# Stochastic Blockmodels for Directed Graphs

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Holland and Leinhardt (1981) proposed the $p_1$ model for the analysis of binary directed graph data in network studies. Such a model provides information about the "attractiveness" and "expansiveness" of the individual nodes in the network, as well as the tendency of a pair of nodes to reciprocate relational ties. When the nodes are a priori partitioned into subgroups based on attributes such as race and sex, the density of ties from one subgroup to another can differ considerably from that relating another pair of subgroups, thus creating a situation called blocking in social networks. The $p_1$ model completely ignores this extra piece of information and is, therefore, unable to explain the block structure. Blockmodels that are simple extensions of the $p_1$ model are proposed specifically for such data. An iterative scaling algorithm is presented for fitting the model parameters by maximum likelihood. The methodology is illustrated in detail on two empirical examples.

KEY WORDS: Stochastic partitioned directed graph; Blockmodeling technique; Iterative scaling algorithm.

## 1. INTRODUCTION

The uses of directed graphs (or digraphs) to describe social networks linking individuals, corporations, or societies via some relationship has become increasingly popular among statisticians. A digraph consists of (a) a set of $g$ nodes representing the interacting members and (b) a $g \times g$ two-way data matrix $\mathbf{X} = (X_{ij})$, called an adjacency matrix, where

$$X_{ij} = 1 \quad \text{if node } i \text{ relates to node } j$$
$$= 0 \quad \text{otherwise.}$$

It is assumed that there are no self choices, so the diagonal entries $X_{ii}$ are all structural zeros. Such a square two-way table is particular in two aspects. First, there is only a single dichotomous response in each off-diagonal cell; this limited nature of the data poses a very difficult task of modeling the underlying cell probabilities $p_{ij} = \Pr(X_{ij} = 1)$. Second, the row and column attributes defining the two-way table both refer to the same set of nodes.

Holland and Leinhardt (1981) proposed a simple exponential model for analyzing digraphs. Their model, which they call the $p_1$ model, prescribes for each node a pair of parameters pertaining to the row and column characteristics of the node. In addition, there is a parameter to measure the overall density of ties, and another parameter to account for any tendency toward reciprocation between members of a pair of nodes. An equivalent log-linear representation of the $p_1$ model was given by Fienberg and Wasserman (1981a).

In many social networks, individuals are a priori partitioned into subgroups $B_1, \ldots, B_b$ based on nodal attributes such as race, sex, geographic locations, and party affiliation. The adjacency matrix is then composed of $b^2$ submatrices, or blocks, each of which represents ties from individuals in some $B_r$ to individuals in some $B_s$ ($r, s = 1, \ldots, b$). The densities of ties in the $b^2$ blocks may differ considerably, depending on the nature of the subgroups involved. The $p_1$ model completely ignores such nodal information and is, therefore, unable to explain any block structure. When the model is fitted to such data, the $p_{ij}$ corresponding to blocks with high tie density are usually underestimated, whereas those corresponding to blocks with low tie density are overestimated.

To fix ideas, consider the $27 \times 27$ adjacency matrix in Table 1. This is part of a much larger study of strength of ties between students from different socioeconomic backgrounds. The study was conducted by Hansell (1984) at Rutgers University, New Brunswick. It involved 317 fifth- and sixth-grade students in an inner-city Baltimore elementary school. Our example consists of 13 male and 14 female sixth graders from a single classroom. The students were given a roster of their classroom and were asked to indicate their liking for each student by choosing one of the three facial expressions: (a) a big smile and labeled "a lot," (b) a moderate smile and labeled "some," and (c) no smile and labeled "not much." Choice (a) suggests a strong friendship tie and is coded as 1 in the sociomatrix, whereas choices (b) and (c) indicate weak ties and are coded as 0. One substantive question of interest is whether or not same-sex choices tend to be strong ties, and opposite-sex choices are mostly weak ties.

The relevant block information in this example is the sex identity of the student, and the subgroups are $B_1 = \{1, \ldots, 13\}$ and $B_2 = \{14, \ldots, 27\}$, representing the male and female students, respectively. Figure 1 focuses on the block structure. The number of ties in each block and the percentage of ties relative to the block size [e.g., in the $B_1 \times B_1$ block, the size is $13(13 - 1) = 156$] are both given. The proportion of same-sex ties is 113/338 (33.43%), which is considerably higher than the value 44/364 (12.09%) obtained for the opposite-sex ties. The a priori assumption is that a friendship tie is stronger among students of the same sex than among students of the opposite sex. In Section 3 we show that the $p_1$ model can be improved on by a blockmodel that makes use of the extra nodal information about the sex identity of the students.

Another example that we shall discuss in detail in Section 3 is taken from the well-known study by Sampson (1969) of the interpersonal ties among 18 novices of a monastery. Sampson's data include responses to four so-

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*Table 1. Hansell's (1984) Data*

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | $x_{i+}$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 6 |
| 2 | 1 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 |
| 3 | 1 | 1 | | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 7 |
| 4 | 1 | 1 | 1 | | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 12 |
| 5 | 1 | 1 | 0 | 0 | | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | 13 |
| 6 | 0 | 1 | 0 | 0 | 1 | | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 10 |
| 7 | 0 | 0 | 0 | 0 | 1 | 1 | | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4 |
| 8 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 7 |
| 9 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 |
| 10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 12 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 |
| 13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 2 |
| 14 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 1 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 7 |
| 15 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 5 |
| 16 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | 1 | | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 19 |
| 17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 2 |
| 19 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 11 |
| 20 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 1 | 0 | | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 11 |
| 21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | | 0 | 0 | 0 | 1 | 1 | 0 | 5 |
| 22 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | | 1 | 1 | 1 | 0 | 1 | 8 |
| 23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | | 1 | 1 | 0 | 0 | 7 |
| 24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 1 | 0 | 0 | 3 |
| 25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 1 | | 0 | 0 | 8 |
| 26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 | 0 |
| 27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 |
| $x_{+j}$ | 7 | 6 | 3 | 3 | 7 | 7 | 3 | 2 | 6 | 7 | 4 | 3 | 6 | 9 | 12 | 5 | 11 | 10 | 3 | 0 | 10 | 6 | 5 | 9 | 10 | 1 | 2 | $157 = x_{++}$ |

ciometric criteria: affect, esteem, influence, and sanction. Both positive and negative responses were considered. Table 2 presents the data generated by the monks' positive responses to the affect criterion. The corresponding labels in Sampson for these 18 monks are 10, 5, 9, 6, 4, 11, 8, 12, 1, 2, 14, 15, 7, 16, 13, 3, 17, 18, roughly in their order of joining the monastery.

On the basis of his own observations and interpretation of events and personal attributes of the monks, Sampson posited two major antagonistic cliques: (a) the *Loyal Opposition*, consisting of monks 2–6, and (b) the *Young Turks*, consisting of monks 8–14. He also identified two minor cliques: (c) the *Outcasts*, consisting of monks 16–18, and (d) the *Waverers*, consisting of monks 1, 7, and 15. Such a clique formation ultimately led to the resignation and expulsion of 12 of the novices. Using blocking algorithms called BLOCKER (Heil and White 1976) and CONCOR (see McQuitty and Clark 1968; Breiger, Boorman, and Arabie 1975; Schwartz 1977), White, Boorman, and Breiger (1976) reproduced Sampson's first three subgroups; however, they placed the Waverers in subgroups 1 and 3. These are the three subgroups shown in Table 2: $B_1 = \{1, \ldots, 7\}$ are the Loyal Opposition, $B_2 = \{8, \ldots, 14\}$ are the Young Turks, and $B_3 = \{15, \ldots, 18\}$ are the Outcasts. Recently, the same three subgroups were identified by Everett (1982a,b) using a graph theoretic blocking procedure called EBLOC. Minor changes in the compositions of the subgroups were later obtained by Everett (1983a,b) using an extension of EBLOC with values assigned to the observed ties.

Figure 2 gives the compositions of the nine blocks formed from the three subgroups of monks. The diagonal blocks represent the same-clique choices. The figures suggest that the "bonds of positive affect" among the Loyal Opposition and among the Young Turks are about the same. The bond seems to be stronger among the Outcasts; however, the small block size there precludes such distinction. Except for the $B_3 \times B_2$ block representing the ties from the Outcasts to the Young Turks, the cross-clique blocks are examples of "zero blocks" mentioned in traditional blockmodeling literature (e.g., see White et al. 1976), which are blocks with essentially zero tie density.

