7 POSITIONS

Ideas of social role have been important to social theorists since the middle of the century. Social networks provide an ideal environment in which to formalise the theoretical concepts of role and position. There have been two related schools of thought on how best to capture the theoretical concepts involved. In this chapter we shall first give consideration to the ideas of structural equivalence and then look at its generalization to regular equivalence.

In its simplest form structural equivalence examines the direct connections of an actor to other actors in the network. Thus, an actor's position is defined by whom he or she is connected to. There is a lot of empirical evidence that shows that structurally equivalent actors share behavioural patterns. They demonstrate a certain level of homogeneity in a similar way to actors belonging to the same cohesive subgroup. In studies of adoption of innovation it has been noted that structurally equivalent actors have similar adoption patterns. Furthermore we can use structural equivalence to provide a simplification of a network that still captures many of the essential features. Hence it provides a high level description of the relations within the network. Structural equivalence has also been used to formalize the concept of niche.

A simple description of structural equivalence is given by the situation in which one individual substitutes for another. For example, a computer programmer working on a project may fall sick and their role is then taken over by a contract programmer. The new programmer relates to all other members of the project team in the same way as the previous programmer. It follows that the new and the old programmer have exactly the same connections in the work network and, as such, are structurally equivalent and are therefore occupying the same position.

7.1 Intuitive Notions

We recall that a social network may consist of a number of different relations collected on the same set of actors. One of the fundamental aspects of social role is that it is determined over a number of different relations. It follows that any definition of structural equivalence must take account of the multirelational nature of social networks. In addition we must assume that the role structure and positions of individuals are apparent in the relations present in the network data.

The positional approach to network analysis is based upon identifying similar positions and should be contrasted with the relational or cohesive approach of chapter 4. In general, positional analysis methods seek to partition actors into mutually exclusive classes of equivalent actors who share similar structural properties. Formal definitions have been developed on directed and undirected networks. These definitions have then been relaxed so as to allow for the analysis of noisy and valued

data. Intuitively two actors are structurally equivalent if they have identical connections to and from all other actors in the network.

7.2 Structural Equivalence

We shall now give a formal definition of structural equivalence, although it is possible to give a sophisticated mathematical definition we shall give a slightly longer but less technical one. This definition is valid for undirected data that allows self loops. Two actors i and j are structurally equivalent if the following two statements are true for every relation:

1. For every actor k which is different from i and j then whenever i is connected to k j is also connected to k and if i is not connected to k then neither is j
2. If i is connected to itself then so is j, if i is not connected to itself then neither is j. So that both actors share the same relationship with themselves.

Hence for graphs without self-loops the definition reduces to the following. Actors i and j are structurally equivalent if outside of each other they are connected to exactly the same other actors.

The extension to directed data simply deals with both the in coming ties and out going ties separately, this also adds another level of complication in dealing with the relationship between i and j but fundamentally the concept is the same.

Let us now consider some examples on single relationship networks. If we examine

FIGURES 7.1 ,7.2 and 7.3 ABOUT HERE

Figure 7.1 we can easily see that actors 3,4 and 5 are all connected to 1 and 2 and are all therefore structurally equivalent. Notice further that actor 1 is connected to 2,3,4,5 and actor 2 is connected to 1,3,4,5 therefore outside of each other they are both connected to 3,4,5 and so are structurally equivalent. In Figure 7.2 actors 3 and 4 both only receive ties from actors 1 and 2 and are therefore structurally equivalent. Actors 1 and 2 are both connected to 3 and 4 and both receive ties from 5, in addition the connection from actor 1 to 2 is matched by the connection from 2 to 1 so that they too are structurally equivalent. Note that 5 is not structurally equivalent to any of the other actors. Figure 7.3 is the same as Figure 7.2 except that there is a self-loop on actor 4, since this self-loop is not on actor 3 they are no longer structurally equivalent and the only equivalent actors are 1 and 2.

