

Analyzing Social Networks Detailed Instructions on the Examples in the Text

This gives the detailed commands required to reproduce all the examples in the text created using UCINET, E-Net and Netdraw. Note we do not show details for Siena or PNet. We are grateful to Daniel Tischer who has documented most of the examples. Occasionally the outputs will not match exactly, this can be for a number of reasons. Some routines use random number generators and the output is dependent on some random number. This may affect the ordering of the output or some values may be different but any differences should be slight. Secondly newer versions of UCINET may have more efficient or later algorithms and this could marginally affect the results but again any differences will be slight.

Steve, Martin and Jeff

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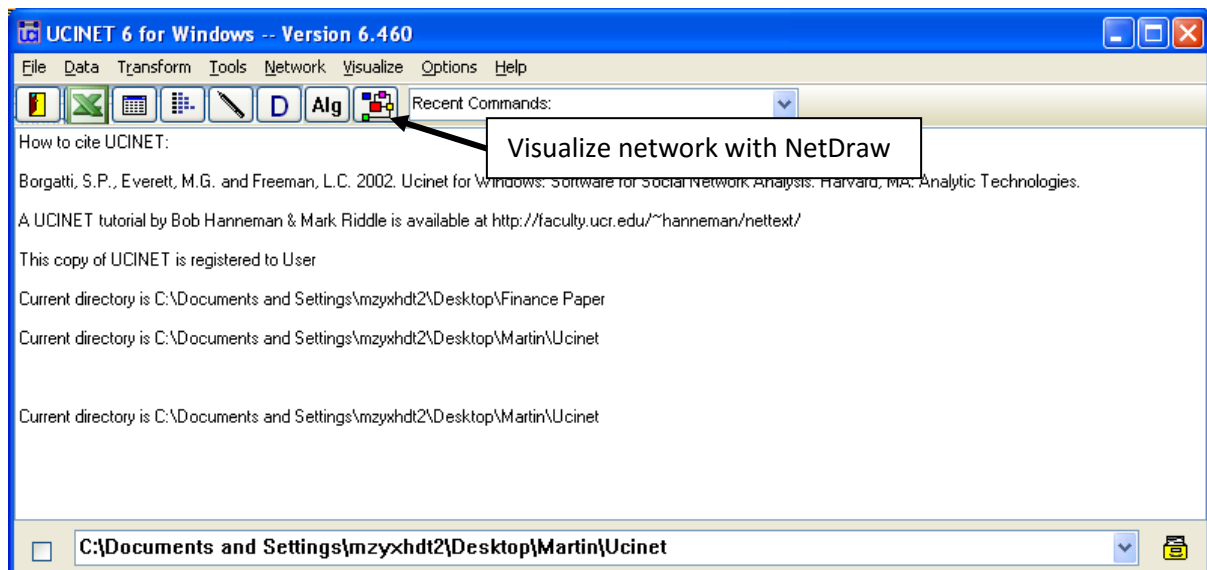
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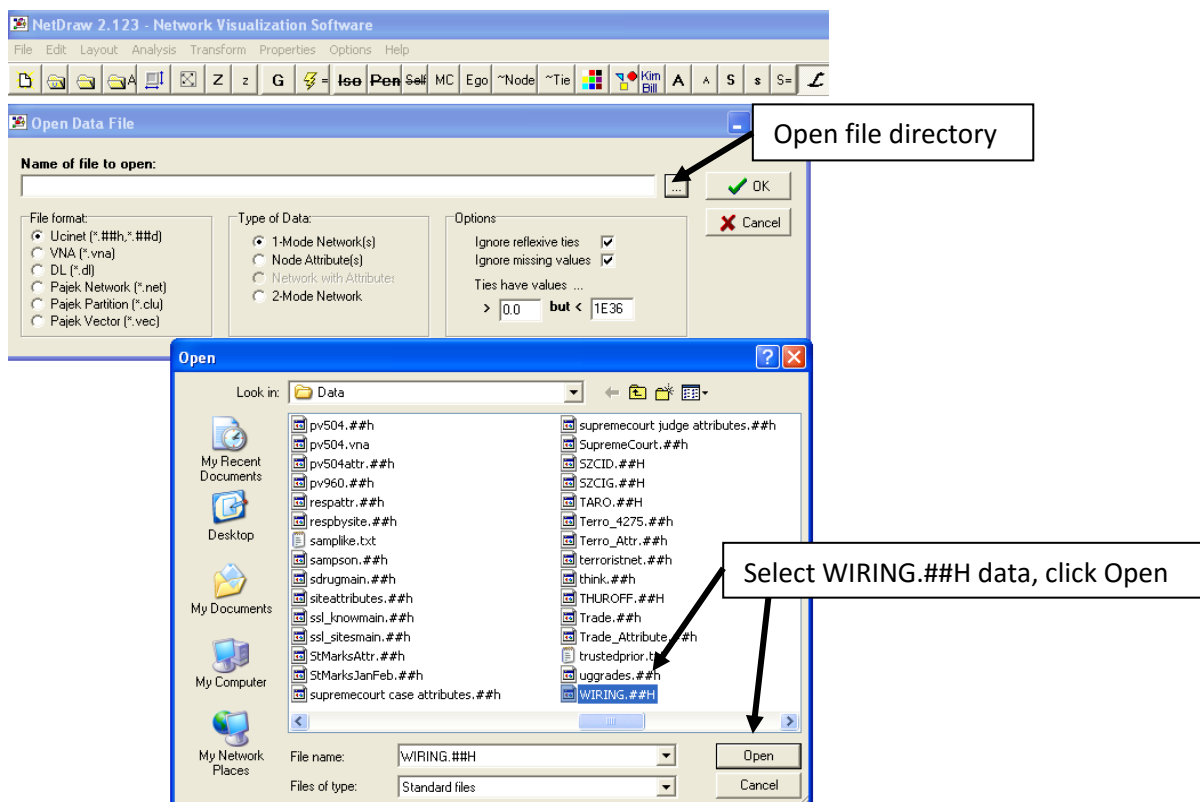
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Section 2.2 Graphs

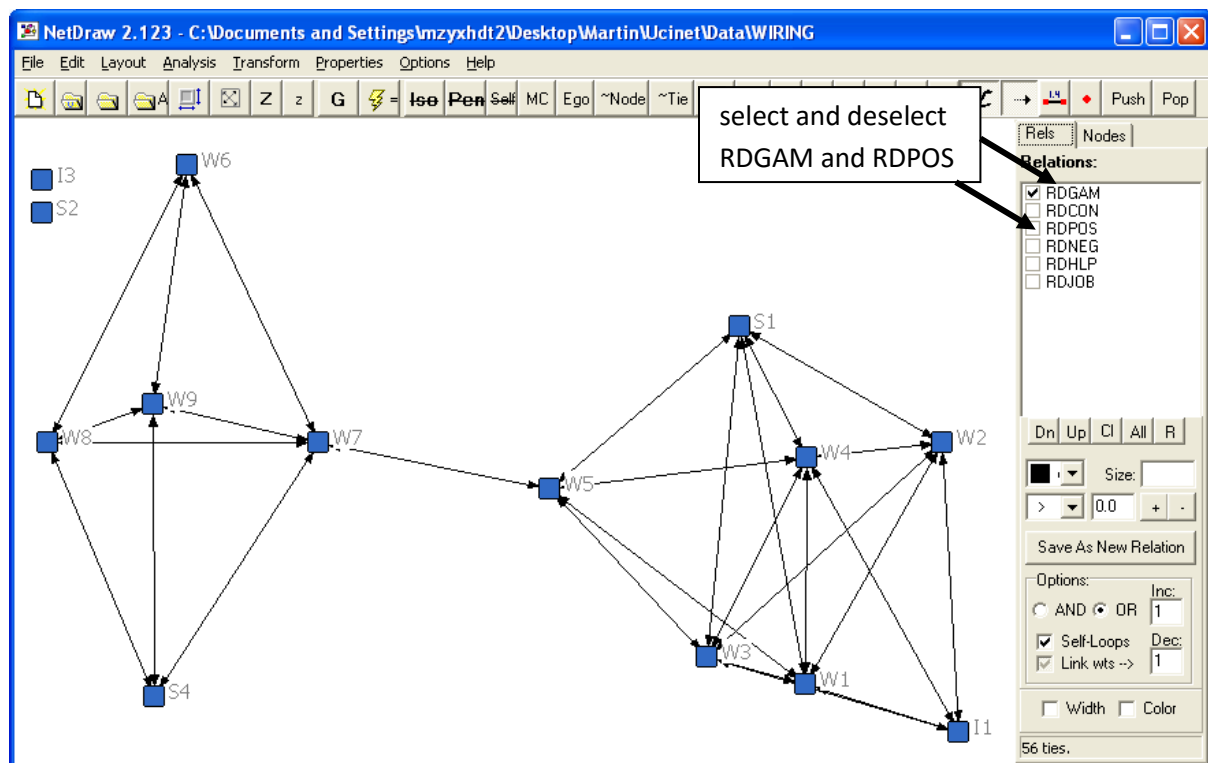
To visualise the “Wiring” dataset open UCINET and run NetDraw:



Open the UCINET dataset “WIRING.##H”



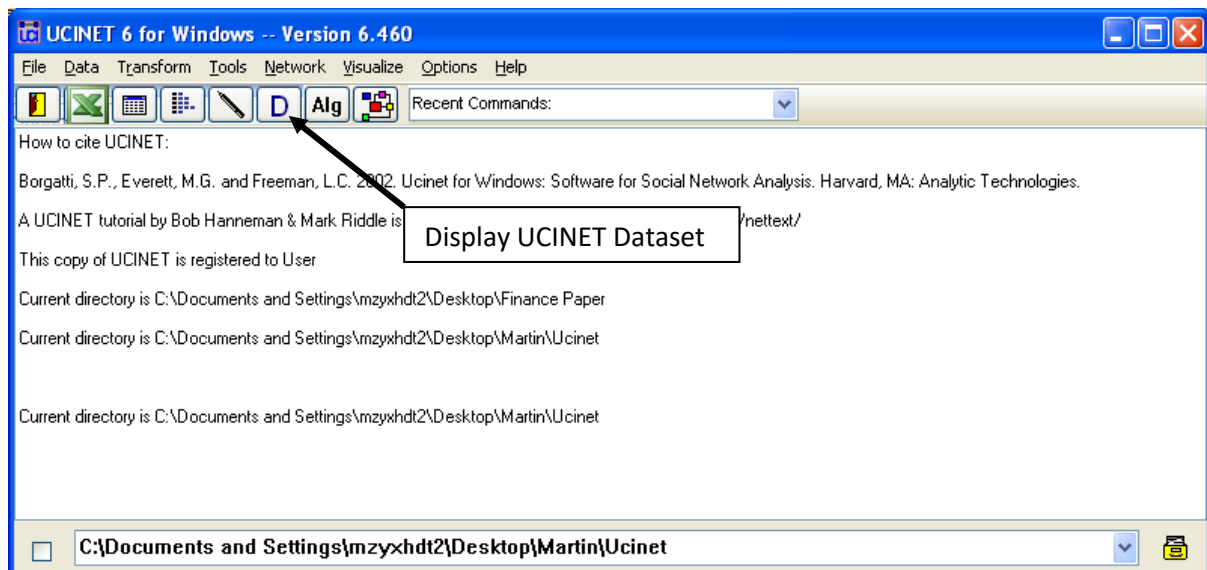
To show the different kinds of social ties in the dataset as illustrated in **Figure 2.2**, select and deselect **RDGAM** (“Plays games”) and **RDPOS** (“Friendship ties”) or any of the other routines.



Follow the same steps to illustrate the **Campnet** dataset to see if your visualization matches **Figure 2.3** in the book

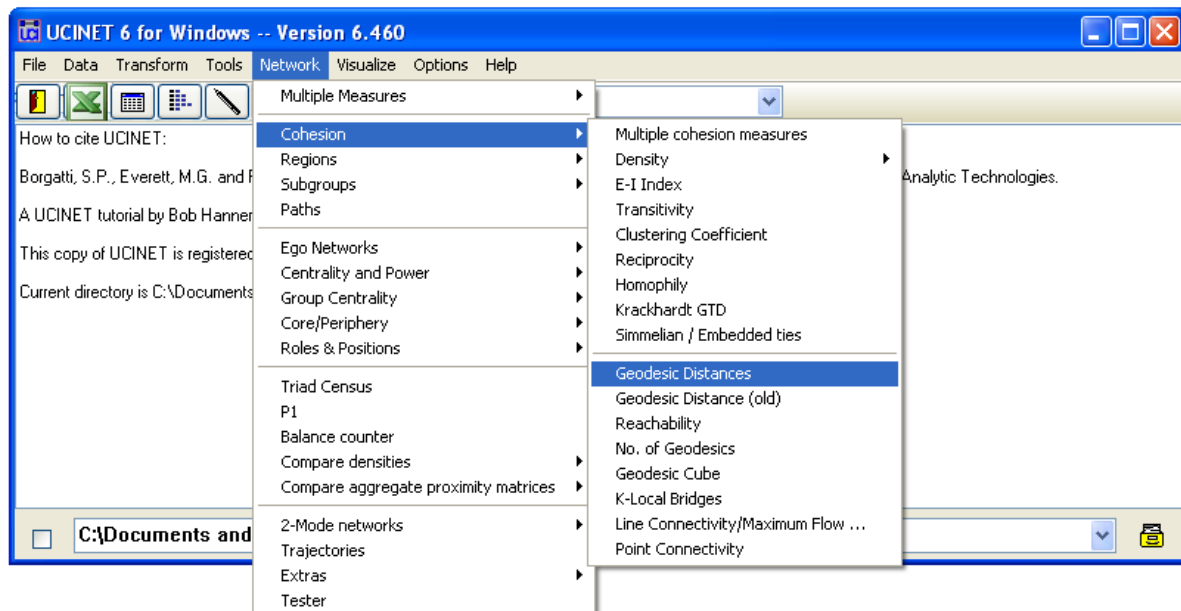
Section 2.4 Adjacency Matrix

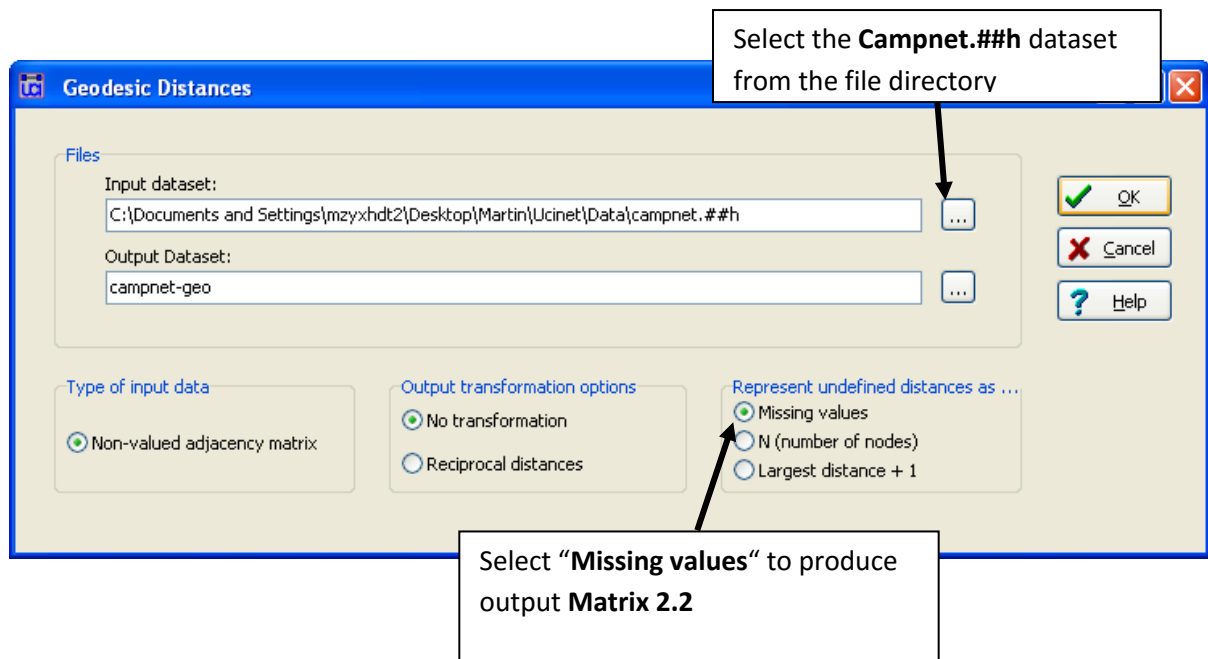
To display the Matrix 2.1 and 2.2 open the UCINET “Display” function



Select the dataset **Wiring.##H** and a new window will open. The first Matrix “**RDGAM**” is the adjacency matrix depicted in **Matrix 2.1**.

To produce output **Matrix 2.2** select the Geodesic Distances routine under **Network|Cohesion|Geodesic Distances** which will open a new window

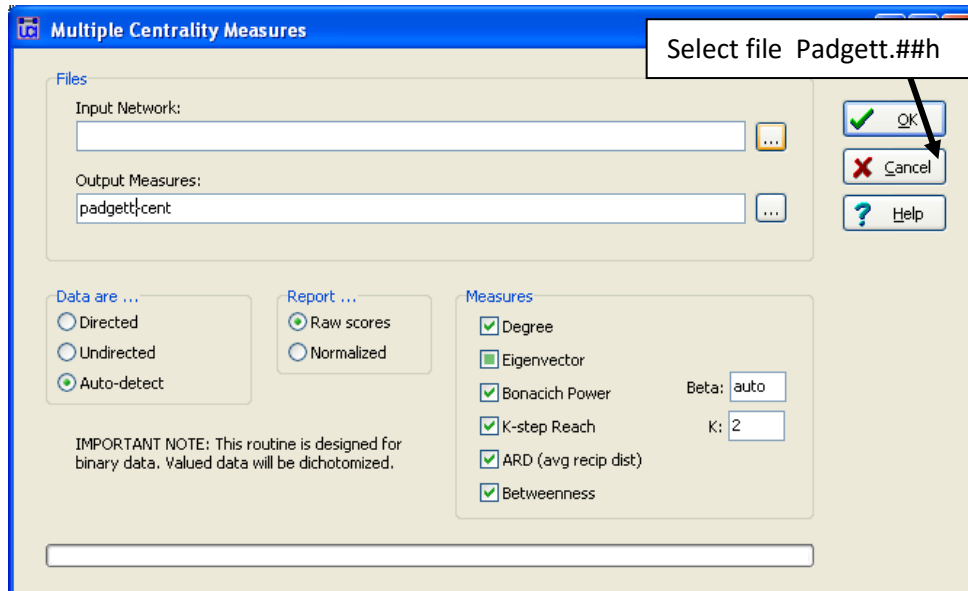




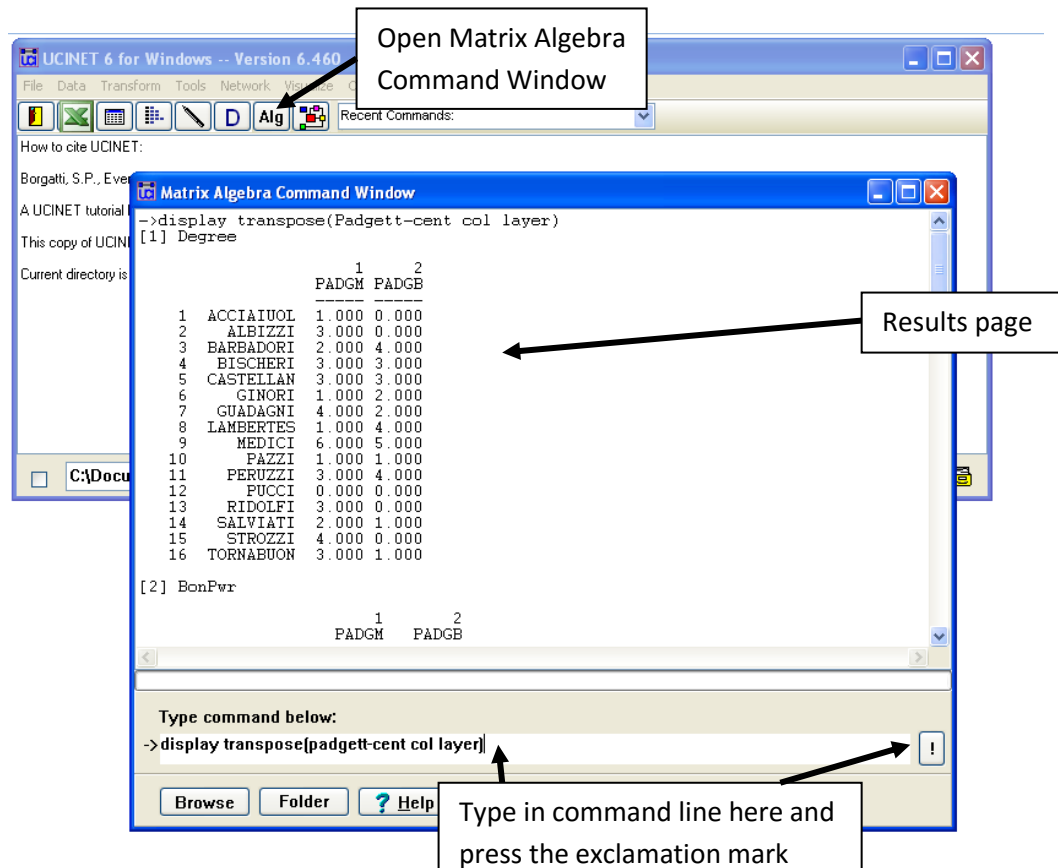
To display **Matrix 2.3** simply follow the steps above.

Section 5.4.1 Transposing

To run the centrality routine described on page 112, open UCINET **Network|Centrality and Power|Multiple Measures** and select the **Padgett.###h** file from the file directory. The measures should be selected as depicted below and the results will be displayed in a new window.

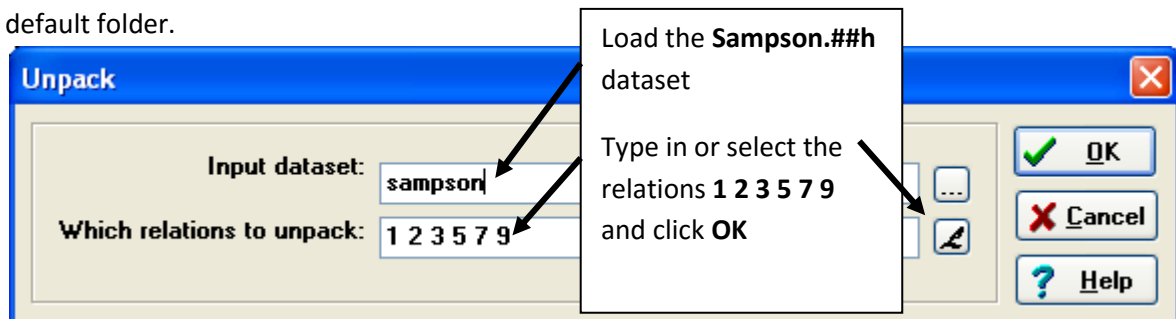


Open the **Matrix Algebra Command Window** **ALG** and type in the command line “**display transpose(Padgett-cent col layer)**”. Click the exclamation mark and the results will appear in the Matrix Algebra Command Window when scrolling down.



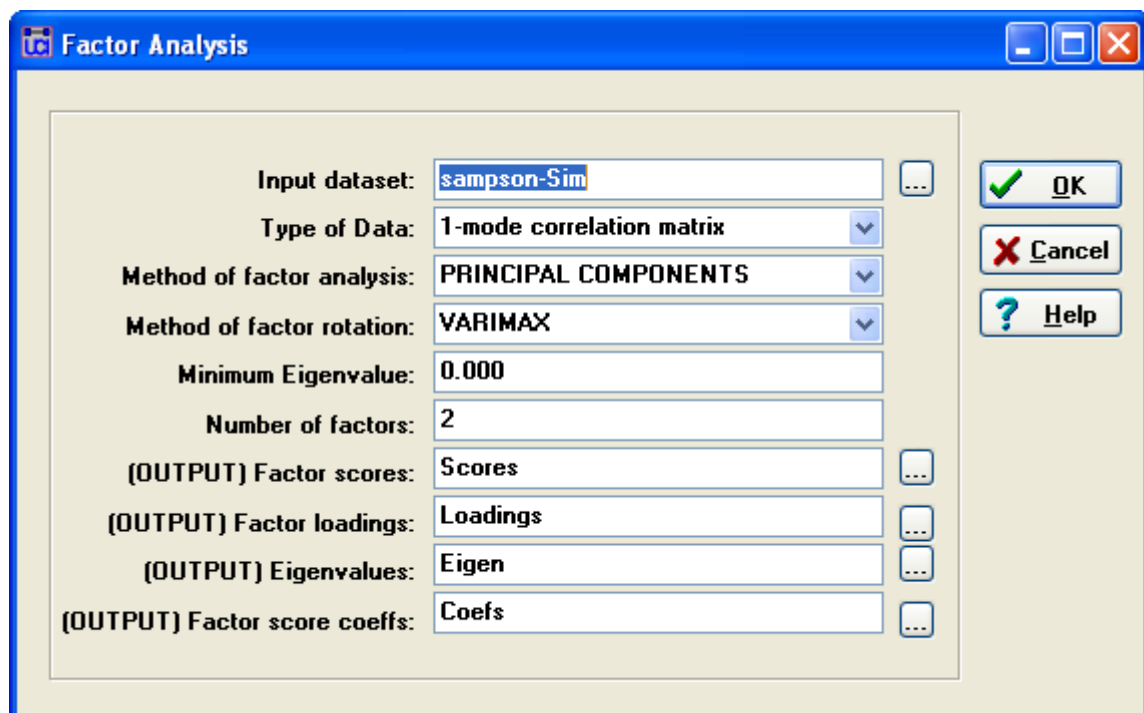
Section 5.4.5 Combining Relations

To create a new relation called positive, first unpack the **Sampson.##h** dataset: go to Data|Unpack and select the **Sampson.##h** file. In the box named “Which relations to unpack” enter **1 2 3 5 7 9** (or select from the dropdown box) and click OK. The individual relations are automatically saved in your default folder.



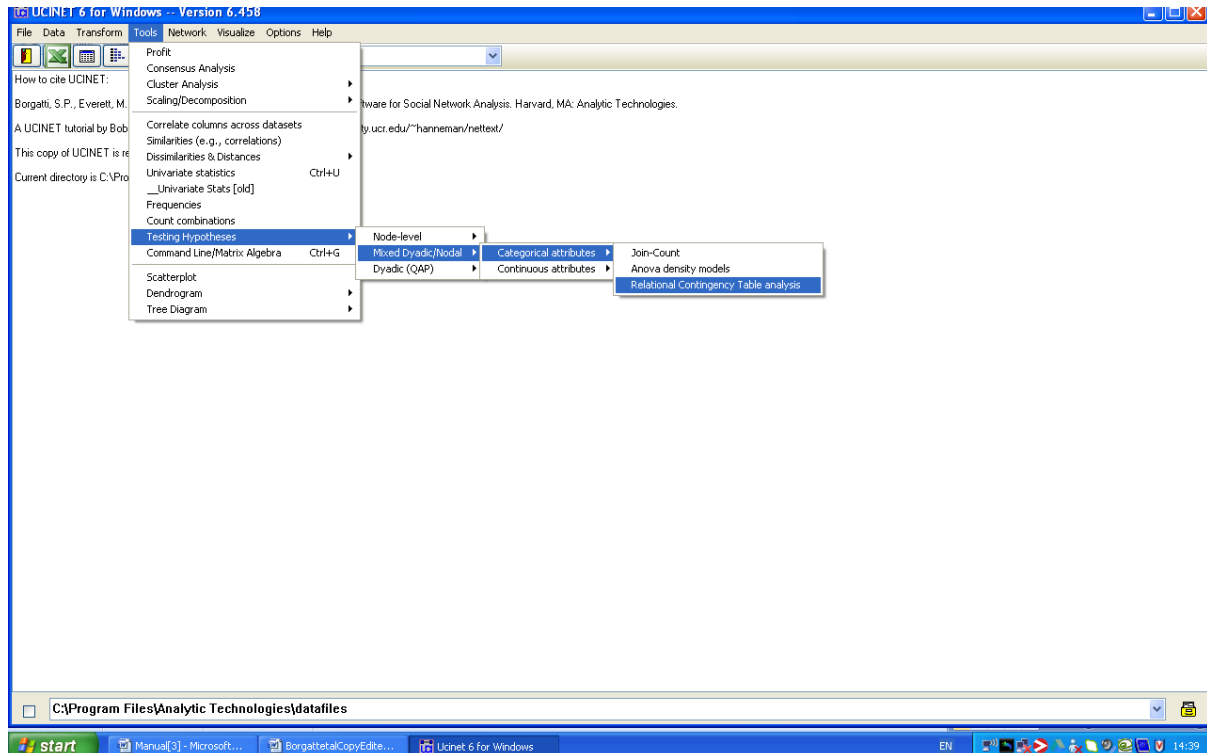
Then open the Matrix Algebra Command Window and type in the command **→positive = add(samplk1 samplk2 samplk3 sampes sampin samprr)**. The new relation is saved as **positive.##h** in your default folder.

To run the Factor Analysis you will need to correlate the matrices. Go to **Tools|Similarities (e.g., correlations)** and load the **Sampson.##h** data. Select the options **correlation** and **MATRICES** and click OK. Then go to **Tools|Scaling/ Decomposition|Factor Analysis** and load the **Sampson.##h** file. Select the options “**1-mode correlation matrix**”, “**PRINCIPAL COMPONENTS**” and “**VARIMAX**” and set the “**Number of factors**” to **2**. Click OK and your results will open in a new window and are headed “**Rotated Factor Loadings**”.

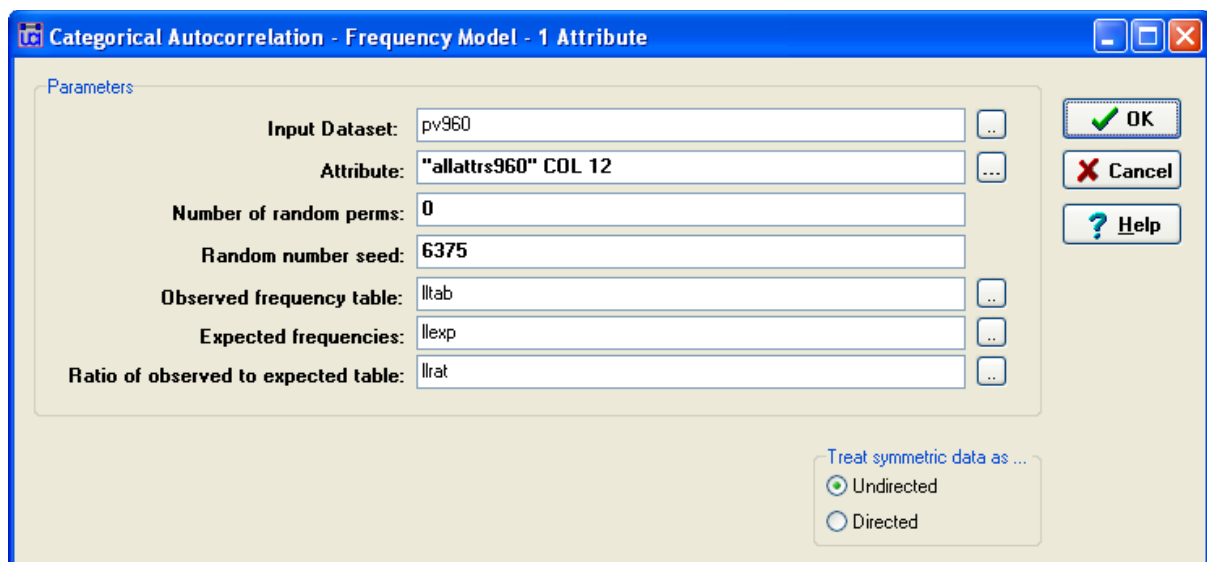


Section 5.4.6 Combining Nodes

There is no procedure to normalize by expected values as shown in matrix 5.7 but this is an output given in another routine Tools|Testing Hypothesis|Missed dyadic/Nodal|Categorical Attributes|Relational Contingency Table analysis



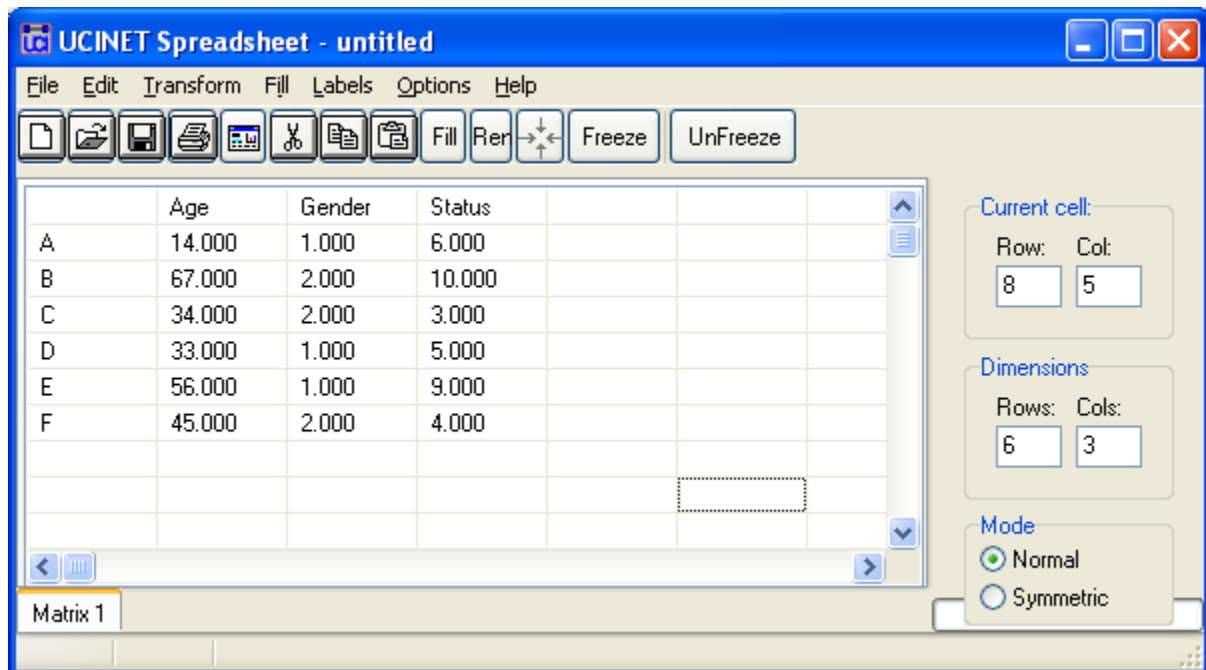
The dataset is PV960 and the departments are in column 12 of the attribute dataset Allattrs960 as we do not want to do the permutation test we set the number of random permutations to 0.



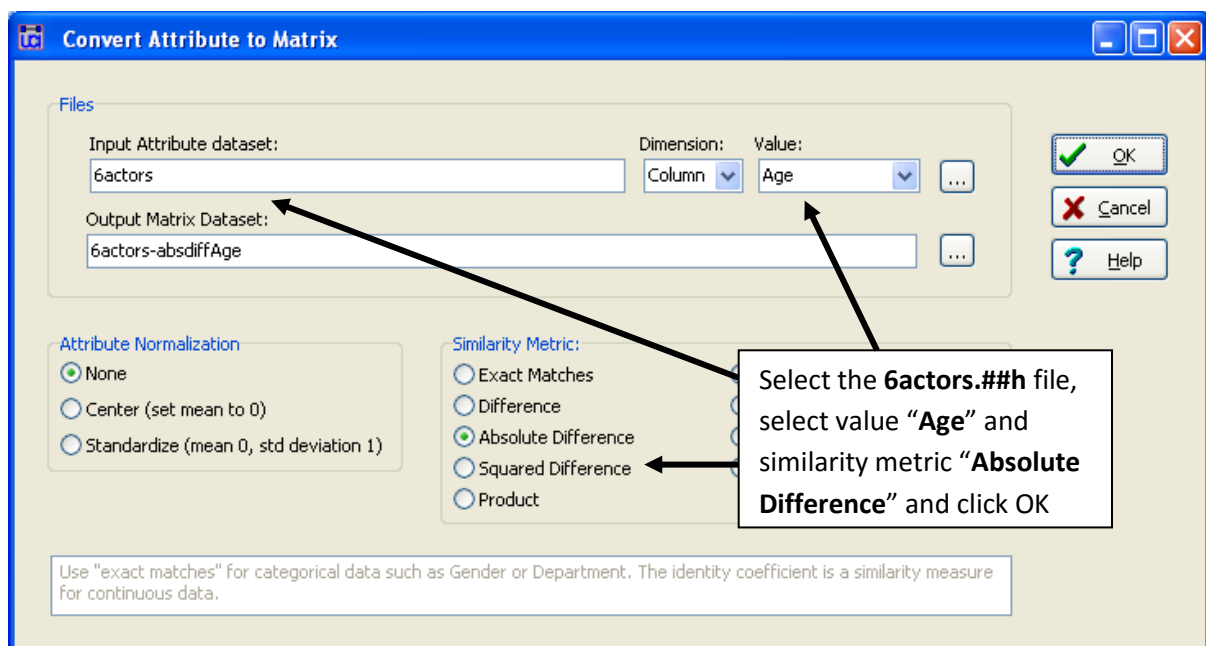
The third matrix in the output is Matrix 5.7 and it is saved in a file called llrat if this is dichotomised at a value of 1.4 and the labels added and then viewed in Netdraw we obtain the network shown in Figure 5.12.