Sampson's data were studied by Holland and Leinhardt (1981), Reitz (1982), Holland, Laskey, and Leinhardt (1983), and Fienberg, Meyer, and Wasserman (1985), using the $p_1$ model and log-linear blockmodels that focus on the clique structure rather than on the individual monks. In particular, a very detailed $p_1$ analysis of Sampson's data was presented by Holland and Leinhardt. These authors demonstrated over the particular example the superiority of the $p_1$ model over some earlier ad hoc techniques used by sociologists. However, as evident from the residual analysis by Holland and Leinhardt (1981; table 5, fig. 6),

| | | $B_1$ | $B_2$ |
|---|---|---|---|
| | | 13 | 14 |
| $B_1$ | 13 | 45 (28.25) | 25 (13.74) |
| $B_2$ | 14 | 19 (10.44) | 68 (37.36) |

*Figure 1. Block Structure of Hansell's (1984) Data: $B_1$, male students; $B_2$, female students.*

Table 2. Sampson's (1969) Data

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | $x_{i+}$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 4 |
| 2 | 0 | | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 |
| 3 | 0 | 1 | | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 |
| 4 | 0 | 1 | 1 | | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 |
| 5 | 0 | 1 | 0 | 1 | | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 |
| 6 | 0 | 1 | 0 | 0 | 0 | | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 |
| 7 | 0 | 0 | 1 | 1 | 1 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 |
| 8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 3 |
| 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 3 |
| 10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 3 |
| 11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 3 |
| 12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | | 1 | 0 | 0 | 0 | 0 | 0 | 3 |
| 13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | | 1 | 0 | 0 | 0 | 0 | 3 |
| 14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | | 0 | 0 | 0 | 0 | 3 |
| 15 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | | 0 | 0 | 1 | 3 |
| 16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | | 1 | 1 | 4 |
| 17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | | 1 | 3 |
| 18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | | 3 |
| $x_{+j}$ | 0 | 6 | 4 | 2 | 4 | 2 | 2 | 6 | 4 | 6 | 2 | 2 | 5 | 1 | 2 | 3 | 2 | 3 | $56 = x_{++}$ |

the $p_1$ model fits the data poorly. Their residual analysis reveals that about one-third of the entries in the three diagonal blocks have large positive residuals with magnitude of at least .70, thus indicating a severe underfitting of the $p_{ij}$ in these blocks. In fact, the $p_1$ model is unable to predict any of the observed ties with a $p_{ij}$ over .5. In Section 3 we exhibit a very simple blockmodel that dramatically improves on the $p_1$ fit.

When attention is focused on the overall block structure rather than the individual nodes of the digraph, Holland et al. (1983) exhibited a simple blockmodel by assuming that (a) the $X_{ij}$ are mutually independent and (b) any $X_{ij}$ and $X_{kl}$ are identically distributed with a common choice probability $p_{rs}$ if $i, k \in B_r$ and $j, l \in B_s$, for some $r, s = 1, \ldots, b$. Assumption (b) says that the pattern of ties in the data is a direct consequence of the density of ties within and across "internally homogeneous" blocks (Breiger 1981). Lorrain and White (1971) characterized homogeneity by means of formal algebraic category theory. Essentially, any pair of nodes $a$ and $b$ in the same block are required to be "structurally equivalent," or node $a$ relates to every other node of the category in exactly the same way as node $b$ does. Assumptions (a) and (b) are simply a stochastic version of this notion of structural equivalence.

| | | $B_1$ | $B_2$ | $B_3$ |
|---|---|---|---|---|
| | | 7 | 7 | 4 |
| $B_1$ | 7 | 19 (45.24) | 2 (4.08) | 1 (3.57) |
| $B_2$ | 7 | 0 (0) | 20 (47.62) | 1 (3.57) |
| $B_3$ | 4 | 1 (3.57) | 4 (14.29) | 8 (66.67) |

*Figure 2. Block Structure of Sampson's (1969) Data: $B_1$, Loyal Opposition; $B_2$, Young Turks; $B_3$, Outcasts.*

The preceding simple blockmodel is in fact a submodel of a class of blockmodels proposed by Fienberg and Wasserman (1981a). In their more general formulation, the $X_{ij}$ in the two assumptions are replaced by the dyads $D_{ij} = (X_{ij}, X_{ji})$, $i < j$. In addition to a choice parameter for each $B_r \times B_s$ block, there is a reciprocity parameter that measures the tendency for nodes in $B_r$ and $B_s$ to reciprocate ties. Generalizations to multiple-relation data were discussed by Fienberg et al. (1981, 1985).

In this article, we are concerned with partitioned digraphs for which both the block information and the individual nodes are of interest. We do not assume internal homogeneity to hold. Thus in Sampson's example the clique formation among the monks as well as their individual behaviors were the subjects of intense investigation by Sampson. In Hansell's example, the individual students were probably of more interest to the parents and school officials than to outside educators, who were primarily interested in how overall friendship choice was related to sex identity.

In Section 2, we propose a class of blockmodels, called the $p_1$ blockmodels, that can answer questions regarding the nodal attributes as well as the individual nodes. Such models generalize the $p_1$ model by incorporating the specific block information into the model in a very simple manner. Maximum likelihood (ML) estimation of the model parameters and approximate likelihood ratio chi-squared tests of hypotheses about the block structure of a digraph are discussed. Although the additional modeling is simple, the resulting blockmodels are not expressible in the form of an ordinary log-linear model; therefore, the standard iterative scaling computer programs for finding the maximum likelihood estimates (MLE's) of the parameters of a log-linear model cannot be directly applied. Using the results of Darroch and Ratcliff (1972), we propose a convergent iterative scaling algorithm for finding the MLE's of the $p_1$ blockmodel parameters.

In Section 3, we apply the simple $p_1$ blockmodeling technology to the two empirical examples. As will be seen there, the $p_1$ blockmodels not only improve on the $p_1$ fits but also yield substantially different interpretations of the data.

## 2. $p_1$ BLOCKMODELS

### 2.1 Derivation of Models

The $p_1$ blockmodels that we advocate are now presented as a generalization of the $p_1$ model of Holland and Leinhardt (1981). Let

$$m_{ij} = \Pr(D_{ij} = (1, 1)), \qquad i < j, \tag{1}$$

$$a_{ij} = \Pr(D_{ij} = (1, 0)), \qquad i \neq j, \tag{2}$$

$$n_{ij} = \Pr(D_{ij} = (0, 0)), \qquad i < j, \tag{3}$$

so that $m_{ij} + a_{ij} + a_{ji} + n_{ij} = 1$ for $i < j$. Assuming that the dyads $D_{ij}$ are mutually independent, Holland and Leinhardt proposed the following basic exponential model for the digraph:

$$p(\mathbf{x}) = \Pr(\mathbf{X} = \mathbf{x}) = K \exp\left[\sum_{i<j} \rho_{ij} x_{ij} x_{ji} + \sum_{i \neq j} \theta_{ij} x_{ij}\right], \tag{4}$$

where

$$\rho_{ij} = \log(m_{ij} n_{ij} / a_{ij} a_{ji}), \qquad i < j, \tag{5}$$

$$\theta_{ij} = \log(a_{ij} / n_{ij}), \qquad i \neq j, \tag{6}$$

$$K = \prod_{i<j} \frac{1}{k_{ij}}, \tag{7}$$

and

$$k_{ij} = 1 + e^{\theta_{ij}} + e^{\theta_{ji}} + e^{\rho_{ij} + \theta_{ij} + \theta_{ji}}. \tag{8}$$

As explained by Holland and Leinhardt (1981), the log-odds ratio $\rho_{ij}$ measures the degree of reciprocation of ties between nodes $i$ and $j$ in the sense that if $\rho_{ij}$ is positive and if $X_{ji} = 1$ ($X_{ji} = 0$), then we are more likely to also observe that $X_{ij} = 1$ ($X_{ij} = 0$). The log-odds $\theta_{ij}$ measures the probability of an asymmetric dyad between nodes $i$ and $j$, given that $X_{ji} = 0$.

Since there is only one observation per cell, a parsimonious modeling will be necessary. Holland and Leinhardt (1981) suggested the following restrictions:

$$\rho_{ij} = \rho, \qquad i < j, \tag{9}$$

$$\theta_{ij} = \theta + \alpha_i + \beta_j, \qquad i \neq j, \tag{10}$$

with the usual side conditions $\alpha_+ = 0$ and $\beta_+ = 0$, where the "+" refers to summation over the appropriate index. These authors referred to $\theta$ as a density parameter, since it governs the density of ones in $\mathbf{X}$. They called $\alpha_i$ the expansiveness parameter and $\beta_i$ the attractiveness parameter of node $i$ because these parameters represent the ability of the node to produce and to attract ties, respectively.

When (9) and (10) are substituted into (4), the $p_1$ model is obtained:

$$p_1(\mathbf{x}) = K \exp\left[\rho m + \theta x_{++} + \sum_i \alpha_i x_{i+} + \sum_j \beta_j x_{+j}\right], \tag{11}$$

where $m = \sum_{i<j} x_{ij} x_{ji}$ is the number of observed mutuals.

The additivity assumption (10) on the choice parameters does not provide any information regarding the block structure of a partitioned digraph; therefore, the application of the $p_1$ model to such data can lead to very misleading results. To gain some insight into the nature of the difficulty, let us examine the likelihood equations in Holland and Leinhardt (1981). The row marginals $X_{i+} = \hat{p}_{i+}$, and the column marginals $X_{+j} = \hat{p}_{+j}$, where $\hat{p}_{ij}$ is the MLE of $p_{ij}$, "smear" the "out-degrees" $X_{i+}$ and the "in-degrees" $X_{+j}$ freely across the nine blocks subject only to the mutuality constraint [Holland and Leinhardt 1981, eq. (28)]. Consequently, some of the cell estimates in the off-diagonal blocks with low tie density are inflated, whereas some of the cell estimates in the diagonal blocks with high tie density are deflated. For example, the $p_1$ analysis of Sampson's data yields relatively low estimates of $p_{ij}$ in most of the three diagonal blocks (in fact, the model is unable to predict any of the ones in the $\mathbf{X}$ matrix with a $p_{ij}$ more than .5!), and many of the cells in the off-diagonal blocks have $p_{ij}$ more than .3, with four cells having $p_{ij}$ more than .4 (see Holland and Leinhardt 1981, table 4).

