



Partitioning signed social networks[☆]

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ABSTRACT

Structural balance theory has proven useful for delineating the blockmodel structure of signed social networks. Even so, most of the observed signed networks are not perfectly balanced. One possibility for this is that in examining the dynamics underlying the generation of signed social networks, insufficient attention has been given to other processes and features of signed networks. These include: actors who have positive ties to pairs of actors linked by a negative relation or who belong to two mutually hostile subgroups; some actors that are viewed positively across the network despite the presence of negative ties and subsets of actors with negative ties towards each other. We suggest that instead viewing these situations as violations of structural balance, they can be seen as belonging to other relevant processes we call mediation, differential popularity and internal subgroup hostility. Formalizing these ideas leads to the relaxed structural balance blockmodel as a proper generalization of structural balance blockmodels. Some formal properties concerning the relation between these two models are presented along with the properties of the fitting method proposed for the new blockmodel type. The new method is applied to four empirical data sets where improved fits with more nuanced interpretations are obtained.

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1. Introduction

Some social relations are signed in the sense of having ties between actors that can be positive or negative. Examples include like/dislike and respect/disrespect for people. Analyses of the network structure of signed relations have to accommodate the additional information contained in the negative part of the signed ties. Structural balance theory, one variant of ‘consistency’ theories, has its origins in the work of Heider (1946). Cartwright and Harary (1956) then formalized Heider’s formulation and provided the foundation for discerning the overall structure of a network of signed ties. This structure for a ‘balanced’ network is given by the first structure theorem described below. A generalization proposed by Davis (1967) leads to the second structure theorem. However, for most observed signed structures for social groups, exact structural balance does not hold. Even so, it is still necessary to delineate the structure of these groups at points in time. Based on the structure theorems, Doreian and Mrvar (1996) proposed an empirical method for establishing the partition structure(s) of a signed relation for groups that is (are) as close to exact balance as is possible. Their

method was subsumed within the rubric of generalized blockmodeling (Doreian et al., 2005). Even though these methods have been useful, the blockmodel structure discerned may not be appropriate for all signed networks for groups. We provide some illustrative examples and then broaden the types of blockmodel that can be specified and identified for signed networks within the generalized blockmodeling framework. We then apply this new blockmodel type to four real data sets and provide commentary on the new results.

2. Structural balance theory and partitions

In Cartwright and Harary’s (1956) generalization of Heider’s (1946) formulation, the difference between sentiment (social) relations and unit formation relations was ignored with attention confined, in effect, to signed social relations. Following Doreian et al. (2005), a binary *signed network* is an ordered pair, (\mathbf{G}, σ) , where:

- (1) $\mathbf{G} = (\mathcal{U}, \mathcal{A})$ is a digraph, without loops, having a set of units (vertices), \mathcal{U} , and a set of arcs, $\mathcal{A} \subseteq \mathcal{U} \times \mathcal{U}$; and
- (2) $\sigma : \mathcal{A} \rightarrow \{p, n\}$ is a sign function. The arcs with the sign p are positive while the arcs with the sign n are negative. Equivalently, consistent with most diagrams of signed networks, $\sigma : \mathcal{A} \rightarrow \{+1, -1\}$.

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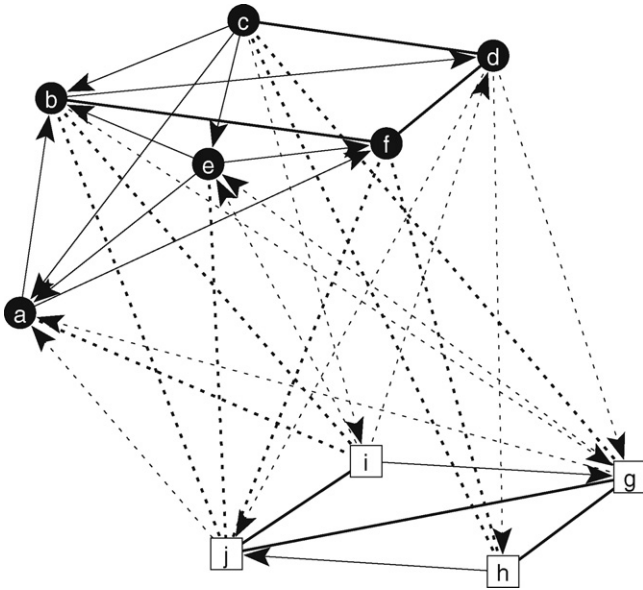


Fig. 1. A balanced signed network with two plus-sets.