Section 5.8 Converting Attributes to Matrices

To run this routine, we must first create attribute datasets in UCINET. To do this open the Matrix spreadsheet editor and enter the information shown below.



Save this attribute file as 6actors.##h. To convert the attributes in matrices, open the procedure Data|Attribute to matrix. Select the file 6actors and select “Age” and “Absolute Difference” to generate Figure 5.14. Change the Value and Similarity Metric as given in the book to generate Figure 5.15 and 5.16.



Section 5.9 Data Export

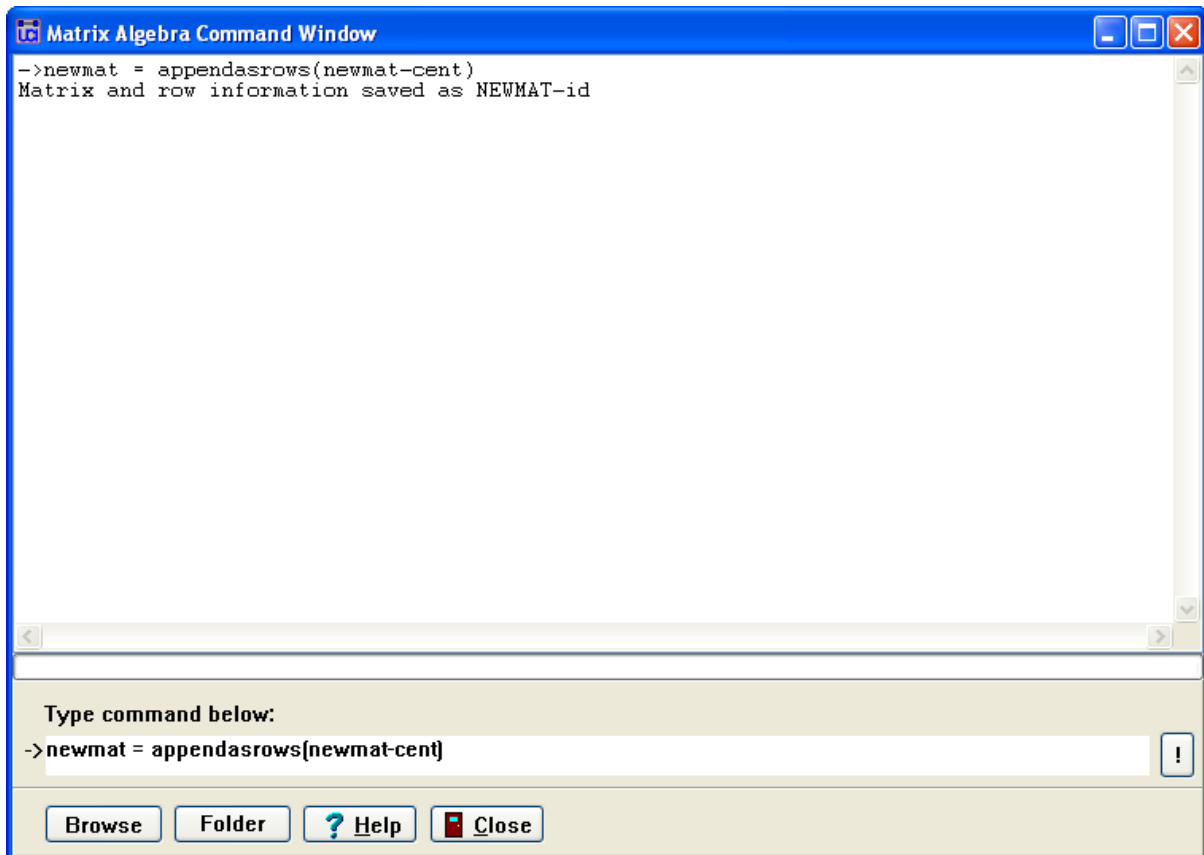
To obtain these results we first need to dichotomise the NEWFRAT data. The data contains rankings and we want to replace the top 5 choices by a one and the rest by a zero. We use Transform|Dichotomise selecting NEWFRAT as the data choosing the k less than or equal to rule and putting 5 in the value box. Note the name of the output dataset is generated automatically as follows.

The screenshot shows the 'Dichotomize' dialog box. In the 'Files' section, 'Input dataset (X):' is set to 'NEWFRAT' and 'Output dataset (Y):' is set to 'NEWFRAT_LE_5'. In the 'Dichotomization rule' section, the rule is 'If x(i,j) Less Than or Equal to value 5 then y(i,j) = 1 else y(i,j) = 0'. In the 'Diagonals of output (Y) matrix:' section, the option 'Set to "else" value' is selected. The 'OK' button is highlighted.

We then run the multiple centrality routine found under Network|Multiple Measures|Node level and we treat the data as undirected by clicking the radio button as follows

The screenshot shows the 'Multiple Centrality Measures' dialog box. In the 'Files' section, 'Input Network:' is set to 'NEWFRAT_LE_5' and 'Output Measures:' is set to 'newmat-cent'. In the 'Data are ...' section, the 'Undirected' radio button is selected. In the 'Report ...' section, the 'Raw scores' radio button is selected. In the 'Measures' section, the following measures are checked: Degree, Eigenvector, Bonacich Power, K-step Reach, ARD (avg recip dist), and Betweenness. The 'Beta' is set to 'auto' and 'K' is set to '2'. An 'IMPORTANT NOTE' at the bottom states: 'This routine is designed for binary data. Valued data will be dichotomized.' The 'OK' button is highlighted.

We then launch the matrix algebra routine and type the command as given in the book and reproduced below



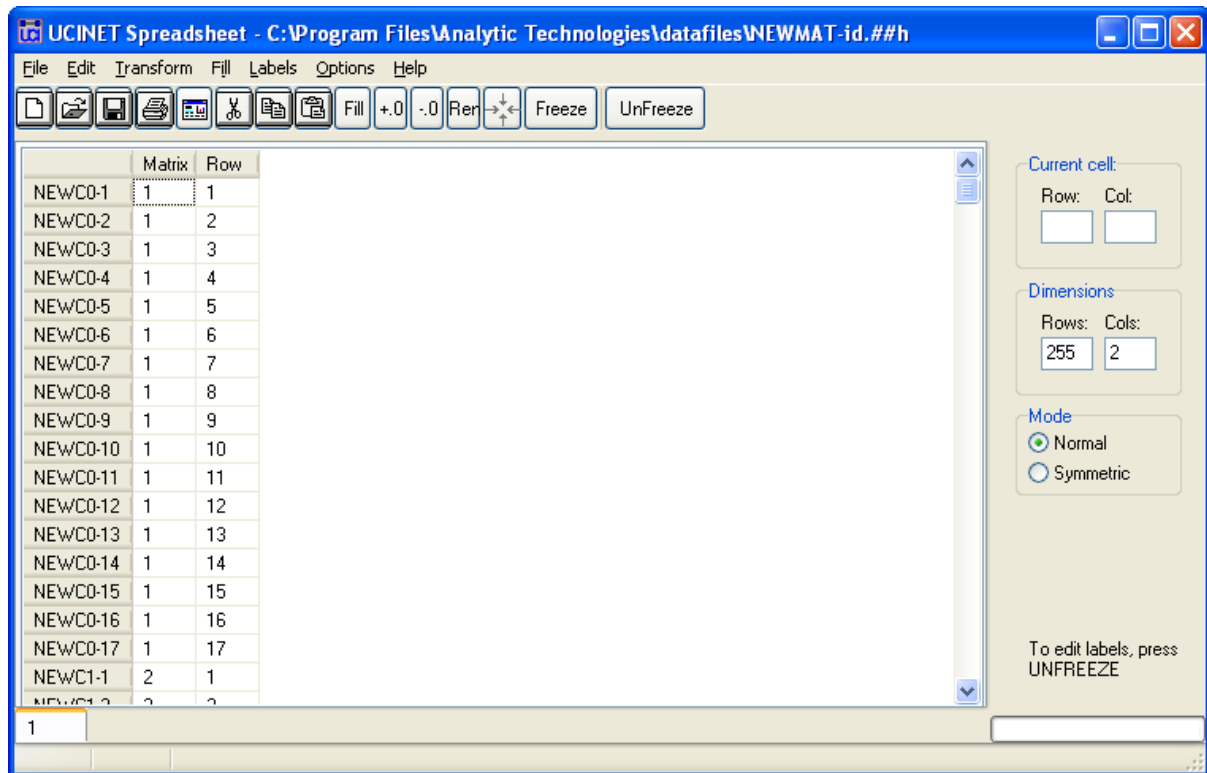
Finally we launch the UCINET spreadsheet editor and load the new file NEWMAT as shown.

The screenshot shows the "UCINET Spreadsheet" window with the file path `C:\Program Files\Analytic Technologies\datafiles\NEWMAT.###h`. The spreadsheet contains the following data:

	Degree	BonPwr	2Step	ARD	Eigenvect	Between
NEWCO-1	6	1219.874	16	11.000	0.193	2.243
NEWCO-2	6	1133.680	15	10.833	0.180	2.058
NEWCO-3	5	1237.819	16	10.500	0.196	0.268
NEWCO-4	5	957.243	16	10.500	0.152	2.179
NEWCO-5	7	1535.068	16	11.500	0.244	1.833
NEWCO-6	7	1281.671	16	11.500	0.203	4.912
NEWCO-7	8	1649.244	16	12.000	0.262	4.064
NEWCO-8	6	1246.119	15	10.833	0.198	1.493
NEWCO-9	8	1672.290	16	12.000	0.265	4.233
NEWCO-10	9	1751.727	16	12.500	0.278	6.758
NEWCO-11	10	2005.343	16	13.000	0.318	7.625
NEWCO-12	10	2070.653	16	13.000	0.328	5.455
NEWCO-13	6	1169.956	16	11.000	0.185	2.233
NEWCO-14	6	1157.809	16	11.000	0.184	2.413
NEWCO-15	9	1688.712	16	12.500	0.268	8.555
NEWCO-16	6	1231.343	16	11.000	0.195	1.971
NEWCO-17	12	2240.207	16	14.000	0.355	15.705
NEWCO-18	8	1534.965	16	12.000	0.242	4.883
NEWCO-19	6	1200.953	16	11.000	0.205	1.702

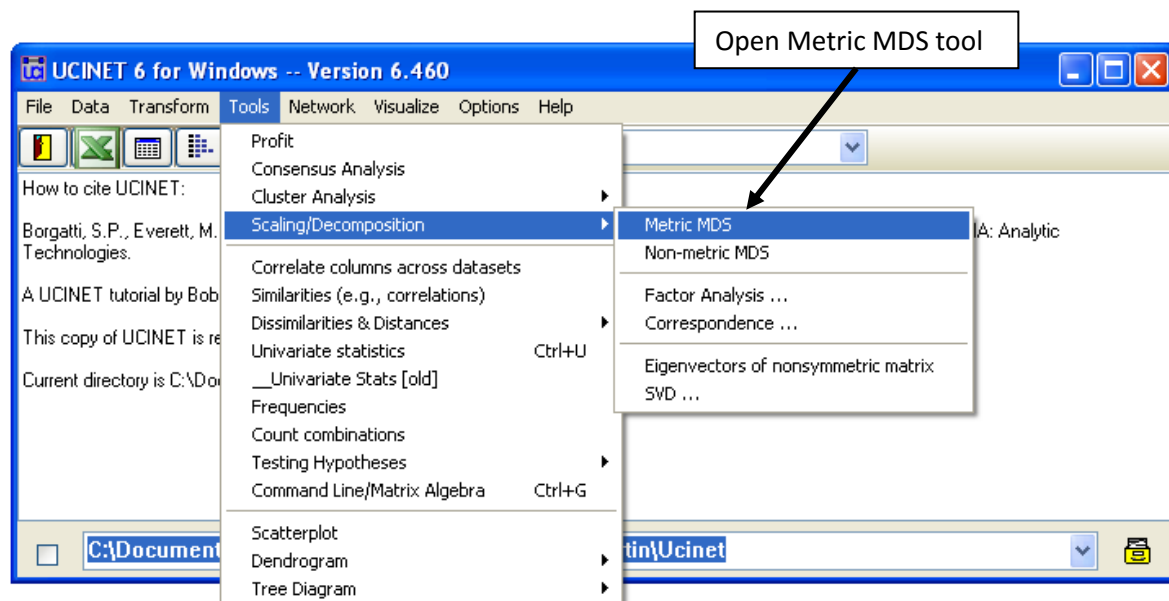
On the right side of the window, there are controls for "Current cell:" (Row: , Col:), "Dimensions:" (Rows: 255, Cols: 6), and "Mode:" (Normal selected, Symmetric). At the bottom right, it says "To edit labels, press UNFREEZE".

We can also view the created file NEWMAT-id in the editor as follows

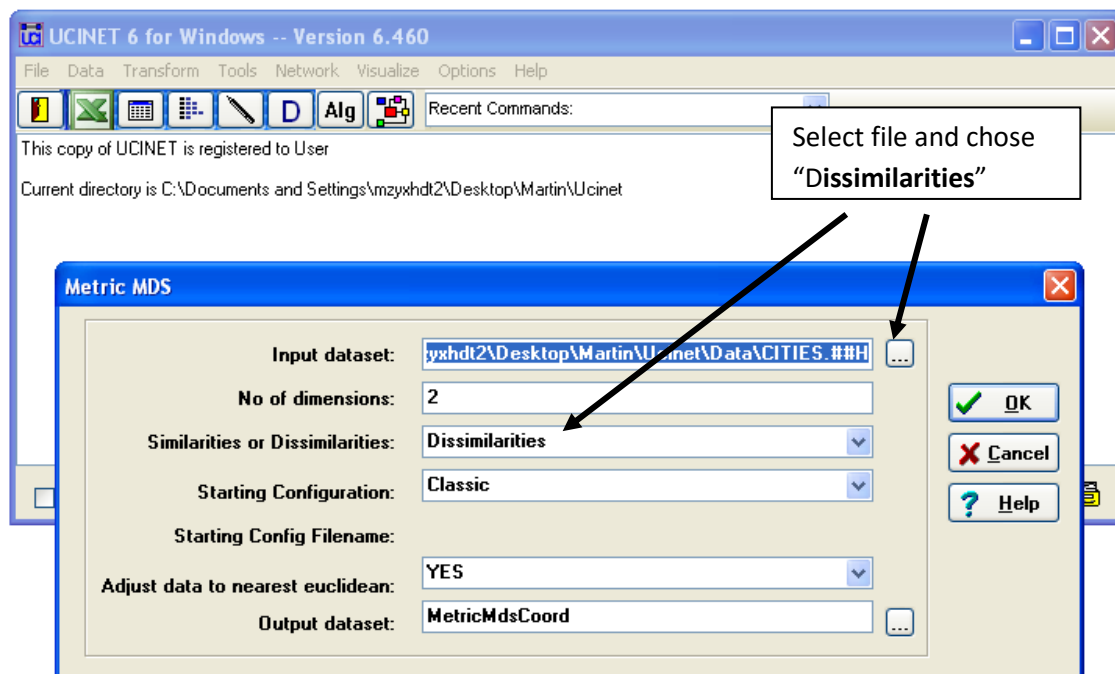


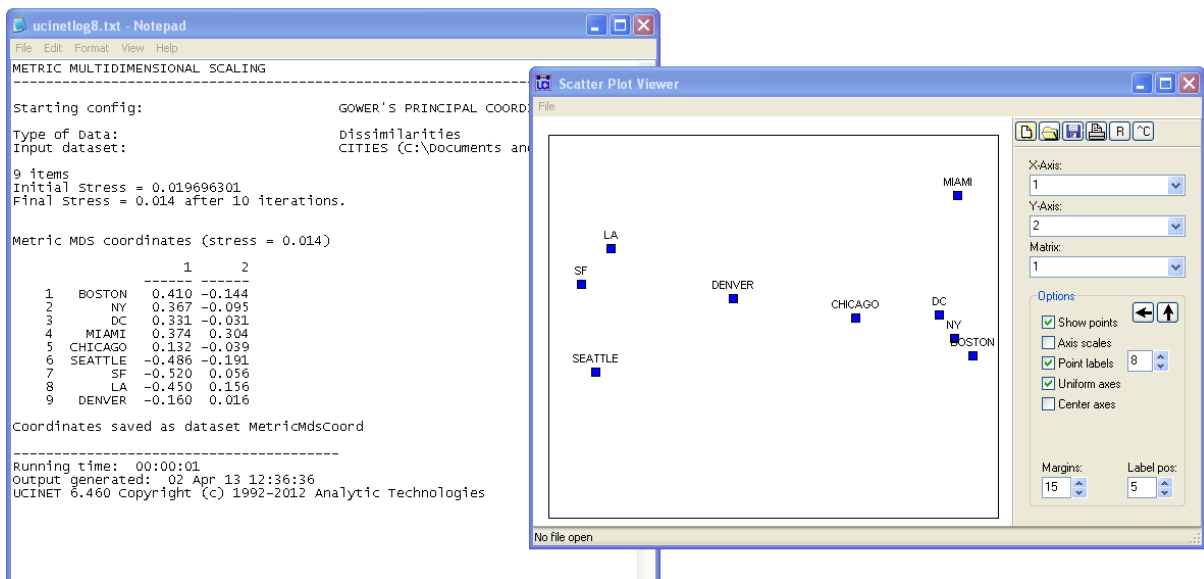
Section 6.2 Multidimensional Scaling

Open the MDS tool in UCINET: **Tools | Scaling/Composition | Metric MDS**



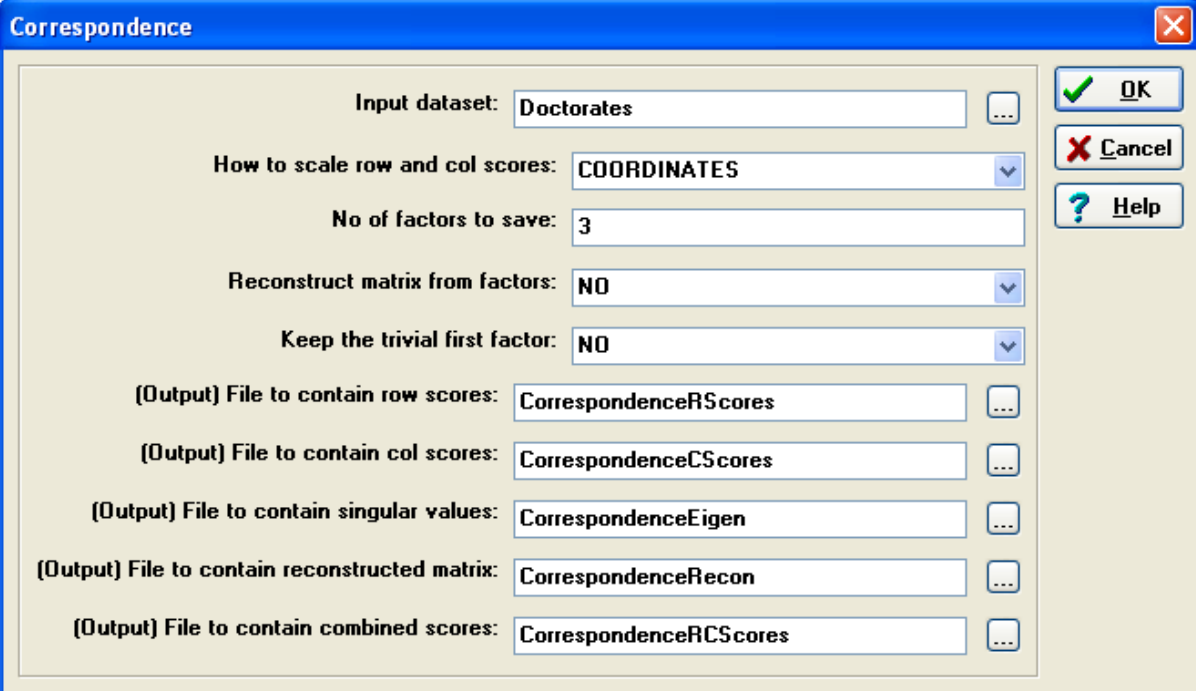
Select the file **CITIES.##h** from the file directory. Keep the number of dimensions at two, but chose the “**Dissimilarities**” option. Click OK and two new windows will open: a UCINET log file which gives you values for “**stress**” and the metric MDS coordinates and a “**Scatter Plot Viewer**” which maps the results as shown in **Figure 6.1**





Section 6.3 Correspondence Analysis

To reproduce Figure 6.2 run Tools|Scaling/Decomposition|Correspondence on the dataset leaving all the defaults alone.



Correspondence

Input dataset: ...

How to scale row and col scores: ▾

No of factors to save:

Reconstruct matrix from factors: ▾

Keep the trivial first factor: ▾

(Output) File to contain row scores: ...

(Output) File to contain col scores: ...

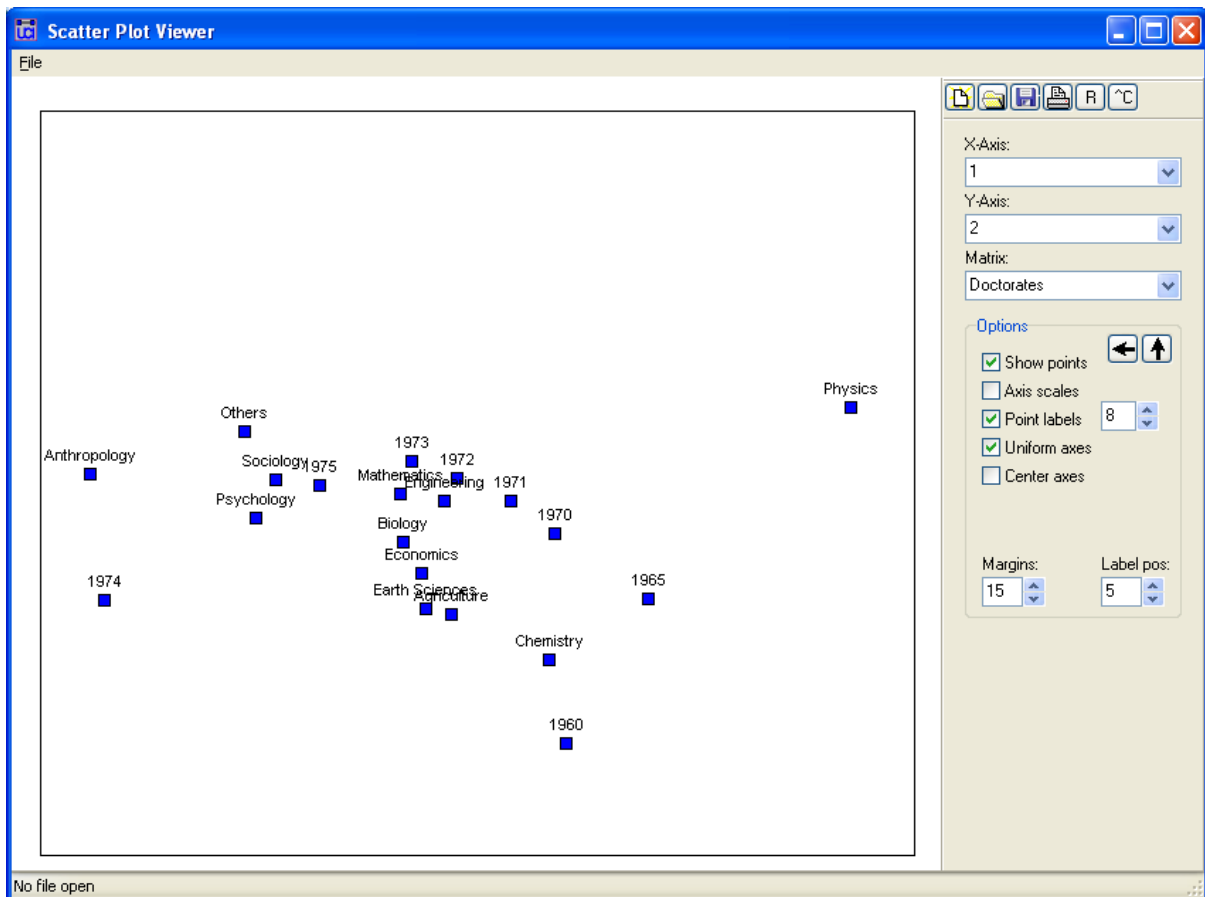
(Output) File to contain singular values: ...

(Output) File to contain reconstructed matrix: ...

(Output) File to contain combined scores: ...

OK Cancel Help

This produces the following as shown in the book.



Section 6.4 Hierarchical Clustering

To run the **Hierarchical Clustering** routine open the tool under **Tools | Cluster Analysis | Hierarchical...** Select your Input dataset **CITIES.##h** and select the **Dissimilarities** option.

Johnson's Hierarchical Clustering

Data

Input dataset: .mzyxhdt2\Desktop\Martin\Scinet\Data\CITIES.##h

Similarities or Dissimilarities: Dissimilarities

Output Partition Matrix: Part

Output Ultrametric Matrix (if desired): None

Parameters

Method: WTD_AVERAGE (average between all pairs)

Graphical dendrogram: Dendrogram

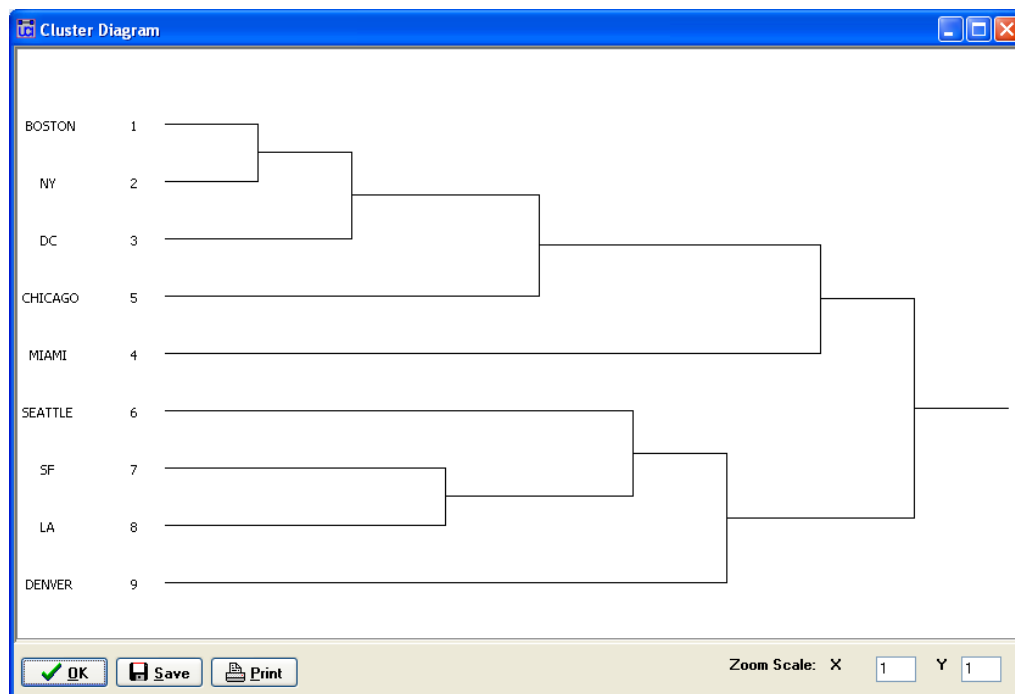
Textual dendrogram: Landscape

Maximum label length: 15

Compute ultrametric proximity matrix: NO

Open the **CITIES.##h** file and select **Dissimilarities**

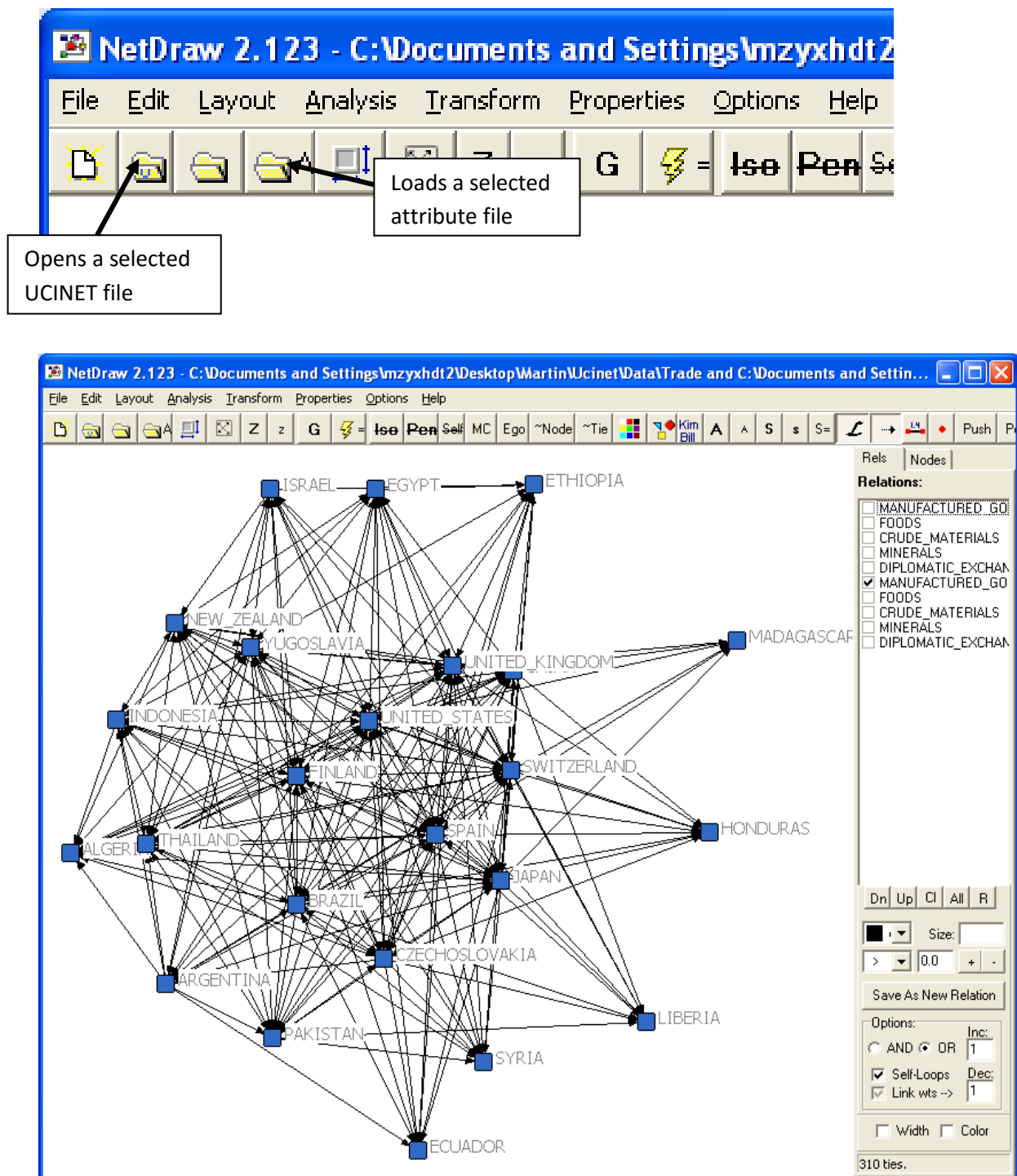
Two new windows will display the output in **Figure 6.5** (**Note:** the order of cities may change, but the clustering remains the same). The Second window will depict the **cluster diagram** shown below which is another way of illustrating the clusters and mergers similar to Figure 6.5.



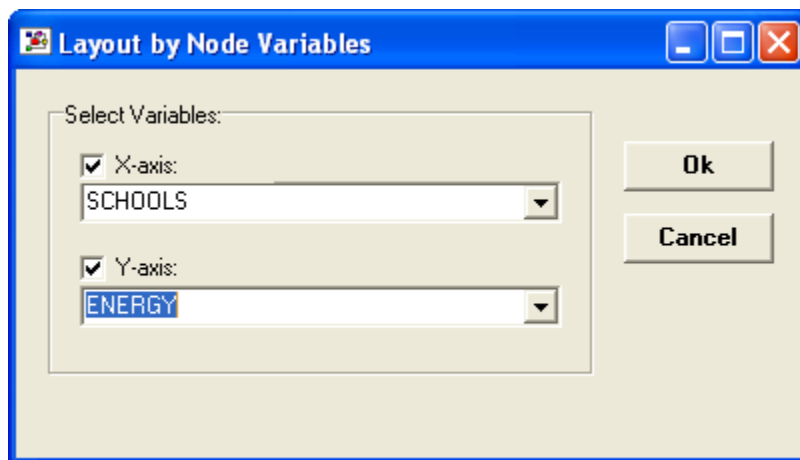
Section 7.2 Layout

7.2.1 Attribute-based scatter plot:

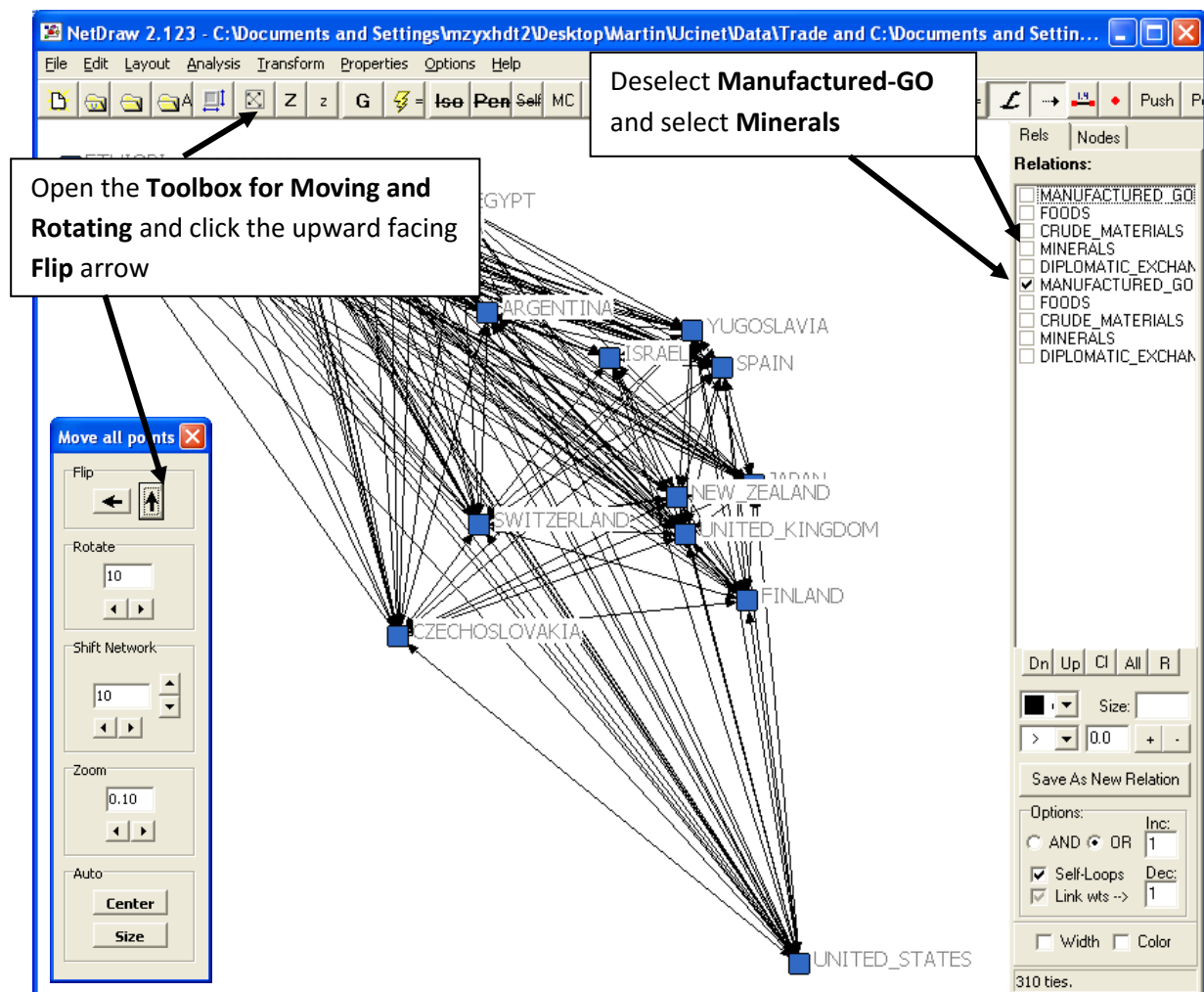
To produce the Attribute-based scatter plot depicted in **Figure 7.3**, open **NetDraw** and open the files **Trade.##h** using the **File|Open|Ucinet dataset|Network** and corresponding attributes **Trade_attribute.##h** using the **File|Open|Ucinet dataset|Attribute data** (you can also simply click the open file buttons marked “u” and “A” in the menu. The output is depicted below.



