, 6, and 8). Each row of Y corresponds to an individual, and each column corresponds to a time point. The first eight subjects are female, and the second eight subjects are male. This is simulated data.

Define a variable that stores gender information.

```
Gender = ['F' 'F' 'F' 'F' 'F' 'F' 'F' 'F' 'M' 'M' 'M' 'M' 'M' 'M' 'M' 'M']';
```

Store the data in a proper table array format to do repeated measures analysis.

```
t = table(Gender,Y(:,1),Y(:,2),Y(:,3),Y(:,4),Y(:,5),...
```

```
'VariableNames',{'Gender','t0','t2','t4','t6','t8'});
```

Define the within-subjects variable.

```
Time = [0 2 4 6 8]';
```

Fit a repeated measures model, where the blood levels are the responses and gender is the predictor variable.

```
rm = fitrm(t,'t0-t8 ~ Gender','WithinDesign',Time);
```

Perform repeated measures analysis of variance.

```
ranovatbl = ranova(rm)
```

```
ranovatbl =

  3x8 table

                       SumSq     DF    MeanSq       F         pValue       pValueGG      pValueHF      pValueLB
                       _____    ___    ______    _____    __________    __________    __________    __________

    (Intercept):Time    881.7     4    220.43    37.539    3.0348e-15    4.7325e-09    2.4439e-10    2.6198e-05
    Gender:Time         17.65     4    4.4125    0.75146       0.56126        0.4877       0.50707       0.40063
    Error(Time)         328.83    56     5.872
```

There are 5 time points, 2 genders, and 16 observations. So, the degrees of freedom for time is (5–1) = 4, for gender-time interaction it is (5–1)*(2–1) = 4, and for error it is (16–2)*(5–1) = 56. The small p-value of 2.6198e–05 indicates that there is a significant effect of time on blood pressure. The p -value of 0.40063 indicates that there is no significant gender-time interaction.

Specify the Within-Subjects Model

Load the sample data.

Try it in MATLAB

```
load repeatedmeas
```

The table between includes the between-subject variables age, IQ, group, gender, and eight repeated measures y1 through y8 as responses. The table within includes the within-subject variables w1 and w2. This is simulated data.

Fit a repeated measures model, where the repeated measures y1 through y8 are the responses, and age, IQ, group, gender, and the group-gender interaction are the predictor variables. Also specify the within-subject design matrix.

```
rm = fitrm(between,'y1-y8 ~ Group*Gender + Age + IQ','WithinDesign',within);
```

Perform repeated measures analysis of variance.

```
ranovatbl = ranova(rm)
```

```
ranovatbl =

  7x8 table

                       SumSq     DF     MeanSq       F         pValue       pValueGG      pValueHF      pValueLB
                       _____    ____    ______    _____    __________    __________    __________    __________

    (Intercept):Time    6645.2     7    949.31     2.2689      0.031674      0.071235      0.056257       0.14621
    Age:Time            5824.3     7    832.05     1.9887      0.059978       0.10651      0.090128       0.17246
    IQ:Time             5188.3     7    741.18     1.7715      0.096749       0.14492       0.12892       0.19683
    Group:Time           15800    14    1128.6     2.6975     0.0014425      0.011884     0.0064346      0.089594
    Gender:Time         4455.8     7    636.55     1.5214       0.16381       0.20533       0.19258       0.23042
    Group:Gender:Time   4247.3    14    303.38    0.72511       0.74677         0.663       0.69184       0.49549
    Error(Time)          64433    154    418.39
```