FIGURE 7.4 ABOUT HERE

Figure 7.4 is a multirelational example. In relation R_1 actors 1 and 2 are structurally equivalent and so are actors 3,4 and 5. However in relations R_2 and R_3 1 and 2 are structurally equivalent and so are 3 and 5 but 4 is not structurally equivalent to any other actor in either relation. It follows that the structurally equivalent actors are 1 and 2 as one pair and 4 and 5 as another pair.

Another way of thinking about structural equivalence is that if we remove the labels that identify two structurally equivalent actors, i and j say, on a diagram then it will no longer be possible to tell which was which. This is because they have exactly the

same pattern of relationships over all relations. If we look back at Figure 7.1 and remove the labels 3 and 5 then we have no way of knowing which label belongs to which vertex. This would not be the case if labels 2 and 3 were removed, we know that the actor of degree 4 is 2 and the one of degree 2 is 3. A consequence of this is that structurally equivalent actors are identical with respect to any structural property. They have the same degree, the same centrality, they are on the same number of cycles etcetera. They are truly substitutable for each other.

To extend the definition to valued data we simply insist that the identical connections to other actors have identical values. If in Figure 7.2 actors 1 and 2 are structurally equivalent and the edge (1,3) has a value of 5.0 then the edge (2,3) must have a value 5.0, furthermore if the edge (1,2) has a value of 7.0 then so must the edge (2,1).

7.3 Profile Similarity

Our definition of structural equivalence is an ideal mathematical model and would rarely occur in real data. It does provide a theoretical framework on which we can base measures that try and capture the degree to which actors are structurally equivalent to each other. This will allow us to analyze data that contains measurement error, respondent variability and all the other inevitable inaccuracies associated with collecting real data. We first observe that structural equivalence is a local property, in as much that to determine whether a pair of actors are structurally equivalent we only need to know the set of actors to whom each are connected. If these sets are identical, with special consideration given to elements of the set which are the actors being compared, then they are structurally equivalent. The rows and columns of the adjacency matrix of the relation contain all the relevant information and can be used to determine the sets of alters and are known as profiles. The profile of actor i in an undirected single relation is simply the ith row (or column as this is the same) of the adjacency matrix. For directed data the profile is the ith row concatenated with the ith column. We illustrate this with some examples. In Figure 7.1 the profile of actor 3 is (1,1,0,0,0) this shows that actor 3 is adjacent to actors 1 and 2 and not adjacent to itself nor actors 4 and 5. Consider actor 2 in Figure 7.2. The second row of the adjacency matrix is (1,0,1,1,0) and the second column is (1,0,0,0,1). The fact that 2 is not connected to itself is recorded in the second entry of both the row and column vectors, that is this value has been noted twice. The profile is therefore (1,0,1,1,0,1,0,0,0,1). Once we have the profiles we can compare them and check whether they satisfy the structural equivalence definition. To do so they need to be identical except for the entries that correspond to the actors that are compared. Hence if we are comparing profile of actor i with that of actor j we need to pay particular attention to the jth entry of the i profile and the jth entry of the i profile.

If the two profiles compared in this way are not identical then the actors are not structurally equivalent. It would be useful to know how similar the two vectors are to each other and to do this we could use any of the standard measures for comparing vectors. These include, but are not limited to, matches, correlation and Euclidean distance. One advantage of using the existing comparison methods for vectors is that they can be applied to valued data. When we compare two profile vectors we have to make sure that we meet all the conditions of structural equivalence. Suppose that we are going to use matching to compare the profile of row i with the profile of row j. For each element except the ith and jth entry in each row or column that makes up the profile we match the corresponding element in each vector. We then match the ith

entry in row i with the jth entry in row j and the jth entry in row i with the ith entry in row j repeating the process for the corresponding column entries. This process is known as reciprocal swapping and is applied regardless of the method of comparing vectors.