Then select the attributes as coordinates option from the **Layout|Attribs as Coordinates** which will open the following window. Select **Schools** on the X-Axis and **Energy** on the Y-Axis and click okay. The output is shown below.



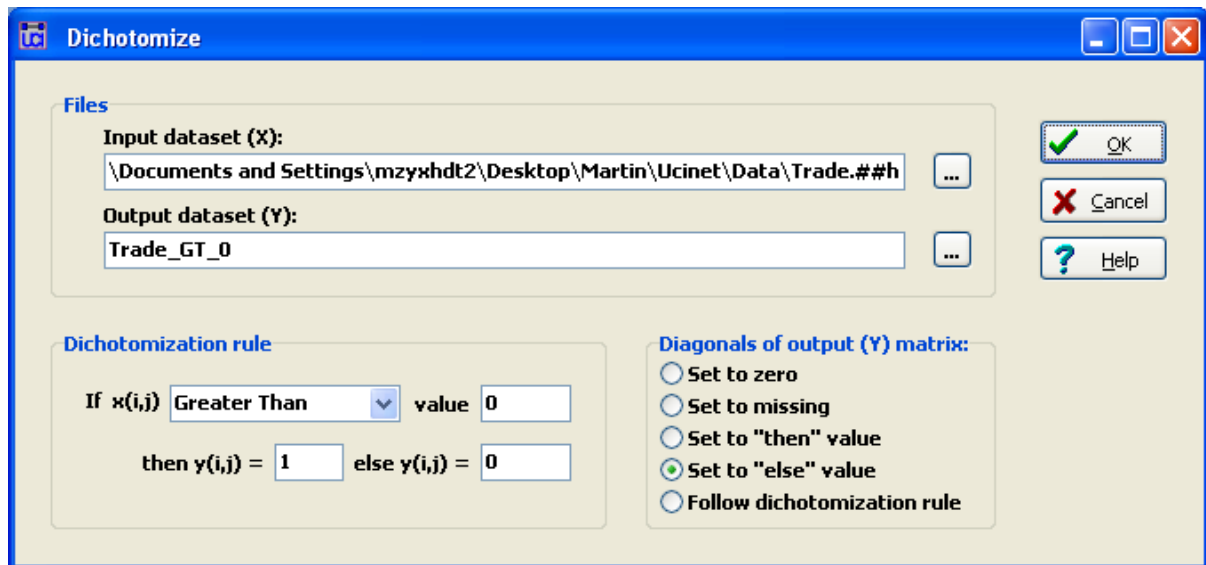
This picture displayed below shows an attribute-based scatter plot for the **Trade.##h** network and the attribute selections Schools and Energy. However you may recognise that it is not the same picture as in **Figure 7.3**. To get the output shown in 7.3, simply deselect the **Relations** option “**Manufactured-GO**” in the right hand menu and select the “**Minerals**” option instead.



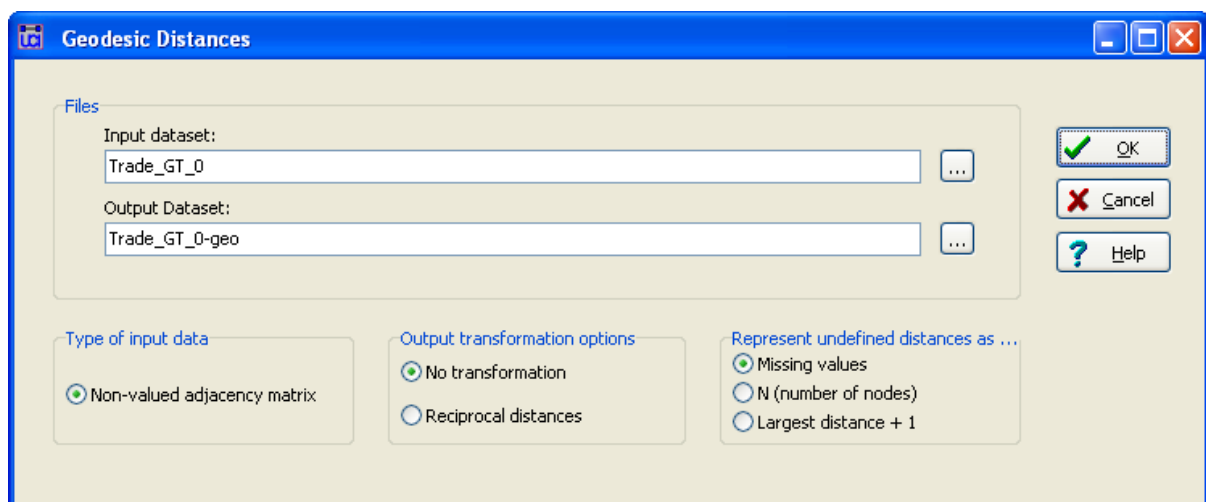
The outcome you generate is upside down so you need to select the **Toolbox for moving, rotating etc.** and click the upward facing arrow and you will see the same output as shown in **Figure 7.3**

7.2.2 Ordination:

To produce figure 7.5, begin with dichotomizing the **Trade.##h** dataset using the tool **Tranform|Dichotomize** ensuring that the options shown below are selected.



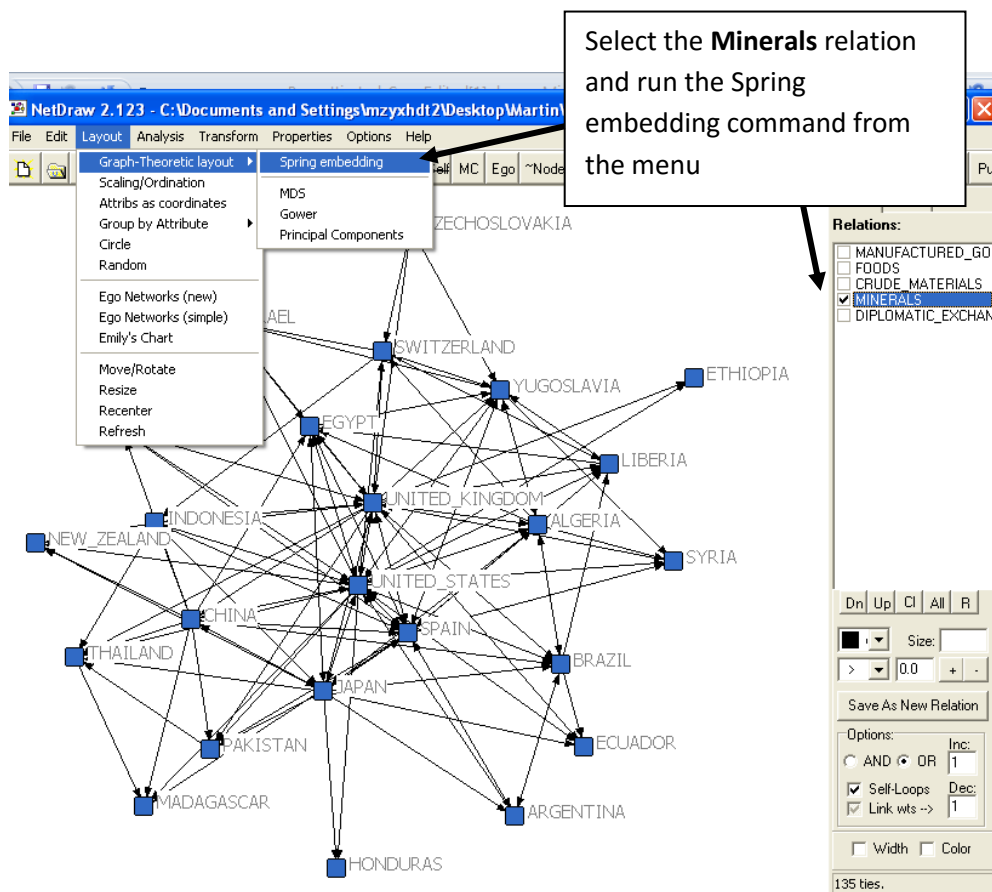
Then run the **Network|Cohesion|Geodesic Distances** routine on the output dataset “**Trade_GT_0**” ensuring that undefined distances are represented as “**Missing Values**”



Now open the new output dataset file “**Trade_GT_0-geo**” in Netdraw

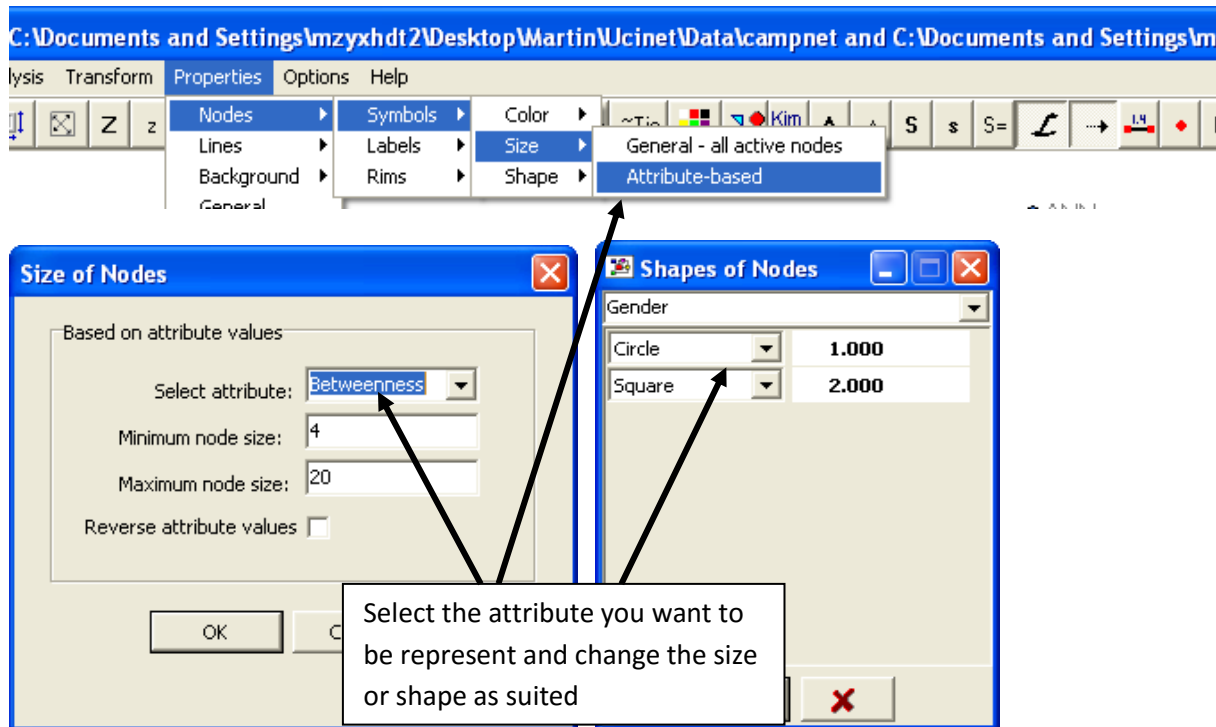
Section 7.2.3 Graph layout algorithms

Figure 7.5 is produced in NetDraw. Load the Trade.##h file in NetDraw and select the Mineral relations in the right-hand menu. Then go to Layout|Graph-Theoretic layout|Spring embedding and click OK. The visualisation will change and become more visible as a result as shown below.



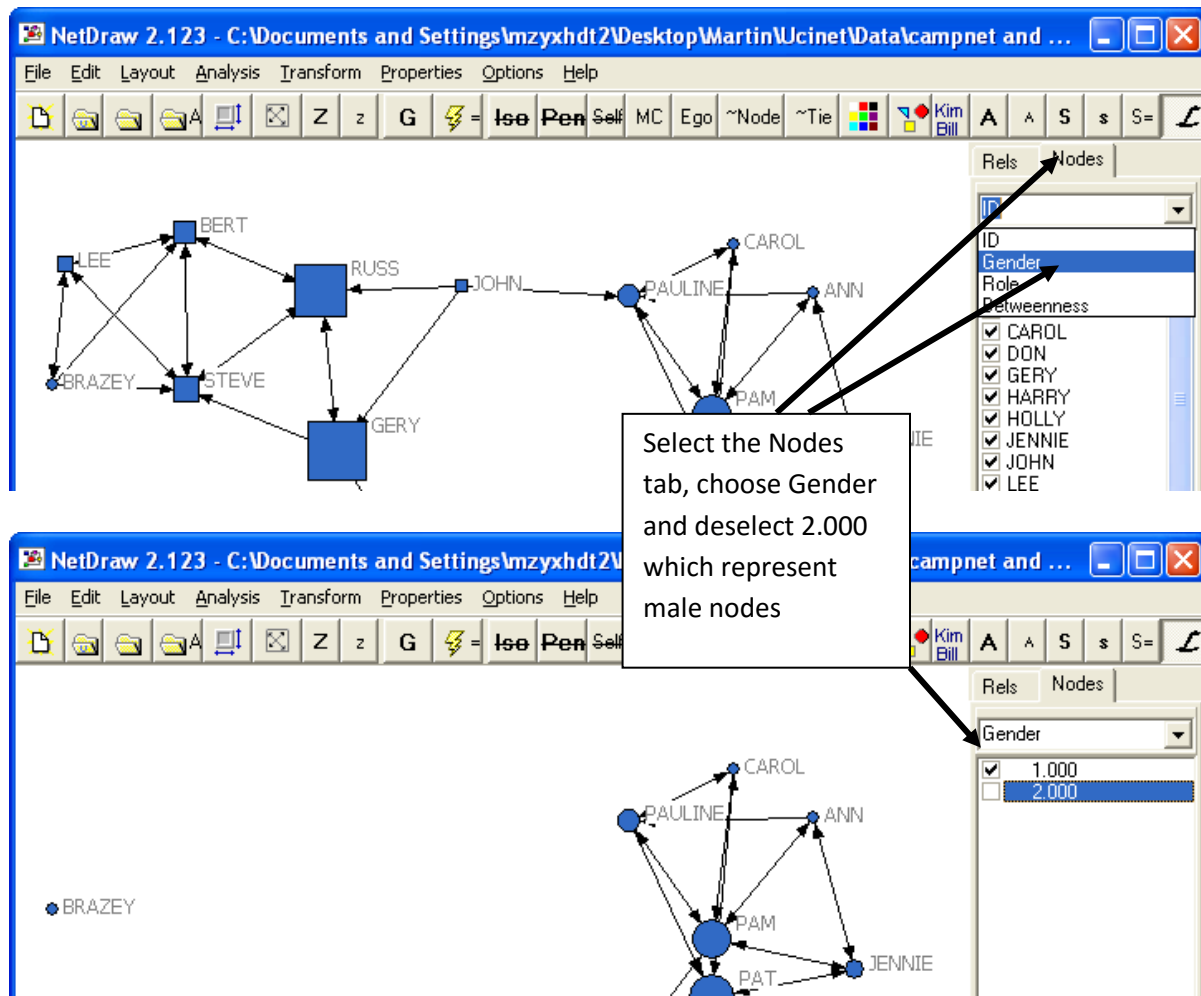
Section 7.3 Embedding Node Attributes

To draw **Figure 7.6** open the **Campnet.##h** (network) and **campattr.##h** (attribute) files; you will see the same figure as **Figure 2.3**. Select **Properties|Nodes|Symbols|Size|Attribute-based** and select **“Betweenness”** from the scroll down menu to visualize the betweenness centrality of each node. Click Okay and you should see the size of the nodes changing. To change the node shape, repeat the process opening **Properties|Nodes|Symbols|Shape|Attribute-based** and select gender.



Section 7.4 Node Filtering

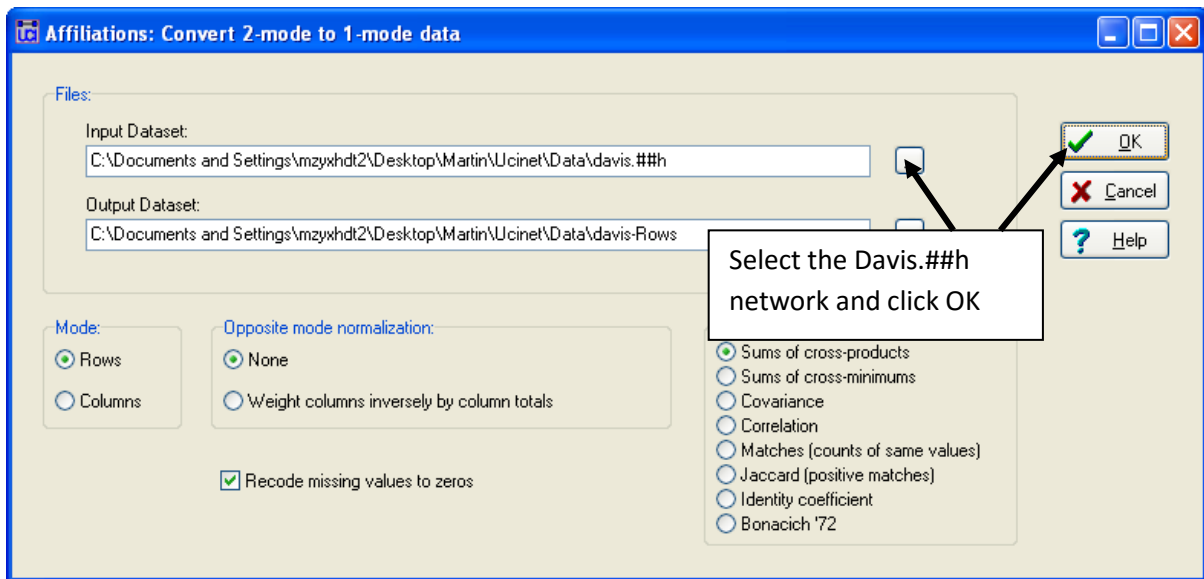
To deselect males to be shown in the network, simply select the “**Nodes**” tab in the upper right hand corner, select **Gender** from the menu and deselect “**2.000**” .



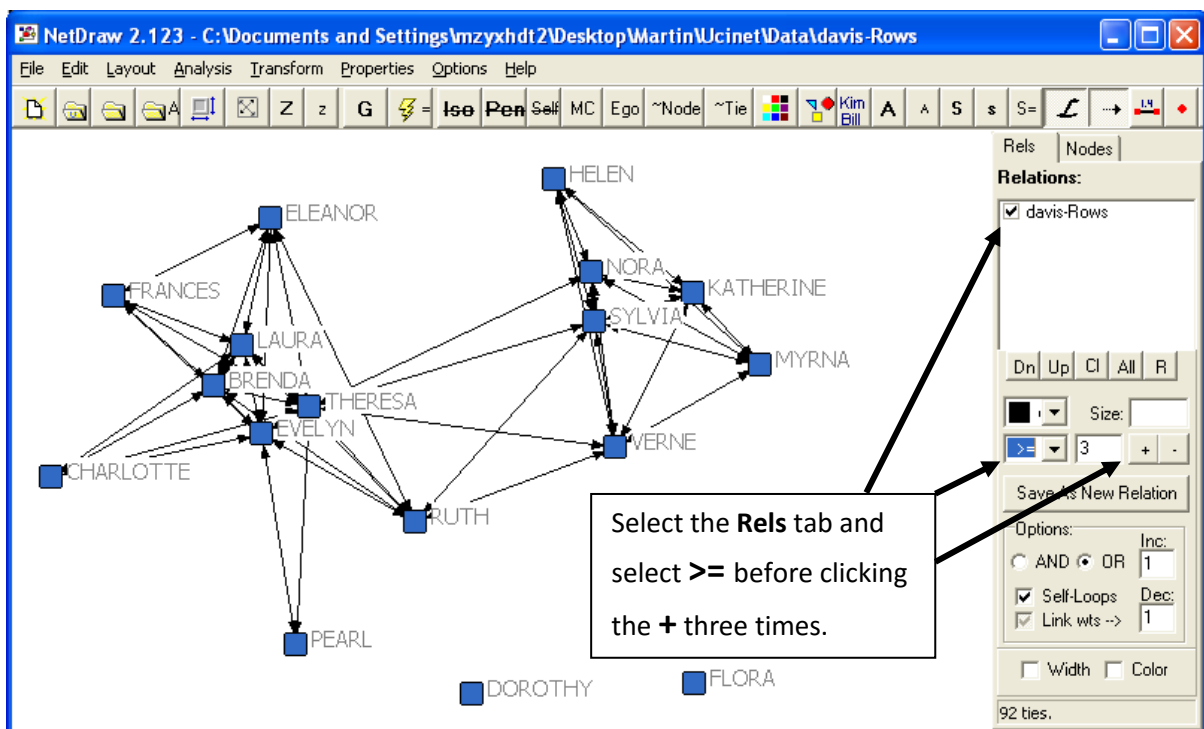
Section 7.6 Embedding Tie Characteristics

7.6.1 Tie Strength

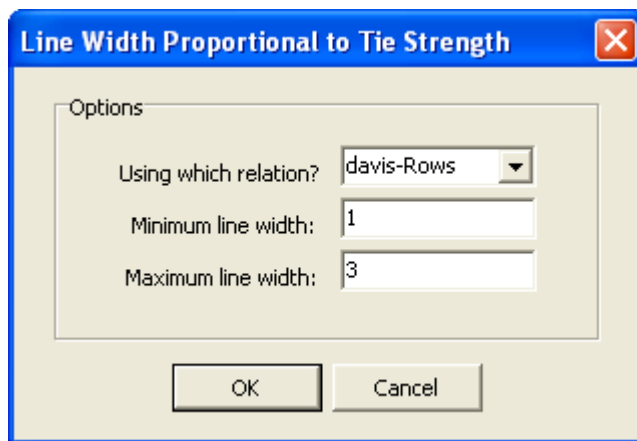
To transform the two-mode **Davis.##h** women-events dataset into a one-mode woman-by-woman dataset run **data|affiliations (2-mode to 1-mode)** and select the **Davis.##h** network. Click okay.



The output will be similar to that depicted in **Figure 7.12**. To suppress weak ties select the **Rels** tab on the right, select “>=” from the drop box and click three times on the + button. This will remove the weak ties and give you the output visible in **Figure 7.13**.

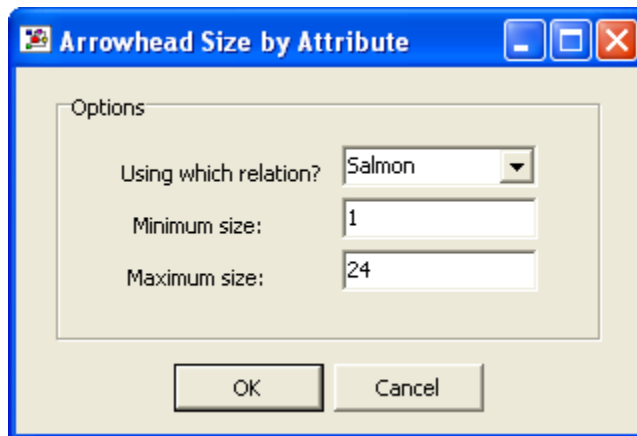


To produce **Figure 7.14** simply restore the weak ties (by re-setting the three to 0) and then open the “Line Width Proportional to Tie Strength” box **Properties|Lines|Size|Tie Strength**. Select the Davis-Rows relation and enter Minimum and Maximum line width (**minimum=1; maximum=3** in this case) and click OK.



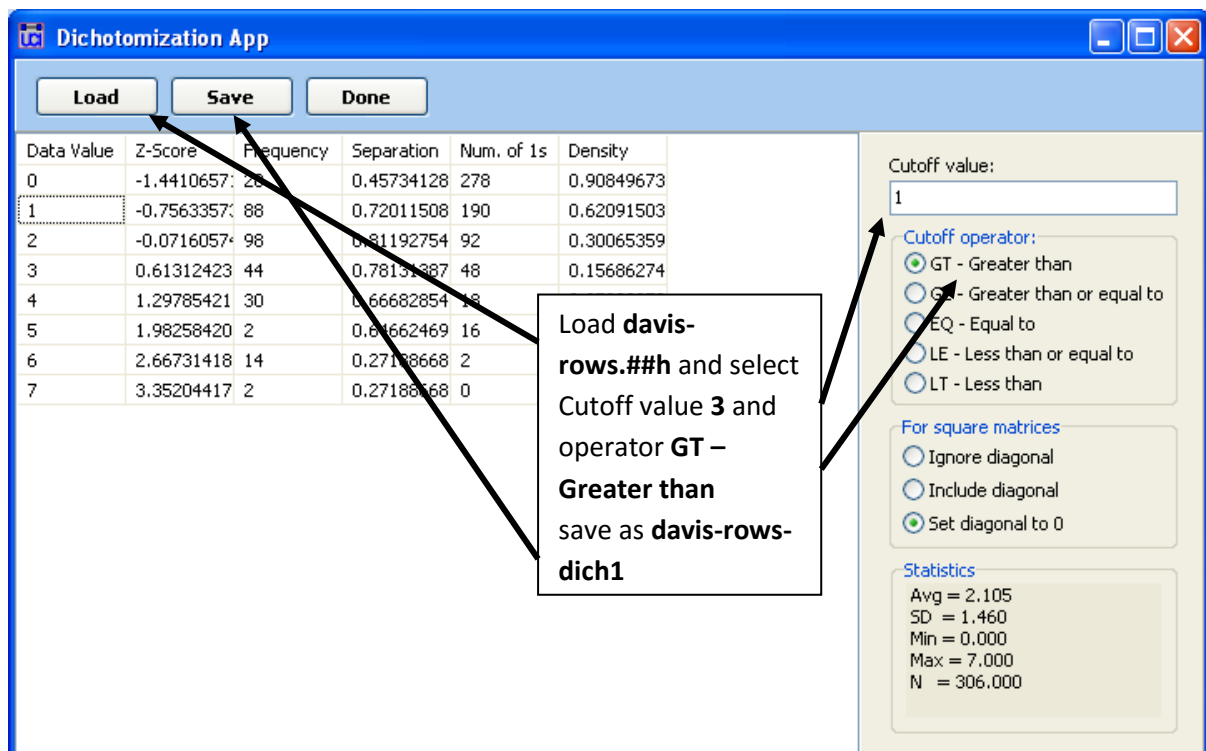
Your network now shows strong ties as thick black lines whereas weak ties remain thin.

To increase arrow head size first load the dataset Salmon into Netdraw turn-off the labels and now select Properties|Lines|Arrow heads|Size|by Ties Strength change the minimum to 1 and the maximum to 24 in the box that opens up as follows.



Clicking OK reproduces Figure 7.15

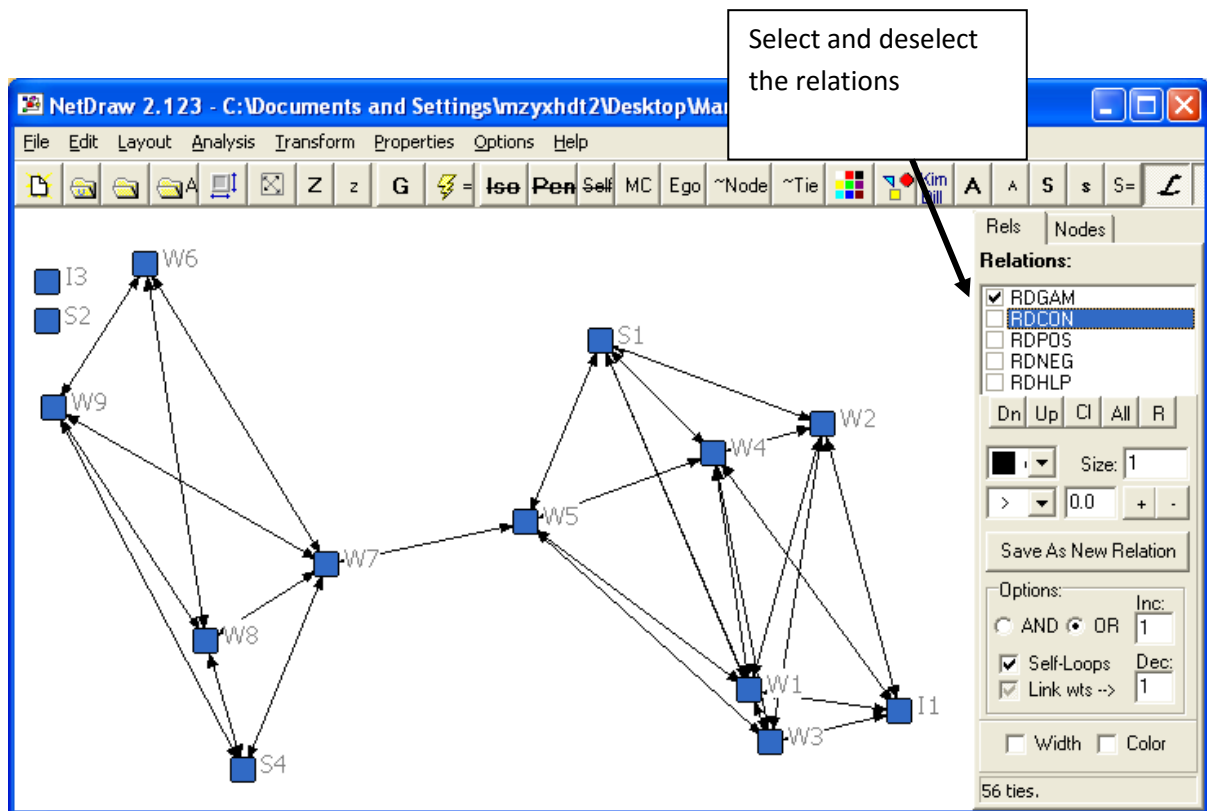
To produce the series of **Figures 7.16a-d** open the two-mode davis-Rows.##h in the Transform|Dichotomize interactive procedure. For 7.16a elect the **Cutoff** value **1** and **GT – Greater than** options and save as **davis-Rows-dich1.##h**. To create 7.16b, 7.16c and 7.16d simply adjust the **Cutoff** value and save as **davis-Rows-dich2.##h** etc.



Open the 4 files in **NetDraw** and select and deselect what network you want to visualise in the **Rels-** menu on the right side.

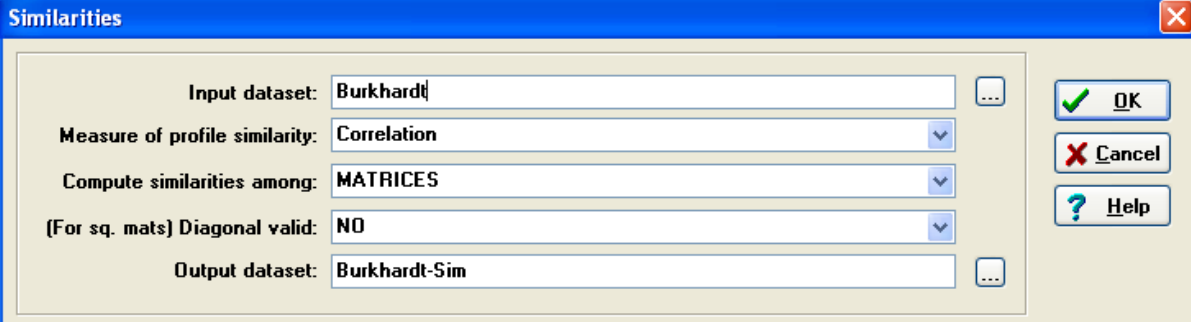
7.6.2 Type of tie

To visualise **Figures 7.17** and **7.18** simply load the **WIRING.##h** file in **NetDraw** and select and deselect the relations you want to visualise. **RDGAM** refers to the Game-playing relation in **Figure 7.17** and **RDCON** visualises **Figure 7.18**.



Section 7.7 Visualizing Network Change

To create the correlation matrix run Tools|Similarities (Eg correlations) on the Burkhardt dataset making sure you select correlation as the measure of similarity and you compute the similarities among matrices as follows. The output will be matrix 7.1




The 'Similarities' dialog box is shown with the following settings:

- Input dataset: Burkhardt
- Measure of profile similarity: Correlation
- Compute similarities among: MATRICES
- (For sq. mats) Diagonal valid: NO
- Output dataset: Burkhardt-Sim

Buttons on the right: OK, Cancel, Help.

