matrix dissimilarity — Compute similarity or dissimilarity measures

Syntax

```
matrix dissimilarity matname = [varlist] [if] [in] [, options]
```

<table>
<thead>
<tr>
<th>options</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>measure</td>
<td>similarity or dissimilarity measure; default is L2 (Euclidean)</td>
</tr>
<tr>
<td>observations</td>
<td>compute similarities or dissimilarities between observations; the default</td>
</tr>
<tr>
<td>variables</td>
<td>compute similarities or dissimilarities between variables</td>
</tr>
<tr>
<td>names(varname)</td>
<td>row/column names for matname (allowed with observations)</td>
</tr>
<tr>
<td>allbinary</td>
<td>check that all values are 0, 1, or missing</td>
</tr>
<tr>
<td>proportions</td>
<td>interpret values as proportions of binary values</td>
</tr>
<tr>
<td>dissim(method)</td>
<td>change similarity measure to dissimilarity measure</td>
</tr>
</tbody>
</table>

where method transforms similarities to dissimilarities by using

```
<table>
<thead>
<tr>
<th>method</th>
<th>formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>oneminus</td>
<td>( d_{ij} = 1 - s_{ij} )</td>
</tr>
<tr>
<td>standard</td>
<td>( d_{ij} = \sqrt{s_{ii} + s_{jj} - 2s_{ij}} )</td>
</tr>
</tbody>
</table>
```

Description

matrix dissimilarity computes a similarity, dissimilarity, or distance matrix.

Options

measure specifies one of the similarity or dissimilarity measures allowed by Stata. The default is L2, Euclidean distance. Many similarity and dissimilarity measures are provided for continuous data and for binary data; see [MV] measure_option.

observations and variables specify whether similarities or dissimilarities are computed between observations or variables. The default is observations.

names(varname) provides row and column names for matname. varname must be a string variable with a length of 32 or less. You will want to pick a varname that yields unique values for the row and column names. Uniqueness of values is not checked by matrix dissimilarity. names() is not allowed with the variables option. The default row and column names when the similarities or dissimilarities are computed between observations is obs#, where # is the observation number corresponding to that row or column.

allbinary checks that all values are 0, 1, or missing. Stata treats nonzero values as one (excluding missing values) when dealing with what are supposed to be binary data (including binary similarity measures). allbinary causes matrix dissimilarity to exit with an error message if the values are not truly binary. allbinary is not allowed with proportions or the Gower measure.
proportions is for use with binary similarity measures. It specifies that values be interpreted as proportions of binary values. The default action treats all nonzero values as one (excluding missing values). With proportions, the values are confirmed to be between zero and one, inclusive. See [MV] measure_option for a discussion of the use of proportions with binary measures. proportions is not allowed with allbinary or the Gower measure.

dissim(method) specifies that similarity measures be transformed into dissimilarity measures. method may be oneminus or standard. oneminus transforms similarities to dissimilarities by using \( d_{ij} = 1 - s_{ij} \) (Kaufman and Rousseeuw 1990, 21). standard uses \( d_{ij} = \sqrt{s_{ii} + s_{jj} - 2s_{ij}} \) (Mardia, Kent, and Bibby 1979, 402). dissim() does nothing when the measure is already a dissimilarity or distance. See [MV] measure_option to see which measures are similarities.

Remarks and examples

Commands such as cluster singlelinkage, cluster completelinkage, and mds (see [MV] cluster and [MV] mds) have options allowing the user to select the similarity or dissimilarity measure to use for its computation. If you are developing a command that requires a similarity or dissimilarity matrix, the matrix dissimilarity command provides a convenient way to obtain it.

The similarity or dissimilarity between each observation (or variable if the variables option is specified) and the others is placed in matname. The element in the \( i \)th row and \( j \)th column gives either the similarity or dissimilarity between the \( i \)th and \( j \)th observation (or variable). Whether you get a similarity or a dissimilarity depends upon the requested measure; see [MV] measure_option.

If there are many observations (variables when the variables option is specified), you may need to increase the maximum matrix size; see [R] matsize. If the number of observations (or variables) is so large that storing the results in a matrix is not practical, you may wish to consider using the cluster measures command, which stores similarities or dissimilarities in variables; see [MV] cluster programming utilities.

When computing similarities or dissimilarities between observations, the default row and column names of matname are set to obs#, where # is the observation number. The names() option allows you to override this default. For similarities or dissimilarities between variables, the row and column names of matname are set to the appropriate variable names.

The order of the rows and columns corresponds with the order of your observations when you are computing similarities or dissimilarities between observations. Warning: If you reorder your data (for example, using sort or gsort) after running matrix dissimilarity, the row and column ordering will no longer match your data.

Another use of matrix dissimilarity is in performing a cluster analysis on variables instead of observations. The cluster command performs a cluster analysis of the observations; see [MV] cluster. If you instead wish to cluster variables, you can use the variables option of matrix dissimilarity to obtain a dissimilarity matrix that can then be used with clustermat; see [MV] clustermat and example 2 below.

Example 1

Example 1 of [MV] cluster linkage introduces data with four chemical laboratory measurements on 50 different samples of a particular plant. Let’s find the Canberra distance between the measurements performed by lab technician Bill found among the first 25 observations of the labtech dataset.
matrix dissimilarity — Compute similarity or dissimilarity measures

. use http://www.stata-press.com/data/r13/labtech
. matrix dissim D = x1 x2 x3 x4 if labtech=="Bill" in 1/25, canberra
. matrix list D

symmetric D[6,6]

obs7    obs18    obs20    obs22    obs23    obs25
obs7   0
obs18  1.3100445  0
obs20  1.1134916  .87626565  0
obs22  1.452748  1.0363077  1.0621064  0
obs23  1.0380665  1.4952796  .81602718  1.6888123  0
obs25  1.4668898  1.5139834  1.4492336  1.0668425  1.1252514  0

By default, the row and column names of the matrix indicate the observations involved. The Canberra distance between the 23rd observation and the 18th observation is 1.4952796. See [MV] measure_option for a description of the Canberra distance.