For directed valued signed networks, σ is defined so that it maps elements in \mathcal{A} to valued positive and negative numbers.

A semiwalk is defined for a signed directed network in the same way as they are unsigned graphs. For $x_i \in \mathcal{U}$ and $a_{ij} \in \mathcal{A}$, with a_{ij} signed, a semiwalk from x_1 to x_n is an alternating sequence of units and arcs: $x_1, (a_{12}$ or $a_{21}), x_2, (a_{23}$ or $a_{32}), \dots, x_{n-1}, (a_{n-1n}$ or $a_{nn-1}), x_n$. Units and arcs can be repeated and if all of the arcs point in the same direction, the semiwalk is a walk. In addition, the sign of a semiwalk is defined as the product of the signs of the arcs it contains. A semiwalk of a signed directed network is *positive* iff it contains an even number of negative arcs and is *negative* otherwise. A signed network (\mathbf{G}, σ) is defined as *balanced* if every closed semiwalk is positive.

The first structure theorem is due to Cartwright and Harary:

Theorem 1. For a balanced signed network, (\mathbf{G}, σ) , the set of units, \mathcal{U} , can be partitioned into two subsets (clusters) so that every positive arc joins units of the same subset and every negative arc joins units of different subsets.

Davis (1967) observed that human groups often split into more than two mutually hostile subgroups and provided a generalization of Theorem 1. In his re-formulation, a signed network is balanced (clusterable in his terminology) if it contains no closed semiwalk with exactly one negative arc. The second structure theorem, due to Davis, is:

Theorem 2. For a balanced signed network (in the sense of Davis), (\mathbf{G}, σ) , the set of units, \mathcal{U} , can be partitioned into two or more subsets (clusters) so that every positive arc joins units of the same subset and every negative arc joins units of different subsets.

Following Davis, we use the term ‘plus-set’ for the clusters of the structure theorems and let k denote the number of them. For the first structure theorem, $k = 2$ and for the second theorem $k \geq 2$. In general, we refer to the k -balance of a signed network and consider a signed network to be k -balanced if it has a partition structure consistent with either structure theorem.

2.1. An artificial signed network

Consider the directed signed network shown in Fig. 1 that is consistent exactly with the first structure theorem. For clarity, pairs of

Table 1
Partitioned signed network matrix for balanced network

	a	b	c	d	e	f	g	h	i	j
a	0	1	0	0	0	1	0	0	-1	0
b	0	0	0	1	0	1	-1	0	-1	-1
c	1	1	0	1	1	0	-1	-1	-1	0
d	0	0	1	0	0	1	-1	-1	0	-1
e	1	1	0	0	0	1	0	0	0	-1
f	0	1	0	1	0	0	0	-1	0	-1
g	-1	0	-1	0	-1	0	0	1	0	1
h	0	0	-1	0	0	-1	1	0	0	1
i	-1	-1	0	-1	-1	0	1	0	0	1
j	-1	-1	0	0	-1	-1	1	0	1	0

reciprocated arcs are shown as edges with the unreciprocated arcs keeping their arrow heads showing their direction. The partition of the vertices is $\{a-f\}$ and $\{g-j\}$ with all of the positive arcs contained within the plus-sets and all of the negative arcs linking vertices in distinct plus-sets. In setting up a blockmodel for a directed signed network, there are two block types. A *positive* block has only positive or null ties and a *negative* block has only negative or null ties. The blockmodel, based on structural balance theory, specifies positive blocks on the main diagonal and negative blocks off the main diagonal. When the Doreian and Mrvar partitioning method, described below and implemented in Pajek (Batagelj and Mrvar, 1998)¹, is applied to the network of Fig. 1 the exact partition is returned and is shown in Table 1. The block structure of Table 1 is

positive	negative
negative	positive

consistent with structural balance. The ellipses and squares of Fig. 1 represent units in their plus-sets.