To better describe a partitioned digraph, we must include an interaction term in (10) to account for the a priori block structure. Owing to the limitation of digraph data, such an interaction term must be as parsimonious as possible. A simple solution is proposed here. We assign to each $B_k \times B_l$ block a parameter $\lambda_{kl}$. Let

$$d_{ijkl} = 1 \quad \text{if the } (i, j) \text{ cell is in the } B_k \times B_l \text{ block}$$
$$= 0 \quad \text{otherwise.}$$

We propose a nonadditive model as follows:

$$\theta_{ij} = \theta + \alpha_i + \beta_j + \sum_{k,l} d_{ijkl} \lambda_{kl}. \tag{12}$$

To identify the block parameters, we impose the constraints $\lambda_{k+} = 0$ and $\lambda_{+l} = 0$ for $k, l = 1, \ldots, b$. Substituting (9) and (12) into (4), we obtain the following $p_1$ blockmodel:

$$p_1(\mathbf{x} \mid \boldsymbol{\lambda}) = K \exp\left[\rho m + \theta x_{++} + \sum_{k,l} \lambda_{kl} x_{++}(B_k \times B_l) + \sum_i \alpha_i x_{i+} + \sum_j \beta_j x_{+j}\right], \tag{13}$$

where $\boldsymbol{\lambda}$ denotes the vector of block parameters $\lambda_{kl}$, and $x_{++}(B_k \times B_l)$ is the observed total in the $B_k \times B_l$ block.

The $p_1$ blockmodel (13) is a full blockmodel with the maximum number of identifiable block parameters, namely $(b - 1)^2$. In Hansell's (1984) example, $b = 1$; hence the

full $p_1$ blockmodel with a single identifiable block parameter will be needed for the data. In Sampson's example, $b = 3$ and there are four free block parameters in the full model. Again, for reasons of parsimony, we prefer simpler submodels by restricting subsets of the $\lambda_{kl}$ to be equal. For instance, we may use a simple submodel for Sampson's data with a single block parameter to differentiate the diagonal blocks from the off-diagonal ones. In fact, as we shall show in Section 3, this "1 df" $p_1$ blockmodel fits the data almost as well as the full four-parameter blockmodel.

To describe submodels with various restrictions on the block parameters, we suggest a more convenient reparameterization of the $p_1$ blockmodels. Suppose there are $h \leq (b-1)^2$ identifiable block parameters $\lambda_1, \ldots, \lambda_h$ associated with a $p_1$ blockmodel. Let $U_s$ denote the union of the $B_k \times B_l$ blocks with the same block parameter $\lambda_s$, and let $x_{++}(U_s)$ denote the observed sum of ties in $U_s$ ($s = 1, \ldots, h$). The class of $p_1$ blockmodels that we shall discuss are given by

$$p_1(\mathbf{x} \mid \boldsymbol{\lambda}) = K \exp\Bigg[\rho m + \theta x_{++} + \sum_s \lambda_s x_{++}(U_s) + \sum_i \alpha_i x_{i+} + \sum_j \beta_j x_{+j}\Bigg]. \quad (14)$$

For example, we can express the simple submodel for Sampson's data in the form of (14), with $h = 1$ and a single $U$ block consisting of the $B_1 \times B_1$, $B_2 \times B_2$, and $B_3 \times B_3$ blocks.

We may interpret $\theta$ and the $\lambda_s$ in (14) in the following manner. Let $L$ denote the union of all of the $B_k \times B_l$ blocks not in any one of $U_1, \ldots, U_h$. If we let $\rho$, $\boldsymbol{\alpha}$, and $\boldsymbol{\beta}$ all equal 0, then the $X_{ij}$ in $L$ and the $X_{ij}$ in $U_s$ are iid Bernoulli variables with success probabilities $p_L$ and $p_s$, respectively. In this case, $\theta = \text{logit}(p_L)$ and $\theta + \lambda_s = \text{logit}(p_s)$. Therefore, $\theta$ governs the density of ties in $L$, and $\lambda_s$ represents the difference of choice densities between the $L$ and $U_s$ blocks on a log-odds scale.

We emphasize that in our formulation of the $p_1$ blockmodels, we do not make any assumptions about the nature of the $U$ and $L$ blocks. In particular, it is not necessary for the $L$ block to consist of zero blocks. The densities of ties in the $U$ and $L$ blocks are governed by $\theta$ and $\lambda_s$. We do not specify the values or signs of these parameters; instead, we estimate them by the ML method.

The interpretations of the main-effects $\alpha_i$ and $\beta_j$ are similar to those of their $p_1$ counterparts. Take $\alpha_i$, for example, where $i$ is in $B_k$. Since $\theta_{ij} - \theta_{i'j} = \alpha_i - \alpha_{i'}$ for any $i'$ in $B_k$ and $j$ in any one of $B_1, \ldots, B_b$, $\alpha_i$ is interpretable as an expansiveness parameter adjusted for group membership $B_k$. Thus if $\alpha_i$ is large and positive (negative), then node $i$ will tend to produce more (fewer) ties than do the other nodes in $B_k$. The interpretation of $\beta_j$ as an adjusted attractiveness parameter follows a similar argument.

## 2.2 Maximum Likelihood Estimation

The parameters of a $p_1$ blockmodel with block parameter vector $\boldsymbol{\lambda}$ consist of $\rho$, $\theta$, $\boldsymbol{\lambda}$, $\boldsymbol{\alpha}$, and $\boldsymbol{\beta}$, collectively represented by $\boldsymbol{\pi}$. To obtain the MLE $\hat{\boldsymbol{\pi}}$ of $\boldsymbol{\pi}$, we first derive the likelihood equations. Since the model is a member of the exponential family, these equations can be obtained by equating the sufficient statistics with their expectations. From (14), the sufficient statistics are $M = \sum_{i<j} X_{ij}X_{ji}$, $\{X_{++}(U_s)\}$, $\{X_{i+}\}$, and $\{X_{+j}\}$; hence the likelihood equations are

$$m = E(M) = \hat{m}_{++} \quad (15)$$

$$x_{++}(U_s) = E(X_{++}(U_s)) = \hat{p}_{++}(U_s), \qquad s = 1, \ldots, h, \quad (16)$$

$$x_{i+} = E(X_{i+}) = \hat{p}_{i+}, \qquad i = 1, \ldots, g, \quad (17)$$

$$x_{+j} = E(X_{+j}) = \hat{p}_{+j}, \qquad j = 1, \ldots, g, \quad (18)$$

where $\hat{p}_{ij} = \hat{m}_{ij} + \hat{a}_{ij}$. The exponential parameter vector $\boldsymbol{\pi}$, which implicitly appears in the preceding equations, is related to the dyadic probabilities as follows:

$$m_{ij} = (1/k_{ij})\exp(\theta_{ij} + \theta_{ji}), \qquad i < j, \quad (19)$$

$$a_{ij} = (1/k_{ij})\exp(\theta_{ij}), \qquad i \neq j, \quad (20)$$

where $k_{ij}$ is defined in (8) and $\theta_{ij}$ follows the nonadditive model (12).

Notice that when the equations in (16) are omitted from the system of likelihood equations, we obtain the ML equations for the parameters of the $p_1$ model. These additional $h$ equations show clearly how a $p_1$ blockmodel makes use of the block information: It distinguishes the blocks by forcing the fitted cell probabilities in each block to equal to the total observed ties in that block.

The MLE of $\boldsymbol{\pi}$ has to be obtained iteratively from Equations (15)–(18). One approach is to work directly with $\boldsymbol{\pi}$. Algorithms for such an approach typically necessitate evaluating or approximating the second derivative matrix of $\boldsymbol{\pi}$ (e.g., see Wong 1987); hence they can be potentially expensive to use in a large digraph. Additionally, good starting values are essential for convergence. For these reasons, we propose to work with the dyadic probabilities using the generalized iterative scaling procedure of Darroch and Ratcliff (1972). The algorithm is simple to implement; moreover, it converges to the ML solutions for any set of initial dyadic probabilities that satisfy (19) and (20) for some value of $\boldsymbol{\pi}$ (e.g., $m_{ij} = a_{ij} = a_{ji} = n_{ij} = .25$). We can recover $\hat{\boldsymbol{\pi}}$ from these estimated probabilities by first obtaining $\hat{\rho}$ and $\hat{\theta}_{ij}$ from Equations (5) and (6) and then solving the system of linear equations (12) for $\hat{\lambda}$, $\hat{\boldsymbol{\alpha}}$, and $\hat{\boldsymbol{\beta}}$ with $\hat{\theta}_{ij}$ on the left sides of the equations.

The iterative scaling algorithm proceeds in cycles of five steps, which we call the row step, the column step, the block step, the mutual step, and the normalizing step. The details of the steps at the $n$th cycle are given in the Appendix. By omitting the appropriate steps of the algorithm, various submodels of a $p_1$ blockmodel may be easily fitted. For example, if the block step is omitted, the resulting algorithm reduces to the $p_1$ fitting algorithm given by Holland and Leinhardt (1981). In addition, we can fit a submodel with $\alpha_i = 0$, $\beta_j = 0$, or $\rho = 0$ by dropping the row step, the column step, or the mutual step, respectively.

We have experimented with simpler versions of the preceding algorithm. In many instances, we have found that dropping the half powers in the row, column, and block steps can speed up the algorithm considerably, particularly near convergence [see the comments of Fienberg and Wasserman (1981b) in the $p_1$ case]. Additionally, the $n_{ij}$ adjustments appear to be unnecessary. At present, we are investigating the convergence properties of these "quasi" Darroch–Ratcliff algorithms. Our conjecture is that these algorithms, in contrast to the unmodified Darroch–Ratcliff algorithm, are probably not globally convergent; however, if they converge to the ML solutions, then they will converge faster than the unmodified algorithm.

## 2.3 Hypothesis Testing

Approximate likelihood ratio chi-squared tests for the parameters of the $p_1$ model were discussed by Holland and Leinhardt (1981) and Fienberg and Wasserman (1981a). Since a $p_1$ blockmodel is the $p_1$ model with an added block structure, it suffices to consider only hypotheses about the block parameters.