To obtain Figure 7.19 submit the matrix Burkhardt-Sim to the metric mds routine under Tools|Scaling/Decomposition|Metric mds



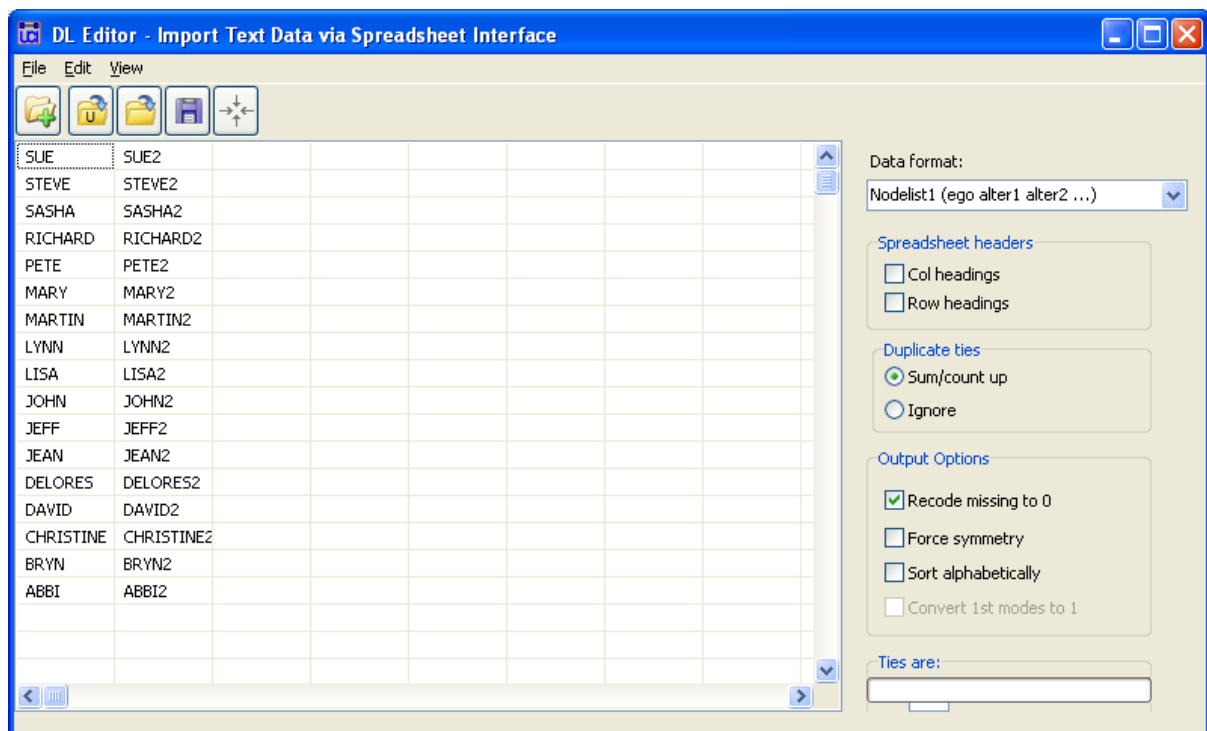
The 'Metric MDS' dialog box is shown with the following settings:

- Input dataset: Burkhardt-Sim
- No of dimensions: 2
- Similarities or Dissimilarities: Similarities
- Starting Configuration: Classic
- Starting Config Filename:
- Adjust data to nearest euclidean: YES
- Output dataset: MetricMdsCoord

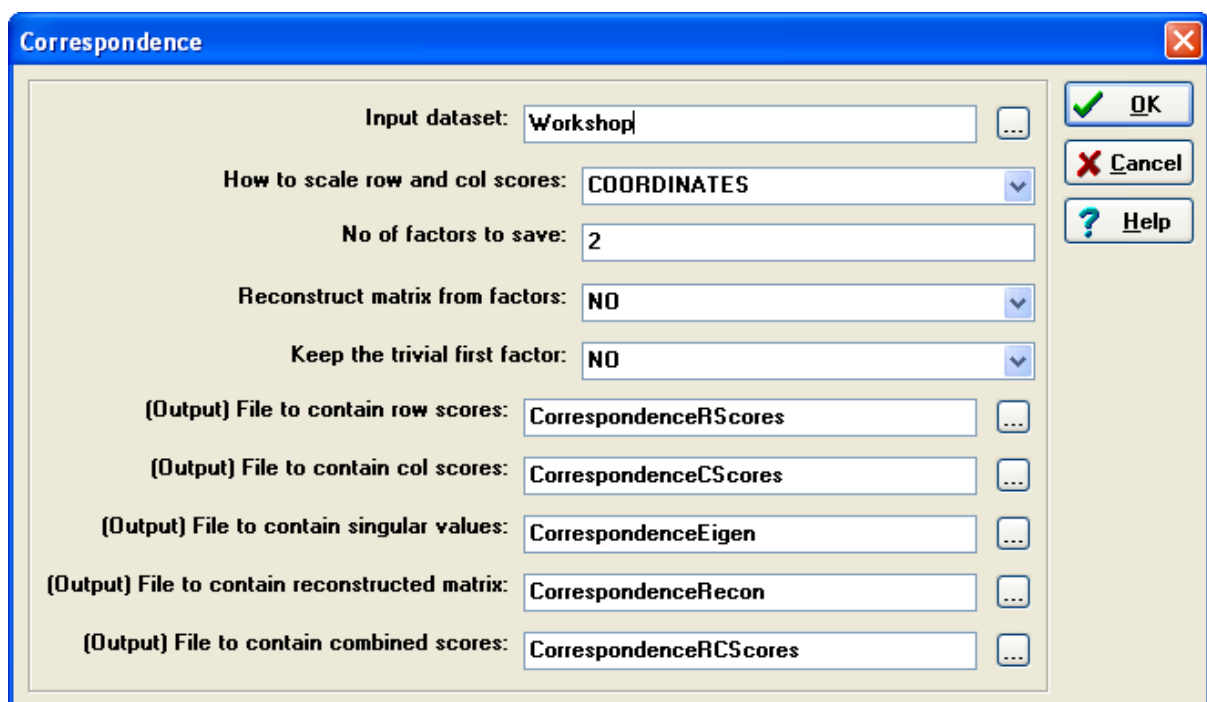
Buttons on the right: OK, Cancel, Help.

To obtain Figures 7.20 and 7.21 simply load Burkhardt into Netdraw and use the Rels tab to see the relations at time T1 and T2 with a cut-off value set at greater than 5.

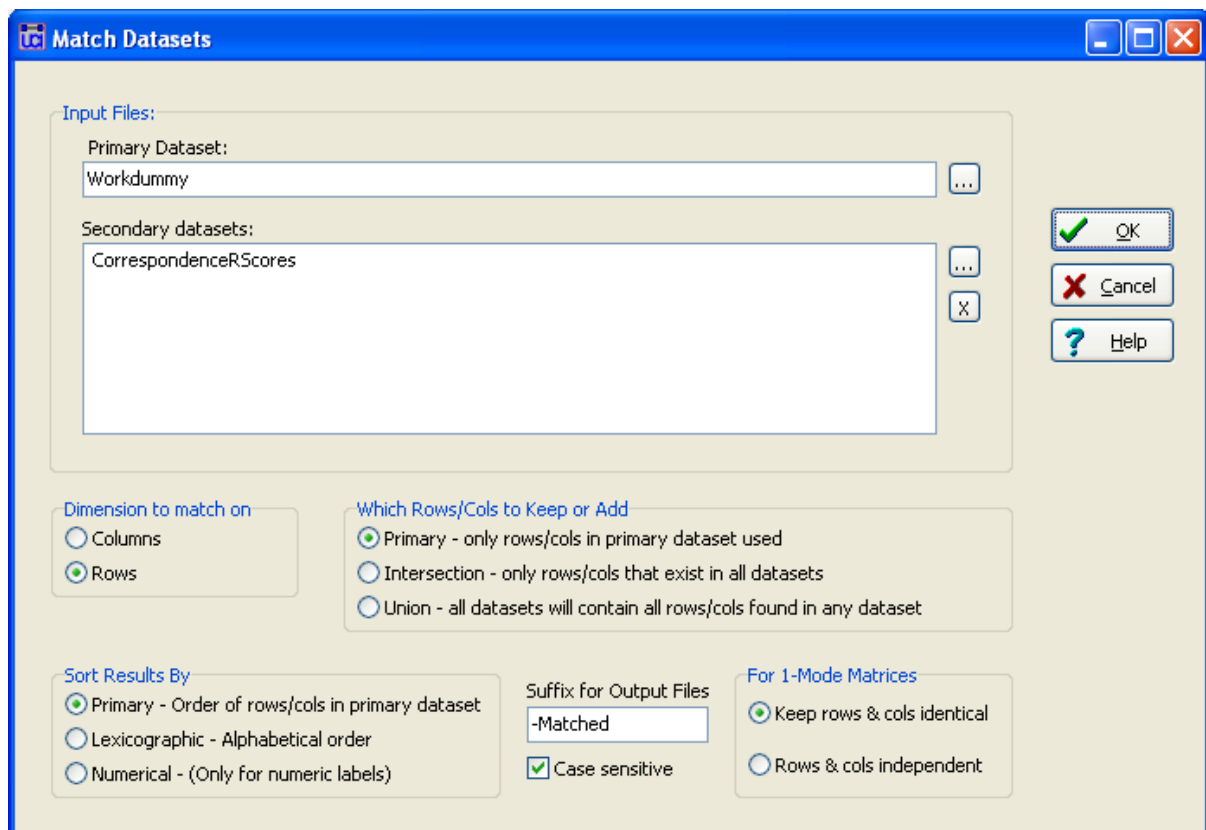
Before running the correspondence analysis on the dataset workshop in order to create Figure 7.23 we need to create a dummy network which will connect each actor at time period one to a copy of themselves in time period 2. This can easily be done using the dl editor as follows.



This is then saved as a UCINET dataset we have called Workdummy. We now run correspondence analysis on the stacked dataset Workshop and we save just two factors ie
Tools|Scaling/Decomposition|Correspondence as follows

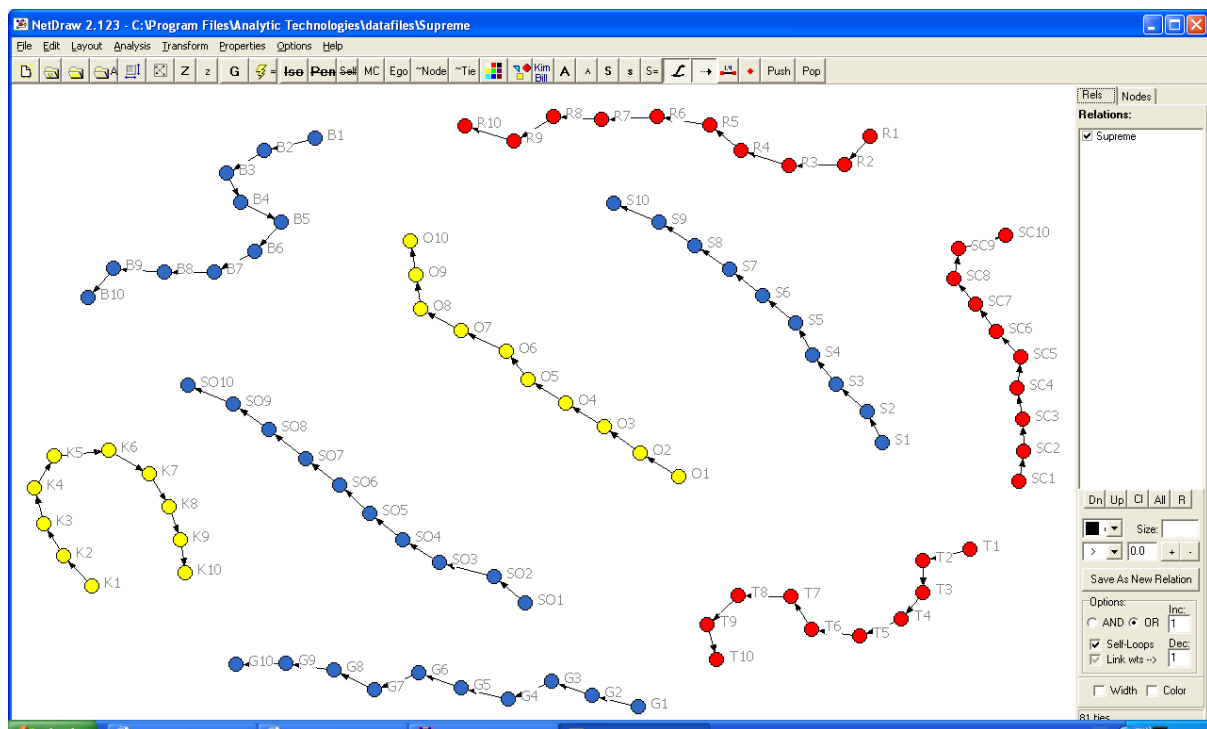


We now should match the co-ordinates to our dummy data to make sure they correspond. To do this run Data|Match Multiple Datasets set Workdummy as the primary and CorrespondenceRScores as the secondary dataset to create a new co-ordinate file called CorrespondenceRScores-matched.

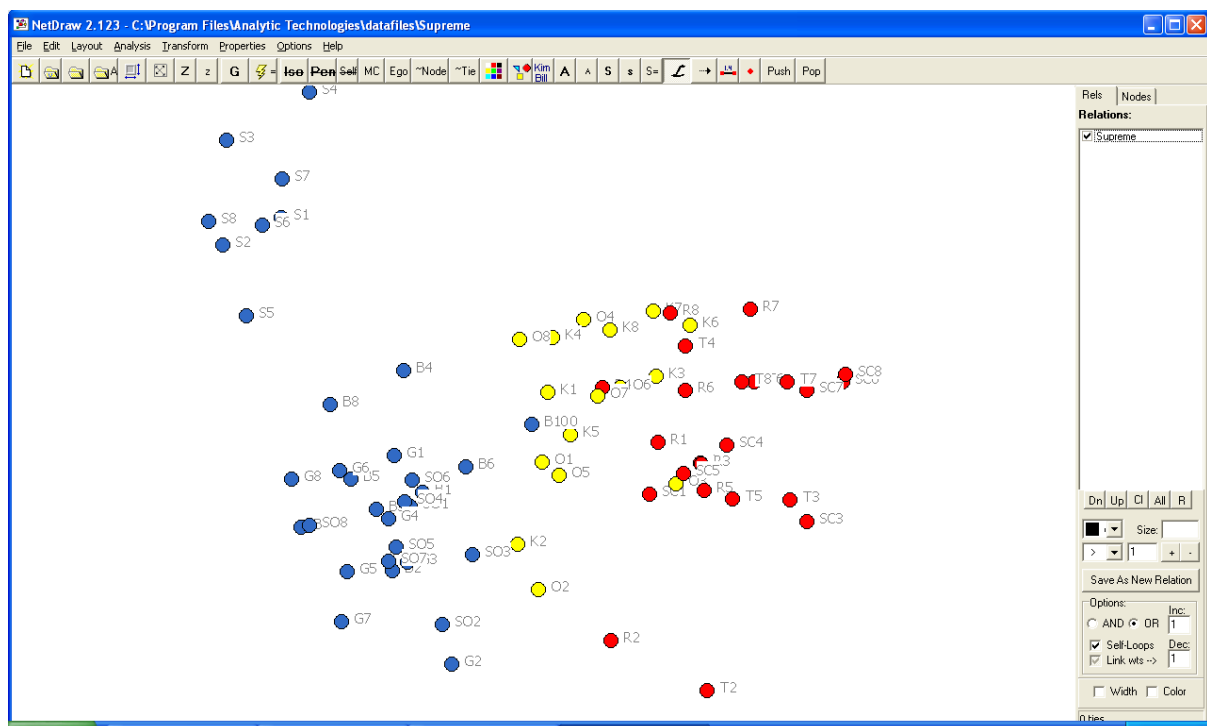


We now open the UCINET dataset Workdummy in Netdraw and then bring in the co-ordinates by using File | Open | Ucinet dataset | Cordinates and selecting CorrespondenceRScores-matched this will give Figure 7.23.

The data for the supreme court for the correspondence analysis is called Supremeall there is also a dataset called supreme which has the connections between all the judges. In Netdraw load supreme and then colour the nodes according to their political persuasion ie leave as Blue S,B,G,SO, colour K and O yellow and T,R SC red. This can easily be done since the trails are in separate components and you can left click to open up a box that covers each trail in turn and colour groups of nodes. Once this is done you get the following.

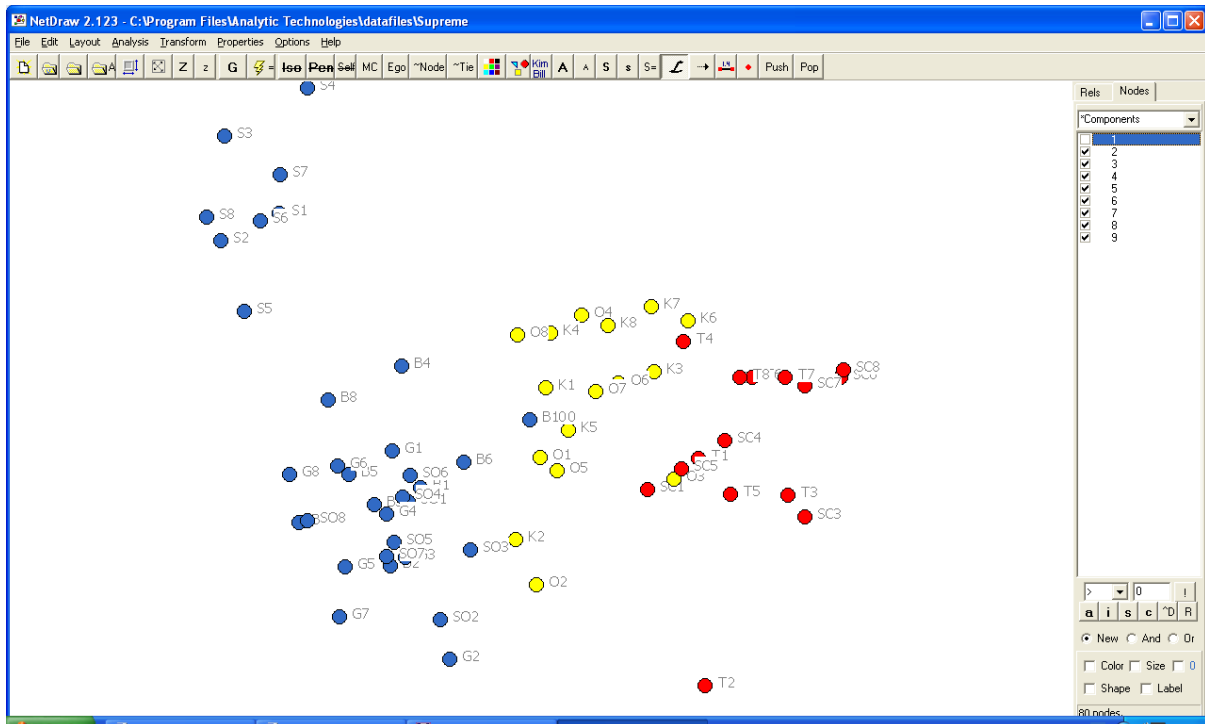


You can now run the correspondence analysis and do the matching as in the previous example and then bring in the coordinates. You may need to flip the diagram but if you view edges greater than zero you obtain Figure 7.24 as below.

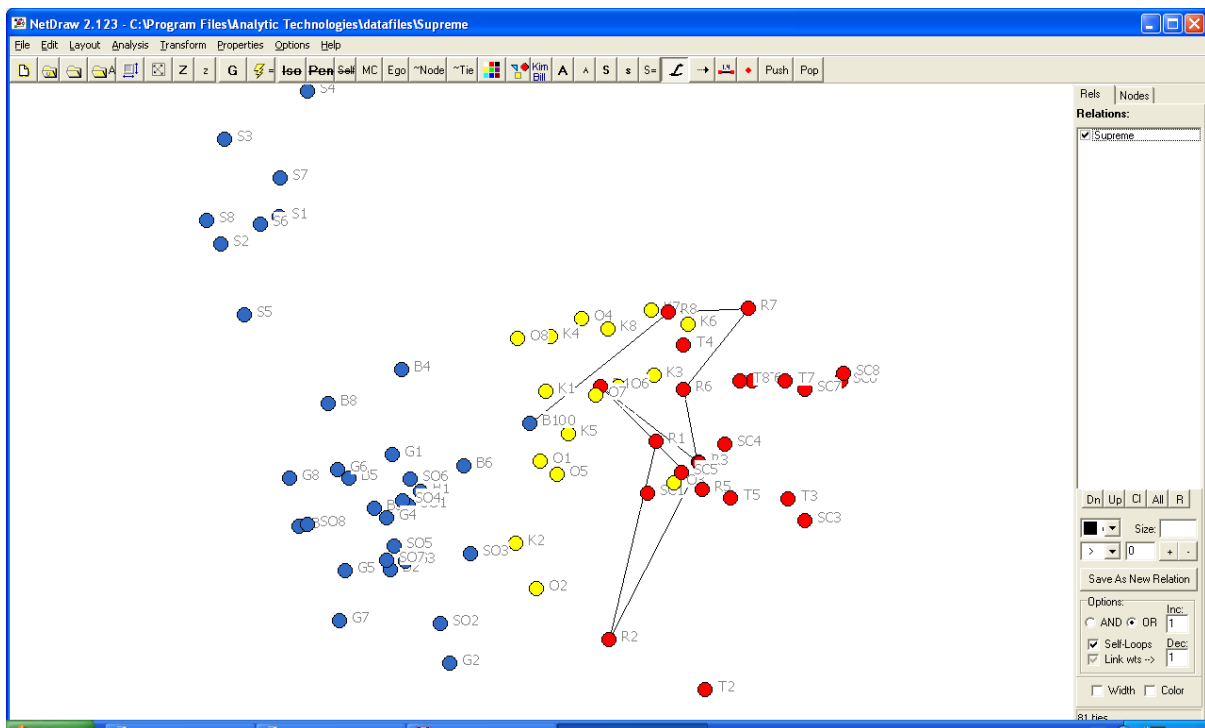


To see just the trail left by Renquist first show all the edges and then run Analysis|components. Now show all the components that are not Renquist (ie all those except component 1) and then colour all

active edges to white using Properties|Lines|Color|General so that you have the following.



If you now click the box to include component 1 you obtain Figure 7.23 as follows.

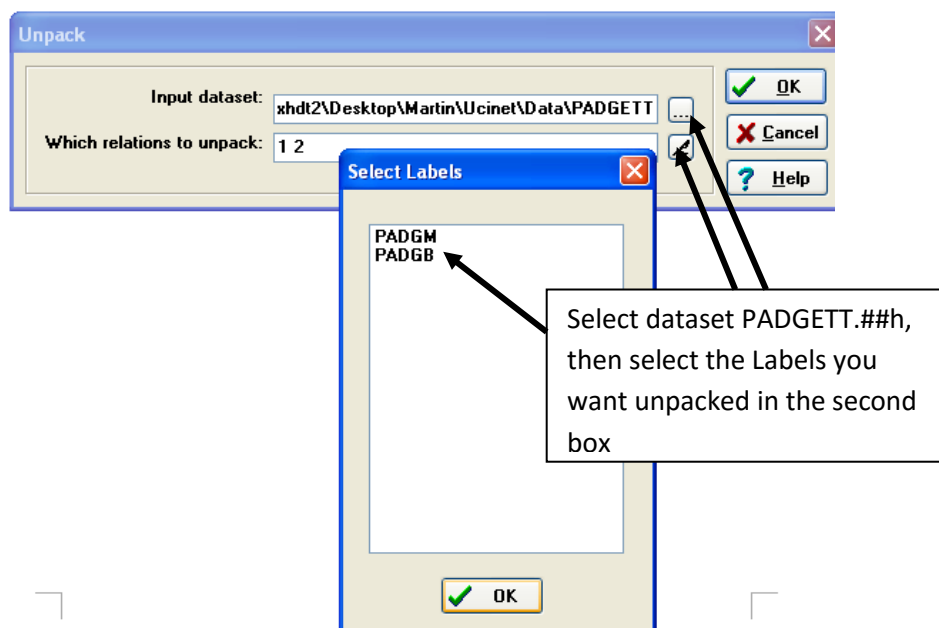


Section 8.3 Dyadic Hypothesis

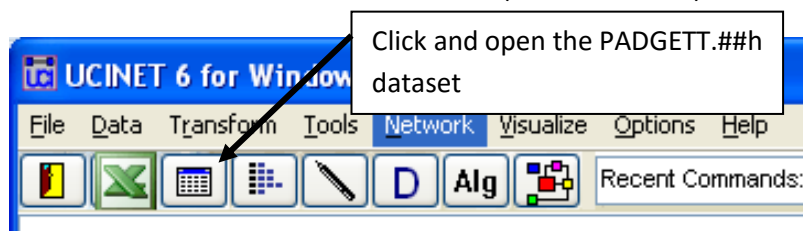
QAP Correlation

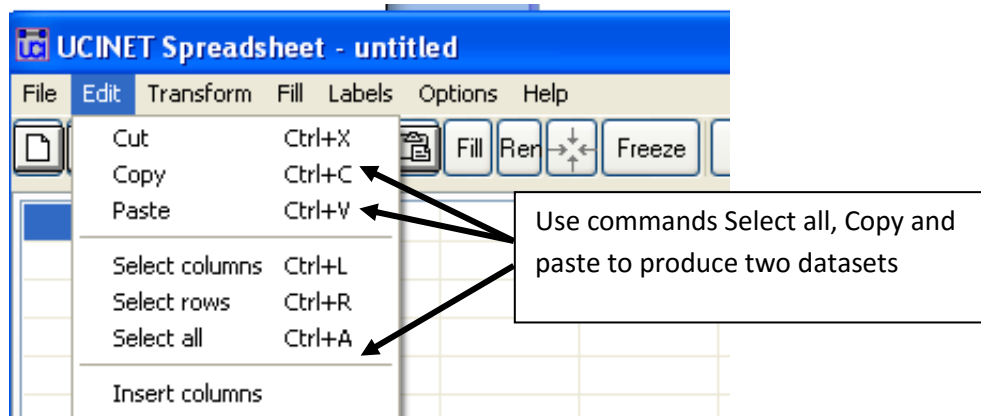
Before running the QAP routine, we must split the **PADGETT.##h** dataset to obtain individual dataset for **Padgm** (marriage network) and **Padgb** (business network). This can be done using a command or manually.

To use the command, select data|unpack and select **Padgett.##h** as input dataset. Afterwards chose the relations you'd like to unpack: **PADGM** and **PADGB** (you can select multiple relations by holding the Ctrl key on your keyboard whilst making the selections). This will create two new dataset files **PADGM.##h** and **PADGB.##h** in your file directory.



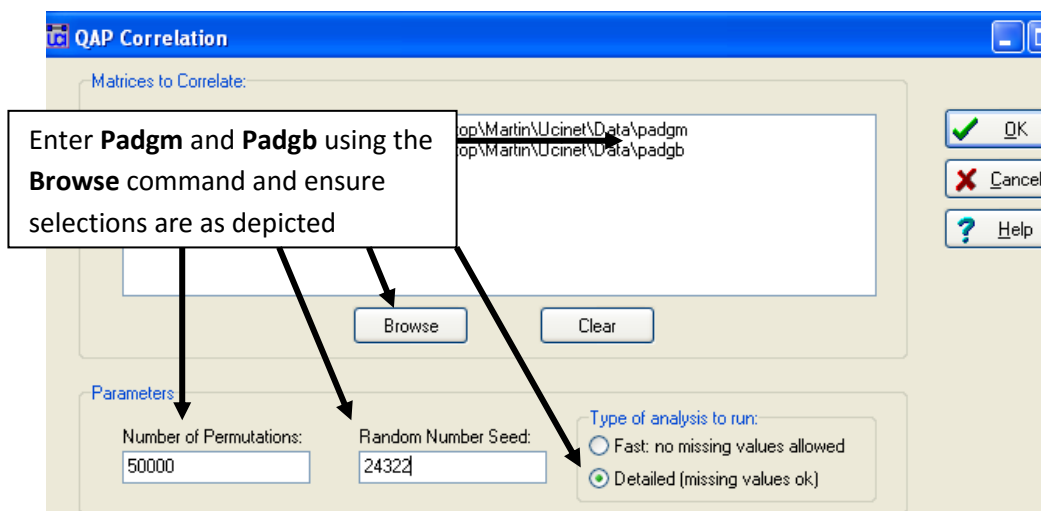
To do this manually, open the Matrix spreadsheet editor and select the **PADGETT.##h** file. The dataset has two tabs PADGM and PADGB (see bottom left).





Using the command order **Ctrl+A** and **Ctrl+C** to copy the data in the **PADGM** tab. Open a new tab and enter **Ctrl+V** to paste the data (you can also use the function “Select all”, “Copy” and “Paste” in the Edit menu). Save this as Padgm. Repeat these steps for the Padgb tab and save it as Padgb.

To run the **QAP** routine on the Padgett and Ansell’s data open UCINET and open **Tools|Testing Hypotheses|Dyadic (QAP)|QAP Correlation** and add both matrices (**Padgm** and **Padgb**) to correlate. Select the option “**Detailed**” in the “**Type of analysis to run**” section and ensure that **Number of Permutations** is set to **50000** and **Random Number Seed** is set to **24322** to replicate the results. Click OK; the UCINET log file will show the same results as in **Figure 8.1**.

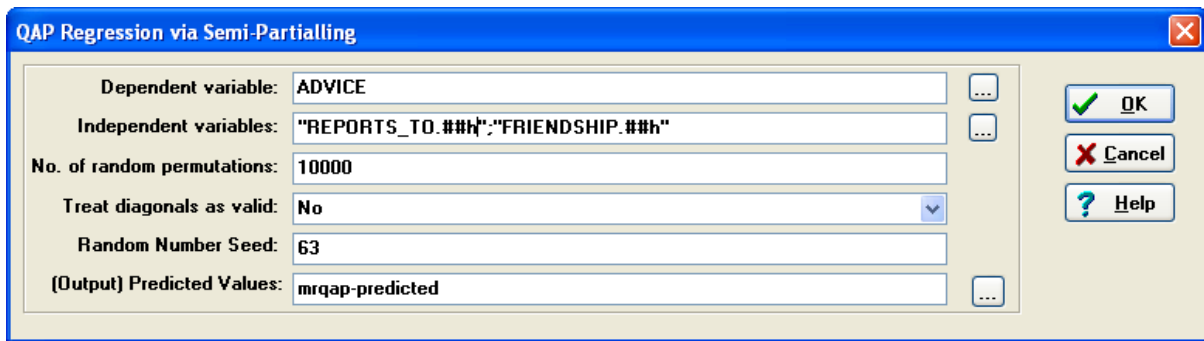


8.3.1 QAP Regression

Before beginning with the routine we must again unpack the dataset we are using **Krack-High-Tec.##h** using the **data|unpack** function in UCINET and selecting all three relations: **ADVICE**, **FRIENDSHIP** and **REPORTS_TO**.

MR-QAP

To perform the QAP Regression, open **Tools|Testing Hypotheses|Dyadic (QAP)|MR-QAP Linear Regression|Semi-Partialling method** and select **ADVICE.##h** as your Dependent variable and **FRIENDSHIP.##h** and **REPORTS_TO.##h** (to make multiple selections press CTRL) as Independent variables. Set the numbers of permutations to **10000** and Random Number Seed to **824** to replicate findings in **Figure 8.2**. Click OK and results will open in a new window.



QAP Regression via Semi-Partialling

Dependent variable:

Independent variables:

No. of random permutations:

Treat diagonals as valid:


Random Number Seed:

(Output) Predicted Values:

OK Cancel Help

LR-QAP

To perform the logistic regression in 8.3 we need to dichotomize the Newcomb (1961) fraternity data so that it only accounts for the top three choices in year one and year two. First of all, **NEWC0** and **NEWC1** need to be unpacked from the **NEWFRAT.###** dataset: **Open data | unpack**, select the **NEWFRAT.###** dataset and unpack **NEWC0** and **NEWC1**.



Select Labels

NEWC0
NEWC1
NEWC2
NEWC3
NEWC4
NEWC5
NEWC6
NEWC7
NEWC8
NEWC10
NEWC11
NEWC12
NEWC13
NEWC14
NEWC15

OK

To dichotomize **NEWC0** and **NEWC1**, open **Transform | Dichotomize interactive**. Load the **NEWC0** file, enter the **Cutoff value** "3" and select **LE- less than or equal to** and save the new matrix as **NEWC0D**. Repeat the step for the **NEWC1** and save it as **NEWC1D**.

Dichotomization App

Load Save Done

Data Value	Z-Score	Frequency	Separation	Num. of 1s	Density
1	-1.6269784	17	-0.4200840	17	0.0625
2	-1.4100479	17	-0.5739440	34	0.125
3	-1.1931175	17	-0.6773651	51	0.1875
4	-0.9761870	17	-0.7514691	68	0.25
5	-0.7592566	17	-0.8043996	85	0.3125
6	-0.5423261	17	-0.8401680	102	0.375
7	-0.3253956	17	-0.8609160	119	0.4375
8	-0.1084652	17	-0.8677218	136	0.5
9	0.1084652	17	-0.8609160	153	0.5625
10	0.3253956	17	-0.8401680	170	0.625
11	0.5423261	17	-0.8043996	187	0.6875
12	0.7592566	17	-0.7514691	204	0.75
13	0.9761870	17	-0.6773651	221	0.8125
14	1.1931175	17	-0.5739440	238	0.875
15	1.4100479	17	-0.4200840	255	0.9375
16	1.6269784	17	0.4200840	272	1

Load NEWC0;
enter 3;
select LE;
save

Cutoff value:
3

Cutoff operator:
☐ GT - Greater than
☐ GE - Greater than or equal to
☐ EQ - Equal to
☒ LE - Less than or equal to
☐ LT - Less than

For square matrices
☐ Ignore diagonal
☐ Include diagonal
☒ Set diagonal to 0

Statistics
 Avg = 8.500
 SD = 4.610
 Min = 1.000
 Max = 16.000
 N = 272.000

The logistic regression routine has a built in system that allows us to construct the reciprocity matrix and the transitivity matrix from a given source matrix. We first load in the dependent variable NEWC1D and the first independent variable NEWC0D under Tools|Testing Hypothesis|Dyadic (QAP)|LR QAP Logistic Regression once this has been loaded we can select reciprocity as a relational effect as follows

LR-QAP -- Logistic Regression QAP (beta version)

Dependent Variable (dyadic):
NEWC1D

Independent Variables (dyadic):
NEWC0D

Source Network:
NEWC0D

Relational Effect:
Reciprocity

Add

Dataset containing node attributes:

Source Attribute:
Source

Attribute-based Effect:
Effect

Add

(Output) Predicted Values:
NEWC1D-pred

(Output) Model fit statistics:
NEWC1D-fit

(Output) Coefficients:
NEWC1D-coef

Options:
 No. of random permutations: 10000
 Random Number Seed: 113735

Statistics to Track:
☐ Betas
☒ T-Statistics

Note: Independent variables can be stacked in a single dataset if no relational effects are being used. Otherwise, enter them as separate datasets

Data are:
☐ Symmetric (undirected)
☒ Non-Symmetric (directed)



OK Cancel Help

If we then click add and repeat to add transitivity we get the following

If we now press OK we get similar results to the ones in the book. The number of permutations are not quite high enough to obtain an exact replication but the significance levels should be very close.

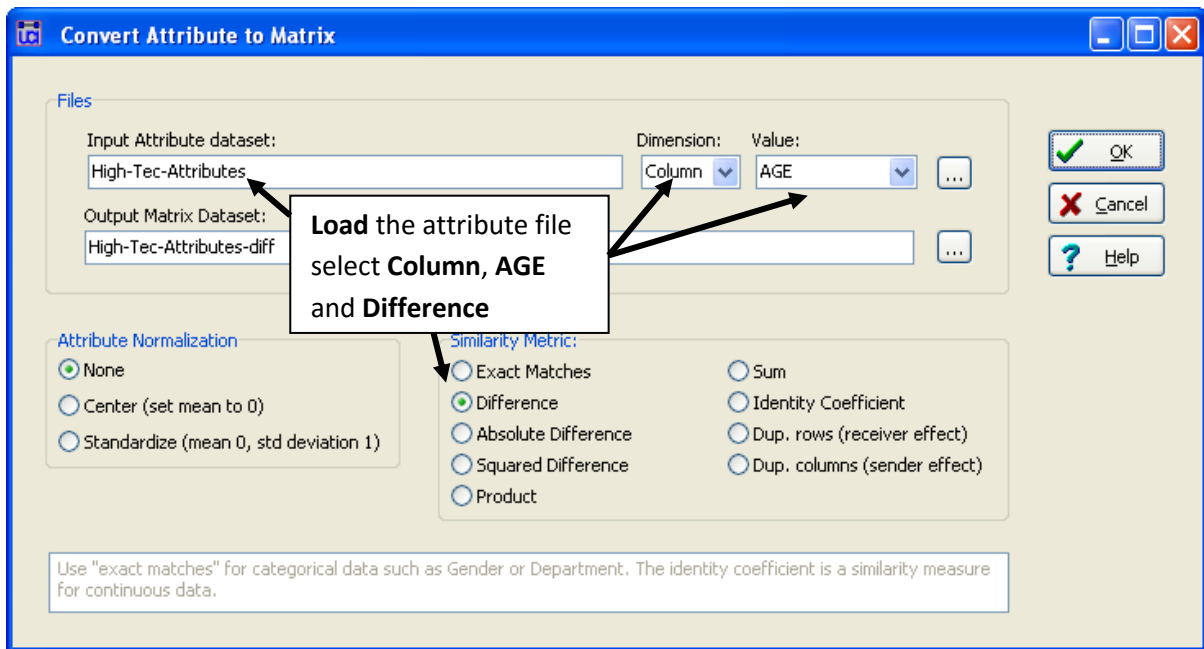
Section 8.4 Dyadic-Monadic Hypotheses

To visualise **Figure 8.4** simply go to **NetDraw** and load the **campnet.##h** file. Turn off the arrowheads

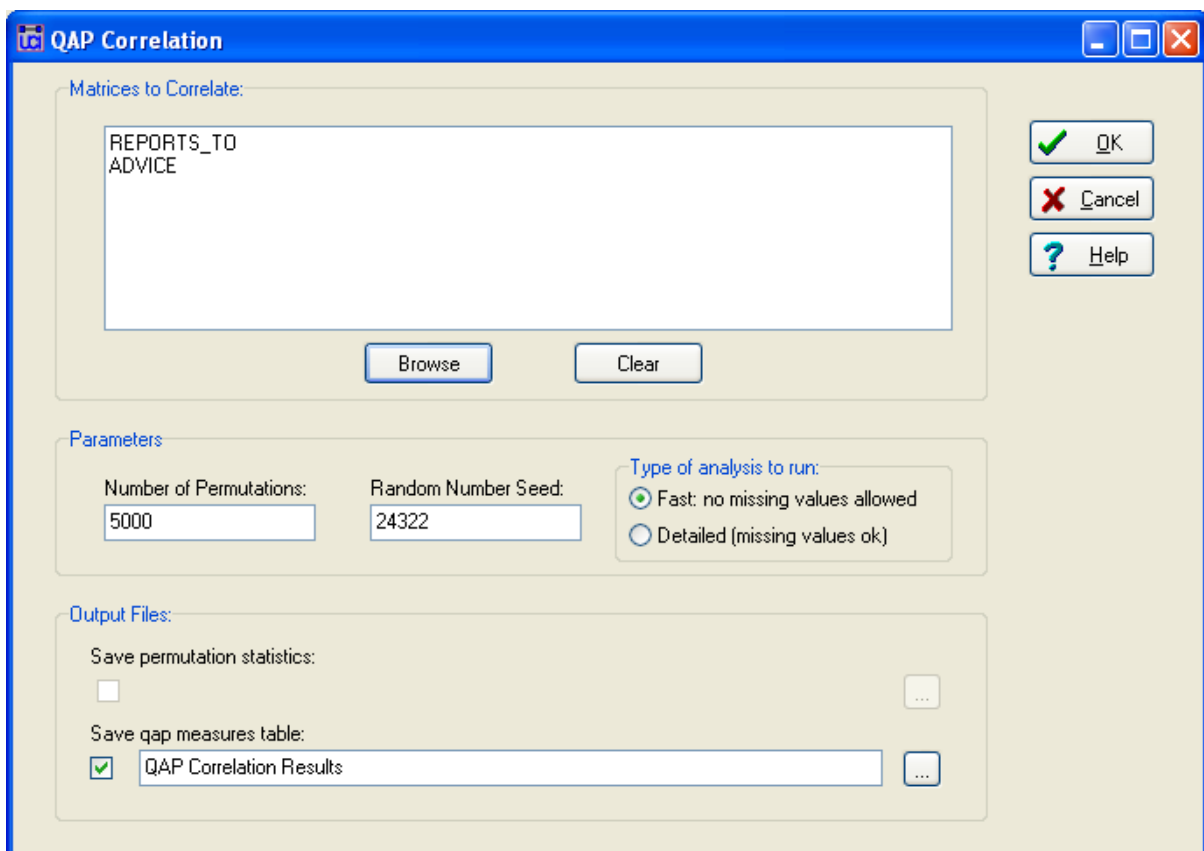
by clicking the  (arrow)-button. Click on the -button in the toolbar and load the **campattr.##h** attribute file. Go to **Properties|Nodes|Symbols|Shape|Attribute-based**, select **Gender** and adjust the shapes (**1** (female) gets a **Circle** / **2** (male) gets a **Square**).