2.2. A second artificial network

One of the empirical predictions of structural balance theory is that signed social networks tend towards balance and that balanced networks are stable. We leave to one side, for the moment, the issue that many empirical networks are not balanced as well as the observation (Doreian and Krackhardt, 2001) that the simple statement regarding the tendency towards balance need not hold. While the idea of a polarized group, such as the one shown in Fig. 1 has some appeal regarding balance, there is little or no scope for mediation – in the sense of having intermediaries positively linked to members of mutually hostile subgroups – in exactly balanced groups. Suppose that the network of Fig. 1 were modified so that there were other actors positively connected to some members in each of the polarized subgroups. This is shown in Fig. 2 with three additional group members, $\{k, l, m\}$, that are viewed as potential mediators. These additional units are represented by diamonds. Table 2 shows this partition structure. This network is a signed network and it is natural to ask how a partitioning approach based on structural balance alone fares.

2.3. A third artificial network

Pushing the ‘mediation’ example further, suppose that the mediators see themselves as competitors for performing mediation and

¹ Note that Pajek is updated regularly and many additional features have been implemented since 1998. Also, an introduction to using this program is provided in de Nooy et al. (2005).

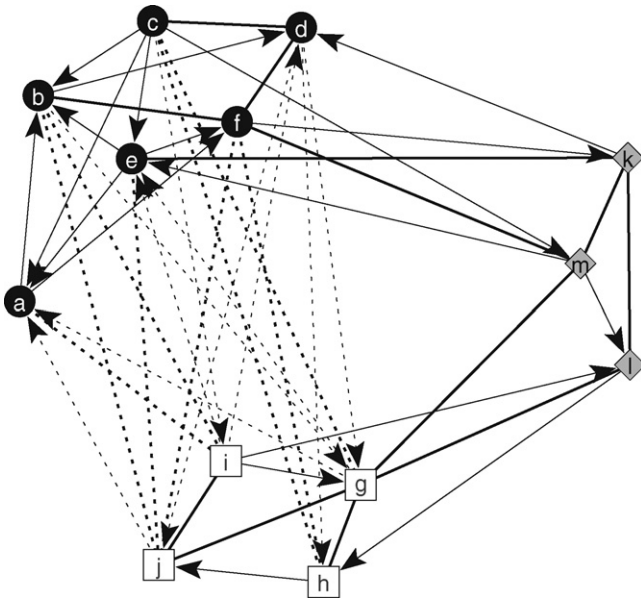


Fig. 2. A balanced signed network plus mediators.

Table 2
Block structure of a signed network with mediators

	a	b	c	d	e	f	g	h	i	j	k	l	m
a	0	1	0	0	0	1	0	0	-1	0	0	0	0
b	0	0	0	1	0	1	-1	0	-1	-1	0	0	0
c	1	1	0	1	1	0	-1	-1	-1	0	0	0	1
d	0	0	1	0	0	1	-1	-1	0	-1	0	0	0
e	1	1	0	0	0	1	0	0	0	-1	1	0	0
f	0	1	0	1	0	0	0	-1	0	-1	1	0	1
g	-1	0	-1	0	-1	0	0	1	0	1	0	1	1
h	0	0	-1	0	0	-1	1	0	0	1	0	0	0
i	-1	-1	0	-1	-1	0	1	0	0	1	0	1	0
j	-1	-1	0	0	-1	-1	1	0	1	0	0	0	0
k	0	0	0	1	1	0	0	0	0	0	0	1	1
l	0	0	0	0	0	0	1	1	0	0	1	0	0
m	0	0	0	0	1	1	1	0	0	0	1	1	0

have only negative ties between them because of this rivalry. The resulting network is shown in Fig. 3 where (km) and (kl) are negative edges and (ml) is a negative arc. The matrix of ties is the same as in Table 2 except all of the ties in the bottom right block are negative. Again, we can ask how well the usual structural balance partitioning works with this network. Before examining the issues raised by the second and third artificial networks, we consider further the nature of structural balance blockmodels of signed social networks.