We then proceed to compare every pair of actors and from this information construct a structural equivalence matrix. The (i,j) entry in this matrix is the profile similarity measure of actor i with actor j. Regardless of how many relations are being considered and whether they were directed or not the structural equivalence matrix is a square symmetric matrix with the same number of rows (and columns) as the number of actors in the data set. It should be noted that if a standard statistical measure such as correlation is used we could not apply classical statistical inference on the results since the independence assumption has been violated. We can however treat the matrix as a proximity measure and apply classification and clustering techniques. This is necessary since one of the goals of positions is to place actors into mutually exclusive equivalence classes.

If we used Euclidean distance then a pair of structurally equivalent actors would yield a distance of zero. Values close to zero would indicate that the actors involved are nearly structurally equivalent. Clearly if we used correlation then structurally equivalent actors will have a correlation coefficient of one. However, in contrast to the Euclidean distance measure, it would also be possible for non-structurally equivalent actors to have a perfect correlation score. This would occur if one profile were a straight multiple of another, in some circumstances this would be desirable; we shall return to this topic later.

An Example In 1968 Sampson collected data on social relations in a contemporary isolated American monastery. Towards the end of his study there was a major crisis, resulting in a number of members being expelled or resigning. Sampson defined four sorts of relation: Affect, Esteem, Influence and Sanction. White, Boorman and Breiger (1976) report these matrices for the period just before the dispute. We shall consider just the Esteem relation which we split into two relations of Esteem and Diesteem. Each noviate ranked the other ranks giving his top three choices for that relation. In all rankings 3 is the highest or first choice and 1 the lowest; ties and no choices were permissible. The matrices are as follows:

Esteem

		1 R	2 B	3 A	4 B	5 P	6 L	7 V	8 W	9 J	10 G	11 H	12 B	13 M	14 A	15 A	16 B	17 E	18 S
1	ROMULAND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	BONAVENTURE	0	0	1	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0
3	AMBROSE	0	0	0	0	3	0	2	0	1	0	0	0	0	0	0	0	0	0
4	BERTHOLD	0	0	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0
5	PETER	2	0	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0
6	LOUIS	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	VICTOR	0	1	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0
8	WINFRID	0	0	0	0	0	0	0	0	3	2	1	0	0	0	0	0	0	0
9	JOHN	0	1	0	0	0	0	3	2	0	0	0	0	0	0	0	0	0	0
10	GREGORY	0	1	0	0	0	0	2	0	3	0	0	0	0	0	0	0	0	0
11	HUGH	0	0	0	0	0	0	0	1	3	2	0	2	0	0	0	0	0	0
12	BONIFACE	0	0	0	0	0	0	0	0	1	3	2	0	0	0	0	0	0	0
13	MARK	0	0	0	0	0	0	0	1	0	3	0	1	0	2	0	0	0	0
14	ALBERT	0	0	0	0	0	0	0	1	0	3	0	2	2	0	0	0	0	0
15	AMAND	0	3	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0
16	BASIL	0	0	0	0	0	0	0	0	3	0	0	0	0	0	2	0	1	1
17	ELIAS	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	2	0	3
18	SIMPLICIUS	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	3	1	0

Disesteem

		1 R	2 B	3 A	4 B	5 P	6 L	7 V	8 W	9 J	10 G	11 H	12 B	13 M	14 A	15 A	16 B	17 E	18 S
1	ROMULAND	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	BONAVENTURE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	2
3	AMBROSE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3	2
4	BERTHOLD	0	0	0	0	0	0	1	0	0	0	0	0	3	0	0	2	2	0
5	PETER	0	0	0	0	0	0	0	0	2	3	1	0	0	0	0	0	0	0
6	LOUIS	0	0	0	0	0	0	0	0	1	3	0	0	0	1	0	2	0	0
7	VICTOR	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	3
8	WINFRID	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	JOHN	0	0	0	0	0	0	0	0	0	2	0	0	3	0	0	1	0	0
10	GREGORY	0	0	0	0	3	0	0	0	0	0	0	0	0	0	1	2	0	0
11	HUGH	0	0	0	0	2	2	0	0	0	0	0	0	0	0	3	0	1	1
12	BONIFACE	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	2	1	1
13	MARK	0	0	0	3	2	0	2	0	0	0	0	0	0	0	0	2	1	0
14	ALBERT	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	2	2	1
15	AMAND	0	0	0	3	0	0	0	0	0	2	0	0	0	0	0	1	0	0
16	BASIL	0	0	0	2	3	0	0	0	0	1	0	0	0	0	0	0	0	0
17	ELIAS	0	0	0	3	2	0	1	0	0	0	0	0	0	0	0	0	0	0
18	SIMPLICIUS	1	0	0	2	2	0	3	0	0	0	0	0	0	0	0	0	0	0