8.4.1 Continuous Attributes

The first step under 8.4.1 is to transform the attributes in a matrix. To do this go to **Data|Attribute to matrix** and load the **High-tec-Attributes.##h** file. Select the **Dimension "Column"**, Value **"AGE"** and select **"Differences"** amongst the **Similarity Matches** options. Save as **High-Tec-Attributes-diff.##h**, click OK and the output in the log file should match that in **Matrix 8.1**.



The second step is to unpack the **REPORTS_TO** relation found in the **Krack-High-Tec.##h** file. Go to **Data|Unpack**, open the file and select option **3** which corresponds with **REPORTS_TO**. To run the QAP correlation illustrated in **Figure 8.5** go to **Tools|Testing Hypotheses|Dyadic (QAP)| QAP Correlation** and load the **High-Tec-Attributes-Diff.##h** and the **REPORTS_TO.##h** matrices. As follows



Pressing OK will reproduce the results in Figure 8.5.

8.4.2 Categorical Attributes

Open the **Data|Attribute** to matrix and select the **Campsex.##h** dataset. Select Dimension “**Column**” and Value “**Sexo**” and double-check that the Similarity Metric is set to “**Exact Matches**”. Click OK and a matrix will open in a new window which will be saved as “**Campsex-sameSexo.##h**”.

ucinetlog18.txt - Notepad

File Edit Format View Help

CONVERT ATTRIBUTE TO MATRIX

Input file: campsex (C:\Documents and Settings\mzy
Dimension: Column
Variable: Sexo

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
	HO	BR	CA	PA	PA	JE	PA	AN	MI	BI	LE	DO	JO	HA	GE	ST	BE	RU
	LL	AZ	RO	M	T	NN	UL	N	CH	LL	E	N	HN	RR	RY	ST	BE	RU
	Y	EY	L			IE	IN	E	AE	L				Y				
1 HOLLY	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
2 BRAZEY	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
3 CAROL	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
4 PAM	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
5 PAT	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
6 JENNIE	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
7 PAULINE	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
8 ANN	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
9 MICHAEL	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
10 BILL	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
11 LEE	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
12 DON	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
13 JOHN	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
14 HARRY	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
15 GERY	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
16 STEVE	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
17 BERT	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
18 RUSS	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1

The 1 correspond to the nodes being of the same sex

Now open the **Tools|Testing Hypotheses|Dyadic (QAP)|QAP Correlation** and insert the **Campsex-sameSexo.##h** and the **Campnet.##h** matrices, select 50000 permutations and make sure the “**Type of analysis to run**” is set to “**Detailed.**” Click OK and a new window will open with the results:

ucinetlog25.txt - Notepad

File Edit Format View Help

QAP results for C:\documents and Settings\mzy\hdt2\Desktop\Martin\ucinet\Data\campnet * C:\Documents and Settings\mzy\hdt2\Desktop\Martin\ucinet\Data\campsex-sameSexo.##h

	1	2	3	4	5	6	7	8
	Obs	Value	significa	Average	Std Dev	Minimum	Maximum	Prop >= 0
1 Pearson Correlation	0.3301	0.0004	-0.0006	0.0761	-0.2019	0.3988	0.0004	0.9998
2 Euclidean Distance	10.488	0.0004	12.1823	0.3676	10.0995	13.1149	0.9998	0.0004
3 Hamming Distance	0.3595	0.0004	0.4854	0.0290	0.3333	0.5621	0.9998	0.0004
4 Match Coef	0.6405	0.0004	0.5146	0.0290	0.4379	0.6667	0.0004	0.9998
5 Jaccard Coef	0.2903	0.0004	0.1484	0.0297	0.0753	0.3245	0.0004	0.9998
6 Goodman-Kruskal Gamma	0.7640	0.0004	-0.0034	0.1953	-0.5172	0.8800	0.0004	0.9998
7 Hubert Gamma	45.0000	0.0004	7.7281	7.1546	2.7666	18.6666	0.0004	0.9998

NOTE: when you have missing data, the significance of the test is based on the significance of the test of Pearson Correlation, otherwise, they should be based on the significance of the test of the other metric.

QAP Correlations

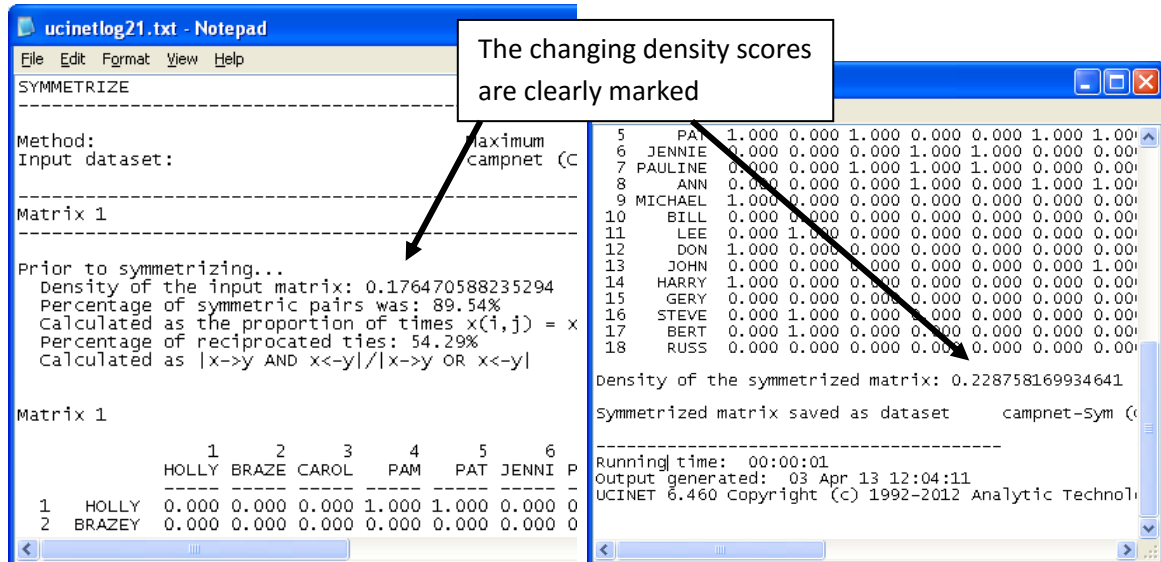
	1	2
	camps	campn
1 campsex-sameSexo	1.000	0.330
2 campnet	0.330	1.000

QAP P-Values

	1	2
	camps	campn
1 campsex-sameSexo	0.000	0.000
2 campnet	0.000	0.000

Values for correlation P-Values

To symmetrise **Campnet.##h** as described in the book open **Transform | Symmetrize...** and select the **Campnet.##h** file. Ensure the setting for method is set to “**Maximum**” and that missing values are handled by “**Choose non-missing values**”. Click OK to see the new matrix. **Note:** The statistics before the new matrix is displayed tells you that the “Density of the input matrix” is 0.1764 (17.6%) amongst other things. At the bottom of the log you can find the density value for the symmetrised matrix which in this case has increase to 0.2287 (22.9%).



Follow the above steps to repeat the **QAP Correlation** but this time select **Campnet-Sym.##h** and the **Campsex-sameSexo.##h** file. Click OK and a new window will open depicting the same results as in **Figure 8.6**.

To generate the output discussed in **Figure 8.7** open the **Network | Ego Networks | Egonet density** procedure and select the **Campnet.##h** dataset. Click OK and a window will open showing three columns (Size, Avg Deg and Density). Now open the **Tools | Testing Hypotheses | Node-level | Regression...** routine and select the **Campnet-egoden.##h** dataset as dependent variable. Because we are interested to regress the Density you have to select **Dependent Column # “3”**. The open **Campatt.##h** as **Independent dataset** and select columns 1 and 2 (enter: **1;2**). These columns refer to the “**Gender**” and “**Role**” attributes. Click OK and a new window will open depicting the output in **Figure 8.7**.

Regression

Dependent dataset: ...

Dependent column #:

Independent dataset: ...

Independent column #:

No of random permutations:

Random Seed:

(Output) Regression Coefficients: ...

(Output) Correlation Matrix: ...

(Output) Inverse of correlation matrix: ...

(Output) Predicted values and residuals: ...

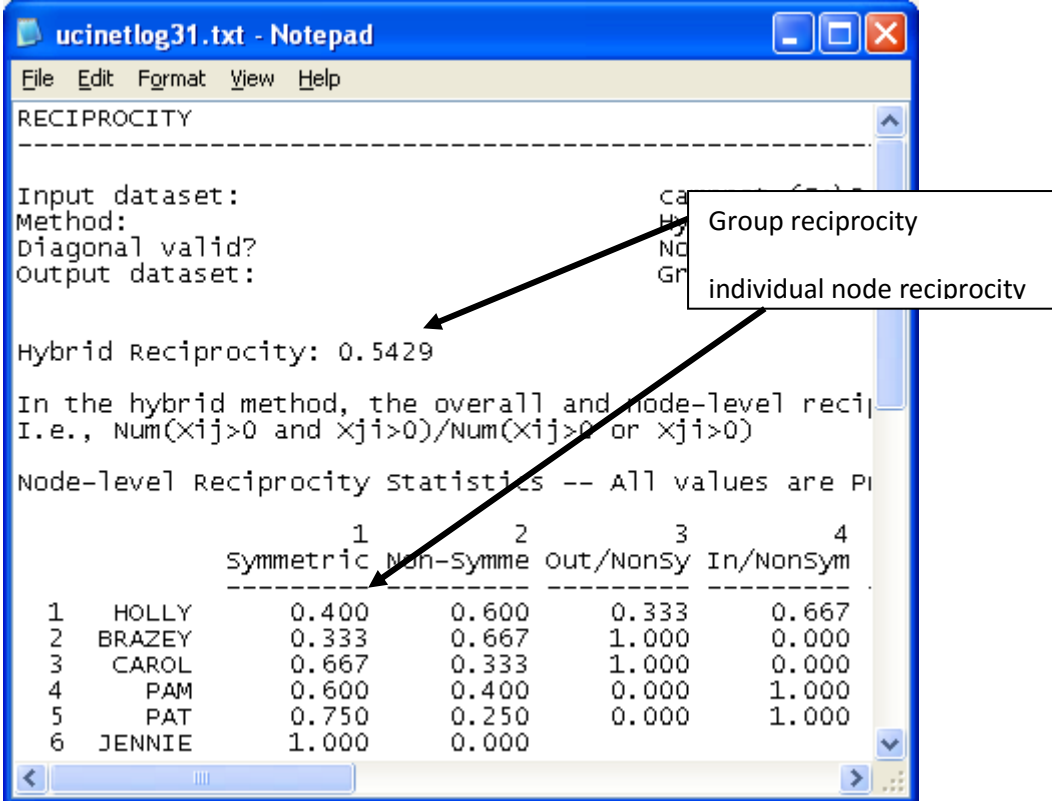
OK

Select the Campnet-egoden.##h file;
Type in column **3**

Select the Campattr.##h file
Type in column **1;2**

Section 9.3 Reciprocity

To run the reciprocity procedure open Network|Cohesion|Reciprocity and select the Campnet.##h dataset. Click OK and a new log file will open depicting the reciprocity value for the network (Hybrid Reciprocity) and individual nodes:



ucinetlog31.txt - Notepad

File Edit Format View Help

RECIPROCITY

Input dataset:
Method:
Diagonal valid?
Output dataset:

Hybrid Reciprocity: 0.5429

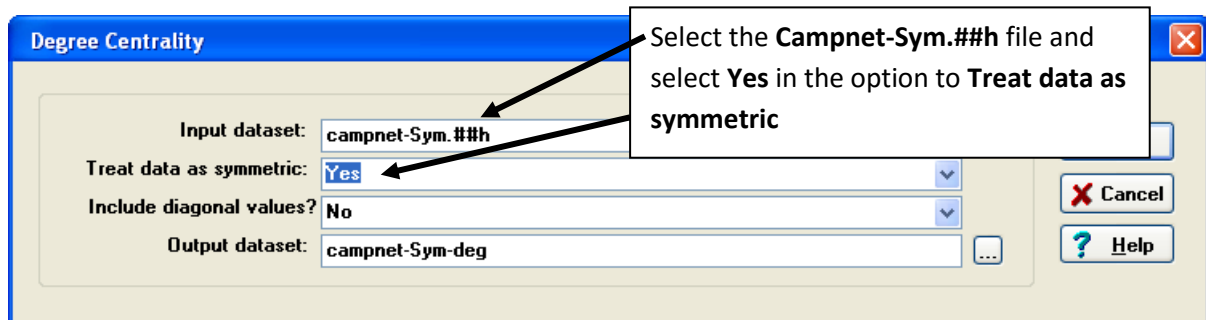
In the hybrid method, the overall and node-level reciprocity are calculated as:
I.e., $\text{Num}(x_{ij} > 0 \text{ and } x_{ji} > 0) / \text{Num}(x_{ij} > 0 \text{ or } x_{ji} > 0)$

Node-level Reciprocity Statistics -- All values are Proportions

		1	2	3	4
		Symmetric	Non-Symme	out/NonSy	In/NonSym
1	HOLLY	0.400	0.600	0.333	0.667
2	BRAZEY	0.333	0.667	1.000	0.000
3	CAROL	0.667	0.333	1.000	0.000
4	PAM	0.600	0.400	0.000	1.000
5	PAT	0.750	0.250	0.000	1.000
6	JENNIE	1.000	0.000		

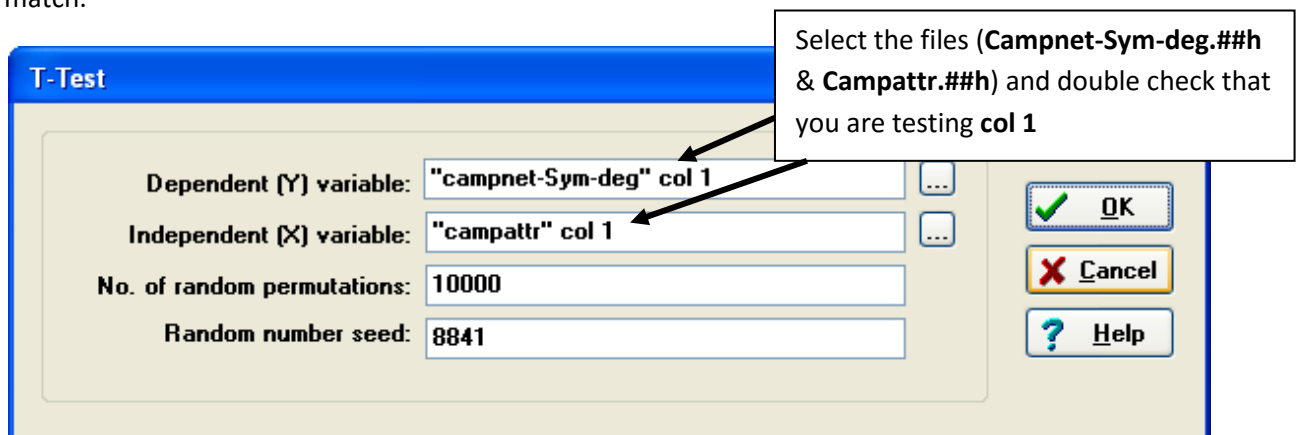
10.3.1 Degree Centrality

To run the Centrality procedure open **Network|Centrality and Power|Degree...** and select the **Campnet-Sym.###h** file. Because we are dealing with a symmetric matrix, select **“Yes”** in the **Treat data as symmetric** box. Click OK and a new window will open showing the same results as in **Figure 10.1**.



(**Note:** if you do not have the file open Transform|Symmetrize and select the Campnet.###h file and select “Maximum” as Symmetrizing Method).

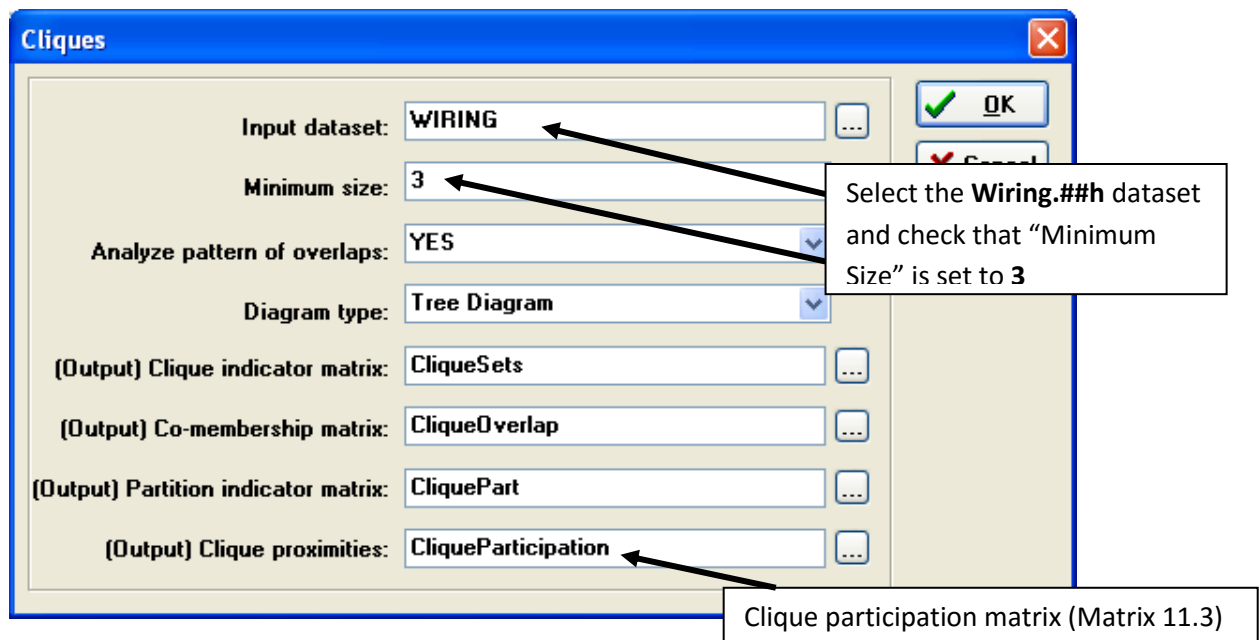
To run the t-Test open **Tools|Testing Hypotheses|Node-level|T-Test...** and select the **Campnet-Sym-deg.###h** dataset column 1 (**col 1**) as dependent variable and **Campattr.###h** column 1 (**col 1**) as independent variable. Click OK and compare your results with those in Figure 10.2; they should match.



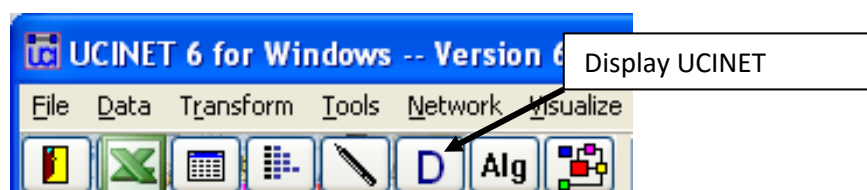
Section 11.2 Cliques

11.2.1 Analyzing clique overlaps

To perform the Cliques routine as discussed in the book go to **Network|Subgroups|Cliques...** and select the **Wiring.##h** dataset. The output in **Matrix 11.1** uses a clique defined as containing **3** or more actors which can be changed in the “**Minimum size**” labelled box. Click OK to see the results in a new log file.



The clique participation matrix in **Matrix 11.1** is generated automatically and saved as **CliqueParticipation.##h**. To open this click on the “**Display UCINET dataset**” button in UCINET and open the **CliqueParticipation.##h** file. (Note: this procedure also automatically generates **Matrix 11.2**, **Matrix 11.3** and **Figure 11.2**)



11.2.2 Bimodal method

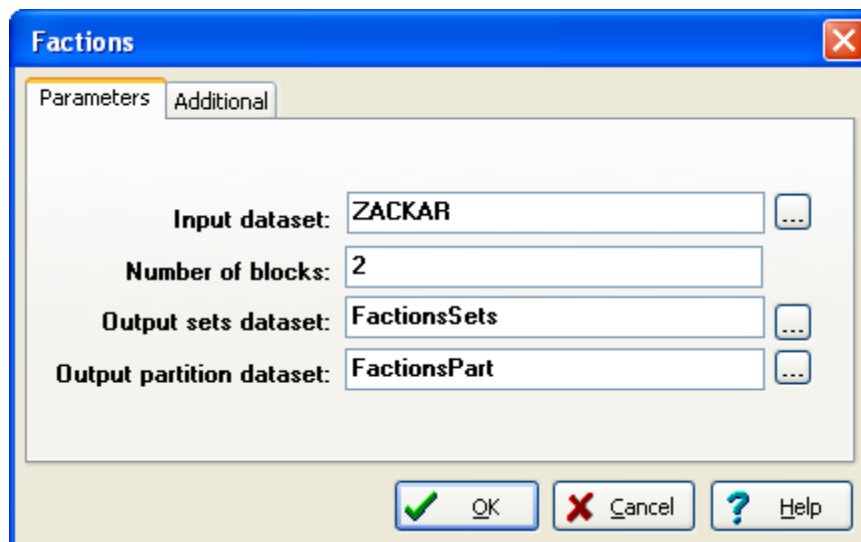
To visualise this network as shown in **Figure 11.3** open **NetDraw** and open the **File|Open|Ucinet Dataset|2-Mode network** and select the **CliqueParticipation.##h** file from the folder. Click OK. You can now change the colours and add the tie strengths as demonstrated earlier.

To produce the hierarchical clustering shown in **Figure 11.4** open **Network|Subgroups|Cliques...** and select the **ZACKAR.##h** file and you can draw the clique participation matrix in **NetDraw** following the steps in the previous example and will receive **Figure 11.5**

Note: doing this routine will overwrite the previous (Wiring) output **CliqueParticipation.##h** unless you change the name.

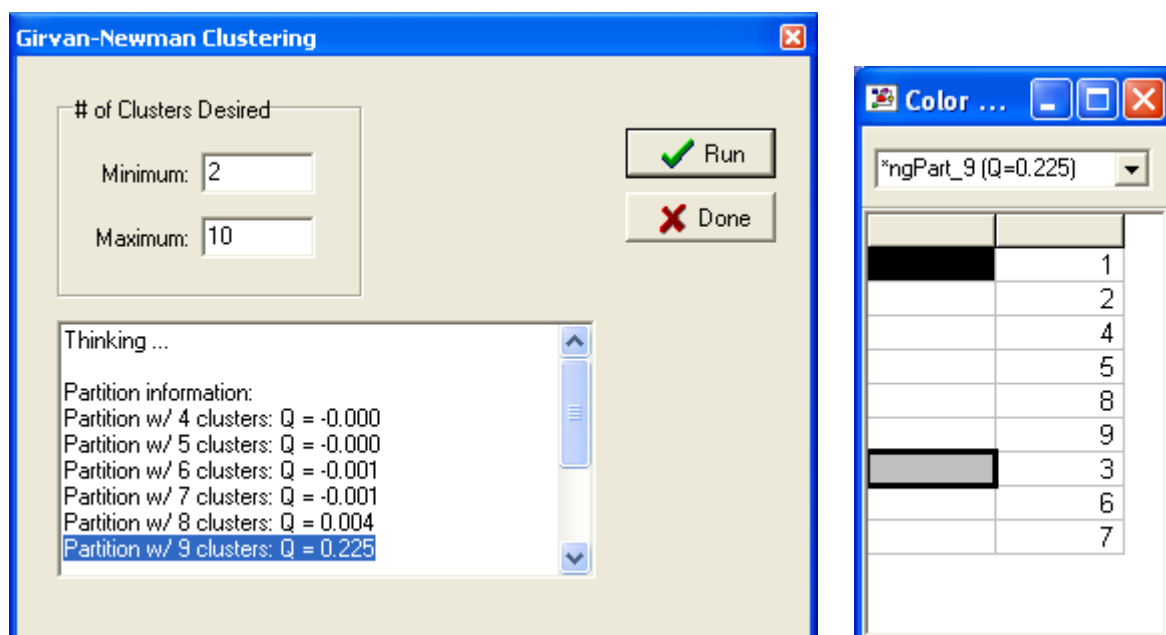
Section 11.3 Factions

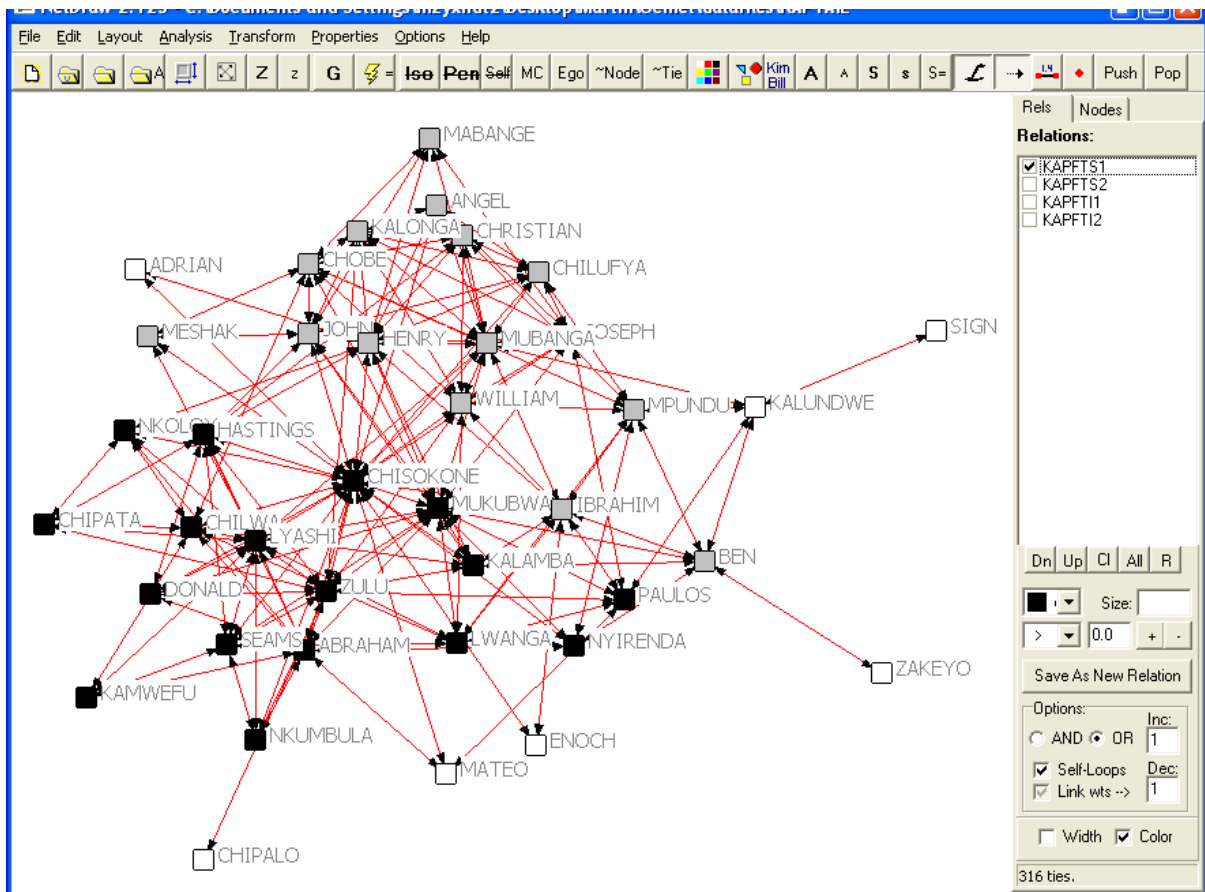
To produce Figure 11.7 open **Network|Subgroups|Factions** and select the **ZACKAR.##h** dataset. Click OK and the output log file should depict **Figure 11.7** (Note: the 1s in figure 11.7 are equal to the 1.000 in the log file).



11.4 Girvan-Newman Algorithm

To run the Girvan-Newman routine, open **NetDraw** and load the **Kaptail.##h** file. Then run **Analysis|Subgroups|Girvan-Newman** and click **Run** to see the Partitions within the window. To colour the partitions as in **Figure 11.8** according to the subgroups given by **Partition w/9 clusters: Q = 0.225**, go to **Properties|Nodes|Symbols|Colours|Attribute based** and select ***ngPart_9 (Q=0.225)** and re-recolor the nodes as shown below which should give you the same outcome as in Figure 11.8





Section 11.5 Directed and Valued Data

To run the routine described in 11.5, go to **Tools | Cluster Analysis | Optimization...** and load the **Camp92.##h** dataset

This is as good as I managed to reproduce figure 11.9 but r-square and groupings are no exact replica (selection and output below)

Combinatorial Optimization Clustering

Input dataset:

Number of clusters:

Fit criterion:

Are diagonal values valid:

Type of data:

Max # of iterations in series:

Length of time in penalty box:

Number of random starts:

Random number seed:

Output partition dataset:

OK Cancel Help

ucinetlog8.txt - Notepad

File Edit Format View Help

Clusters:

```

1: CAROL PAM PAT JENNIE PAULINE JOHN
2: HOLLY ANN MICHAEL BILL DON HARRY
3: BRAZEY LEE GERY STEVE BERT RUSS

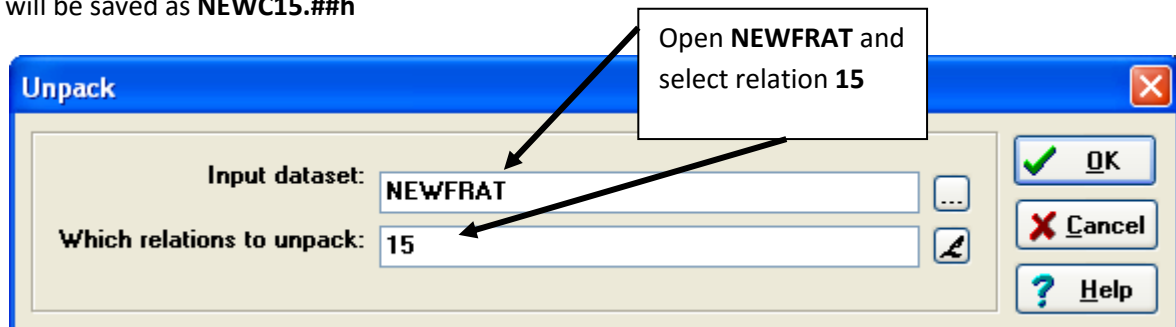
```

Camp92 weeks 2 and 3 rank order of amount of interaction

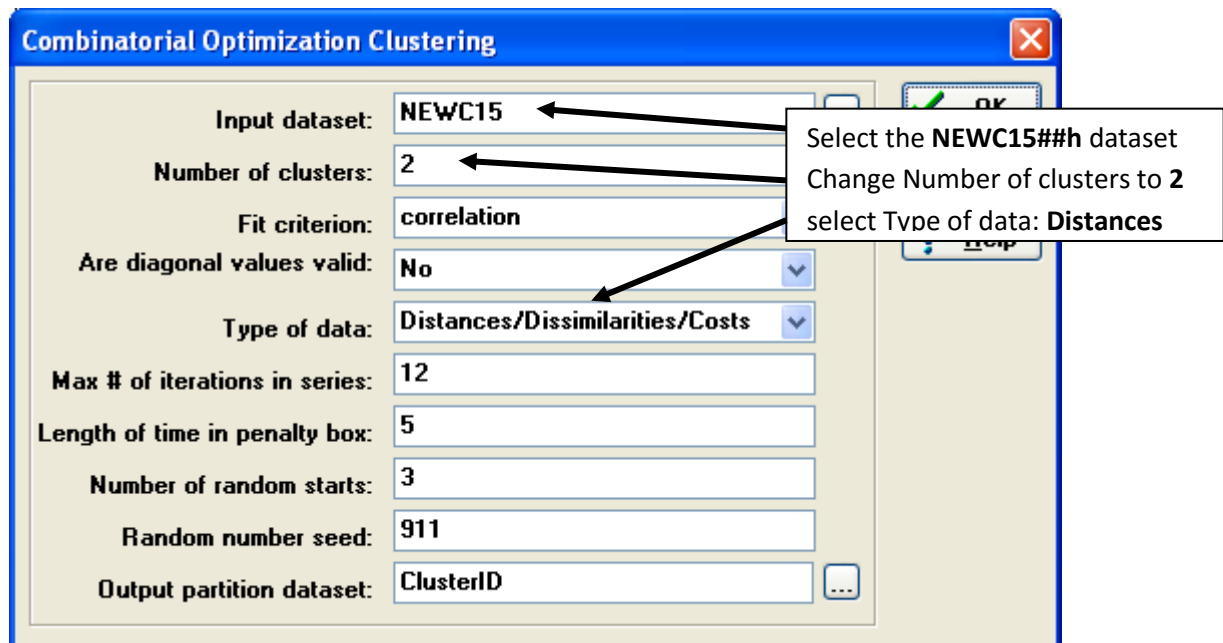
	5 PAT	6 JENNIE	3 CAROL	4 PAM	13 JOHN	7 PAULINE	10 BILL	8 ANN	1 HOLLY	14 HARRY	9 MICHAEL	12 DON	11 LEE	2 BRAZEY	15 GERY	16 STEVE	17 BERT	18 RUSS
5 PAT		1.000	8.000	3.000	11.000	2.000	16.000	14.000	4.000	12.000	9.000	13.000	7.000	10.000	17.000	5.000	6.000	15.000
6 JENNIE	1.000		4.000	2.000	12.000	7.000	16.000	3.000	11.000	13.000	15.000	14.000	10.000	9.000	17.000	5.000	6.000	8.000
3 CAROL	2.000	4.000		1.000	3.000	6.000	16.000	12.000	17.000	5.000	7.000	10.000	11.000	15.000	13.000	8.000	9.000	14.000
4 PAM	3.000	4.000	6.000		7.000	1.000	15.000	2.000	9.000	12.000	8.000	13.000	16.000	5.000	17.000	11.000	10.000	14.000
13 JOHN	9.000	15.000	1.000	5.000		3.000	14.000	16.000	17.000	4.000	8.000	6.000	12.000	11.000	7.000	10.000	13.000	2.000
7 PAULINE	3.000	4.000	5.000	1.000	2.000		17.000	7.000	14.000	13.000	6.000	11.000	12.000	10.000	16.000	9.000	8.000	15.000
10 BILL	10.000	16.000	8.000	15.000	9.000	17.000		13.000	3.000	14.000	2.000	1.000	11.000	4.000	12.000	6.000	7.000	5.000
8 ANN	10.000	1.000	12.000	2.000	16.000	7.000	15.000		8.000	4.000	3.000	5.000	17.000	9.000	13.000	11.000	6.000	14.000
1 HOLLY	4.000	12.000	15.000	8.000	16.000	10.000	11.000	5.000		9.000	3.000	1.000	13.000	2.000	17.000	7.000	6.000	14.000
14 HARRY	14.000	16.000	5.000	11.000	6.000	9.000	12.000	8.000	4.000		1.000	2.000	3.000	17.000	13.000	10.000	7.000	15.000
9 MICHAEL	9.000	13.000	4.000	6.000	14.000	7.000	17.000	8.000	3.000	2.000		1.000	10.000	11.000	15.000	12.000	5.000	16.000
12 DON	12.000	17.000	13.000	14.000	11.000	15.000	10.000	16.000	3.000	2.000	1.000		4.000	9.000	6.000	8.000	5.000	7.000
11 LEE	7.000	15.000	9.000	14.000	11.000	12.000	13.000	17.000	5.000	4.000	8.000	2.000		6.000	16.000	1.000	3.000	10.000
2 BRAZEY	10.000	11.000	12.000	2.000	15.000	5.000	17.000	7.000	1.000	13.000	9.000	8.000	3.000		16.000	6.000	4.000	14.000
15 GERY	15.000	12.000	9.000	13.000	5.000	17.000	10.000	16.000	11.000	14.000	4.000	7.000	8.000	6.000		2.000	3.000	1.000
16 STEVE	8.000	15.000	5.000	12.000	16.000	7.000	17.000	14.000	10.000	13.000	11.000	6.000	3.000	9.000	4.000		1.000	2.000
17 BERT	13.000	11.000	9.000	6.000	17.000	14.000	16.000	15.000	7.000	12.000	10.000	8.000	5.000	4.000	3.000	1.000		2.000
18 RUSS	16.000	11.000	10.000	17.000	6.000	15.000	3.000	14.000	2.000	12.000	13.000	7.000	8.000	9.000	1.000	4.000	5.000	

Section 11.7 Performing a Cohesive Subgraph Analysis

First unpack the dataset “week 15” from the **NEWFRAT.##h** by opening **Data|Unpack**, selecting the **NEWFRAT.##h** dataset and select **15** from the dropdown menu as shown below. The new dataset will be saved as **NEWC15.##h**

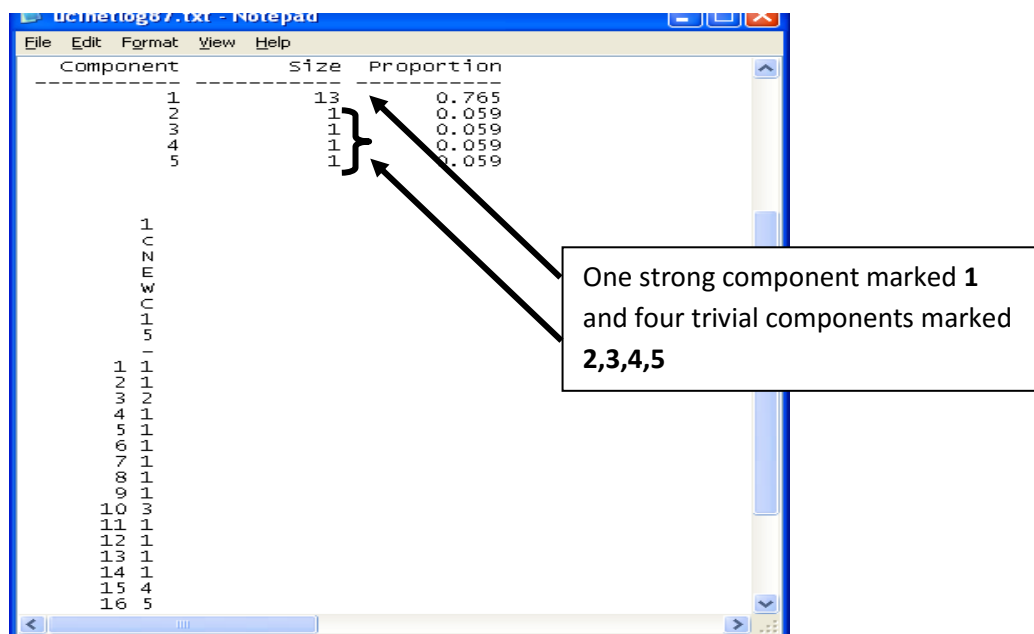


To create **Figure 11.10** go to **Tools|Cluster Analysis|Optimization...** and open the **NEWC15** dataset. Change the settings for **Number of clusters** to “2” and for **Type of data** select “Distances/Dissimilarities/Costs”. Click OK.