Example 2

Example 2 of [MV] cluster linkage presents a dataset with 30 observations of 60 binary variables, a1, a2, ..., a30. In [MV] cluster linkage, the observations were clustered. Here we instead cluster the variables by computing the dissimilarity matrix by using matrix dissimilarity with the variables option followed by the clustermat command.

We use the matching option to obtain the simple matching similarity coefficient but then specify dissim(oneminus) to transform the similarities to dissimilarities by using the transformation \( d_{ij} = 1 - s_{ij} \). The allbinary option checks that the variables really are binary (0/1) data.

. use http://www.stata-press.com/data/r13/homework
. matrix dissim Avars = a*, variables matching dissim(oneminus) allbinary
. matrix subA = Avars[1..5,1..5]
. matrix list subA

symmetric subA[5,5]

a1      a2      a3      a4      a5
a1  0
a2  .4  0
a3  .4  .46666667  0
a4  .3  .3  .36666667  0
a5  .4  .4  .13333333  .3  0

We listed the first five rows and columns of the 60 × 60 matrix. The matrix row and column names correspond to the variable names.

To perform an average-linkage cluster analysis on the 60 variables, we supply the Avars matrix created by matrix dissimilarity to the clustermat averagelinkage command; see [MV] cluster linkage.

. clustermat averagelinkage Avars, clear
obs was 0, now 60
cluster name: _clus_1
. cluster generate g5 = groups(5)
We generated a variable, \( g_5 \), indicating the five-group cluster solution and then tabulated to show how many variables were clustered into each of the five groups. Group five has only one member.

```
list g5 if g5==5
```

The member corresponds to the 13th observation in the current dataset, which in turn corresponds to variable \( a_{13} \) from the original dataset. It appears that \( a_{13} \) is not like the other variables.

**Example 3**

`matrix dissimilarity` drops observations containing missing values, except when the Gower measure is specified. The computation of the Gower dissimilarity between 2 observations is based on the variables where the 2 observations both have nonmissing values.

We illustrate using a dataset with 6 observations and 4 variables where only 2 of the observations have complete data.

```
use http://www.stata-press.com/data/r13/gower, clear
list
```

```
+----+----+----+----+
<table>
<thead>
<tr>
<th>b1</th>
<th>b2</th>
<th>x1</th>
<th>x2</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>0</td>
<td>.76</td>
<td>.75</td>
</tr>
<tr>
<td>2.</td>
<td>.</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>3.</td>
<td>1</td>
<td>.72</td>
<td>.88</td>
</tr>
<tr>
<td>4.</td>
<td>.</td>
<td>.4</td>
<td>.</td>
</tr>
<tr>
<td>5.</td>
<td>0</td>
<td>.</td>
<td>.14</td>
</tr>
<tr>
<td>6.</td>
<td>0</td>
<td>.</td>
<td>.55</td>
</tr>
</tbody>
</table>
```

```
mat dissimilarity matL2 = b* x*, L2
matlist matL2, format(%8.3f)
```

```
+----+----+----+----+
<table>
<thead>
<tr>
<th></th>
<th>obs1</th>
<th>obs3</th>
</tr>
</thead>
<tbody>
<tr>
<td>obs1</td>
<td>0.000</td>
<td></td>
</tr>
<tr>
<td>obs3</td>
<td>1.421</td>
<td>0.000</td>
</tr>
</tbody>
</table>
```

The resulting matrix is \( 2 \times 2 \) and provides the dissimilarity between observations 1 and 3. All other observations contained at least one missing value.
However, with the _gower_ measure we obtain a $6 \times 6$ matrix.

```
. matrix dissimilarity matgow = b1 b2 x1 x2, gower
. matlist matgow, format(%8.3f)
```

<table>
<thead>
<tr>
<th></th>
<th>obs1</th>
<th>obs2</th>
<th>obs3</th>
<th>obs4</th>
<th>obs5</th>
<th>obs6</th>
</tr>
</thead>
<tbody>
<tr>
<td>obs1</td>
<td>0.000</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>obs2</td>
<td></td>
<td>0.000</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>obs3</td>
<td>0.572</td>
<td>0.000</td>
<td>0.000</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>obs4</td>
<td>0.500</td>
<td>0.944</td>
<td>0.000</td>
<td>0.000</td>
<td></td>
<td></td>
</tr>
<tr>
<td>obs5</td>
<td>0.412</td>
<td>1.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>obs6</td>
<td>0.528</td>
<td>0.491</td>
<td>0.708</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
</tr>
</tbody>
</table>

Because all the values for observation 2 are missing, the matrix contains missing values for the dissimilarity between observation 2 and the other observations. Notice the missing value in `matgow` for the dissimilarity between observations 4 and 5. There were no variables where observations 4 and 5 both had nonmissing values, and hence the _Gower_ coefficient could not be computed.

### References


### Also see

- [MV] cluster — Introduction to cluster-analysis commands
- [MV] clustermat — Introduction to clustermat commands
- [MV] mdsmat — Multidimensional scaling of proximity data in a matrix
- [MV] cluster programming utilities — Cluster-analysis programming utilities
- [MV] measure_option — Option for similarity and dissimilarity measures
- [P] matrix — Introduction to matrix commands