Shortly after this data was collected Gregory, Basil, Elias and Simplicius were expelled. Almost immediately John departed voluntarily. A few days later Hugh, Boniface, Mark and Albert left, and within a week Victor and Amand departed. One

month later Romuland also left. Sampson grouped the monks and then named the groups as follows:
{Winifrid, John, Gregory, Hugh, Boniface, Mark, Albert} The Young Turks.
{Bonaventure, Ambrose, Berthold, Peter, Louis} The Loyal Opposition
{Basil, Elias, Simplicius} The Outcasts
{Romuland, Victor, Amand} Indeterminate.
The following structural equivalence matrix was obtained when the Esteem and Disesteem matrices were submitted to the profile similarity routine in UCINET. The data is not symmetric so the profiles use both the rows and columns, since this can be achieved by placing the transpose of a matrix as a new relation and then only taking the rows this is often referred to as 'including the transposes'. Euclidean distances were selected as the choice for measuring the amount of structural equivalence between the profiles. The distances have been rounded up to the nearest whole number.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
	RO	BO	AM	BE	PE	LO	VI	WI	JO	GR	HU	BO	MA	AL	AM	BA	EL	SI
ROMULAND	0	7	7	8	11	7	8	5	9	10	7	7	8	7	7	9	8	8
BONAVENTURE	7	0	5	8	12	8	7	8	10	12	9	8	9	8	9	11	10	10
AMBROSE	7	5	0	9	12	9	7	7	10	11	8	8	10	8	9	10	10	10
BERTHOLD	8	8	9	0	10	10	9	10	11	12	11	10	9	10	10	10	10	11
PETER	11	12	12	10	0	10	12	12	13	13	12	12	13	13	11	12	12	13
LOUIS	7	8	9	10	10	0	10	8	10	12	10	9	10	9	7	10	10	10
VICTOR	8	7	7	9	12	10	0	8	11	12	10	9	11	9	10	11	10	9
WINFRID	5	8	7	10	12	8	8	0	8	9	6	5	8	7	8	8	9	9
JOHN	9	10	10	11	13	10	11	8	0	10	10	10	11	10	9	11	11	11
GREGORY	10	12	11	12	13	12	12	9	10	0	9	9	11	10	11	9	12	12
HUGH	7	9	8	11	12	10	10	6	10	9	0	5	9	7	9	9	10	9
BONIFACE	7	8	8	10	12	9	9	5	10	9	5	0	7	5	9	9	9	9
MARK	8	9	10	9	13	10	11	8	11	11	9	7	0	6	9	9	9	9
ALBERT	7	8	8	10	13	9	9	7	10	10	7	5	6	0	9	9	9	9
AMAND	7	9	9	10	11	7	10	8	9	11	9	9	9	9	0	9	9	9
BASIL	9	11	10	10	12	10	11	8	11	9	9	9	9	9	9	0	7	9
ELIAS	8	10	10	10	12	10	10	9	11	12	10	9	9	9	9	7	0	5
SIMPLICIUS	8	10	10	11	13	10	9	9	11	12	9	9	9	9	9	9	5	0