Specify the model for the within-subject factors. Also display the matrices used in the hypothesis test.

```
[ranovatbl,A,C,D] = ranova(rm,'WithinModel','w1+w2')
```

```
ranovatbl =

  21x8 table

                     SumSq     DF    MeanSq       F         pValue       pValueGG      pValueHF      pValueLB
                     _____    ____    ______    _____    __________    __________    __________    __________

    (Intercept)      3141.7     1    3141.7     2.5034       0.12787       0.12787       0.12787       0.12787
    Age              537.48     1    537.48    0.42828       0.51962       0.51962       0.51962       0.51962
    IQ               2975.9     1    2975.9     2.3712       0.13785       0.13785       0.13785       0.13785
```

```
    Group              20836     2     10418      8.3012    0.0020601    0.0020601    0.0020601    0.0020601
    Gender             3036.3    1     3036.3     2.4194      0.13411      0.13411      0.13411      0.13411
    Group:Gender        211.8    2      105.9    0.084385      0.91937      0.91937      0.91937      0.91937
    Error              27609    22      1255
    (Intercept):w1     146.75    1     146.75     0.23326      0.63389      0.63389      0.63389      0.63389
    Age:w1             942.02    1     942.02      1.4974      0.23402      0.23402      0.23402      0.23402
    IQ:w1              11.563    1     11.563     0.01838      0.89339      0.89339      0.89339      0.89339
    Group:w1           4481.9    2     2240.9       3.562     0.045697     0.045697     0.045697     0.045697
    Gender:w1          270.65    1     270.65      0.4302      0.51869      0.51869      0.51869      0.51869
    Group:Gender:w1    240.37    2     120.19     0.19104      0.82746      0.82746      0.82746      0.82746
    Error(w1)           13841    22     629.12
    (Intercept):w2     3663.8    3     1221.3      3.8381     0.013513     0.020339      0.01575     0.062894
    Age:w2             1199.9    3     399.95      1.2569       0.2964      0.29645      0.29662      0.27432
    IQ:w2              3650.1    3     1216.7      3.8237     0.013744     0.020636     0.016005     0.063351
    Group:w2           5963.8    6     993.96      3.1237    0.0093493     0.015434     0.011278     0.063955
    Gender:w2          2173.1    3     724.38      2.2765     0.087813      0.10134     0.092674      0.14557
    Group:Gender:w2    3339.6    6      556.6      1.7492      0.12345         0.14       0.1294      0.19724
    Error(w2)           21001    66     318.2


A =

  6x1 cell array

    {1x8 double}
    {1x8 double}
    {1x8 double}
    {2x8 double}
    {1x8 double}
    {2x8 double}


C =

  1x3 cell array

    {8x1 double}    {8x1 double}    {8x3 double}


D =

     0
```

Display the contents of A.

```
[A{1};A{2};A{3};A{4};A{5};A{6}]
```

```
ans =

     1     0     0     0     0     0     0     0
     0     1     0     0     0     0     0     0
     0     0     1     0     0     0     0     0
     0     0     0     1     0     0     0     0
     0     0     0     0     1     0     0     0
     0     0     0     0     0     1     0     0
     0     0     0     0     0     0     1     0
     0     0     0     0     0     0     0     1
```

Display the contents of C.

```
[C{1} C{2} C{3}]
```

```
ans =

     1     1     1     0     0
     1     1     0     1     0
     1     1     0     0     1
     1     1    -1    -1    -1
     1    -1     1     0     0
     1    -1     0     1     0
     1    -1     0     0     1
     1    -1    -1    -1    -1
```

Algorithms

`ranova` computes the regular p-value (in the `pValue` column of the `rmanova` table) using the F-statistic cumulative distribution function:

p-value = 1 – fcdf(F,v_1,v_2).

When the compound symmetry assumption is not satisfied, `ranova` uses a correction factor epsilon, ε, to compute the corrected p-values as follows:

p-value_corrected = 1 – fcdf(F,ε^*v_1,ε^*v_2).

The `mauchly` method tests for sphericity (hence, compound symmetry) and `epsilon` method returns the epsilon adjustment values.

See Also

`anova` | `epsilon` | `fitrm` | `manova` | `mauchly`

Topics

Model Specification for Repeated Measures Models

Compound Symmetry Assumption and Epsilon Corrections

Mauchly's Test of Sphericity