A common testing situation in blockmodeling is to assess whether the proposed block structure significantly improves on the $p_1$ fit. This may be accomplished by testing $H_0$: $\boldsymbol{\lambda} = \mathbf{0}$ against $H_1$: $\boldsymbol{\lambda} \neq \mathbf{0}$. Although the log-likelihood of the parameters is directly obtainable from (14), it can be expressed in terms of the dyadic probabilities without explicitly solving for the exponential parameters as follows:

$$L = \sum_{i<j} X_{ij}X_{ji} \log m_{ij} + \sum_{i\neq j} X_{ij}(1 - X_{ji})\log a_{ij} + \sum_{i<j} (1 - X_{ij})(1 - X_{ji})\log n_{ij}. \quad (21)$$

Let $L_{H_i}$ denote $L$ estimated under $H_i$ $(i = 0, 1)$. Then the usual log-likelihood ratio (LLR) statistic for this test is

$$\text{LLR} = -2(L_{H_0} - L_{H_1}). \quad (22)$$

In a $p_1$ blockmodel, the number of parameters grows with the sample size, which is the number of dyads, $\binom{g}{2}$; therefore, the standard asymptotic chi-squared distribution theory for likelihood ratios cannot be applied to LLR. In fact, there is evidence that the asymptotic distribution of LLR may not be chi-squared (see Fienberg and Wasserman 1981b; Haberman 1981; Holland and Leinhardt 1981). In the applications in Section 3, however, we shall assume that LLR is approximately chi-squared distributed with $h$ df, with the understanding that the chi-squared values provide only rough and informal guidelines for the significance testing.

Another testing situation involving $\boldsymbol{\lambda}$ is in the choice of competing blockmodels appropriate for a partitioned digraph. Suppose that there are two competing models and that one is a submodel of the other, which possesses additional $U$ blocks denoted by $U(\lambda_k^*)$, $k \in Q^*$. To see whether the simpler model adequately accounts for the block structure seen in the data, we can test $H_0$: $\lambda_k^* = 0$, $k \in Q^*$, against $H_1$: $\lambda_k^* \neq 0$, $k \in Q^*$, using the LLR test statistic with $|Q^*|$ df, where $|Q^*|$ is the cardinality of $Q^*$. If the test accepts, then $U(\lambda_k^*)$, $k \in Q^*$, are regarded as part of the $L$ block, and the simpler model is adequate for the partitioned digraph.

# 3. EMPIRICAL EXAMPLES

The proposed $p_1$ blockmodeling methodology is now illustrated in detail on the two data sets mentioned in Section 1. We first discuss Hansell's (1984) classroom ex-

*Table 3. Fitted Cell Probabilities Using the $p_1$ Model for Hansell's (1984) Data, Multiplied by 100*

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | 21 | 10 | 11 | 32 | 31 | 9 | 6 | 21 | 25 | 12 | 9 | 21 | 40 | 55 | 22 | 46 | 41 | 11 | 0 | 44 | 24 | 19 | 37 | 46 | 2 | 5 |
| 2 | 9 | | 3 | 3 | 10 | 10 | 2 | 2 | 6 | 8 | 3 | 2 | 6 | 14 | 23 | 7 | 17 | 15 | 3 | 0 | 16 | 7 | 5 | 12 | 17 | 1 | 1 |
| 3 | 31 | 27 | | 11 | 32 | 31 | 11 | 6 | 26 | 34 | 17 | 11 | 27 | 42 | 60 | 25 | 56 | 50 | 11 | 0 | 48 | 25 | 20 | 43 | 48 | 3 | 7 |
| 4 | 55 | 51 | 24 | | 55 | 55 | 25 | 16 | 50 | 59 | 36 | 26 | 51 | 67 | 81 | 47 | 78 | 73 | 25 | 0 | 72 | 48 | 41 | 68 | 71 | 9 | 18 |
| 5 | 62 | 54 | 32 | 35 | | 65 | 30 | 22 | 54 | 60 | 38 | 30 | 54 | 73 | 84 | 56 | 80 | 76 | 34 | 0 | 77 | 57 | 49 | 72 | 78 | 9 | 19 |
| 6 | 48 | 39 | 21 | 23 | 53 | | 19 | 13 | 40 | 45 | 25 | 19 | 39 | 61 | 74 | 41 | 68 | 63 | 22 | 0 | 65 | 43 | 35 | 58 | 67 | 5 | 11 |
| 7 | 17 | 14 | 5 | 5 | 18 | 17 | | 3 | 14 | 18 | 8 | 5 | 14 | 25 | 40 | 13 | 36 | 30 | 5 | 0 | 30 | 13 | 10 | 25 | 29 | 2 | 3 |
| 8 | 30 | 27 | 10 | 10 | 30 | 29 | 11 | | 27 | 35 | 17 | 11 | 27 | 41 | 60 | 23 | 57 | 50 | 10 | 0 | 48 | 24 | 19 | 44 | 47 | 4 | 8 |
| 9 | 13 | 9 | 4 | 5 | 15 | 15 | 4 | 2 | | 12 | 5 | 4 | 9 | 20 | 32 | 10 | 26 | 22 | 5 | 0 | 23 | 11 | 8 | 18 | 25 | 1 | 2 |
| 10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 11 | 4 | 3 | 1 | 1 | 5 | 4 | 1 | 1 | 3 | 4 | | 1 | 3 | 6 | 12 | 3 | 10 | 8 | 1 | 0 | 8 | 3 | 2 | 6 | 8 | 0 | 1 |
| 12 | 12 | 10 | 4 | 4 | 13 | 13 | 4 | 2 | 10 | 13 | 6 | | 10 | 19 | 32 | 10 | 28 | 23 | 4 | 0 | 23 | 10 | 7 | 19 | 22 | 1 | 2 |
| 13 | 9 | 6 | 3 | 3 | 10 | 10 | 2 | 2 | 6 | 8 | 3 | 2 | | 14 | 23 | 7 | 17 | 15 | 3 | 0 | 16 | 7 | 5 | 12 | 17 | 1 | 1 |
| 14 | 35 | 25 | 13 | 14 | 39 | 38 | 12 | 8 | 26 | 28 | 14 | 11 | 25 | | 62 | 26 | 51 | 47 | 14 | 0 | 51 | 30 | 24 | 43 | 54 | 3 | 6 |
| 15 | 26 | 17 | 9 | 9 | 28 | 28 | 8 | 6 | 19 | 17 | 9 | 8 | 17 | 38 | | 16 | 38 | 35 | 9 | 0 | 41 | 22 | 17 | 33 | 44 | 1 | 3 |
| 16 | 85 | 82 | 61 | 63 | 86 | 86 | 61 | 48 | 82 | 86 | 71 | 61 | 82 | 90 | 95 | | 94 | 92 | 62 | 0 | 92 | 82 | 77 | 91 | 92 | 30 | 50 |
| 17 | 5 | 3 | 1 | 1 | 5 | 5 | 1 | 1 | 3 | 3 | 1 | 1 | 3 | 8 | 13 | 3 | | 7 | 1 | 0 | 9 | 4 | 3 | 6 | 10 | 0 | 0 |
| 18 | 10 | 6 | 3 | 3 | 11 | 11 | 3 | 2 | 6 | 6 | 3 | 2 | 6 | 15 | 24 | 6 | 16 | | 3 | 0 | 17 | 8 | 6 | 13 | 19 | 0 | 1 |
| 19 | 50 | 46 | 21 | 21 | 51 | 50 | 22 | 14 | 45 | 54 | 31 | 22 | 46 | 62 | 77 | 43 | 75 | 69 | | 0 | 68 | 43 | 36 | 64 | 67 | 7 | 16 |
| 20 | 50 | 48 | 20 | 17 | 43 | 46 | 22 | 13 | 47 | 57 | 34 | 23 | 48 | 61 | 78 | 26 | 77 | 71 | 17 | | 69 | 41 | 35 | 65 | 66 | 8 | 17 |
| 21 | 25 | 17 | 9 | 9 | 28 | 27 | 8 | 5 | 18 | 18 | 9 | 7 | 17 | 36 | 50 | 17 | 38 | 35 | 9 | 0 | | 22 | 17 | 31 | 42 | 1 | 3 |
| 22 | 37 | 30 | 14 | 16 | 42 | 40 | 14 | 9 | 30 | 36 | 18 | 13 | 30 | 50 | 65 | 32 | 59 | 53 | 16 | 0 | 54 | | 26 | 48 | 56 | 4 | 8 |
| 23 | 32 | 26 | 11 | 13 | 35 | 34 | 11 | 7 | 26 | 32 | 16 | 11 | 26 | 43 | 60 | 27 | 54 | 48 | 12 | 0 | 49 | 27 | | 43 | 50 | 3 | 7 |
| 24 | 14 | 9 | 5 | 5 | 16 | 16 | 4 | 3 | 10 | 10 | 5 | 4 | 9 | 22 | 34 | 10 | 24 | 21 | 5 | 0 | 24 | 12 | 9 | | 27 | 1 | 2 |
| 25 | 41 | 30 | 16 | 17 | 44 | 44 | 15 | 10 | 31 | 32 | 17 | 14 | 30 | 54 | 67 | 30 | 56 | 53 | 17 | 0 | 57 | 36 | 29 | 49 | | 3 | 7 |
| 26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 |
| 27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |

*Table 4. Fitted Cell Probabilities Using the Blockmodel for Hansell's Data, Multiplied by 100*