Since we used Euclidean distance a value of zero would indicate perfect structural equivalence. The only zero values are on the diagonal (actors are structurally equivalent to themselves) and so no two actors are perfectly structurally equivalent. The smallest values are 5 so that the most similar actors are pairs such as Bonaventure and Ambrose or Albert and Boniface. The least similar actors have a score of 13, for example Peter and John. To obtain some form of structurally equivalent groups we can submit this matrix to either a

FIGURE 7.4 ABOUT HERE

multidimensional scaling routine or an hierarchical clustering method. Figure 7.4 is the dendrogram associated with a single-link clustering of the structural equivalence matrix given above. The following groupings are obtained from this clustering at the level 8.674.
{Bonaventure, Ambrose, Berthold, Victor}
{Romuland, Winfrid, Hugh, Boniface, Mark, Albert}
{Louis, Amand}
{Basil, Elias, Simplicius}

Peter, John and Gregory are each singletons and have not been taken into any clusters at this level. Each group is consistent with Sampson's assignment in as much as none of the members of the three major groupings are placed together. It also has to be remembered that this is an analysis of just one pair of the relations and so is not as rich in data as taking all the relations.

7.4 BLOCKMODELS

Once we have identified a partition of the nodes based upon structural equivalence we can use this information to provide a simplified or reduced matrix. We first arrange the rows and columns of the adjacency matrix so that structurally equivalent actors are grouped together. This grouping induces blocks within the matrix figure 7.5 shows this process for the network given in figure 7.1.

FIGURE 7.5

We note that the blocks consist of either all zero or all ones. We could therefore replace each block by a zero or a one without loosing any information. This gives rise to a new and smaller adjacency matrix which represents a reduced graph. We call these the image matrix and image graph respectively. The blocked adjacency matrix and image graph for Figure 7.5 are given in Figure 7.6

This process is called blockmodelling. For pure structural equivalence the blocks are either all ones or all zeros and these are called one block and zero blocks respectively. The core-periphery models of chapter 6 are a special case of this in which we insist that the core interactions are a one block and the peripheral interactions are a zero block. For real data the blocks will not be perfect, the zero blocks will be predominately filled with zeros and the one blocks should contain nearly all ones. The extent to which this is true is a measure of how well the method has managed to partition the data into structurally equivalent blocks. In the following we have repeated the profile analysis on the Sampson esteem data but we dichotomized the data first.

		1 2	3	4	5	7	1 0	8	9	1 4	1 1	1 2	1 3	1 6	5	1 6	1 7	1 8
		R	B	A	B	P	V	G	W	J	A	H	B	M	L	A	B	E	S
1	ROMUL_10																		
2	BONAVEN_5			1		1									1				
3	AMBROSE_9					1	1			1									
4	BERTH_6					1									1				
5	PETER_4	1			1										1				
7	VICTOR_8		1		1	1													
10	GREG_2		1				1			1									
8	WINF_12							1		1		1							
9	JOHN_1		1				1		1										
14	ALBERT_16							1	1				1	1					
11	HUGH_14							1	1	1			1						
12	BONI_15							1		1		1							
13	MARK_7							1	1		1		1						
6	LOUIS_11		1	1															
15	AMAND_13		1											1	1				
16	BASIL_3									1						1		1	1
17	ELIAS_17							1								1	1		1
18	SIMP_18							1									1	1	