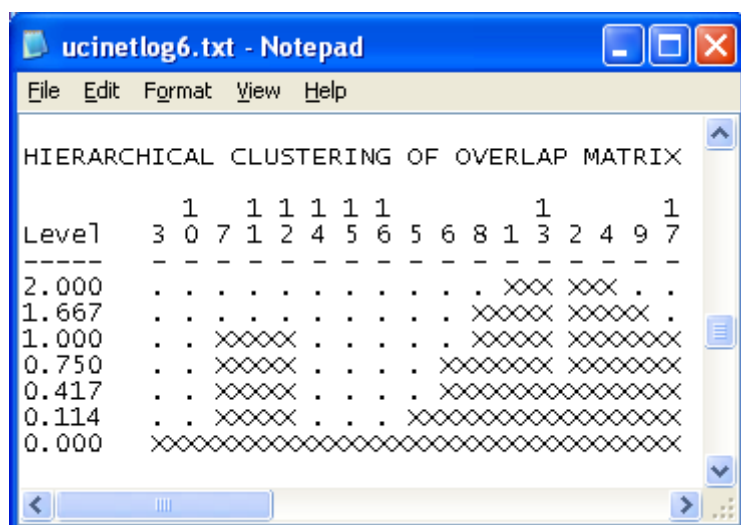


To dichotomize the **NEWC15** go to **Transform|Dichotomize interactive** and load **NEWC15.##h**. Select a **Cutoff** value of “5” and **LE – less than or equal to** and save dataset as **NEWC15D**. The log file in a new window will display **Matrix 11.6**.

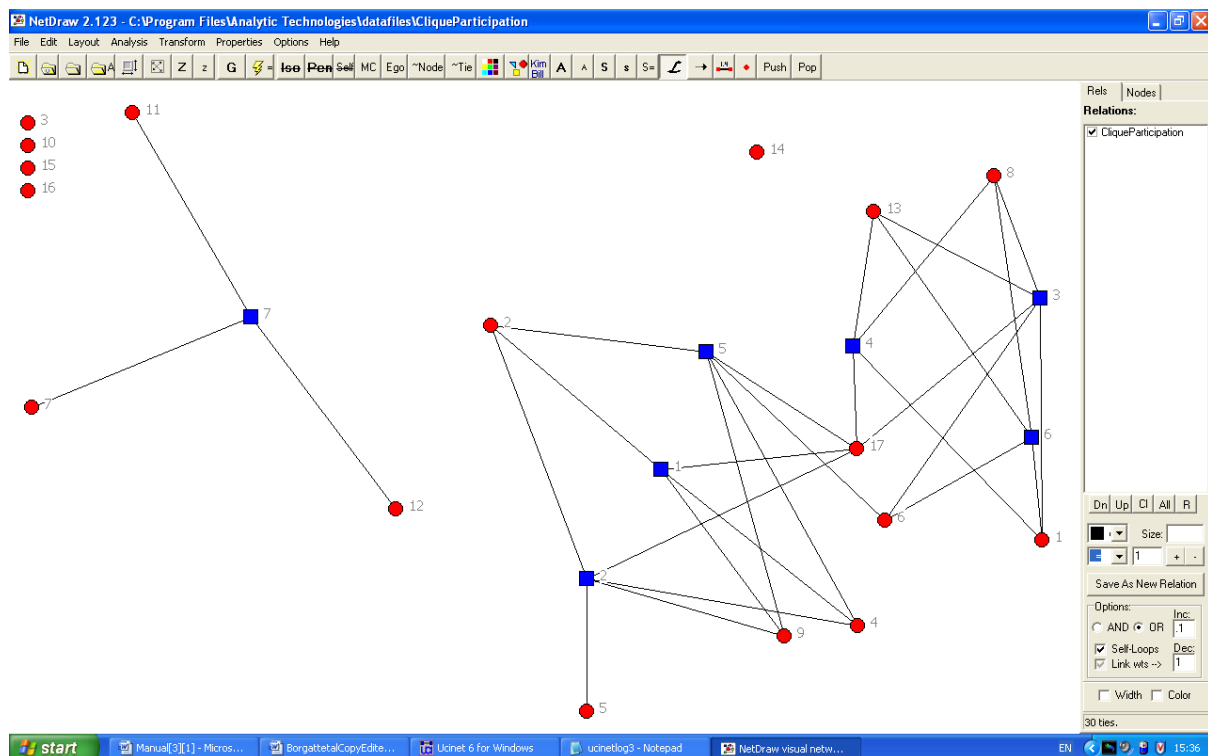
Run the component analysis by going to **Network|Regions|Components...|Binary graph** and select the **NEWC15D.##h** dataset. Run the component analysis on strong component by selecting “**Strong Component**” on the bottom left. The outcome shows the one large and four trivial strong components described in the book:



To perform the clique analysis go to **Network | Subgroups | Cliques...** and select the **NEWC15D.##h** dataset keeping the minimum size set to **3**. The log file will show the same results as in **Figure 11.11**. The discussion below figure 11.11 is based on the Hierarchical Clustering of the overlap Matrix shown below which clearly indicates that 3,10,14,15,16 are only part of the cluster at level 0.



If we now take the matrix cliqueparticipation into netdraw as a 2-mode dataset and look just at clique membership ie set a cut-off value of one we obtain the following



This clearly shows the split in the main group on the right as described in the book.

Follow the same procedure to run the Example on the “top three” and “top seven” choices to replicate the findings (**Note:** use the **Transform | Dichotomize interactive** command and change the **Cutoff** point to “3” and “7”).

Section 12.3 Profile Similarity

First we need to create a version of the **Sampson.##h** dataset that only contains the esteem and disesteem matrices. To do that, go to **Data | Filter/Extract | Submatrix** input the Sampson dataset and select the Esteem and Disesteem matrices as follows

If you do not know the numbers of the matrices these can be selected by clicking the \mathcal{L} on the right of the window.

To run the procedure go to **Network|Roles & Positions|Structural|Profile...** and open **Sampson-Ext.###h** and select the option “Methods of handling diagonal values” **Reciprocal2 (double count)** as depicted below:

Structural Equivalence Via Profile Similarity

Input dataset: Sampson-Ext

Include transpose in calculations: Yes

Method of handling diagonal values: Reciprocal2 (double count)

Measure of profile similarity/distance: EUCLIDEAN DISTANCE

For binary data: Convert to geodesic distances: NO

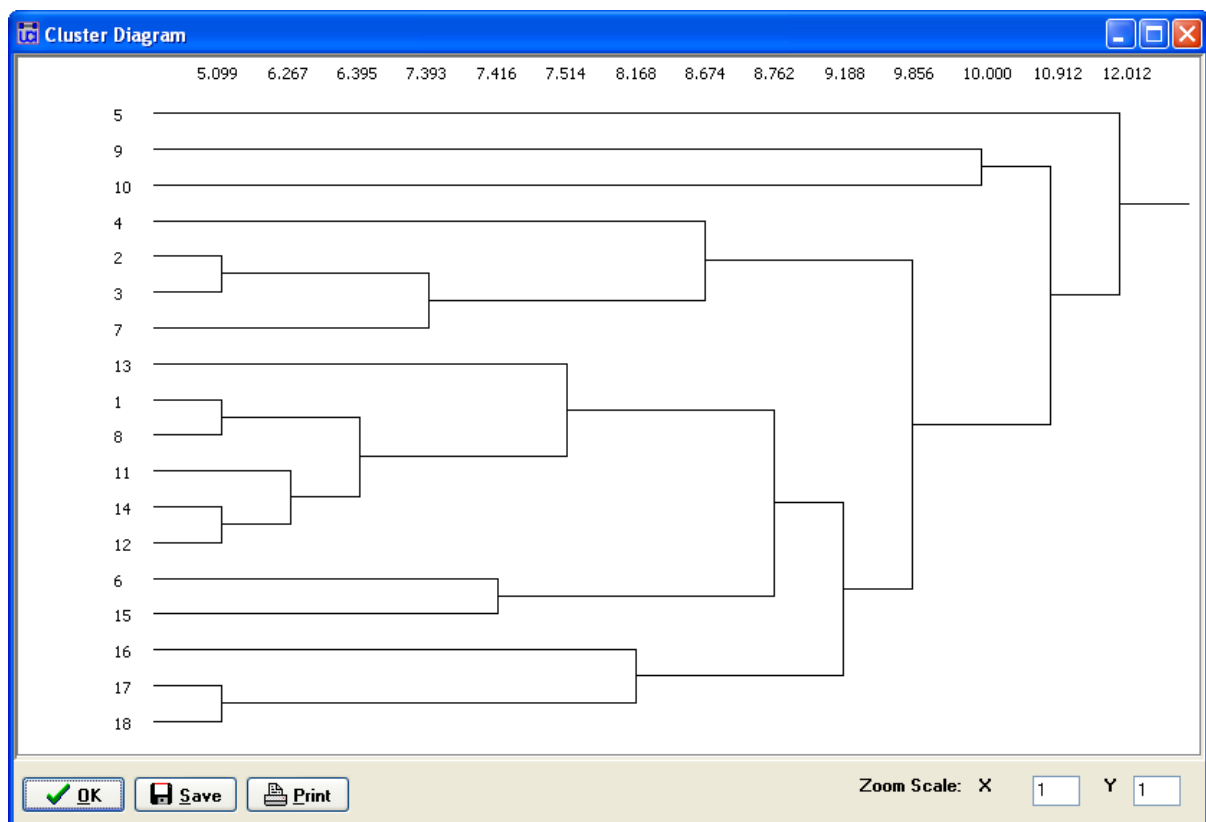
Diagram Type: Dendrogram

(Output) Equivalence matrix: SE

(Output) Partition dataset: SEPart

OK Cancel Help

The results will be shown in a new log file **Structural Equivalence matrix** for the Esteem and Disesteem matrices (visible in **Matrix 12.3**) and a **hierarchical clustering of the equivalence matrix** (**Figure 12.2**) and are accompanied by a **Cluster Diagram**:



Section 12.4 Blockmodels

First we begin by dichotomizing the **SAMPSON-Ext** using the **Transform|Dichotomize** procedure and save the new datasets as **SAMPSON-Ext_GT_0** as follows

We now run profile similarity on this selecting correlation and our method for handling the diagonal is reciprocal1 which ignores the repeated reciprocal pairing in the transpose as follows:

We can see a four split in the clustering diagram in the output log at the level 0.122 the partitions are saved in the dataset SEPart and this is not displayed but we can view this and it would look like this

DISPLAY

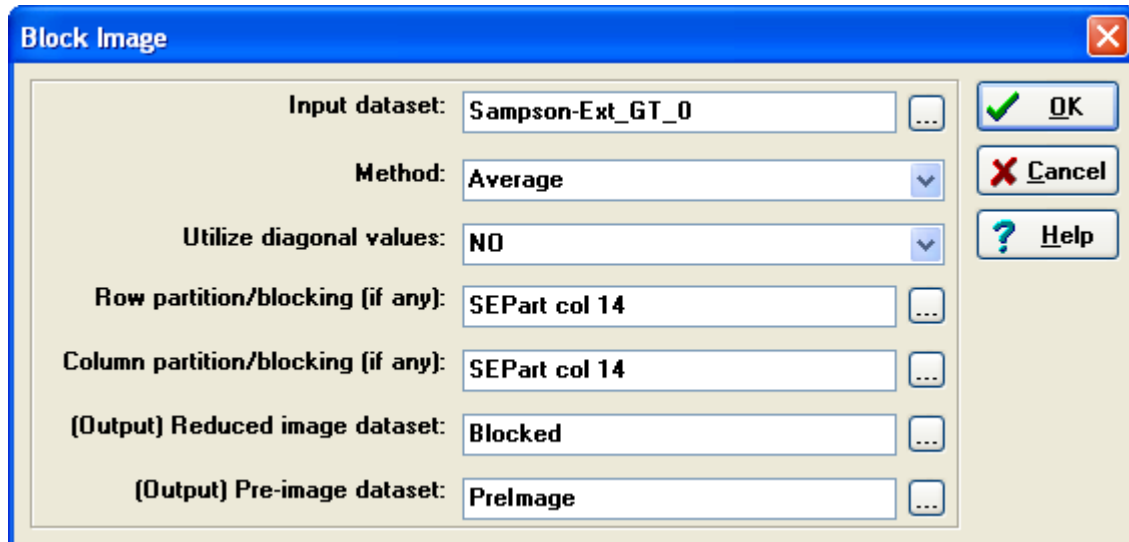
Input dataset: SEPart (C:\Program Files\Analytic
Technologies\datafiles\SEPart

Partition Indicator Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
	0.	0.	0.	0.	0.	0.	0.	0.	0.	0.	0.	0.	0.	0.	0.	-0	-0
	83	64	61	46	43	41	37	36	35	30	24	23	13	12	10	.0	.0
	2	0	6	8	9	0	7	0	8	5	1	9	5	2	6	21	67
	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
1	1	1	1	1	1	1	1	1	4	5	5	7	7	7	7	7	18
2	2	2	2	2	2	2	3	3	3	3	3	3	3	7	7	7	18
3	3	3	3	3	3	3	3	3	3	3	3	3	3	7	7	7	18
4	4	4	4	4	4	4	4	4	4	5	5	7	7	7	7	7	18
5	5	5	5	5	5	5	5	5	5	5	5	7	7	7	7	7	18
6	6	6	6	6	6	6	6	6	6	6	15	15	15	15	18	18	18
7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	18
8	8	12	12	12	12	12	12	14	14	14	14	14	14	14	14	18	18
9	9	9	9	9	9	10	10	10	10	10	10	10	14	14	14	18	18
10	10	10	10	10	10	10	10	10	10	10	10	10	14	14	14	18	18
11	11	11	11	12	12	12	12	14	14	14	14	14	14	14	14	18	18
12	12	12	12	12	12	12	12	14	14	14	14	14	14	14	14	18	18
13	13	13	14	14	14	14	14	14	14	14	14	14	14	14	14	18	18
14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	18	18
15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	18	18
16	16	16	16	16	18	18	18	18	18	18	18	18	18	18	18	18	18
17	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18
18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18

18 rows, 17 columns, 1 levels.

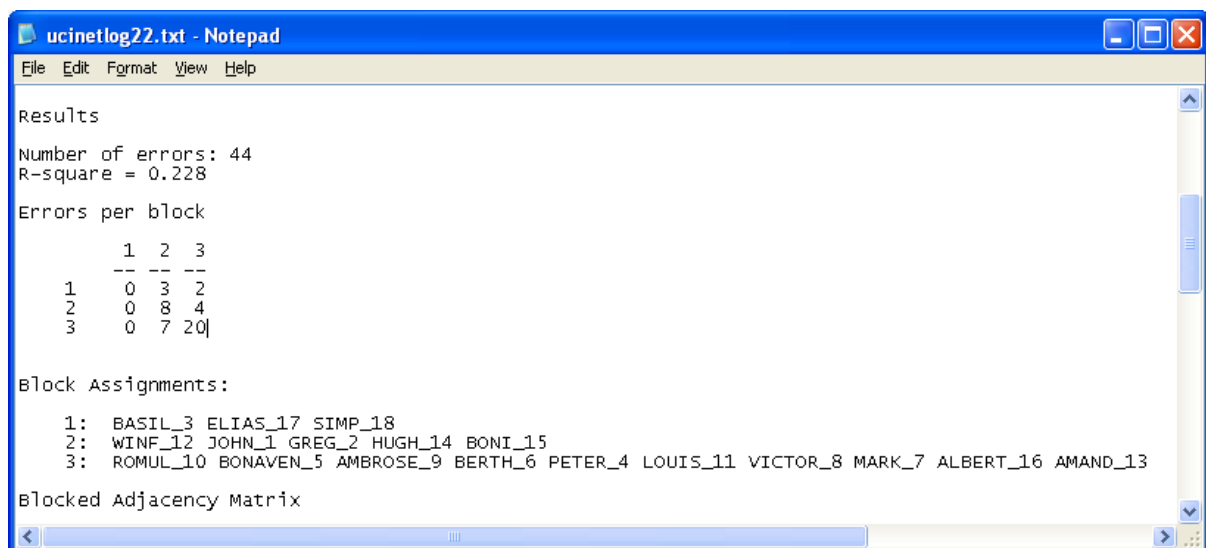
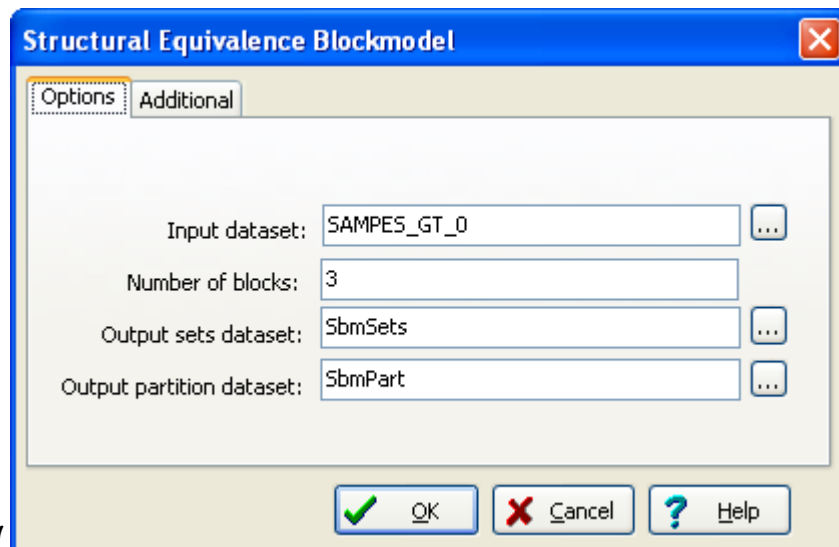
Note that column 14 with the label 0.122 contains the split to interpret this actor 1 is in the group labelled 7 along with 2,3,4,5 and 7; actor 6 is in the group labelled 15 along with 15. The groups are labelled by the highest number of the actor that they contain. We use column 14 of this matrix to get the blockmodel. This is done using Transform|Aggregate (including CSS)|Block. We select Sampson-Ext_GT_0 as our dataset and SEPart col 14 for the partition as follows:



Running this gets the blockmodel shown in Figure 12.4.

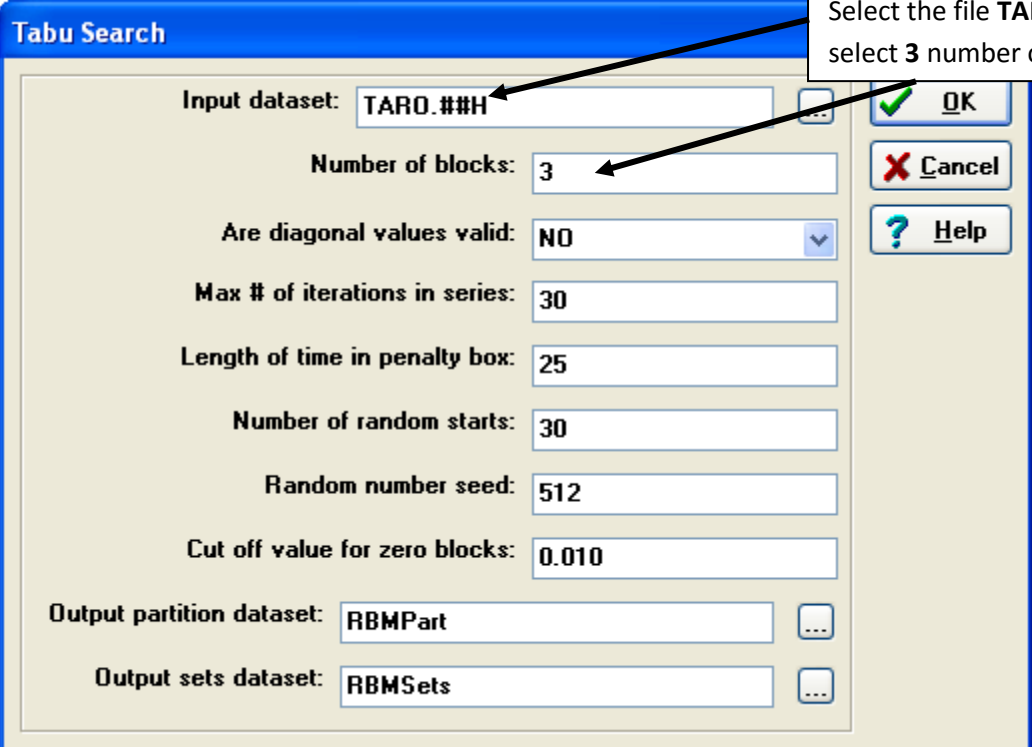
Section 12.5 The Direct Method

To run the structural equivalence ptimization routine go to **Network|Roles & Positions|Structural|Optimization...** and select the dichotomized Sampson esteem relation “**SAMPES_GT_0**”. The optimised outcome of the routine will not be identical to that in **Matrix 12.5** but similar.



Section 12.6 Regular Equivalence

To run the procedure described in **Matrix 12.7** go to **Network|Roles & Positions|Maximum Regular|Optimization...** and load the **TARO.##h** file. Select “**3**” blocks and click OK to see the outcome (which will be similar but not the same) in a new log file.



The screenshot shows the 'Tabu Search' dialog box with the following fields and values:

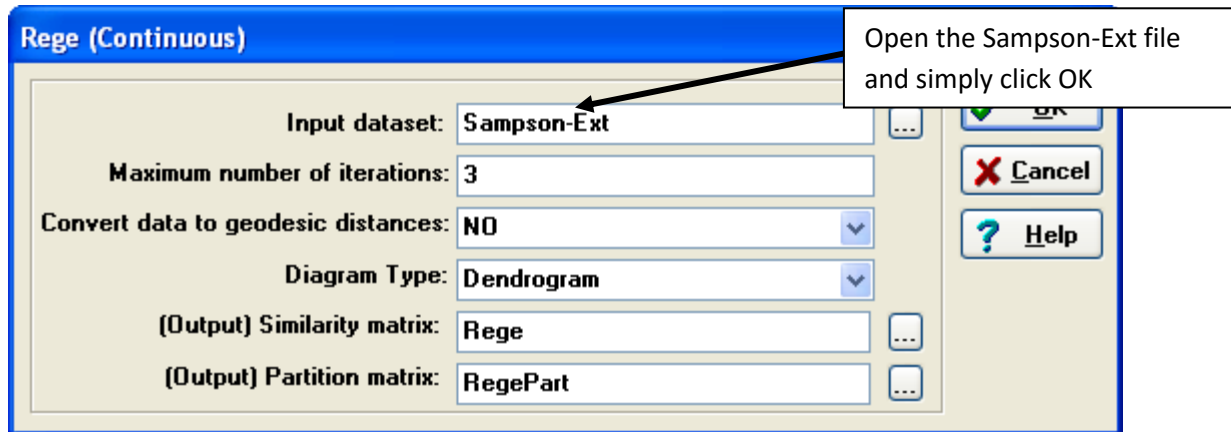
- Input dataset: TARO.##H
- Number of blocks: 3
- Are diagonal values valid: NO
- Max # of iterations in series: 30
- Length of time in penalty box: 25
- Number of random starts: 30
- Random number seed: 512
- Cut off value for zero blocks: 0.010
- Output partition dataset: RBMPart
- Output sets dataset: RBMSets

Annotations with arrows point to the 'Input dataset' field and the 'Number of blocks' field, with a text box stating: 'Select the file **TARO.##h** and select **3** number of blocks'.

Buttons on the right: OK, Cancel, Help.

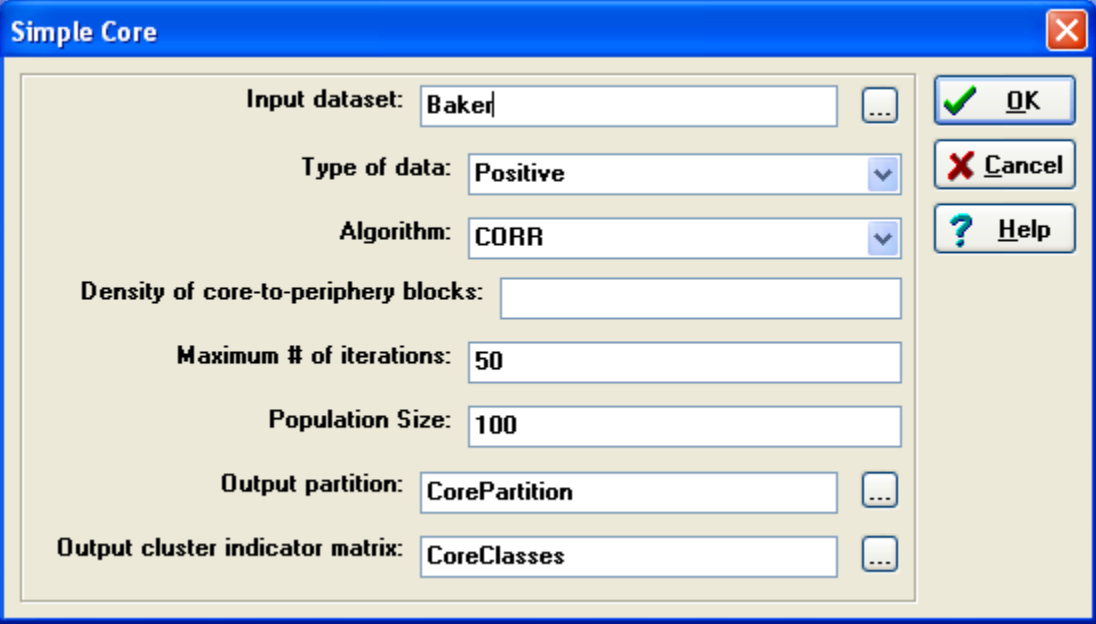
Section 12.7 REGE

To run the REGE routine go to **Network|Roles & Positions|Maximum Regular|REGE...** and select the **Sampson-Ext** file (this file should contain valued and not dichotomized data!). Keep the standard setting and click okay to receive the output described in the book.



Section 12.8 Core-Periphery Models

Simply run Network|Core/Periphery|Categorical on the Baker data with the defaults ie



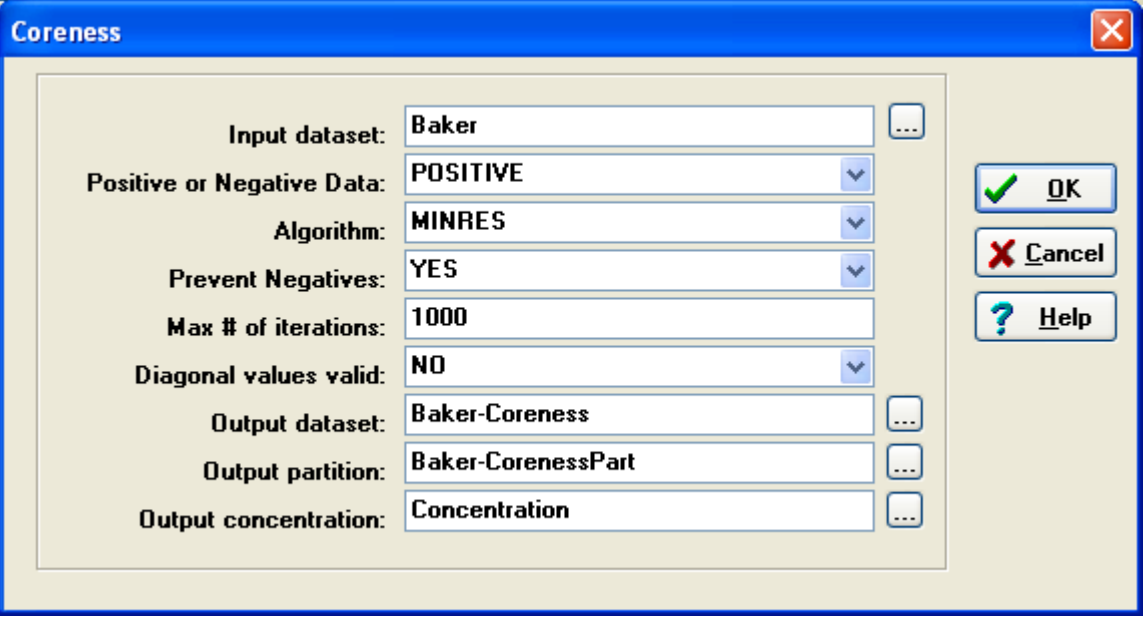
The 'Simple Core' dialog box is shown with the following settings:

- Input dataset: Baker
- Type of data: Positive
- Algorithm: CORR
- Density of core-to-periphery blocks: (empty)
- Maximum # of iterations: 50
- Population Size: 100
- Output partition: CorePartition
- Output cluster indicator matrix: CoreClasses

Buttons on the right: OK, Cancel, Help.

The output will be as in matrix 12.8.

For the continuous run Network|Core/Periphery|Continuous with the defaults as follows.



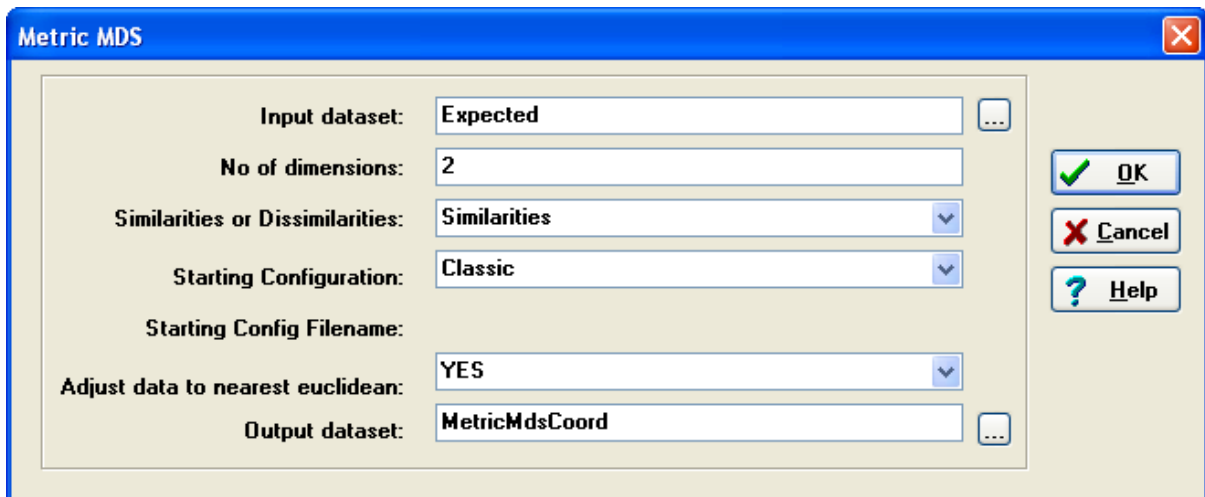
The 'Coreness' dialog box is shown with the following settings:

- Input dataset: Baker
- Positive or Negative Data: POSITIVE
- Algorithm: MINRES
- Prevent Negatives: YES
- Max # of iterations: 1000
- Diagonal values valid: NO
- Output dataset: Baker-Coreness
- Output partition: Baker-CorenessPart
- Output concentration: Concentration

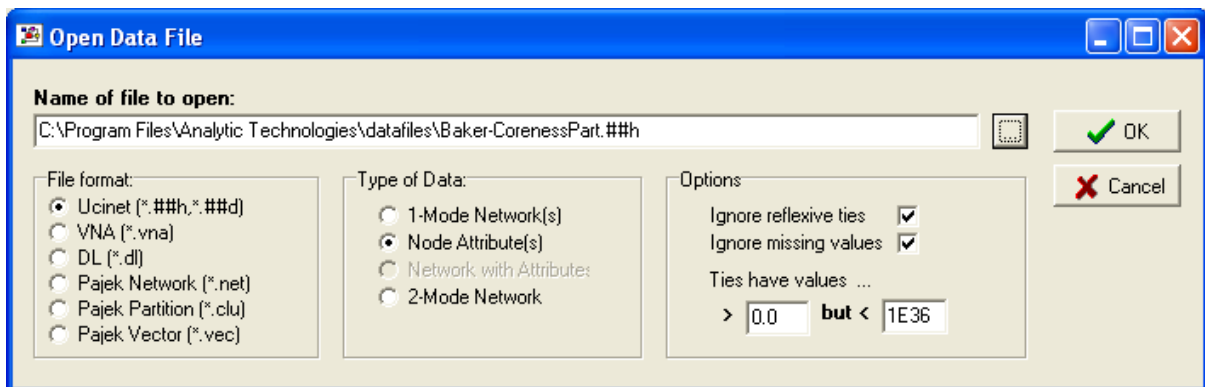
Buttons on the right: OK, Cancel, Help.

