**matrix dissimilarity** — Compute similarity or dissimilarity measures

### Syntax

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

#### options

<table>
<thead>
<tr>
<th>option</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

- **oneminus** \( d_{ij} = 1 - s_{ij} \)
- **standard** \( d_{ij} = \sqrt{s_{ii} + s_{jj} - 2s_{ij}} \)

### 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.

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

Remarks and examples

Commands such as \texttt{cluster singlelinkage}, \texttt{cluster completelinkage}, and \texttt{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 \texttt{matrix dissimilarity} command provides a convenient way to obtain it.

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

If there are many observations (variables when the \texttt{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 \texttt{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 \texttt{matname} are set to \texttt{obs#}, where \# is the observation number. The \texttt{names()} option allows you to override this default. For similarities or dissimilarities between variables, the row and column names of \texttt{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 \texttt{sort} or \texttt{gsort}) after running \texttt{matrix dissimilarity}, the row and column ordering will no longer match your data.

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

\textbf{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.
. 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

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

We listed the first five rows and columns of the 60 x 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, `g5`, 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.

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

```
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.
```

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></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></td>
<td></td>
<td></td>
</tr>
<tr>
<td>obs5</td>
<td>0.412</td>
<td>1.000</td>
<td>0.708</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

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