Density / average value within blocks

		1 7	2 14	3 15	4 18
1	7	0.3333	0.0238	0.2500	0.0000
2	14	0.0952	0.4762	0.0000	0.0000
3	15	0.2500	0.0714	0.5000	0.0000
4	18	0.0000	0.1429	0.3333	1.0000

```
                                 1      1 1 1 1      1    1 1 1
                  1 2 3 4 5 7    0 8 9 4 1 2 3    6 5    6 7 8
                  R B A B P V    G W J A H B M    L A    B E S
                 ---------------------------------------------
 1  ROMUL_10    |               |                  |       |       |
 2 BONAVEN_5    |               |                  |       | 1 1 1 |
 3 AMBROSE_9    |               |                  |   1   |   1 1 |
 4   BERTH_6    |           1   |              1   |       | 1 1   |
 5   PETER_4    |               | 1   1   1        |       |       |
 7  VICTOR_8    |               |         1        |       |   1 1 |
                ---------------------------------------------------
10    GREG_2    |         1     |                  |   1   | 1     |
 8   WINF_12    |               |                  |       |       |
 9    JOHN_1    |               | 1            1   |       | 1     |
14 ALBERT_16    |         1     |                  |       | 1 1 1 |
11   HUGH_14    |         1     |                  | 1 1   |   1 1 |
12   BONI_15    |         1     |                  | 1     | 1 1 1 |
13    MARK_7    |       1 1 1   |                  |       | 1 1   |
                ---------------------------------------------------
 6  LOUIS_11    |               | 1   1 1          |       | 1     |
15  AMAND_13    |       1       | 1                |       | 1     |
                ---------------------------------------------------
16   BASIL_3    |       1 1     | 1                |       |       |
17  ELIAS_17    |       1 1 1   |                  |       |       |
18   SIMP_18    | 1     1 1 1   |                  |       |       |
                 ---------------------------------------------
```

Density / average value within blocks

```
             1      2      3      4
             7     14     15     18
        ------ ------ ------ ------
 1  7  0.0333 0.1190 0.0833 0.5000
 2 14  0.1667 0.0476 0.2857 0.5714
 3 15  0.0833 0.2857 0.0000 0.3333
 4 18  0.5000 0.0476 0.0000 0.0000
```

FIGURE 7.7

The results show four groups and this results in sixteen blocks in each of the two relations. The density of each of the blocks is given below each relation. Of the thirty two blocks only eight are perfect of which seven are zero blocks and one is a one block. This is fairly common when analyzing data of this type. The blockmodel allows us to uncover structural properties of the data. We can see for example that none of the groups have any esteem for the outcasts (except themselves!) and also that there is a high level of disesteem from each of the groups to the outcasts. This confirms that Sampson was correct in his observation and that calling this group the outcasts was justified.

In general one looks for certain patterns in the blockmodel that equate to known structures. Core-periphery is one such pattern. Another common pattern is to have the one blocks on the diagonal in the image matrix, these equate to cohesive subgroups and the blockmodel gives additional insight into the interactions between these groups.

For valued data we would expect the blocks to contain similar values. So that instead of one and zero blocks we may have a five block (say), that is a block in

which each value is a five. The image matrix will now consist of entries that are the average of all of the values in the blocks. We can again judge how good the blockmodel is by looking at the variation in the values in each block. The standard deviation is one obvious way to do this and this is reported in software programs such as UCINET.

Finally when using profile structural equivalence it is common practice to first convert the data to geodesic distances. Two actors that are structurally equivalent in the original data will still be structurally equivalent in the geodesic distance matrix. One reason for doing the conversion is that the geodesic distance matrix contains information about how well an actor is connected into the whole network and not just their local neighbourhood. This is particularly useful for sparse networks but at a penalty of making the interpretation of the results more difficult.

7.5 THE DIRECT METHOD

We have constructed our blockmodels by first performing a profile analysis and then using this to partition our adjacency matrix. An alternative is to use a direct method to partition the data. As already mentioned we are able to assess how close a partition is to an ideal blockmodel by examining the entries of each block. To compare two different partitions on the same data we just need count the number of changes that are required to make the blockmodel fit the ideal structure of zeros and ones. We call this the fit and we can now try to optimise the fit over all the possible assignments of actors to different groups. One disadvantage of this approach is that we have to specify the number of groups. For valued data it is not possible to simply count the number of errors and more sophisticated fit functions are used but the principle remains the same. We demonstrate the direct method on the dichotomized