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | 40 | 21 | 23 | 56 | 56 | 19 | 13 | 42 | 44 | 24 | 19 | 40 | 19 | 35 | 9 | 29 | 23 | 3 | 0 | 24 | 9 | 6 | 19 | 25 | 1 | 1 |
| 2 | 21 | | 6 | 6 | 23 | 22 | 5 | 3 | 14 | 16 | 7 | 5 | 14 | 5 | 11 | 2 | 9 | 7 | 1 | 0 | 7 | 2 | 2 | 5 | 7 | 0 | 0 |
| 3 | 54 | 45 | | 24 | 57 | 56 | 20 | 13 | 45 | 52 | 28 | 20 | 45 | 23 | 41 | 10 | 35 | 29 | 3 | 0 | 29 | 10 | 7 | 23 | 28 | 1 | 2 |
| 4 | 77 | 70 | 44 | | 79 | 79 | 43 | 30 | 70 | 76 | 53 | 43 | 70 | 46 | 67 | 23 | 61 | 54 | 9 | 0 | 54 | 25 | 19 | 47 | 53 | 2 | 5 |
| 5 | 83 | 75 | 54 | 57 | | 85 | 51 | 40 | 76 | 78 | 58 | 50 | 75 | 52 | 71 | 31 | 64 | 58 | 12 | 0 | 58 | 30 | 23 | 51 | 59 | 2 | 6 |
| 6 | 73 | 62 | 39 | 42 | 76 | | 36 | 27 | 64 | 66 | 43 | 35 | 62 | 37 | 57 | 20 | 49 | 43 | 7 | 0 | 43 | 19 | 14 | 36 | 44 | 1 | 3 |
| 7 | 34 | 26 | 11 | 12 | 37 | 36 | | 6 | 27 | 32 | 15 | 10 | 26 | 12 | 24 | 5 | 19 | 15 | 1 | 0 | 15 | 5 | 3 | 12 | 15 | 0 | 1 |
| 8 | 53 | 44 | 20 | 22 | 55 | 54 | 20 | | 45 | 52 | 28 | 20 | 44 | 23 | 41 | 9 | 35 | 29 | 3 | 0 | 29 | 10 | 7 | 24 | 28 | 1 | 2 |
| 9 | 30 | 20 | 9 | 10 | 32 | 32 | 8 | 5 | | 24 | 11 | 8 | 20 | 8 | 17 | 4 | 13 | 11 | 1 | 0 | 11 | 4 | 2 | 8 | 11 | 0 | 1 |
| 10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 11 | 10 | 7 | 2 | 3 | 11 | 11 | 2 | 1 | 7 | 8 | | 2 | 7 | 3 | 6 | 1 | 4 | 3 | 0 | 0 | 3 | 1 | 1 | 3 | 3 | 0 | 0 |
| 12 | 27 | 20 | 8 | 9 | 29 | 28 | 7 | 4 | 20 | 25 | 11 | | 20 | 8 | 18 | 3 | 14 | 11 | 1 | 0 | 11 | 3 | 2 | 9 | 11 | 0 | 1 |
| 13 | 21 | 14 | 6 | 6 | 23 | 22 | 5 | 3 | 14 | 16 | 7 | 5 | | 5 | 11 | 2 | 9 | 7 | 1 | 0 | 7 | 2 | 2 | 5 | 7 | 0 | 0 |
| 14 | 13 | 9 | 3 | 4 | 14 | 14 | 3 | 2 | 9 | 11 | 5 | 3 | 9 | | 83 | 42 | 73 | 69 | 23 | 0 | 73 | 49 | 39 | 64 | 76 | 3 | 9 |
| 15 | 7 | 5 | 2 | 2 | 8 | 8 | 2 | 1 | 5 | 6 | 2 | 2 | 5 | 56 | | 25 | 58 | 55 | 13 | 0 | 61 | 33 | 25 | 50 | 63 | 2 | 4 |
| 16 | 79 | 73 | 45 | 47 | 79 | 79 | 46 | 32 | 73 | 79 | 58 | 46 | 73 | 98 | 99 | | 99 | 98 | 88 | 0 | 98 | 96 | 93 | 98 | 99 | 50 | 74 |
| 17 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 11 | 21 | 3 | | 11 | 1 | 0 | 13 | 5 | 3 | 9 | 15 | 0 | 0 |
| 18 | 2 | 1 | 0 | 0 | 2 | 2 | 0 | 0 | 1 | 1 | 1 | 0 | 1 | 22 | 38 | 8 | 25 | | 3 | 0 | 26 | 10 | 7 | 18 | 28 | 0 | 1 |
| 19 | 30 | 25 | 9 | 9 | 29 | 30 | 9 | 5 | 25 | 31 | 14 | 9 | 25 | 85 | 93 | 70 | 90 | 87 | | 0 | 88 | 69 | 60 | 84 | 88 | 11 | 25 |
| 20 | 30 | 25 | 9 | 8 | 27 | 29 | 9 | 5 | 24 | 31 | 14 | 9 | 25 | 83 | 92 | 54 | 90 | 87 | 34 | | 87 | 65 | 57 | 84 | 86 | 11 | 25 |
| 21 | 7 | 5 | 2 | 2 | 8 | 8 | 2 | 1 | 5 | 6 | 2 | 2 | 5 | 54 | 71 | 26 | 57 | 53 | 13 | 0 | | 33 | 24 | 48 | 62 | 2 | 4 |
| 22 | 16 | 12 | 4 | 4 | 17 | 16 | 4 | 2 | 12 | 15 | 6 | 4 | 12 | 74 | 85 | 50 | 79 | 75 | 27 | 0 | 77 | | 43 | 70 | 79 | 5 | 12 |
| 23 | 12 | 9 | 3 | 3 | 12 | 12 | 3 | 2 | 9 | 12 | 5 | 3 | 9 | 65 | 80 | 42 | 73 | 68 | 20 | 0 | 70 | 44 | | 62 | 72 | 3 | 9 |
| 24 | 3 | 2 | 1 | 1 | 3 | 3 | 1 | 0 | 2 | 3 | 1 | 1 | 2 | 33 | 50 | 13 | 36 | 32 | 6 | 0 | 37 | 17 | 12 | | 40 | 1 | 2 |
| 25 | 17 | 12 | 4 | 5 | 19 | 18 | 4 | 3 | 12 | 15 | 6 | 4 | 12 | 77 | 87 | 49 | 79 | 76 | 29 | 0 | 80 | 57 | 47 | 72 | | 4 | 11 |
| 26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 |
| 27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |

ample (Table 1). As explained in Section 2.1, the only $p_1$ blockmodel for this simple $2 \times 2$ block structure (Fig. 1) is the 1 df blockmodel that differentiates the same-sex ($B_1 \times B_1$, $B_2 \times B_2$) blocks from the opposite-sex ($B_1 \times B_2$, $B_2 \times B_1$) blocks by a single block parameter $\lambda$. To assess the strength of the sex effect, we fit the $p_1$ block model to the data and employ the approximate chi-squared test procedure of Section 2.3 to test $H_0$: $\lambda = 0$ against $H_1$: $\lambda \neq 0$. The LLR statistic (see Sec. 2.3) gives a value of 61.49, which is very significant if the distribution of the test statistic under $H_0$ is assumed to have a chi-squared distribution with 1 df. The estimated overall choice density for the same-sex blocks is $\hat{\theta} + \hat{\lambda} = -.95$, and that for the opposite-sex blocks is $\hat{\theta} = -2.80$. The significant positive value of $\lambda$ suggests that friendship is stronger among students of the same sex than among students of the opposite sex. When the $p_1$ model is fitted to the data, we obtain $\hat{\theta} = -1.84$. This larger value of $\theta$ is expected, since the $p_1$ model regards the same-sex and opposite-sex blocks as one single block.

Tables 3 and 4 give the fitted $p_1$ and blockmodel ML cell probabilities. In the same-sex blocks, the blockmodel cell estimates are uniformly at least as large as the $p_1$ ones; the situation is reversed in the opposite-sex blocks. This observation is consistent with the fact that $\lambda$ is significantly positive.

Figure 3 presents the stem-and-leaf displays of the residuals $X_{ij} - \hat{p}_{ij}$ of the two fits side by side. For both of these fits, the majority of the residuals are concentrated between the stems (tenths digits) $-1$ and 0. About half (50.8%) of the blockmodel residuals are between the stems $-0$ and 0; only 41.7% of the $p_1$ residuals are in this range. The $p_1$ fit leads to more large positive residuals (underfitting) than does the blockmodel fit. For example, there are 49 $p_1$ residuals greater than .70 [this is an arbitrary cutoff value used by Holland and Leinhardt (1981) to flag

*Table 5. Maximum Likelihood Estimates of Main Effects for Hansell's (1984) Data*

| | Blockmodel | | $p_1$ Model | |
|---|---|---|---|---|
| Student | $\hat{\alpha}_i$ | $\hat{\beta}_i$ | $\hat{\alpha}_i$ | $\hat{\beta}_i$ |
| 1 | .19 | .48 | .05 | .40 |
| 2 | −1.24 | .21 | −1.35 | .31 |
| 3 | .49 | −1.05 | .48 | −1.00 |
| 4 | 1.56 | −1.10 | 1.52 | −1.20 |
| 5 | 1.70 | .34 | 1.58 | .11 |
| 6 | 1.09 | .41 | .96 | .23 |
| 7 | −.33 | −.99 | −.34 | −.85 |
| 8 | .51 | −1.62 | .53 | −1.53 |
| 9 | −.75 | .20 | −.86 | .26 |
| 10 | −∞ | .54 | −∞ | .69 |
| 11 | −1.97 | −.48 | −2.01 | −.28 |
| 12 | −.69 | −.97 | −.71 | −.80 |
| 13 | −1.24 | .21 | −1.35 | .31 |
| 14 | .20 | 1.07 | .22 | .86 |
| 15 | −.54 | 1.94 | −.44 | 1.66 |
| 16 | 3.59 | −.37 | 2.99 | −.67 |
| 17 | −2.80 | 1.68 | −2.37 | 1.59 |
| 18 | −1.95 | 1.41 | −1.54 | 1.31 |
| 19 | 1.47 | −1.17 | 1.32 | −1.17 |
| 20 | 1.48 | −∞ | 1.45 | −∞ |
| 21 | −.52 | 1.38 | −.35 | 1.19 |
| 22 | .56 | .12 | .57 | .03 |
| 23 | .24 | −.24 | .39 | −.23 |
| 24 | −1.37 | 1.11 | −1.00 | 1.04 |
| 25 | .50 | 1.33 | .40 | 1.06 |
| 26 | −∞ | −2.63 | −∞ | −2.00 |
| 27 | −∞ | −1.60 | −∞ | −1.16 |