3. Blockmodels of signed social networks

The generalized blockmodeling approach is a direct method that analyzes the network data rather than some transformation of them. It requires a criterion function that is optimized by a relocation algorithm. See Doreian et al. (2005) for details of this approach to delineating network structure. The criterion function for signed networks is designed in terms of the structure theorems via a count of elements that are not consistent with an ideal k -balance partition. These inconsistencies take the form of negative ties within

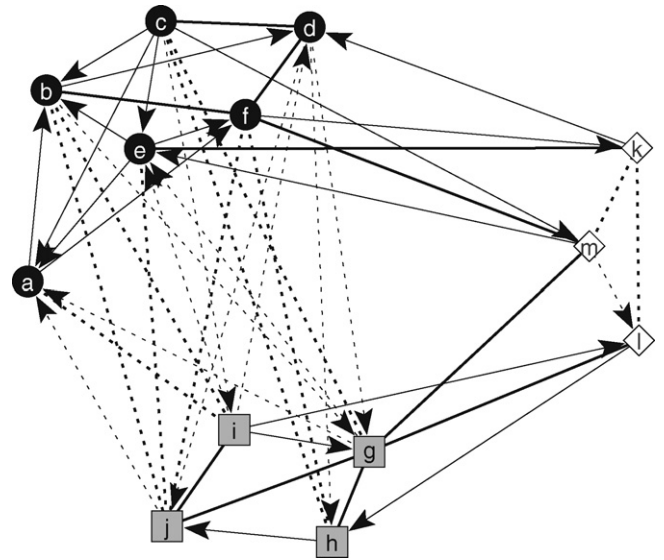


Fig. 3. A balanced signed network plus mutually hostile mediators.

plus-sets and positive ties between plus-sets. In essence, they form a line index of imbalance Harary et al. (1965). Let \mathcal{N} be the total number of negative ties within plus-sets and let \mathcal{P} be the total number of positive ties between plus-sets. A straightforward criterion function is defined as

$$P(\mathbf{C}) = \mathcal{N} + \mathcal{P}$$

Here, the two types of inconsistencies are treated equally: the criterion function simply counts of all inconsistencies regardless of their type. This is the line index of imbalance proposed by Harary et al. (1965). A slightly more general criterion function is

$$P(\mathbf{C}) = \alpha\mathcal{N} + (1 - \alpha)\mathcal{P}$$

where $0 \leq \alpha \leq 1$. With $\alpha = 0.5$, the two inconsistencies are equally weighted. For $0 \leq \alpha < 0.5$, positive inconsistencies are more important and for $0.5 < \alpha \leq 1$, the negative inconsistencies are considered as more consequential than positive ones.

The clustering problem is as follows:

Determine the clustering \mathbf{C}^* for which

$$P(\mathbf{C}^*) = \min_{\mathbf{C} \in \Phi} P(\mathbf{C})$$

where \mathbf{C} is a clustering of a given set of units \mathcal{U} , Φ is the set of all possible clusterings and $P : \Phi \rightarrow \mathbb{R}$ is the criterion function.

Finally the relocation method, as a local optimization procedure, is specified as

Determine the initial clustering \mathbf{C} ;

repeat:

if in the neighborhood of the current clustering \mathbf{C} there exists a clustering \mathbf{C}' such that $P(\mathbf{C}') < P(\mathbf{C})$

then move to clustering \mathbf{C}'

The neighborhood is determined by two transformations: moving a unit from one cluster to another cluster; and interchanging two units between different clusters. This procedure, with $\alpha = 0.5$, identified the unique partition shown in Table 1.

When the value of the criterion function is plotted against k , the curve has a concave up shape with a unique minimum value, $P(\mathbf{C}^{\min})$. The intuition for this is clear. If all of the vertices of the network are in a single plus-set, all the negative ties will be inconsistencies. Similarly, if every vertex is a singleton (in its own plus-set) all the positive ties will be inconsistencies. Between these extremes, some combination of the positive and negative ties will