		1 1 1		1 1 1								1		1 1
		0 1 2 8 9		8 6 7		4 6 2 3 5 1 5 7 3 4								
		G H B W J		S B E		B L B A P R A V M A								
10	GREG_2		1			1				1				
11	HUGH_14	1	1 1 1											
12	BONI_15	1 1	1											
8	WINF_12	1 1	1											
9	JOHN_1		1			1				1				
18	SIMP_18	1			1 1									
16	BASIL_3		1	1	1				1					
17	ELIAS_17	1		1 1					1					
4	BERTH_6					1		1						
6	LOUIS_11						1 1							
2	BONAVEN_5					1	1 1							
3	AMBROSE_9		1				1		1					
5	PETER_4				1 1		1							
1	ROMUL_10													
15	AMAND_13					1 1				1				
7	VICTOR_8				1	1	1							
13	MARK_7	1	1 1								1			
14	ALBERT_16	1	1 1						1					

FIGURE 7.8

esteem data. Figure 7.8 is a three block optimization and we see that it has identified the outcasts but that two of the young turks are now in the loyal opposition. In this example since the monks were asked only to rank their top three choices then it is not possible for the larger blocks to have all ones. This means that the larger blocks

cannot be made to fit well with the consequence that the technique struggles to find good solutions. The user needs to be aware that regardless of the inherent structure the method produces an answer, and that this answer may not be particularly good, it is simply the best of a bad set. It is always good practice to examine the results carefully to see if they fit the model well.

One of the expectations we had of the structural equivalence model was that actors who are structurally equivalent would exhibit similar behaviours. This did happen to a significant extent with the Sampson data. All members of the outcasts were expelled and both the direct and the profile similarity method identified these as structurally equivalent. The young turks all left and again these were identified using the structurally equivalent models The four core members of the loyal opposition remained and each method placed three of these together and one method included all four.

7.6 REGULAR EQUIVALENCE

One of the restrictions of structural equivalence is that actors need to be connected to the same actors. Whilst it is true that this is necessary when considering adoption of innovation or diffusion it is not necessary when we consider similarity of behaviour. David Krackhardt for example looked at turnover of staff in a number of fast food outlets. He examined whether people with similar patterns of advice seeking exhibited similar turnover patterns. Clearly he could not use structural equivalence since the actors were in different restaurants and so could not be connected to each other. In his study he used a generalization of structural equivalence called regular equivalence. Regular equivalence relaxes the strict condition on the one blocks in blockmodelling. Rather than having blocks that have a one in every row and column we simply require at least one one in each row and column. An example of a regular blockmodelling is given in Figure 7.9. The blockmodel has zero blocks as in structural equivalence and we note that one of the blocks is a one block but the other blocks each have at least one one in every row and every column. In structural equivalence if two actors were equivalent they had

FIGURE 7.9 HERE

to be connected to exactly the same others. Hence two teachers are structurally equivalent if they teach the same students. In regular equivalence the teachers have to teach at least one student each (and not all students)and equally the students all need at least one teacher.

To find a regular equivalence we can use methods similar to structural equivalence. The direct method simply needs a small change to the fit measure but in all other respects is the same as for structural equivalence.

As an example we consider the taro data these data represent the relation of gift-giving (taro exchange) among 22 households in a Papuan village collected by Schwimmer in 1973. He points out how these ties function to define the appropriate persons to mediate the act of asking for or receiving assistance among group members. We submitted the data to the UCINET direct regular equivalence optimization routine selecting three groups. The routine returned a perfect solution that is one which each block satisfies the condition for regular equivalence. The solution is given in Figure 7.10