The output contains the values as shown in Table 12.3 with a recommended split of 8 core nodes.

The Δ matrix is saved as "Expected" and this needs to be submitted to the metric-mds program under Tools|Scaling/Decomposition|Metric MDS ie



In netdraw load the Baker dataset and turn off the arrows by clicking the arrow head button on the tool bar marked with an arrow →. Next load the dataset created by the coreness routine which indicates which actors are in the core namely BakerCorenessPart as shown below



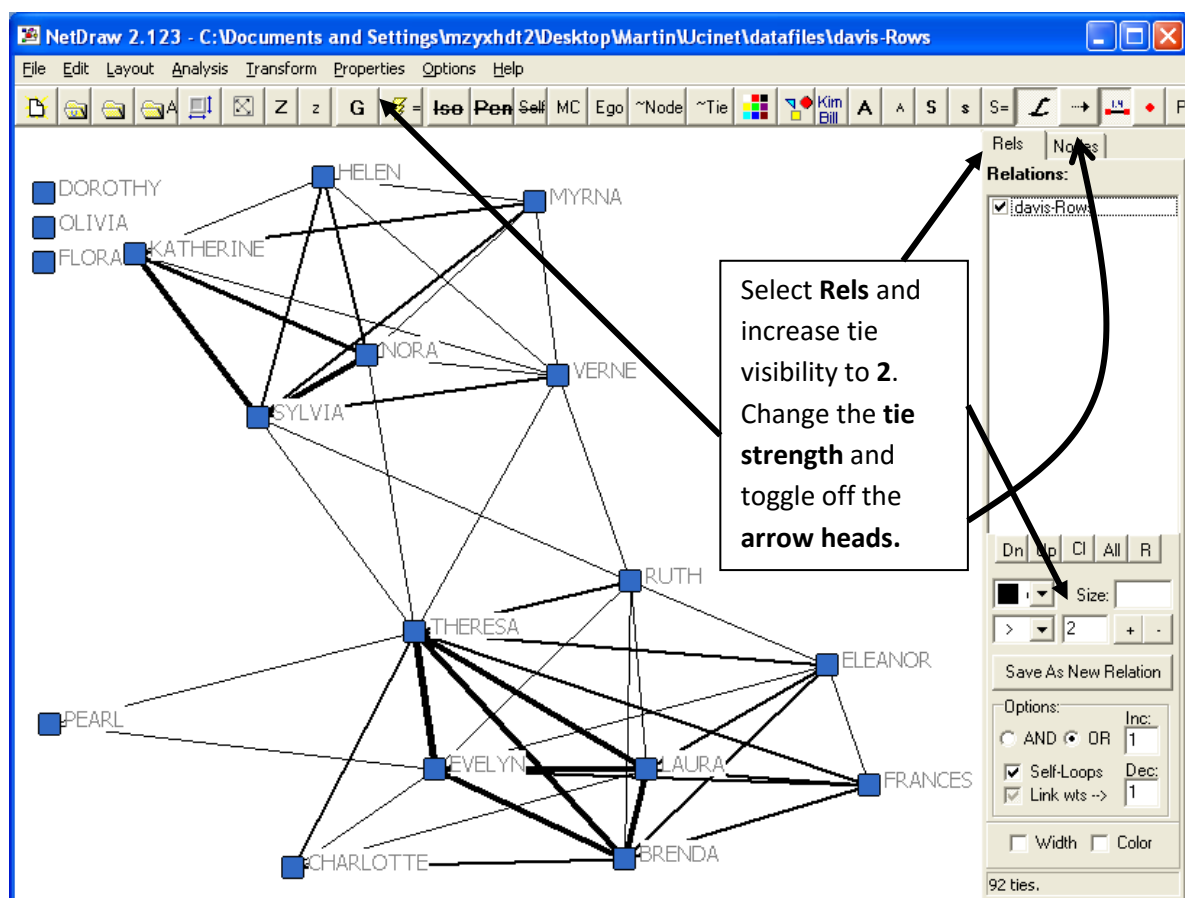
Use this attribute to both colour and shapes the nodes. Finally (and this needs to be done last) position the nodes using the created co-ordinates MetricMdsCoord. This is done by clicking File|Open|Ucinet dataset|coordinates and then selecting MetricMdsCorod



Section 13.2 Converting to One-Mode Data

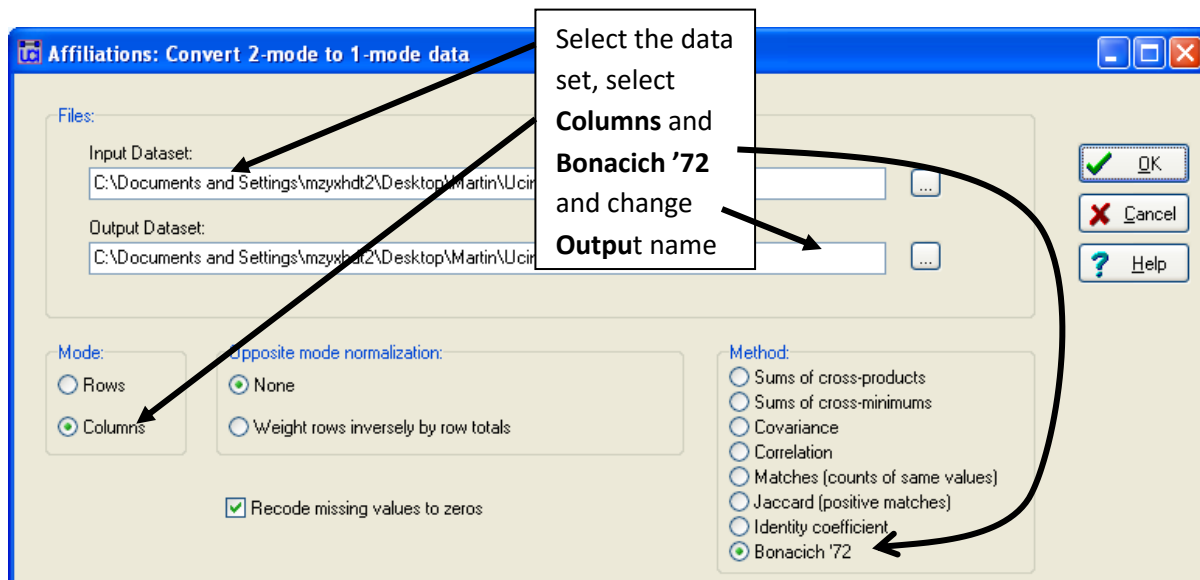
To convert a Two-Mode data set, like the **davis.##h** data into a One-Mode matrix, simply go to **Data|Affiliations (2-mode to 1-mode)** and open the **davis.##h** file and click OK. The output log file should match Matrix 13.2 and the matrix is saved as **davis-Rows.##h**.

To visualise the network, open **NetDraw** and select the **davis-Rows.##h** file. The result will show a relatively dense network because most of the women have attended at least one event together. Therefore we are increasing the minimum tie strength to “two” in the options for **Rels** to the right. Then go to **Property|Lines|Size|Tie strength** to represent the number of events attended in the thickness of the tie and turn off the **arrow heads** by clicking the arrow-symbol in the **toolbar**. The result should be similar to **Figure 13.1**.



The **event-by-event matrix 13.3** is generated like the woman-by-woman matrix by loading the **davis.##h** dataset in the Affiliations (2-mode to 1-mode) procedure; however, this time we need to collect the Mode “**Columns**” in the bottom left corner. The output will be saved as **davis-Columns.##h**.

The event-by-event **matrix 13.4** is generated in the same way but with the selection of **Bonacich '72** made in the Methods box. Please be aware that this will **overwrite** the previous result **davis-Columns.##h** unless the output dataset is renamed (for example into **davis-Column72.##h**). The resulting log file is shown below.



ucinetlog65.txt - Notepad

File Edit Format View Help

		1	2	3	4	5	6	7	8	9	10	11	12	13
		E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	E13
1	E1	1.000	0.841	1.000	0.783	1.000	1.000	0.569	1.000	0.299	0.000	0.000	0.000	0.000
2	E2	0.841	1.000	1.000	0.783	1.000	1.000	0.569	1.000	0.500	0.000	0.000	0.000	0.000
3	E3	1.000	1.000	1.000	1.000	1.000	0.795	0.586	0.564	0.240	0.000	0.000	0.000	0.000
4	E4	0.783	0.783	1.000	1.000	1.000	0.699	0.634	0.475	0.387	0.000	0.000	0.000	0.000
5	E5	1.000	1.000	1.000	1.000	1.000	0.776	0.680	0.634	0.205	0.000	0.000	0.000	0.000
6	E6	1.000	1.000	0.795	0.699	0.776	1.000	0.564	0.634	0.333	0.316	0.366	0.274	0.431
7	E7	0.569	0.569	0.586	0.634	0.680	0.564	1.000	0.536	0.274	0.531	0.464	0.586	0.569
8	E8	1.000	1.000	0.564	0.475	0.634	0.634	0.536	1.000	0.436	0.523	0.138	0.564	0.414
9	E9	0.299	0.500	0.240	0.387	0.205	0.333	0.274	0.436	1.000	0.613	0.564	0.654	1.000
10	E10	0.000	0.000	0.000	0.000	0.000	0.316	0.531	0.523	0.613	1.000	0.657	1.000	1.000
11	E11	0.000	0.000	0.000	0.000	0.000	0.366	0.464	0.138	0.564	0.657	1.000	0.613	0.586
12	E12	0.000	0.000	0.000	0.000	0.000	0.274	0.586	0.564	0.654	1.000	0.613	1.000	1.000
13	E13	0.000	0.000	0.000	0.000	0.000	0.431	0.569	0.414	1.000	1.000	0.586	1.000	1.000
14	E14	0.000	0.000	0.000	0.000	0.000	0.431	0.569	0.414	1.000	1.000	0.586	1.000	1.000


rows, 14 columns, 1 levels.

ode matrix saved as: davis-columns (C:\Documents and Settings\mzyxhdt2\...

Again the event-by-event (**davis-Column.###**) matrix can be visualised repeating the steps used to visualise the woman-by-woman matrix and represent tie-strength by line thickness. Enter **0.5** to set the **minimum tie-strength** visualised in the network (because we have normalised the dataset using **Bonacich '72** values are between 0 and 1 and we select a cut-off point of 0.5).

Section 13.4 Bipartite Networks

To create a bipartite network from a two-mode dataset simply run Transform|Graph Theoretic|Bipartite



Bipartite

Input 2-mode dataset: ...

Value to fill within-mode ties:

Make result symmetric? ▼

Prefix for row entities:

Prefix for column entities:

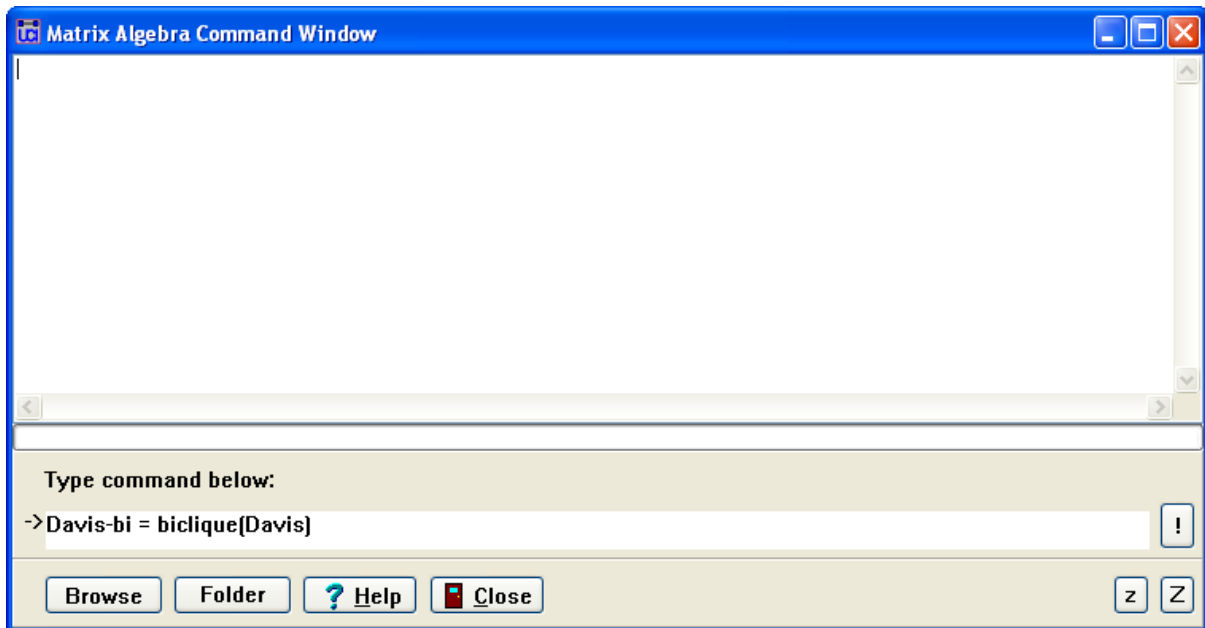
Output dataset: ...

OK Cancel Help

This will create the dataset Davis-Bip as shown in Matrix 13.5.

Section 13.5 Cohesive Subgroups

Unfortunately automated bi-cliques has not been fully implemented but it is available as a command in matrix algebra in versions later than 6.487. The command has the form $\rightarrow \text{biclique}(\text{filename } x \ y)$ where x is the minimum size of mode 1 (the rows) and y is the minimum size of mode 2 (the columns) if these are omitted it has a default of 3 for each mode. The output has each bi-clique as a column with the nodes in the rows and a 1 in row i column j indicating that node i is a member of bi-clique j . To find the (3,3) bi-cliques of the Davis data we run matrix algebra and then type $\rightarrow \text{Davis-bi} = \text{biclique}(\text{Davis})$ as follows



If we display Davis-bi we get

		1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2																							
		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8	9	0	1	2		
		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
1	EVELYN	0	1	0	0	1	1	1	1	0	0	0	1	0	0	1	0	0	1	0	0	0	0		
2	LAURA	0	0	0	0	0	1	1	0	1	1	1	1	0	0	1	1	0	0	0	0	0			
3	THERESA	1	1	0	0	1	1	1	1	1	1	1	0	0	0	1	1	1	1	0	0	0			
4	BRENDA	0	0	0	0	0	1	1	1	1	1	1	1	0	0	0	1	1	1	0	0	0			
5	CHARLOTTE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0			
6	FRANCES	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
7	ELEANOR	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0			
8	PEARL	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
9	RUTH	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0			
10	VERNE	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1			
11	MYRNA	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0			
12	KATHERINE	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	1	0			
13	SYLVIA	1	0	1	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	1	1			
14	NORA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1			
15	HELEN	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	1			
16	DOROTHY	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
17	OLIVIA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
18	FLORA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
19	E1	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0			
20	E2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0			
21	E3	0	0	0	0	0	0	1	1	0	0	1	1	0	0	1	1	1	1	0	0	0			
22	E4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	1	0	0	0			
23	E5	0	0	0	0	1	1	1	1	1	1	1	1	0	0	1	1	1	1	0	0	0			
24	E6	0	1	0	0	0	1	1	1	0	1	1	1	0	0	1	0	0	0	0	0	0			
25	E7	1	0	0	0	0	0	0	0	1	1	1	0	1	0	0	1	1	0	0	0	1			
26	E8	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0			
27	E9	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1			
28	E10	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	1	0			
29	E11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
30	E12	0	0	1	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	1	1			
31	E13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0			
32	E14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0			

We now create the co-membership matrix by running Data|Affiliations on this output.

Affiliations: Convert 2-mode to 1-mode data

Files:

Input Dataset: ...

Output Dataset: ...

Mode:

☒ Rows

☐ Columns

Opposite mode normalization:

☒ None

☐ Weight columns inversely by column totals

☒ Recode missing values to zeros

Method:

☒ Sums of cross-products

☐ Sums of cross-minimums

☐ Covariance

☐ Correlation

☐ Matches (counts of same values)

☐ Jaccard (positive matches)

☐ Identity coefficient

☐ Bonacich '72

OK Cancel Help

Finally running Tools|Cluster Analysis|Hierarchical and selecting similarities and the simple average method as shown below gives Figure 13.4.

Johnson's Hierarchical Clustering

Data

Input dataset: ...

Similarities or Dissimilarities: ...

Output Partition Matrix: ...

Output Ultrametric Matrix (if desired): ...

Parameters

Method: ...

Graphical dendrogram: ...

Textual dendrogram: ...

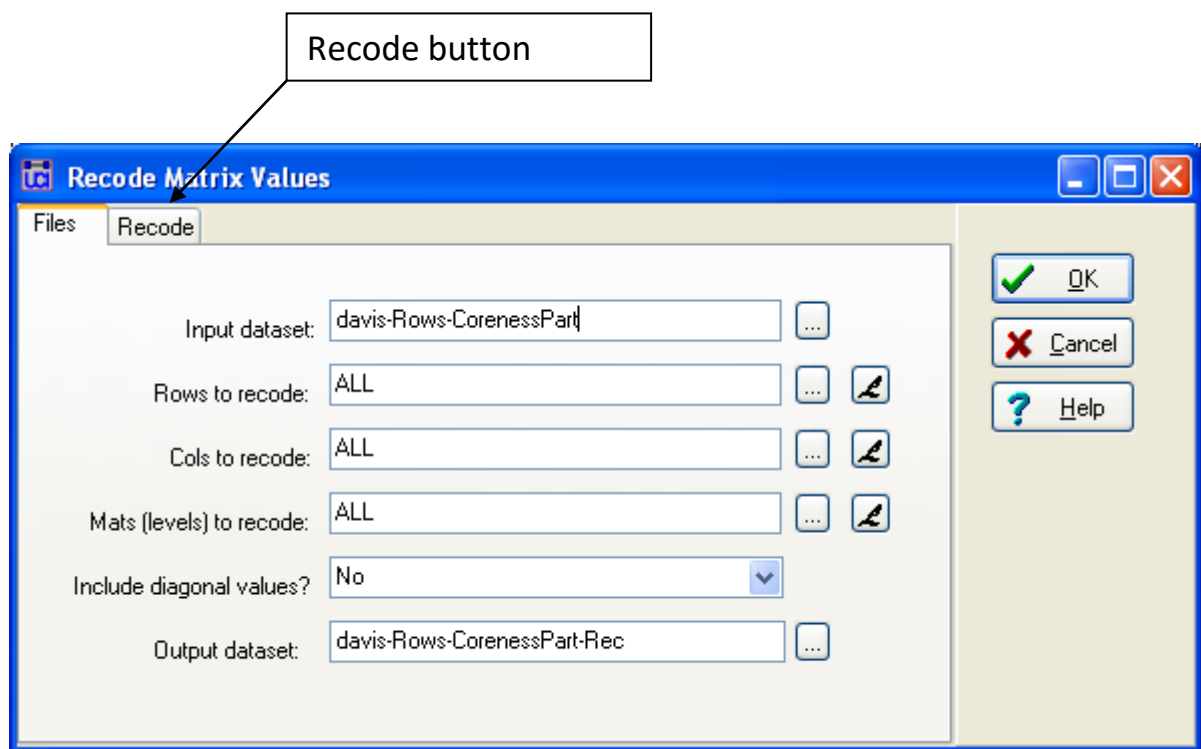
Maximum label length: ...

Compute ultrametric proximity matrix: ...

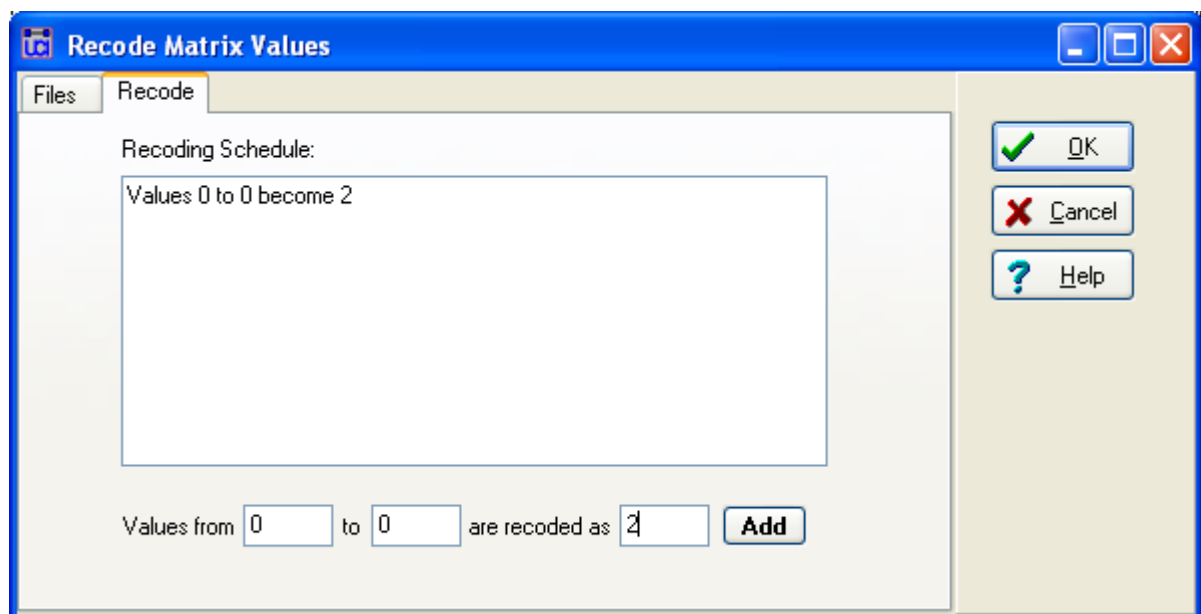
OK Cancel Help

Section 13.6 Core-Periphery Models

The first thing to do is create davis-Rows and davis-Columns as described in section 13.2. Now run the continuous core-periphery routine on each of these as shown in section 12.8. We now need to recode the two files davis-Rows-corenessPart and davis-Columns-corenessPart. Run Transform|Recode to bring up the following and type in or select the first dataset as shown

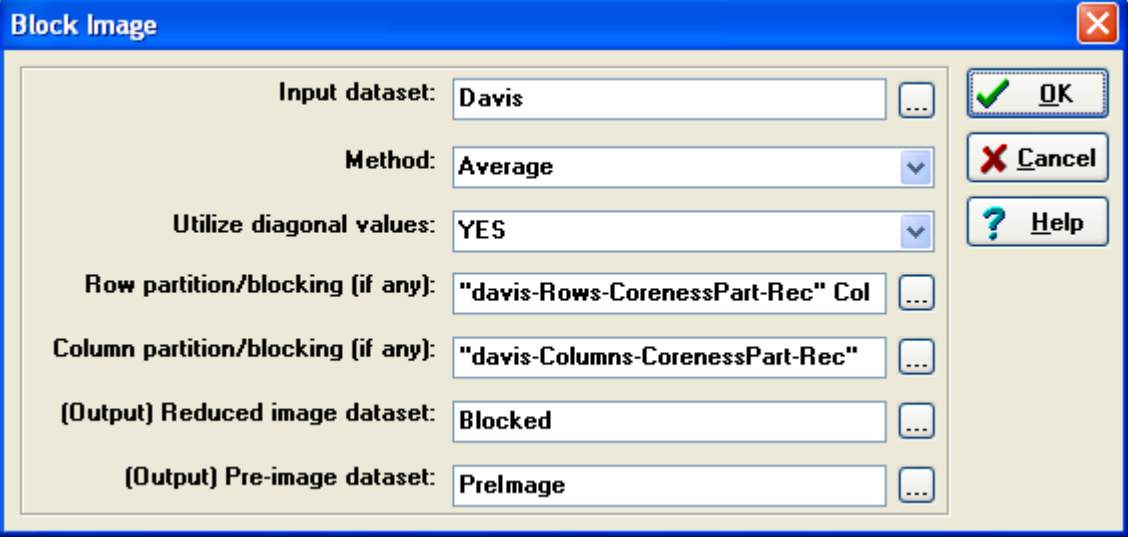


Click on the recode button to show the following window complete the values boxes as shown click add then run the routine.



You need to repeat the same procedure davis-Columns-CorenessPart. We can no use these to get a core-periphery partition of Davis. Run Transform|Aggregate|Block with input data as Davis with the row partition as davis-Rows-CorenessPart-Rec and the column partition as davis-Columns-

CorenessPart-Rec as shown below.



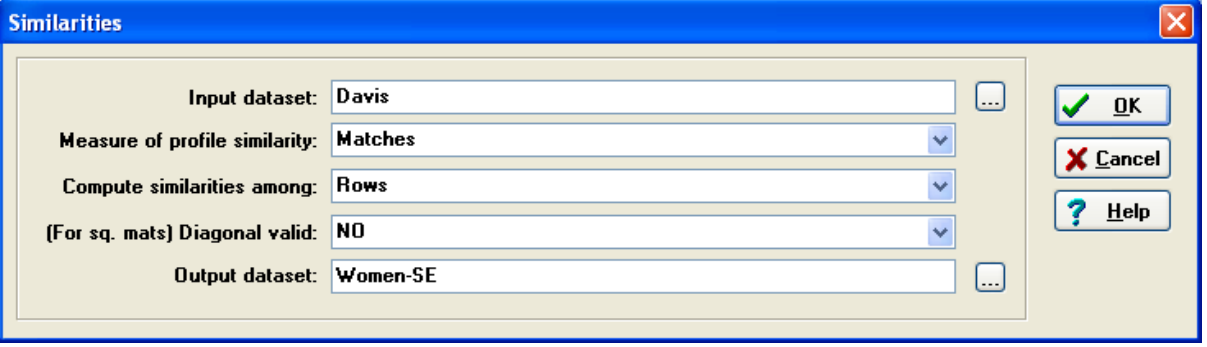
The 'Block Image' dialog box has a blue title bar with a close button. It contains several input fields and buttons. The 'Input dataset' field is set to 'Davis'. The 'Method' dropdown is set to 'Average'. The 'Utilize diagonal values' dropdown is set to 'YES'. The 'Row partition/blocking (if any)' field is set to '"davis-Rows-CorenessPart-Rec" Col'. The 'Column partition/blocking (if any)' field is set to '"davis-Columns-CorenessPart-Rec"'. The '(Output) Reduced image dataset' field is set to 'Blocked'. The '(Output) Pre-image dataset' field is set to 'PreImage'. On the right side, there are three buttons: 'OK' with a green checkmark, 'Cancel' with a red X, and 'Help' with a question mark.

Input dataset:	Davis	...
Method:	Average	▼
Utilize diagonal values:	YES	▼
Row partition/blocking (if any):	"davis-Rows-CorenessPart-Rec" Col	...
Column partition/blocking (if any):	"davis-Columns-CorenessPart-Rec"	...
(Output) Reduced image dataset:	Blocked	...
(Output) Pre-image dataset:	PreImage	...

If you now click OK you will get the core-periphery image as shown in Figure 13.5.

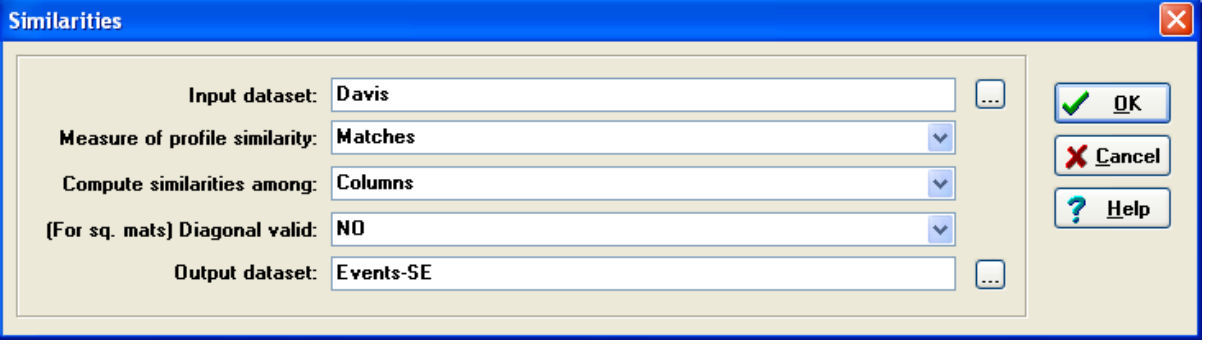
Section 13.7 Equivalence

The structural equivalence for the women and events are found by running Tools|Similarities and we label the output as women-SE when we calculate matches across the rows and Events-SE when we calculate across the columns as follows



The 'Similarities' dialog box has a blue title bar with a close button. It contains several input fields and buttons. The 'Input dataset' field is set to 'Davis'. The 'Measure of profile similarity' dropdown is set to 'Matches'. The 'Compute similarities among' dropdown is set to 'Rows'. The '(For sq. mats) Diagonal valid' dropdown is set to 'NO'. The 'Output dataset' field is set to 'Women-SE'. On the right side, there are three buttons: 'OK' with a green checkmark, 'Cancel' with a red X, and 'Help' with a question mark.

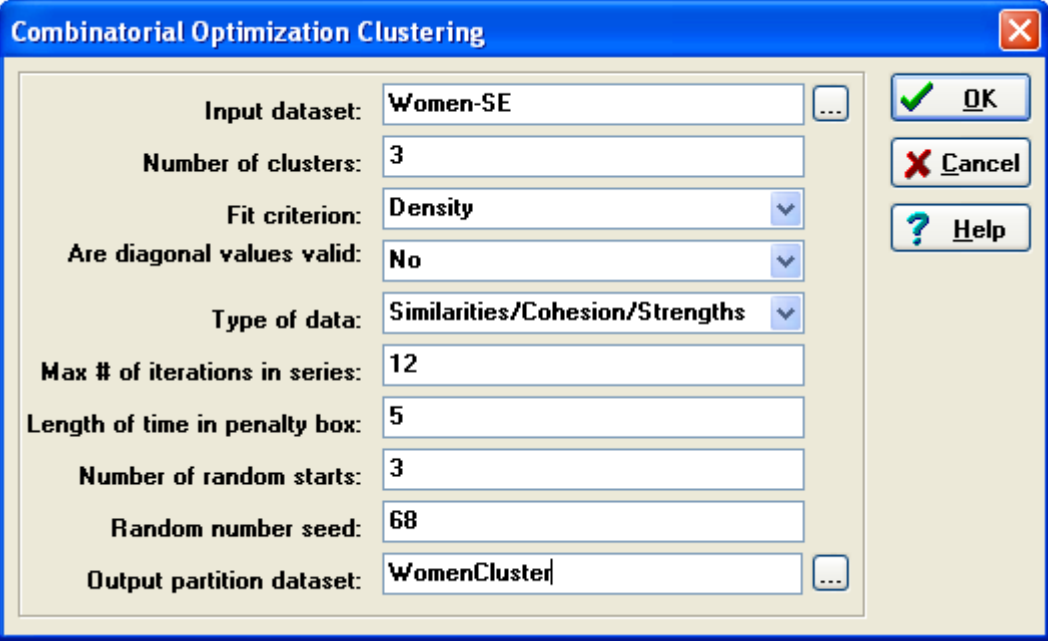
Input dataset:	Davis	...
Measure of profile similarity:	Matches	▼
Compute similarities among:	Rows	▼
(For sq. mats) Diagonal valid:	NO	▼
Output dataset:	Women-SE	...



The 'Similarities' dialog box has a blue title bar with a close button. It contains several input fields and buttons. The 'Input dataset' field is set to 'Davis'. The 'Measure of profile similarity' dropdown is set to 'Matches'. The 'Compute similarities among' dropdown is set to 'Columns'. The '(For sq. mats) Diagonal valid' dropdown is set to 'NO'. The 'Output dataset' field is set to 'Events-SE'. On the right side, there are three buttons: 'OK' with a green checkmark, 'Cancel' with a red X, and 'Help' with a question mark.

Input dataset:	Davis	...
Measure of profile similarity:	Matches	▼
Compute similarities among:	Columns	▼
(For sq. mats) Diagonal valid:	NO	▼
Output dataset:	Events-SE	...

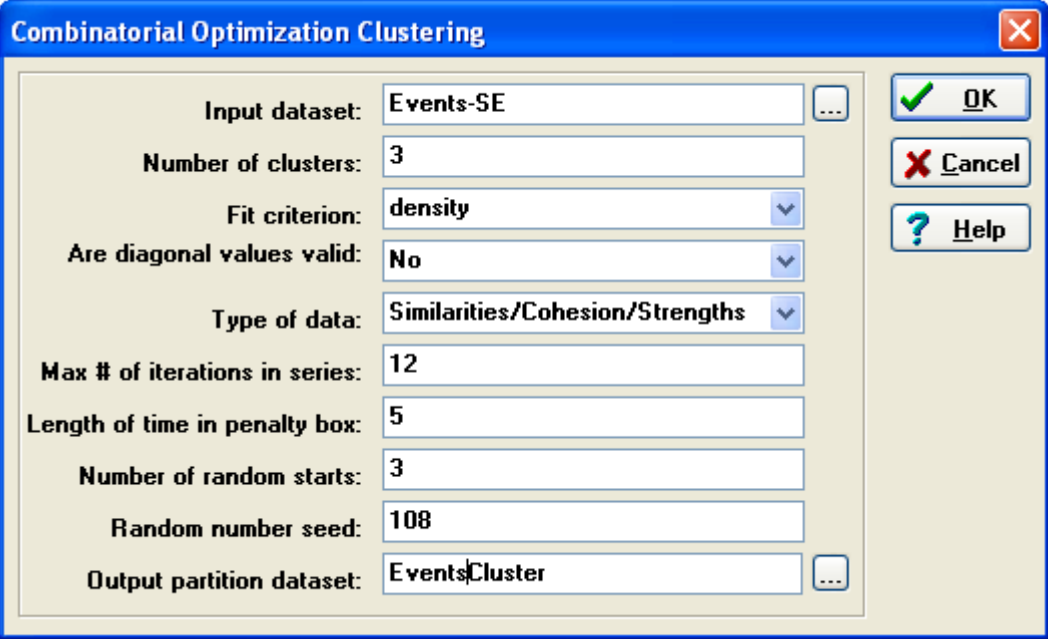
We then submit the output of each of these to the Tools|Cluster Analysis|Optimization selecting 3 clusters and calling the output dataset WomenCluster



The screenshot shows the 'Combinatorial Optimization Clustering' dialog box. The 'Input dataset' is 'Women-SE'. The 'Number of clusters' is set to 3. The 'Fit criterion' is 'Density'. The 'Are diagonal values valid' checkbox is unchecked, with 'No' selected in the dropdown. The 'Type of data' is 'Similarities/Cohesion/Strengths'. The 'Max # of iterations in series' is 12. The 'Length of time in penalty box' is 5. The 'Number of random starts' is 3. The 'Random number seed' is 68. The 'Output partition dataset' is 'WomenCluster'. On the right, there are buttons for 'OK' (with a green checkmark), 'Cancel' (with a red X), and 'Help' (with a question mark).