Table 3
Best structural balance partition with mediators

	a	b	c	d	e	f	k	m	g	h	i	j	l
a	0	1	0	0	0	1	0	0	0	0	-1	0	0
b	0	0	0	1	0	1	0	0	-1	0	-1	-1	0
c	1	1	0	1	1	0	0	1	-1	-1	-1	0	0
d	0	0	1	0	0	1	0	0	-1	-1	0	-1	0
e	1	1	0	0	0	1	1	0	0	0	0	-1	0
f	0	1	0	1	0	0	1	1	0	-1	0	-1	0
k	0	0	0	1	1	0	0	1	0	0	0	0	<i>1</i>
m	0	0	0	0	1	1	1	0	<i>1</i>	0	0	0	<i>1</i>
g	-1	0	-1	0	-1	0	0	<i>1</i>	0	1	0	1	1
h	0	0	-1	0	0	-1	0	0	1	0	0	1	0
i	-1	-1	0	-1	-1	0	0	0	1	0	0	1	1
j	-1	-1	0	0	-1	-1	0	0	1	0	1	0	0
l	0	0	0	0	0	0	<i>1</i>	0	1	1	0	0	0

be inconsistencies which will be fewer than for either extreme. More formally, Let k be the number of plus-sets in a partition with $1 \leq k \leq n$. Partitions with k and $k + 1$ plus-sets are said to be adjacent. Doreian et al. (2005) established the following result.

Theorem 3. For any signed network, (G, σ) , there will be a unique lowest value, denoted by $P(C^{\min})$, of the criterion function that occurs for partitions with a single number, k , of plus-sets or for adjacent partitions.

This implies that a unique minimized value of the criterion function can be obtained by searching partitions in terms of k and that it is not necessary to examine partitions for every value of k . This does not imply that there is a unique partition with the minimized value of $P(C^{\min})$.

4. Relaxing the structural balance blockmodel

When the signed network shown in Fig. 2 is partitioned according to structural balance $P(C^{\min}) = 2.5$ for $k = 2$. With $\alpha = 0.5$ this implies five ties are inconsistent with structural balance. (For $k = 3$ there are six optimal partitions, each with 4.5 as the value of the criterion function. From Theorem 3, the unique partition for $k = 2$ is the best possible partition under structural balance.) The partition structure is given in Table 3 where the five inconsistent ties are bolded and italicized. The partition in Table 3 is problematic because it does not reflect the known structure shown in Table 2. Two of the potential mediators $\{k, m\}$ have been pulled into one of the two initial plus-sets while the remaining mediator $\{l\}$ has been pulled into the other initial plus-set. This means that, for k and m , all of their positive ties to and from vertices of the second plus-set are now inconsistencies while all of the positive ties from l to members of the other plus-set are inconsistencies relative to structural balance². The partitioning task becomes one of seeking a blockmodel specification that retrieves the known structure of Fig. 2 where the block structure is clear:

positive	negative	positive
negative	positive	positive
positive	positive	positive

² If the potential mediators had been tied to a greater extent to one plus-set or the other, they would be pulled to that plus-set.

Table 4
Best structural balance partition with mutually hostile mediators

	a	b	c	d	e	f	k	m	g	h	i	j	l
a	0	1	0	0	0	1	0	0	0	0	-1	0	0
b	0	0	0	1	0	1	0	0	-1	0	-1	-1	0
c	1	1	0	1	1	0	0	1	-1	-1	-1	0	0
d	0	0	1	0	0	1	0	0	-1	-1	0	-1	0
e	1	1	0	0	0	1	1	0	0	0	0	-1	0
f	0	1	0	1	0	0	1	1	0	-1	0	-1	0
k	0	0	0	1	1	0	0	<i>-1</i>	0	0	0	0	<i>1</i>
m	0	0	0	0	1	1	<i>-1</i>	0	<i>1</i>	0	0	0	<i>1</i>
g	-1	0	-1	0	-1	0	0	<i>1</i>	0	1	0	1	1
h	0	0	-1	0	0	-1	0	0	1	0	0	1	0
i	-1	-1	0	-1	-1	0	0	0	1	0	0	1	1
j	-1	-1	0	0	-1	-1	0	0	1	0	1	0	0
l	0	0	0	0	0	0	<i>1</i>	0	1	1	0	0	0

This shows why a partition based on structural balance cannot return the known structure of the network because delineating the structure of Table 2 requires the presence of positive blocks off the main diagonal. Similarly, when the structural balance partitioning is used for Fig. 3, it does not delineate the known partition. The best partition is for $k = 2$ with $P(C) = 3.5$ for $k = 2$. With $\alpha = 0.5$ this implies seven inconsistencies with structural balance. This partition shown in Table 4 is the same but the inconsistencies with structural balance differ. The inconsistencies are bolded and italicized and the known block structure

positive	negative	positive
negative	positive	positive
positive	positive	negative

is not identified. The departures from structural balance includes the negative diagonal block as well as positive off-diagonal blocks.