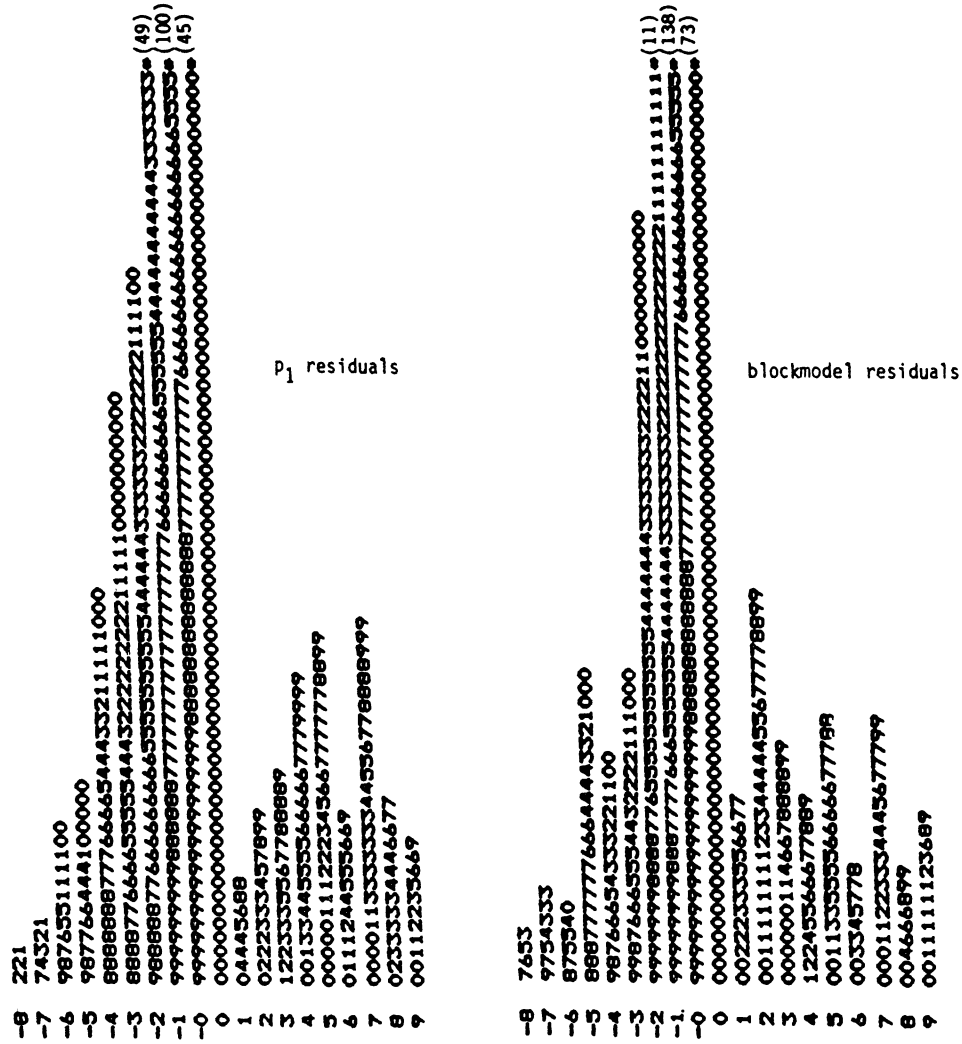


*Figure 3. Stem-and-Leaf Displays of $p_1$ and Blockmodel Residuals for Hansell's (1984) Data. The numbers in parentheses indicate the number of leaves at a certain stem position omitted from the displays.*

an unexpected tie] and only 40 in the case of the blockmodel. The sum of absolute $p_1$ residuals is 170.76; a smaller value of 145.86 is obtained for the blockmodel residuals. Figure 3 shows that the distribution of the blockmodel residuals is fairly symmetric about 0, although the right tail is slightly heavier than the left one. On the other hand, the distribution of the $p_1$ residuals is bimodal, with the major mode corresponding to underfitting in the same-sex blocks and the minor mode corresponding to overfitting in the opposite-sex blocks.

We next compare the estimated reciprocity and main effects of the two fits. The $p_1$ fit gives $\hat{\rho} = 1.37$, whereas the blockmodel fit gives a much smaller value of .81. The block structure, therefore, has explained away about 41% of the reciprocation seen in the $p_1$ model. The LLR statistic for testing $H_0$: $\rho = 0$ against $H_1$: $\rho \neq 0$ yields a value of 3.19, which is smaller than the usual .05 critical value of the chi-squared distribution with 1 df.

Table 5 compares the estimated main effects. The two sets of expansiveness parameters do not differ much from each other. But large differences are found in the attractiveness parameters. Both fits indicate that the expansiveness and attractiveness of the students are only moderately associated (the sample correlation coefficient between $\alpha_i$ and $\beta_i$ is $-.50$ for the $p_1$ fit and $-.41$ for the blockmodel fit).

Now we carry out a parallel analysis on Sampson's monastery data (Table 2). Unlike Hansell's (1984) simple example, there are several $p_1$ blockmodels that are suitable for Sampson's block structure (Fig. 2). Table 6 contains the results of the $p_1$ fit and some blockmodel fits, including the full $p_1$ blockmodel with four distinct block parameters. The fit of each of the blockmodels is much better than that of the $p_1$ model based on the criteria used in the table. The LLR statistic for testing the difference between blockmodel (2) and the $p_1$ model, for example, yields a very significant chi-squared value of 72.69 on 1 df. Table 6 shows that the simplest of these blockmodels, namely blockmodel (2), which distinguishes the same-clique blocks from the cross-clique blocks by a single block parameter $\lambda$, fits the data almost as well as the other three. This model implies that the bonds of positive affect in the three

*Table 6. Summary of Some Blockmodel Fits to Sampson's (1969) Data*

| Model | Block structure | Sum of absolute residuals | Number of absolute residuals greater than .70 | Log-likelihood | Estimated $\rho$ |
|---|---|---|---|---|---|
| 1 | $p_1$ model | 85.13 | 38 | −118.46 | 3.14 |
| 2 | $\lambda$ / $\lambda$ / $\lambda$ | 51.88 | 19 | −82.12 | 1.52 |
| 3 | $\lambda$ / $\lambda_1$ $\lambda$ / $\lambda_1$ | 51.56 | 19 | −81.26 | 1.57 |
| 4 | $\lambda_2$ / $\lambda_3$ | 51.47 | 19 | −80.66 | 1.58 |
| 5 | Saturated blockmodel | 51.52 | 19 | −80.51 | 1.56 |

cliques are comparable in magnitude; moreover, this magnitude is different from that associated with monks from different cliques. The estimated choice density for the same-clique blocks is $\hat{\theta} + \hat{\lambda} = -.53$; that for the cross-clique blocks is $\hat{\theta} = -3.88$. Therefore, the strength of same-clique affect is significantly stronger than that of cross-clique affect.

An interesting conclusion from Table 6 is that there is no significant evidence that the Outcasts have preferential affect for the Young Turks. This may be justified by comparing blockmodels (2) and (3) and testing $H_0$: $\lambda_1 = 0$ against $H_1$: $\lambda_1 \neq 0$. The LLR statistic gives a very nonsignificant chi-squared value of 1.72 on 1 df. Therefore, the $B_3 \times B_2$ block should be regarded as a member of the cross-clique blocks (or the *zero blocks*).

Table 7 gives the fitted ML cell probabilities under blockmodel (2). Except for the first column of zero estimates, the entries in Table 7 are very different from their $p_1$ counterparts in Table 4 of Holland and Leinhardt (1981). In the same-clique blocks, the blockmodel cell estimates are uniformly larger than their $p_1$ estimates. Only 10 of the observed ties in these blocks have estimated cell probabilities of less than .5 (recall that the $p_1$ model is unable to predict any of the observed ties in the adjacency matrix with a $p_{ij}$ of more than .5). In the cross-clique blocks, uniformly smaller cell estimates are produced by the blockmodel.