Input dataset:	Women-SE
Number of clusters:	3
Fit criterion:	Density
Are diagonal values valid:	No
Type of data:	Similarities/Cohesion/Strengths
Max # of iterations in series:	12
Length of time in penalty box:	5
Number of random starts:	3
Random number seed:	68
Output partition dataset:	WomenCluster

This leads to a partition of the rows as shown in Figure 13.7, we repeat the process for the columns.



The screenshot shows the 'Combinatorial Optimization Clustering' dialog box. The 'Input dataset' is 'Events-SE'. The 'Number of clusters' is set to 3. The 'Fit criterion' is 'density'. The 'Are diagonal values valid' checkbox is unchecked, with 'No' selected in the dropdown. The 'Type of data' is 'Similarities/Cohesion/Strengths'. The 'Max # of iterations in series' is 12. The 'Length of time in penalty box' is 5. The 'Number of random starts' is 3. The 'Random number seed' is 108. The 'Output partition dataset' is 'EventsCluster'. On the right, there are buttons for 'OK' (with a green checkmark), 'Cancel' (with a red X), and 'Help' (with a question mark).

Input dataset:	Events-SE
Number of clusters:	3
Fit criterion:	density
Are diagonal values valid:	No
Type of data:	Similarities/Cohesion/Strengths
Max # of iterations in series:	12
Length of time in penalty box:	5
Number of random starts:	3
Random number seed:	108
Output partition dataset:	EventsCluster

Finally to get the blockmodel shown in Figure 13.8 we apply the clustering to the rows and columns of Davis using Transform|Aggregate (including CSS)|Block using the clusters found above as follows

Block Image

×

Input dataset: Davis

Method: Average

Utilize diagonal values: Yes

Row partition/blocking (if any): WomenCluster col 1

Column partition/blocking (if any): EventsCluster col 1

(Output) Reduced image dataset: Blocked

(Output) Pre-image dataset: Prelmage

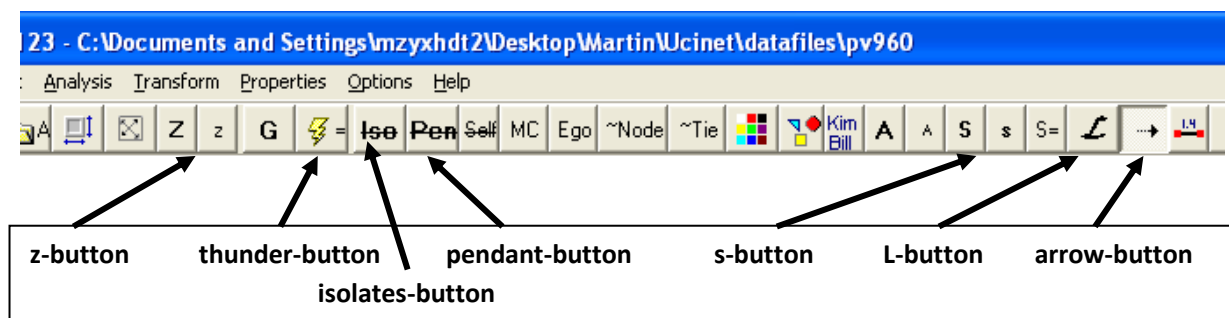
✓ OK

✗ Cancel

? Help

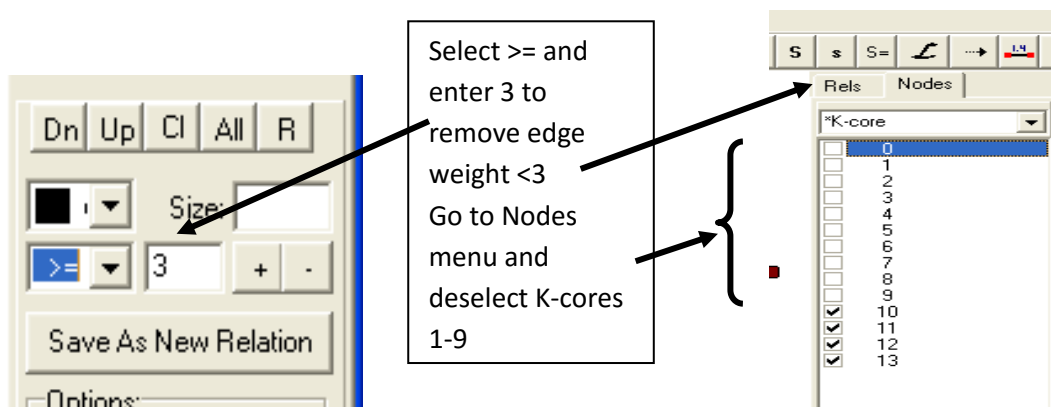
Section 14.2 Reducing the Size of the Problem

To visualise the **PV960.##h** dataset as in **Figures 14.1** and **14.2** open the matrix in **NetDraw**. Once loaded (**Note:** this may take longer than with small matrices) you may have to zoom out using the **z-button** in the **toolbar** and reorganise the network by clicking the **thunderbolt-button** (if you hold your mouse over the button it should say “layout w/ noder repulsion and equal edge length bias”). Following this you should see a less square network. Now turn off the node labels (**L-button** in the toolbar) and the arrow heads (**arrow-button** next to L-button), and reduce the size of the nodes by clicking repeatedly on the **s-button**. Finally click on the **pendant-button** to delete pendants (nodes with degree 1).



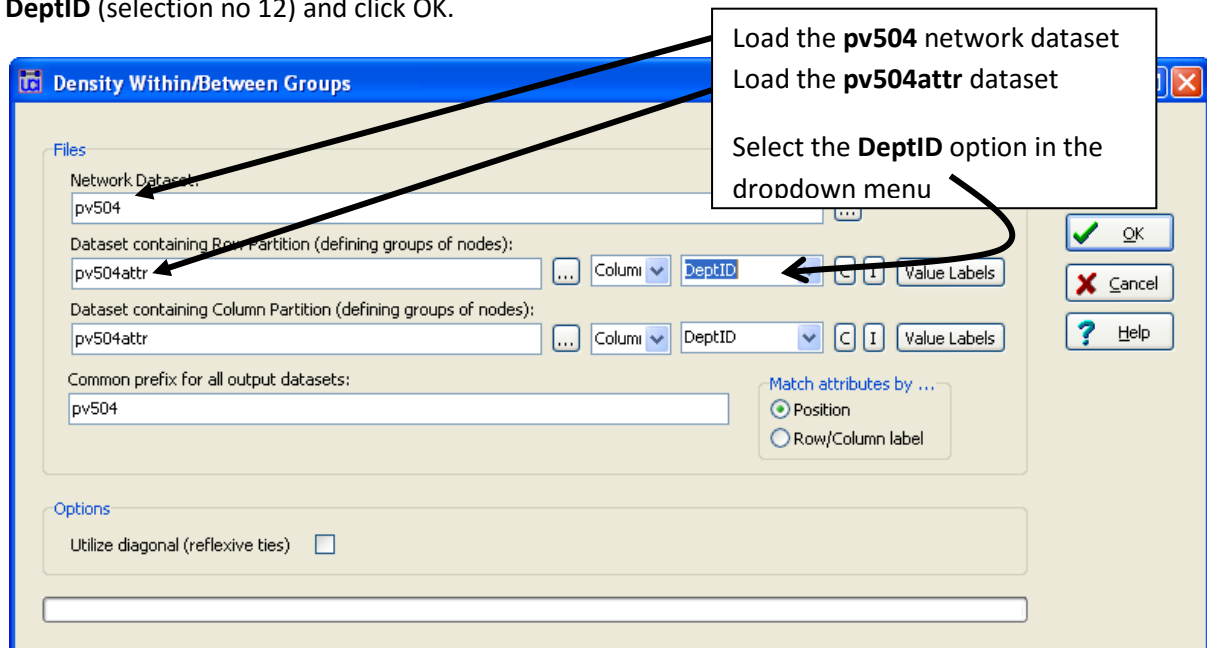
For **Figure 14.2**, simply remove edge weights of less than “3” as done previously in the **Rels-** menu to the right. Then remove the isolates by clicking on the **isolate-button** and NewDraw will visualise Figure 14.2.

To illustrate **Figure 14.3** click **Analysis|K-cores**. Now go to the **Nodes**-menu to the right and select ***K-core**. Remove the ticks in the first 9 boxes and reorganise the network by click on the **thunderbolt-button**.



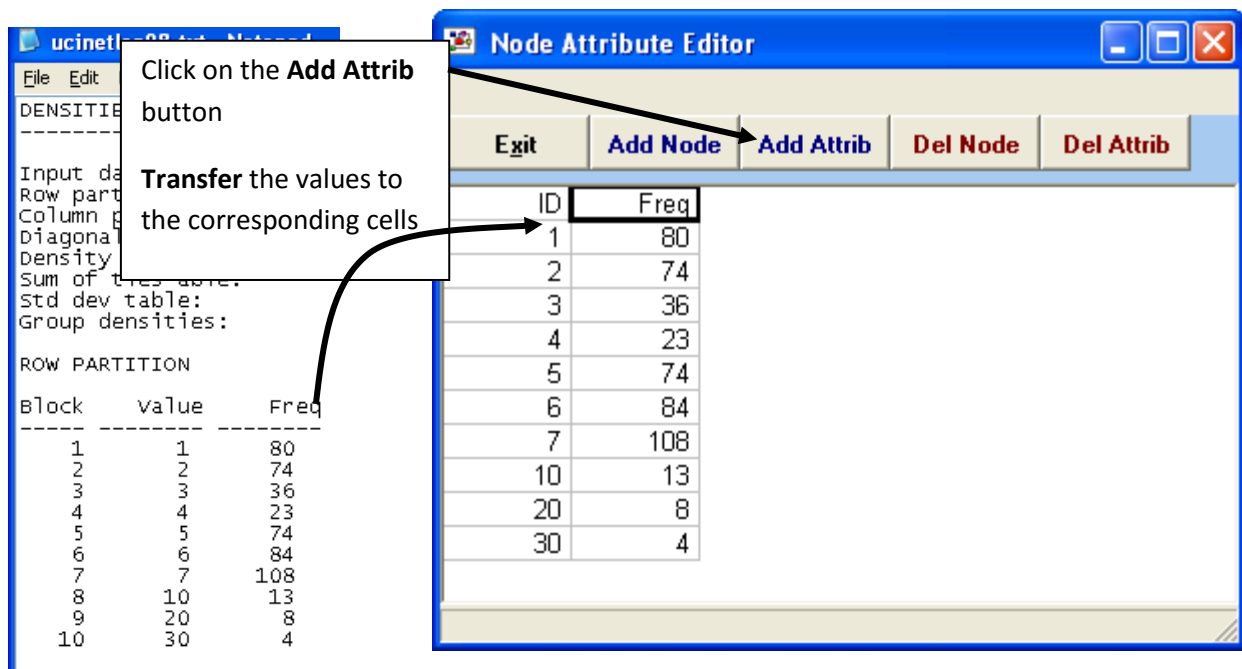
Section 14.2.4 Aggregation

To run the Group by Density routine go to **Network|Cohesion|Density|Density by Groups** and open the **pv504.###** dataset. Load **pv504attr.###** dataset which contains the row partition and select **DeptID** (selection no 12) and click OK.



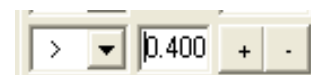
A new log file will open and the results shown in **Matrix 14.1** can be found about half way down the log file in a matrix titled “**Density (prop of ties) / Average tie strength**”. (Note: keep the log file open)


To visualise this relation as shown in **Figure 14.4** go to **NetDraw** and open the **pv504-den.###** dataset. To adjust the **node size** by using the average department size we must create an **attribute** file. To do this go to **Transform|Node attribute editor**. The editor will display a column named **ID** and list the **10** departments. Click the **Add Attrib** button and transfer the **Freq**-values displayed in the **log file** under **ROW PARTITIONING** (towards the top of the log file) into the **corresponding cells** in the **Node attribute editor**. Close the editor by clicking on **Exit**.



Now go to **Properties | Nodes | Symbols | Size | Attribute based** and select the **Freq** attribute. Adjust **Maximum node size** to **"10"** and click **OK**. Now set the shape of symbols to circles (**Properties | Nodes | Symbols | Shape | General - all active nodes**). Remove connections that are

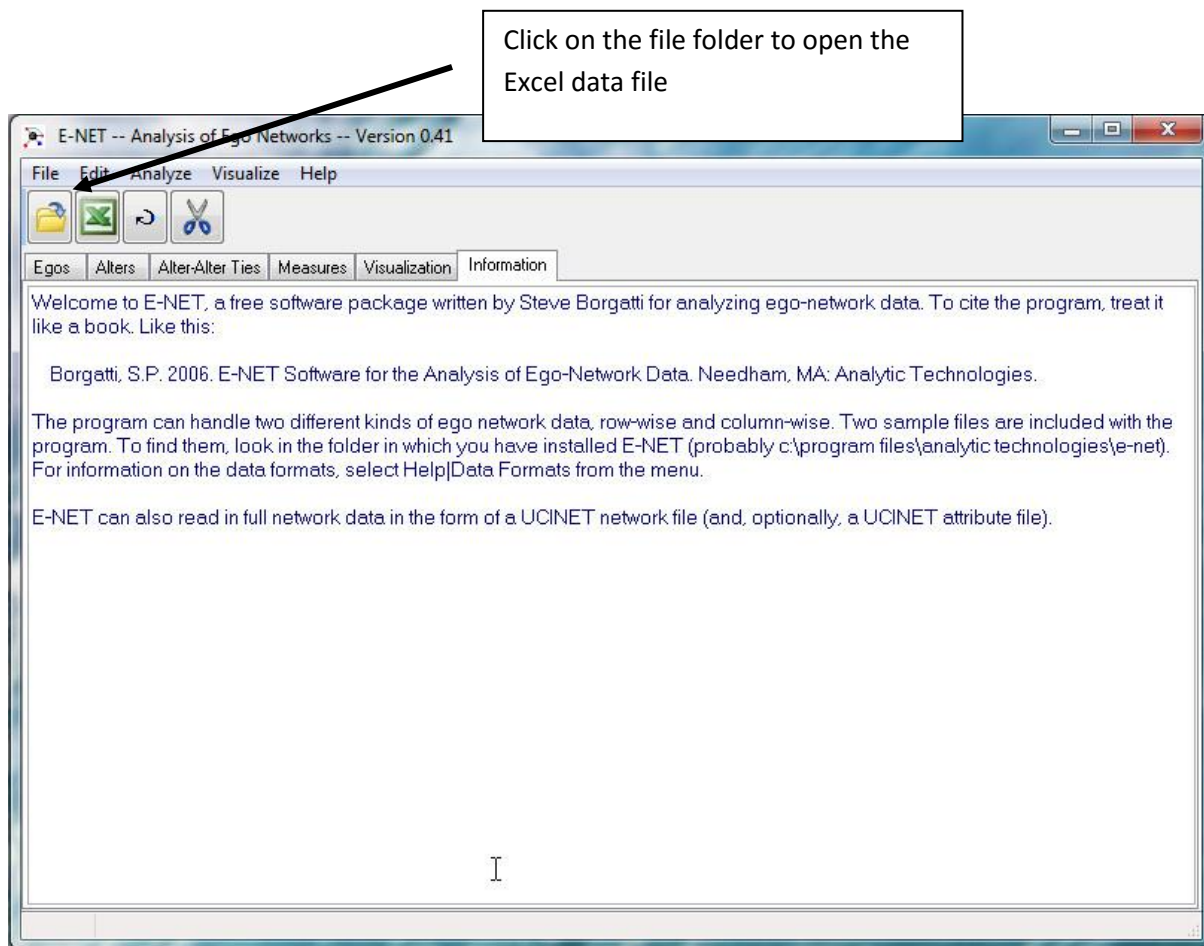
smaller than **0.4** by going into the **Rels**-menu and adjust the selection to



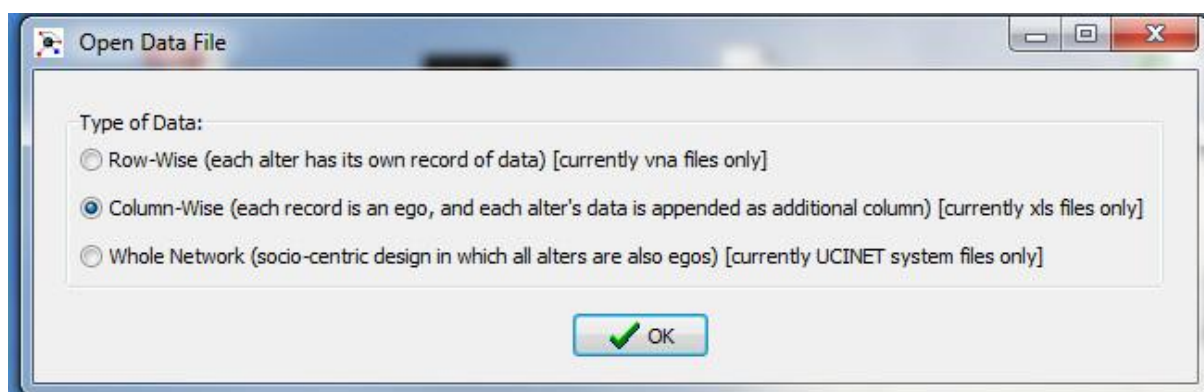
and press the **thunderbolt**-button (Note: you may want to **flip** the network by going into  and by clicking the left-facing arrow-button).

Section 15.5 Example 2 of an ego network study

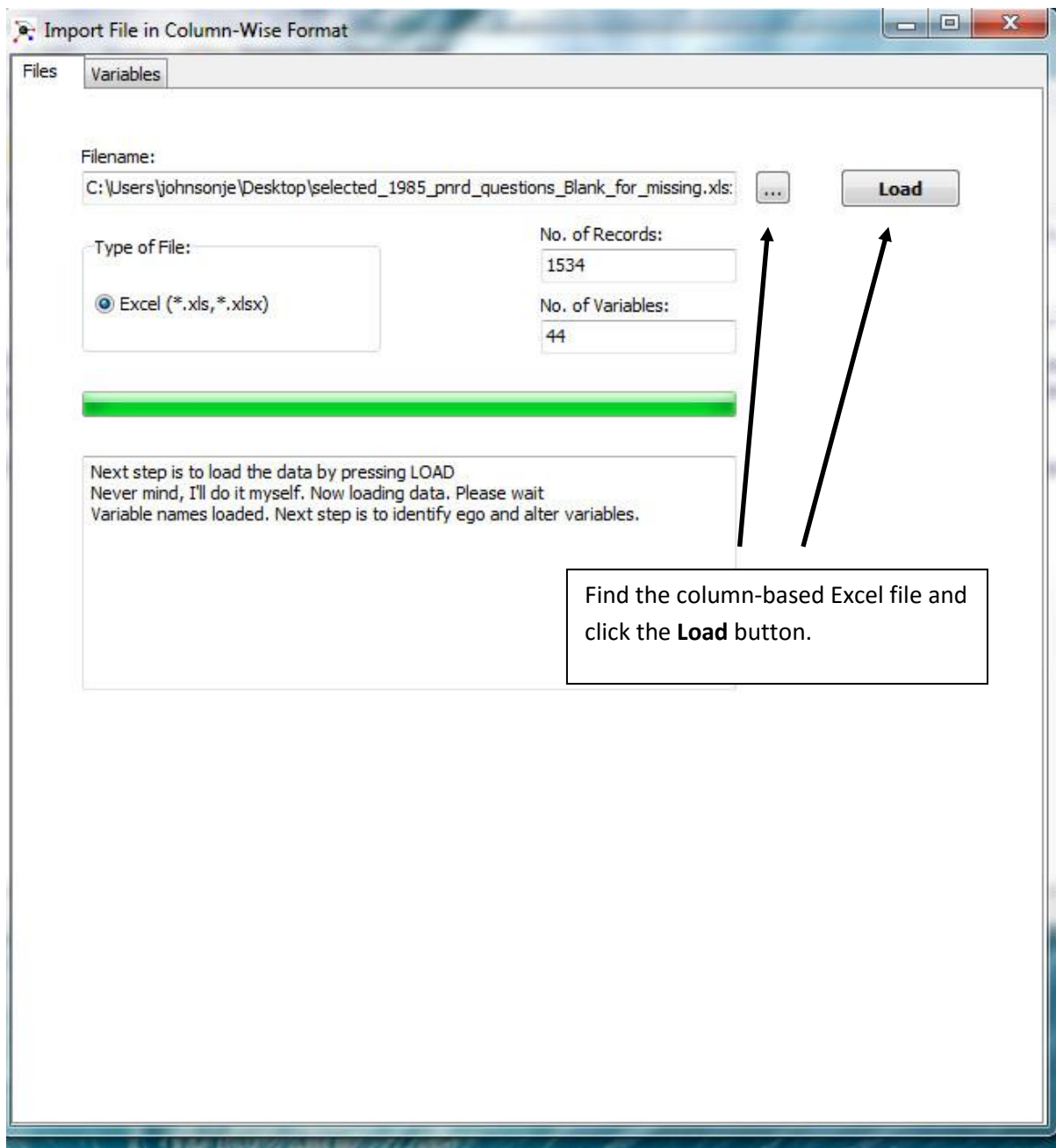
To run the structural holes measures on the GSS column-based data format an Excel data file can be directly opened by E-Net.



This will open a screen asking the type of data you wish to open. Note that each of the data types will read only specific file types. Since this is a column-wise data format it is an Excel file type.



Click **OK** and a separate window will query about for the location of the file to be loaded.



The file will be loaded into a separate window and then you will need to select the variables to be used in the analysis. In this case we will load all variables.

Import File in Column-Wise Format

Files Variables

Variables in Source File:

- id_Original
- sex
- race
- degree
- rincome
- rdclose1
- age1
- sex1
- educ1
- race1
- relig1
- rdclose2
- age2
- sex2
- educ2
- race2
- relig2
- rdclose3
- age3
- sex3
- educ3
- race3
- relig3
- rdclose4
- age4
- sex4
- educ4
- race4
- relig4
- rdclose5
- age5
- sex5
- educ5
- race5

>

<

Ego Variables:

OK

Cancel

Ego-Alter Ties and Perceptions:

>

<

Alter-Alter Ties

☒ Ignore zeros

Use "Auto" button to automatically identify the different kinds of data

Auto

Format of Alter data:

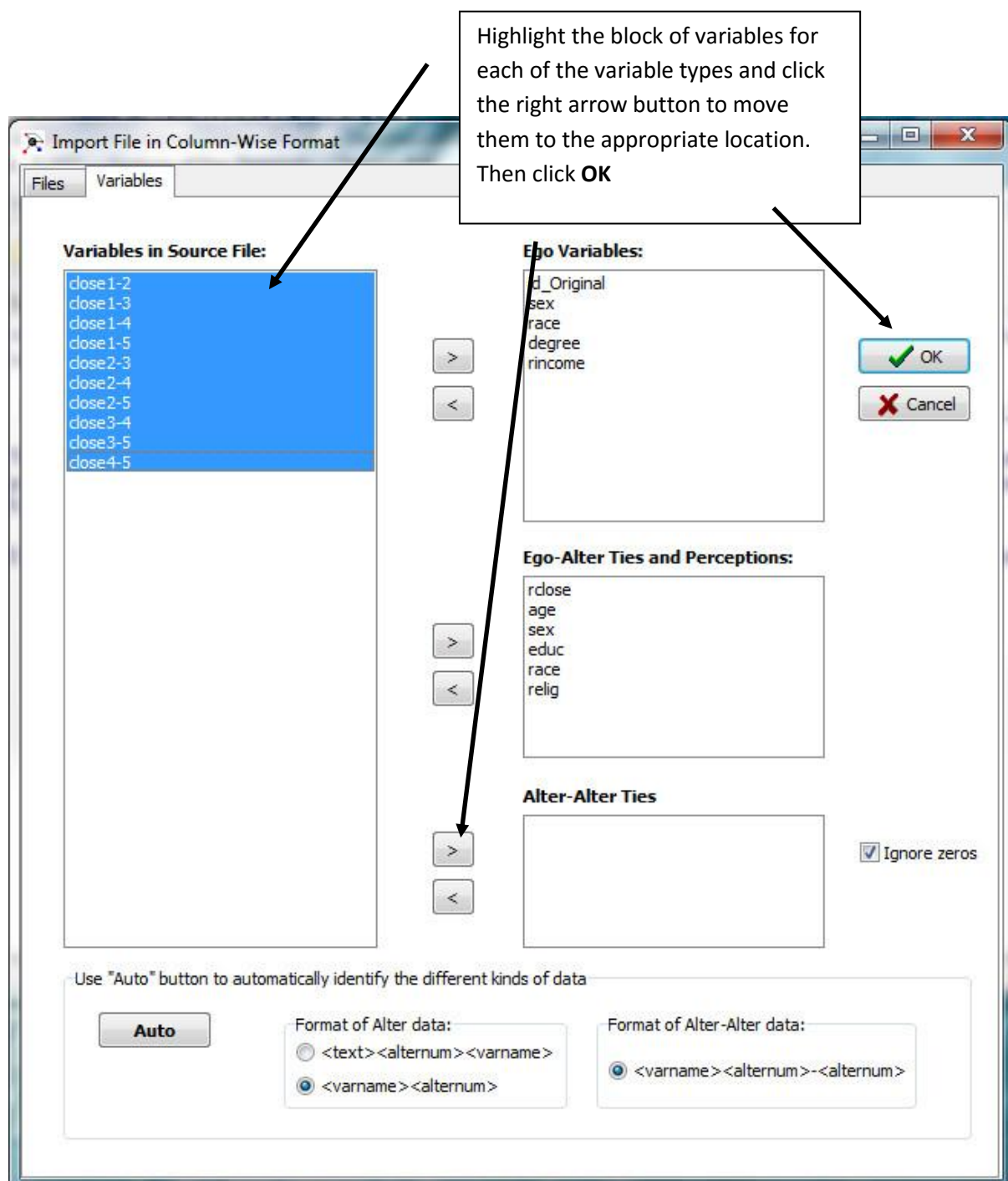
☐ <text><altnum><varname>

☒ <varname><altnum>

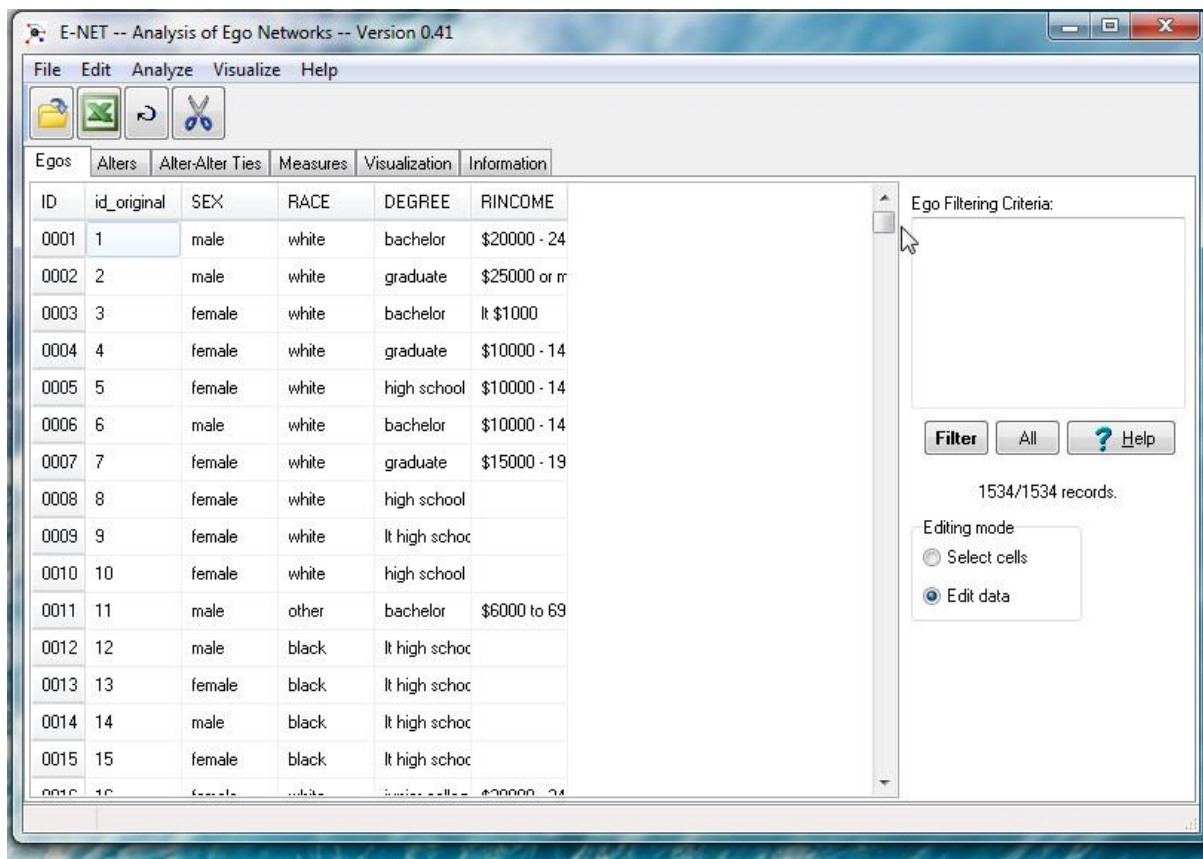
Format of Alter-Alter data:

☒ <varname><altnum>-<altnum>

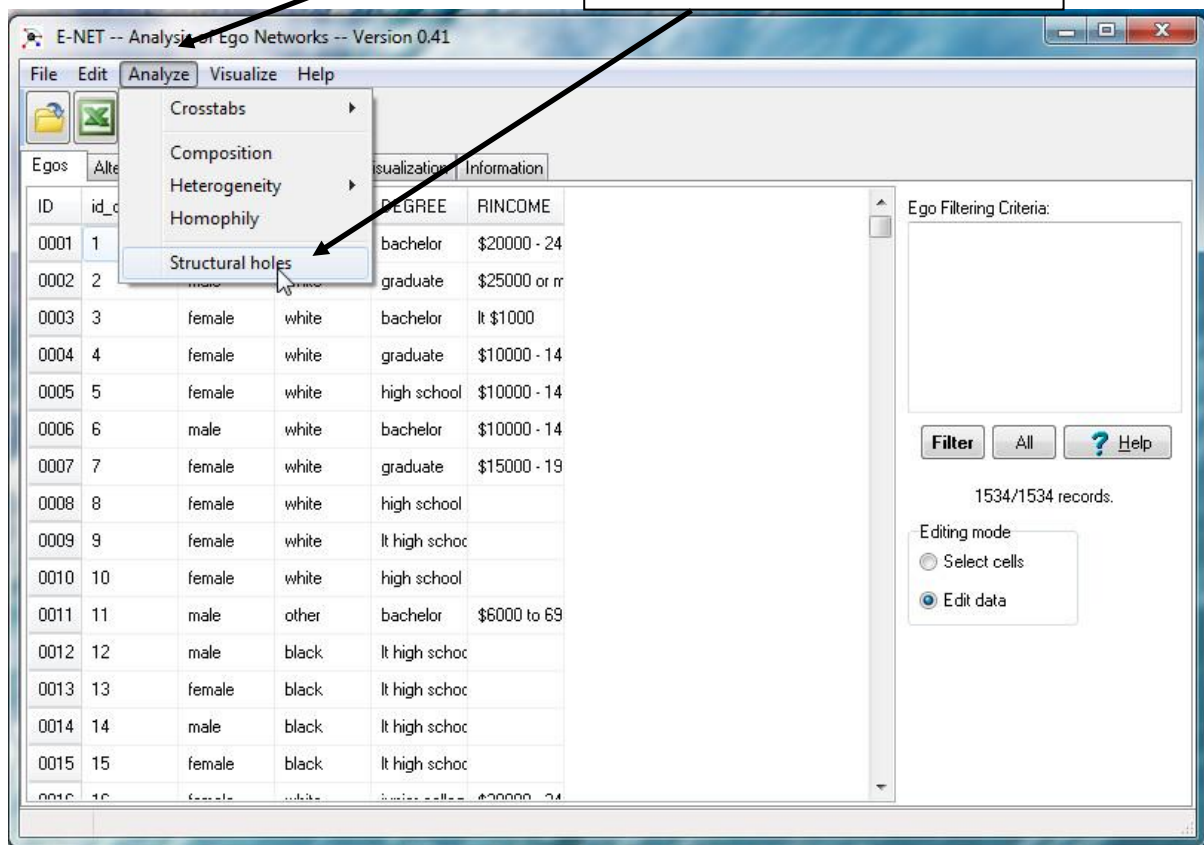
Highlight the variables on the left and click on the arrow in the middle to move the different types of variables into their appropriate box.



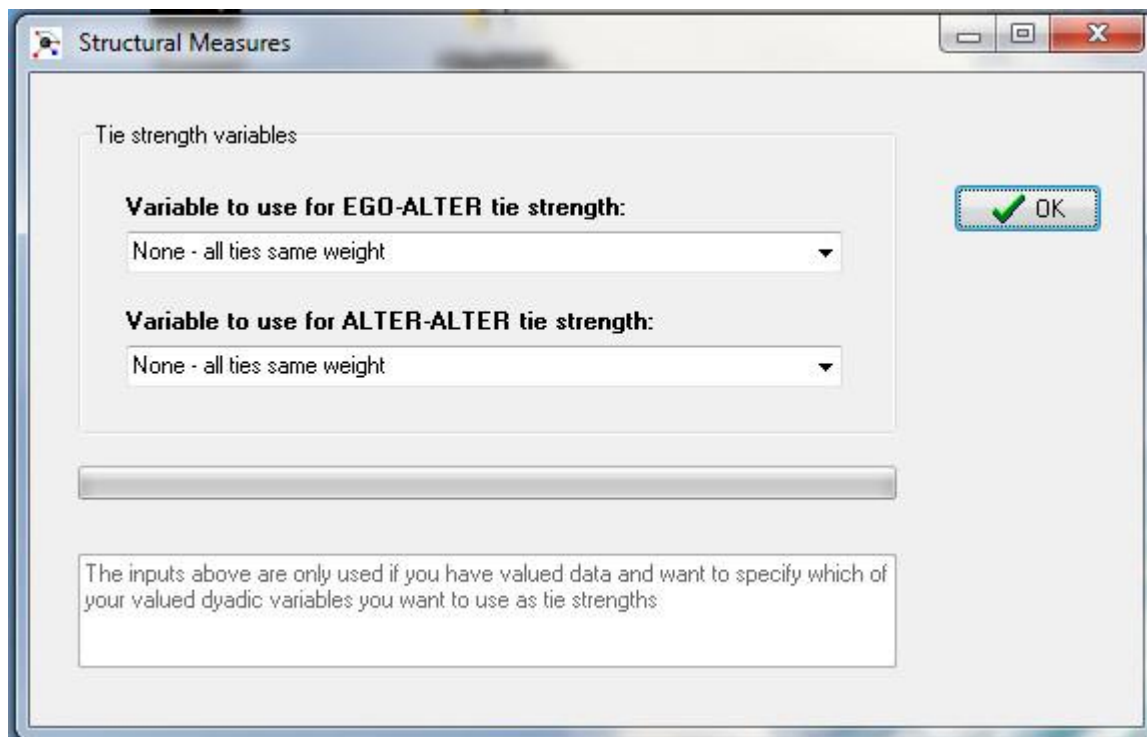
Data will be imported and is now ready for analysis and visualization.



To analyse the data click on the **Analysis Menu**. And then click on **Structural holes**.



A window will then query about how you want to handle the strength of EGO-ALTER and ALTER-ALTER ties. For this analysis there is no weighting. Click **OK** to proceed with the analysis.



E-NET -- Analysis of Ego Networks -- Version 0.41

File Edit Analyze Visualize Help

Egos Alters Alter-Alter Ties Measures Visualization Information

ID	SH:Degree	SH:Density	SH:Effsize	SH:Efficiency
0001	5	0.000	5.000	1.000
0002	5	0.000	5.000	1.000
0003	5	0.000	5.000	1.000
0004	5	0.000	5.000	1.000
0005	5	0.000	5.000	1.000
0006	4	0.000	4.000	1.000
0007	5	0.000	5.000	1.000
0008	5	0.000	5.000	1.000
0009	2	0.000	2.000	1.000
0010	2	0.000	2.000	1.000
0011	3	0.000	3.000	1.000
0012				
0013	3	0.000	3.000	1.000
0014	2	0.000	2.000	1.000
0015				

Editing mode

☐ Select cells

☒ Edit data