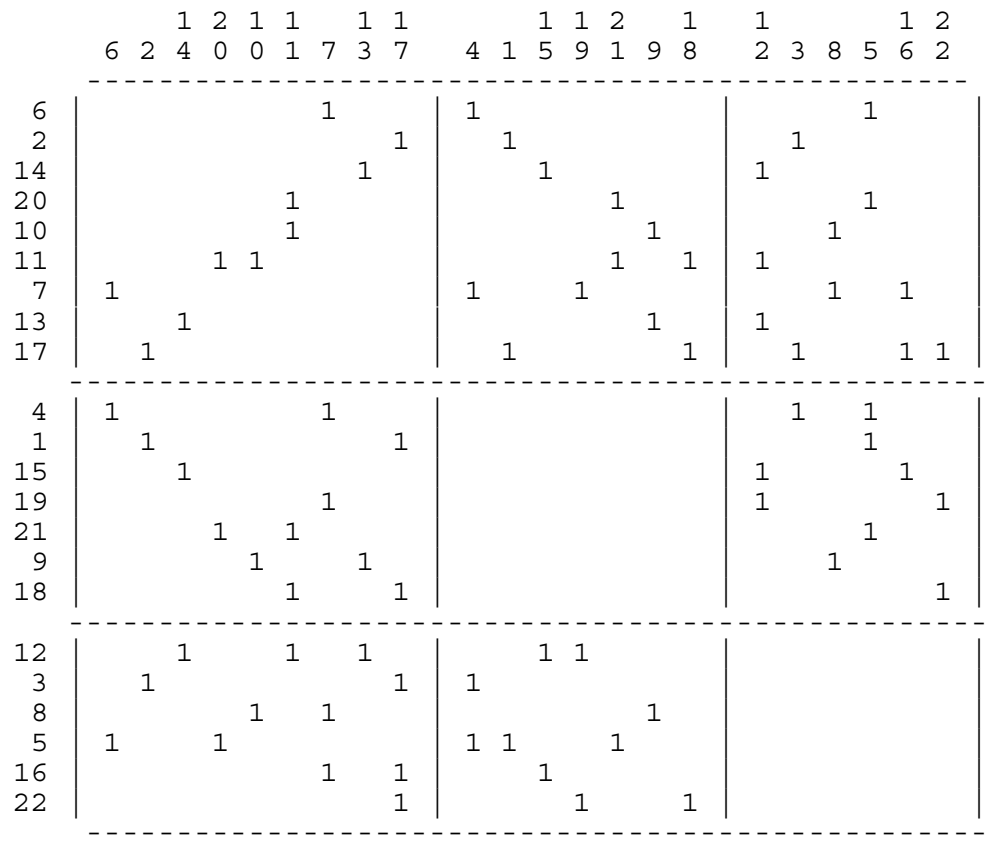

Figure 7.10

This three group solution consists of a group that exchanges within itself and with the other two groups. The two other groups only exchange outside of their groups. This suggests a status orientated where the top group exchanges with everyone else but the lower group exchange with the top and the other group but not with themselves.

7.7 REGE

The extension of profile similarity to regular equivalence is not as simple. Unlike structural equivalence where the measure is derived by comparing all all actors we now have to simultaneously compare profiles with the best possible matches. This a far more complicated process since we need to match against other actors that are potentially equivalent, and this will not be known until the process is completed. This problem is solved by iteratively moving towards an equivalence matrix and using the interim scores to as equivalence measures between iterations. The algorithm REGE accomplishes this, we do not present the details here but we will note some important facts which anyone using REGE needs to know. Firstly for binary data the algorithm only works on directed data (valued is no problem). Secondly the similarity values produced can be difficult to interpret in absolute terms. They are usually used to partition the data using a clustering routine, as was the case for profile structural equivalence. As with structural profile equivalence if you have binary data then some analysts suggest converting the binary matrix to a geodesic distance matrix. This may be the only course of action if you have undirected binary data.

To see how REGE can be used we return to the Sampson esteem data. Blah blah.

Step 1

Regular or structural
If regular go to 6
Step 2
Binary or valued.
If valued go to 5
Step 3
If approximate number of groups known and these are small (less than 10) use direct method. If successful stop.
Step 4
Use profile on binary data. If successful stop. If not convert to geodesic distances.
Step 5
Use profile. Stop.
Step 6
If approximate number of groups known and these are small (less than 10) use direct method. If successful stop.
Step7
If binary undirected convert to geodesic distances.
Step 8
Run REGE, if failed and binary convert to geodesic distances and repeat.