Figure 4 presents the stem-and-leaf displays of the $p_1$ and blockmodel-(2) residuals side by side. The contrast between the bimodality of the $p_1$ residuals and the symmetric cluster of the blockmodel residuals at about 0 is indeed striking. Sixty percent of the blockmodel residuals

*Table 7. Fitted Cell Probabilities Using Blockmodel (2) for Sampson's (1969) Data, Multiplied by 100*

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | 86 | 63 | 31 | 63 | 31 | 31 | 21 | 9.9 | 21 | 3.4 | 3.4 | 15 | 1.4 | 2.2 | 7.4 | 2.2 | 8.0 |
| 2 | 0 | | 69 | 38 | 69 | 38 | 38 | 9.8 | 4.4 | 9.8 | 1.5 | 1.5 | 6.7 | .6 | 1.2 | 5.2 | 1.2 | 4.6 |
| 3 | 0 | 86 | | 34 | 65 | 34 | 34 | 11 | 4.7 | 11 | 1.6 | 1.6 | 7.2 | .6 | 1.1 | 4.3 | 1.1 | 4.1 |
| 4 | 0 | 82 | 57 | | 57 | 27 | 27 | 12 | 5.2 | 12 | 1.7 | 1.7 | 7.9 | .7 | 1.1 | 4.1 | 1.1 | 4.2 |
| 5 | 0 | 86 | 65 | 34 | | 34 | 34 | 11 | 4.7 | 11 | 1.6 | 1.6 | 7.2 | .6 | 1.1 | 4.3 | 1.1 | 4.1 |
| 6 | 0 | 82 | 57 | 27 | 57 | | 27 | 12 | 5.2 | 12 | 1.7 | 1.7 | 7.9 | .7 | 1.1 | 4.1 | 1.1 | 4.2 |
| 7 | 0 | 82 | 57 | 27 | 57 | 27 | | 12 | 5.2 | 12 | 1.7 | 1.7 | 7.9 | .7 | 1.1 | 4.1 | 1.1 | 4.2 |
| 8 | 0 | 4 | 1.2 | .3 | 1.2 | .3 | .3 | | 59 | 77 | 33 | 33 | 69 | 17 | .5 | 2.4 | .5 | 2.1 |
| 9 | 0 | 4 | 1.2 | .3 | 1.2 | .3 | .3 | 74 | | 74 | 30 | 30 | 66 | 15 | .5 | 2.1 | .5 | 1.9 |
| 10 | 0 | 4 | 1.2 | .3 | 1.2 | .3 | .3 | 77 | 59 | | 33 | 33 | 69 | 17 | .5 | 2.4 | .5 | 2.1 |
| 11 | 0 | 4.4 | 1.3 | .4 | 1.3 | .4 | .4 | 70 | 50 | 70 | | 25 | 61 | 12 | .5 | 1.9 | .5 | 1.9 |
| 12 | 0 | 4.4 | 1.3 | .4 | 1.3 | .4 | .4 | 70 | 50 | 70 | 25 | | 61 | 12 | .5 | 1.9 | .5 | 1.9 |
| 13 | 0 | 4 | 1.2 | .3 | 1.2 | .3 | .3 | 76 | 58 | 76 | 31 | 31 | | 16 | .5 | 2.2 | .5 | 2 |
| 14 | 0 | 4.7 | 1.4 | .4 | 1.4 | .4 | .4 | 68 | 47 | 68 | 23 | 23 | 58 | | .5 | 2.0 | .5 | 2 |
| 15 | 0 | 14 | 4.5 | 1.2 | 4.5 | 1.2 | 1.2 | 17 | 7.8 | 17 | 2.6 | 2.6 | 12 | 1.1 | | 83 | 51 | 80 |
| 16 | 0 | 25 | 9 | 2.6 | 9 | 2.6 | 2.6 | 29 | 15 | 29 | 5.2 | 5.2 | 21 | 2.2 | 75 | | 75 | 92 |
| 17 | 0 | 14 | 4.5 | 1.2 | 4.5 | 1.2 | 1.2 | 17 | 7.8 | 17 | 2.6 | 2.6 | 12 | 1.1 | 51 | 83 | | 80 |
| 18 | 0 | 15 | 4.9 | 1.4 | 4.9 | 1.4 | 1.4 | 17 | 8.1 | 17 | 2.7 | 2.7 | 12 | 1.1 | 61 | 87 | 61 | |

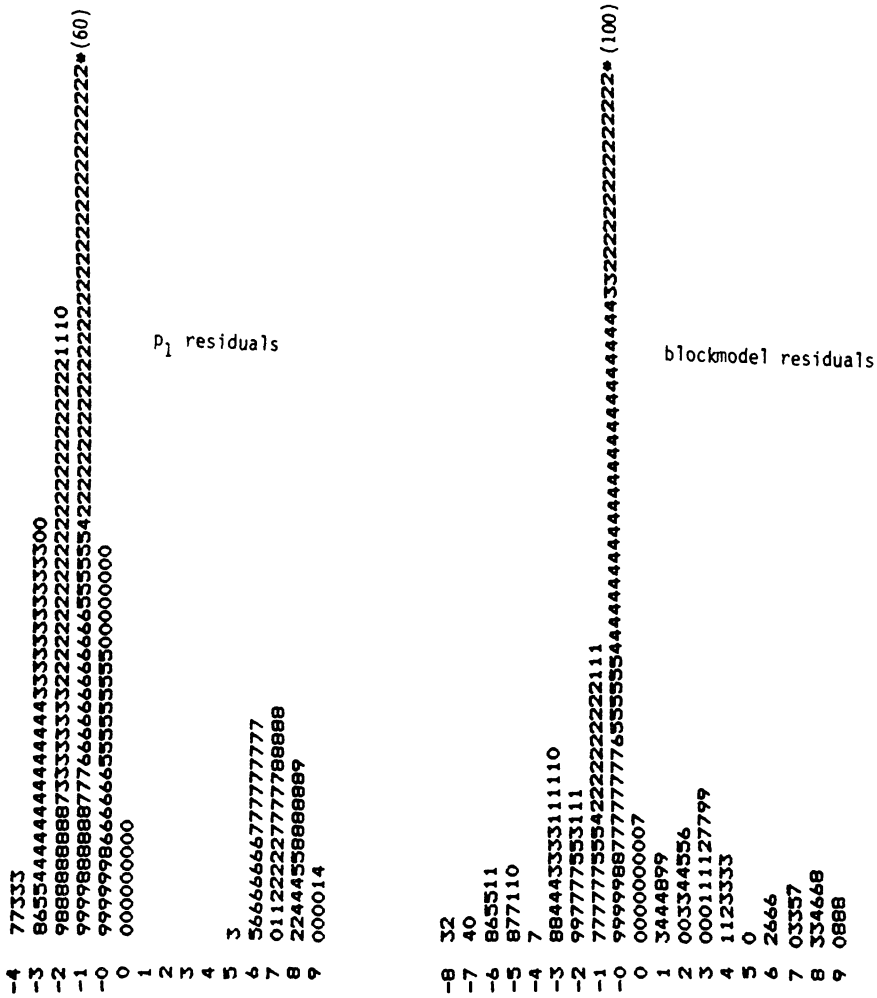


*Figure 4. Stem-and-Leaf Displays of $p_1$ and Blockmodel Residuals for Sampson's (1969) Data. The numbers in parentheses indicate the number of leaves at a certain stem position omitted from the displays.*

are between the stems $-0$ and 0; only 12.8% of the $p_1$ residuals are in this range. Figure 5 highlights the exceptionally small and large blockmodel residuals with absolute magnitude greater than .7. There are 19 of them. The $p_1$ fit, on the other hand, produces a total of 38 (see Holland and Leinhardt 1981, fig. 6). The sum of absolute residuals is reduced from 85.13 in the $p_1$ case to 51.88 in the case of blockmodel (2), a 39.06% reduction.

Next we compare the estimated reciprocity and main effects of the two fits. The $p_1$ fit gives $\hat{\rho} = 3.14$; this figure is reduced to 1.52 in the case of the blockmodel fit. Again, as in Hansell's (1984) example, the blockmodel has explained away about 52% of the tendency toward reciprocation predicted by the $p_1$ model. Interestingly enough, a comparable value of 1.01 was obtained by Holland et al. (1983) using the blockmodel mentioned in Section 1.

Table 8 compares the estimated main effects. There are three major differences between these two sets of estimates. First, the $\hat{\alpha}_i$ under the blockmodel are larger in absolute magnitude than their $p_1$ counterparts in 14 of the 18 monks. As in the $p_1$ analysis, however, these $\hat{\alpha}_i$ are small relative to the $\hat{\beta}_i$. The LLR test of $H_0$: $\alpha_i = 0$ for all $i$ yields an approximate chi-squared value of 7.16 (6.83 in the $p_1$ case) on 17 df. Therefore, a simpler blockmodel with $\alpha_i = 0$ for all $i$ should fit the data well.

Second, under the $p_1$ model, there are more monks with

*Table 8. Maximum Likelihood Estimates of Main Effects for Sampson's (1969) Data, Multiplied by 100*

| | Blockmodel (2) | | $p_1$ Model | |
|---|---|---|---|---|
| Monk | $\hat{\alpha}_i$ | $\hat{\beta}_i$ | $\hat{\alpha}_i$ | $\hat{\beta}_i$ |
| 1 | .95 | $-\infty$ | 1.15 | $-\infty$ |
| 2 | −.04 | 1.36 | −.73 | 1.25 |
| 3 | .11 | .11 | −.30 | .49 |
| 4 | .24 | −1.21 | .22 | −.62 |
| 5 | .11 | .11 | −.30 | .49 |
| 6 | .24 | −1.21 | .22 | −.62 |
| 7 | .24 | −1.21 | .22 | −.62 |
| 8 | −.93 | 1.59 | −.73 | 1.25 |
| 9 | −.79 | .72 | −.30 | .49 |
| 10 | −.93 | 1.59 | −.73 | 1.25 |
| 11 | −.62 | −.43 | .22 | −.62 |
| 12 | −.62 | −.43 | .22 | −.62 |
| 13 | −.86 | 1.17 | −.53 | .89 |
| 14 | −.51 | −1.33 | .49 | −1.53 |
| 15 | .68 | −.88 | .22 | −.62 |
| 16 | 1.34 | .40 | .48 | −.25 |
| 17 | .68 | −.88 | .22 | −.62 |
| 18 | .67 | .48 | −.05 | .00 |

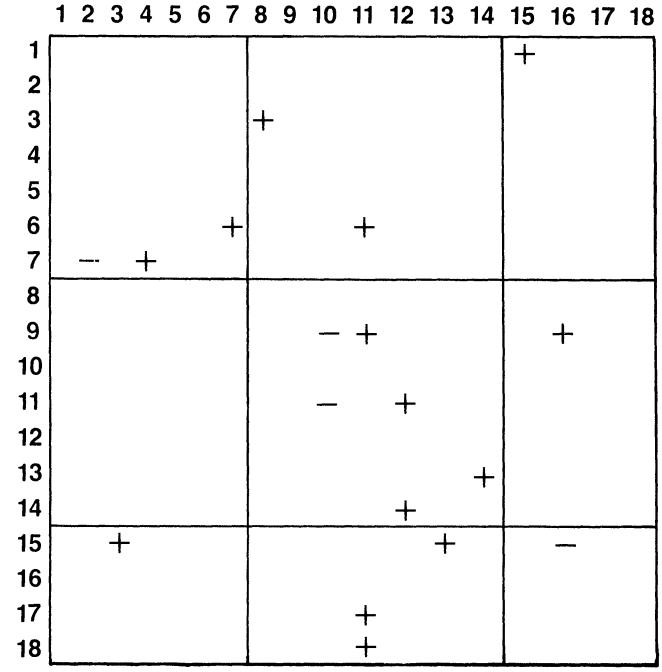


*Figure 5. Coded Residuals From Blockmodel (2) Fit to Sampson's (1969) Data: −, a residual less than or equal to −.7; +, a residual equal to or greater than .7.*

the same estimated main effects (e.g., monks 4, 6, 7, 11, 12, 15, and 17). Under blockmodel (2), no two monks from different cliques possess the same main effects. This phenomenon may be explained by the fact that the blockmodel estimates depend on the additional block constraints (16). The additional constraint has explained away much of the apparent association between the monks' expansiveness and attractiveness characteristics concluded from the $p_1$ fit, as Figure 6 shows (the sample correlation coefficient between $\hat{\alpha}_i$ and $\hat{\beta}_i$ is $-.96$ for the $p_1$ fit and $-.40$ for the blockmodel fit).

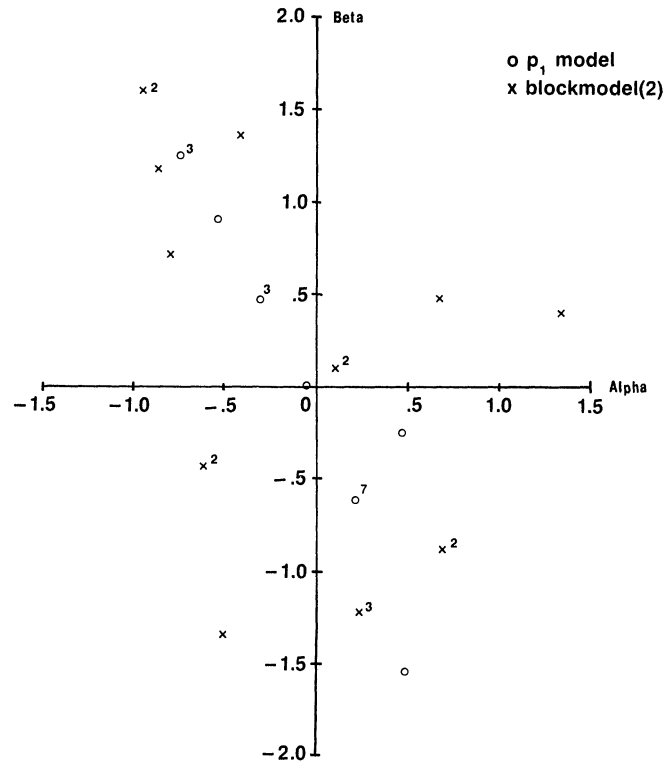


*Figure 6. Plot of $\hat{\beta}_i$ Versus $\hat{\alpha}_i$ for Sampson's (1969) Data.*

Through the detailed comparative analyses of the two empirical examples, we have demonstrated the considerable flexibility and power of our blockmodeling approach. In particular, we have shown via Sampson's example that $p_1$ analysis of a partitioned digraph with one or more pronounced low tie density blocks can lead to very misleading results; in this situation, even a simple $p_1$ blockmodel with a single block parameter can dramatically improve on the $p_1$ fit.

## APPENDIX: AN ITERATIVE SCALING ALGORITHM FOR $p_1$ BLOCKMODELS

Here we provide the details of the iterative scaling algorithm mentioned in Section 2.2. In the following, $p_{ij}^{(n)} = a_{ij}^{(n)} + m_{ij}^{(n)}$ and $q_{ij}^{(n)} = 1 - p_{ij}^{(n)}$.

The row step:

$$m_{ij}^{(n+1)} = m_{ij}^{(n)}(E_i^{(n)}E_j^{(n)})^{1/2}$$

$$a_{ij}^{(n+1)} = a_{ij}^{(n)}(E_i^{(n)}F^{(n)})^{1/2}$$

$$n_{ij}^{(n+1)} = n_{ij}^{(n)}F^{(n)},$$

where $E_i^{(n)} = x_{i+}/p_{i+}^{(n)}$ and $F^{(n)} = (g(g-1) - x_{++})/q_{++}^{(n)}$.

The column step:

$$m_{ij}^{(n+2)} = m_{ij}^{(n+1)}(G_i^{(n+1)}G_j^{(n+1)})^{1/2}$$

$$a_{ij}^{(n+2)} = a_{ij}^{(n+1)}(G_j^{(n+1)}F^{(n+1)})^{1/2}$$

$$n_{ij}^{(n+2)} = n_{ij}^{(n+1)}F^{(n+1)},$$

where $G_j^{(n+1)} = x_{+j}/p_{+j}^{(n+1)}$.

The block step: Let

$$Q = \{1, \ldots, h\}$$

$$C_k^{(n+2)} = \sum_{U_k} x_{ij} \Big/ \sum_{U_k} p_{ij}^{(n+2)}, \qquad k \in Q$$

$$C_L^{(n+2)} = \sum_{L} x_{ij} \Big/ \sum_{L} p_{ij}^{(n+2)}.$$

For each $(i, j)$ cell in $U_k$, $k \in Q$,

$$m_{ij}^{(n+3)} = m_{ij}^{(n+2)}(C_k^{(n+2)}C_l^{(n+2)})^{1/2}$$

if the $(j, i)$ cell is in $U_l$, some $l \in Q$

$$= m_{ij}^{(n+2)}(C_k^{(n+2)}C_L^{(n+2)})^{1/2}$$

if the $(j, i)$ cell is in $L$

$$a_{ij}^{(n+3)} = a_{ij}^{(n+2)}(C_k^{(n+2)}F^{(n+2)})^{1/2}$$

$$a_{ji}^{(n+3)} = a_{ji}^{(n+2)}(C_l^{(n+2)}F^{(n+2)})^{1/2}$$

if the $(j, i)$ cell is in $U_l$, some $l \in Q$

$$= a_{ji}^{(n+2)}(C_L^{(n+2)}F^{(n+2)})^{1/2}$$

if the $(j, i)$ cell is in $L$

$$n_{ij}^{(n+3)} = n_{ij}^{(n+2)}F^{(n+2)}.$$

For each $(i, j)$ cell in $L$,

$$m_{ij}^{(n+3)} = m_{ij}^{(n+2)} C_L^{(n+2)}$$

if the $(j, i)$ cell is in $L$

$$= m_{ij}^{(n+2)} (C_k^{(n+2)} C_L^{(n+2)})^{1/2}$$

if the $(j, i)$ cell is in $U_k$, some $k \in Q$

$$a_{ij}^{(n+3)} = a_{ij}^{(n+2)} (C_L^{(n+2)} F^{(n+2)})^{1/2}$$

$$a_{ji}^{(n+3)} = a_{ji}^{(n+2)} (C_L^{(n+2)} F^{(n+2)})^{1/2}$$

if the $(j, i)$ cell is in $L$

$$= a_{ji}^{(n+2)} (C_k^{(n+2)} F^{(n+2)})^{1/2}$$

if the $(j, i)$ cell is in $U_k$, some $k \in Q$

$$n_{ij}^{(n+3)} = n_{ij}^{(n+2)} F^{(n+2)}.$$

The mutual step:

$$m_{ij}^{(n+4)} = m_{ij}^{(n+3)} H^{(n+3)}$$

$$a_{ij}^{(n+4)} = a_{ij}^{(n+3)} M^{(n+3)}$$

$$n_{ij}^{(n+4)} = n_{ij}^{(n+3)} M^{(n+3)},$$

where $H^{(n+3)} = 2m/m_{++}^{(n+3)}$ and $M^{(n+3)} = (\binom{g}{2} - m)/(\binom{g}{2} - \frac{1}{2} m_{++}^{(n+2)})$.

The normalizing step:

$$m_{ij}^{(n+5)} = m_{ij}^{(n+4)} / R_{ij}^{(n+4)}$$

$$a_{ij}^{(n+5)} = a_{ij}^{(n+4)} / R_{ij}^{(n+4)}$$

$$n_{ij}^{(n+5)} = n_{ij}^{(n+4)} / R_{ij}^{(n+4)},$$

where $R_{ij}^{(n+4)} = m_{ij}^{(n+4)} + a_{ij}^{(n+4)} + a_{ji}^{(n+4)} + n_{ij}^{(n+4)}$.

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