There is another structural feature that can be part of a relaxed balance blockmodel: actors who are viewed positively regardless of the presence of ‘balance’ effects. If there are three clusters of actors, say C_1, C_2 and C_3 , with the ties between C_1 and C_3 mutually negative, it is possible that the actors in C_2 are viewed positively by actors in C_1 and C_3 . Such occurrences would appear as a positive off-diagonal block.

Our proposal for relaxing the specification of the structural balance is simple:

- Keep the presence of positive and negative blocks in the blockmodel;
- Remove the specification of positive blocks on the main diagonal and negative blocks off the main diagonal;
- Allow both block types to appear anywhere in the block structure; and
- Continue using the same criterion function, $P(C)$, as for structural balance partitioning.

We call this the *relaxed structural balance blockmodel* and apply the same relocation algorithm to delineate structures as close to this (new) ideal blockmodel type. If there is an exact partition of a signed network into positive and negative blocks, where the positive and negative blocks can be anywhere in the blockmodel, the network is defined as a *relaxed balanced network*. The networks shown in Figs. 2 and 3 have relaxed balanced structures. Using this procedure with the new type of blockmodel allows us to delin-

ate it exactly (without inconsistencies) using Pajek (Batagelj and Mrvar, 1998). All analyses reported here were done using Pajek Version 1.23.

Unfortunately, using a relaxed balance blockmodel and fitting it with the same relocation algorithm comes at a price: Theorem 3 no longer holds. Instead of the pattern described by Theorem 3, the values of $P(\mathbf{C})$ in relation to k behaves like that the $P(\mathbf{C})$ for structural equivalence. More formally, let $P(\mathbf{C}_k)$ denote the optimal value of $P(\mathbf{C})$ for partitions of the vertices into k clusters.

Theorem 4. For establishing optimal partitions of a signed network when using the relaxed structural balance blockmodel, the values of $P(\mathbf{C}_k)$ decline monotonically as k increases.

Proof. Consider an optimal partition with k clusters with $P(\mathbf{C}_k) = c_k$. Consider next, an optimal partition with $k + 1$ clusters that has been obtained from the k -cluster partition by splitting a cluster of that partition. This split induces splits in the blocks for the split cluster. Denote the new criterion function by $P(\mathbf{C}_{k+1}) = c_{k+1}$. Consider an off-diagonal block split into two sub-blocks. If this was a negative block split into two negative sub-blocks the same +1's will remain inconsistencies and $c_{k+1} = c_k$. However, if a sub-block of a negative block is now a positive block then there must be more +1's than -1's and the criterion function will drop below c_k . Hence $P(\mathbf{C}_{k+1}) < P(\mathbf{C}_k)$. Taking both types of change following the split of a cluster, $P(\mathbf{C}_{k+1}) = c_{k+1} \leq P(\mathbf{C}_k) = c_k$. A similar argument holds for a positive block split into two sub-blocks with the role of +1's and -1's reversed. For the diagonal blocks there will be a split into four sub-blocks and a similar argument holds for them as for the off-diagonal blocks. Suppose that there is an optimal partition into $k + 1$ clusters that is not nested inside an optimal partition into k clusters and that, for this partition, $P(\mathbf{C}_{k+1}) = d_{k+1}$. By the above argument, an optimal partition with k clusters can be split to create a partition where $P(\mathbf{C}_{k+1}) = c_{k+1}$. If $d_{k+1} > c_{k+1}$ then the partition is not optimal. It follows that $d_{k+1} \leq c_{k+1}$. \square

4.1. Signed dual networks

The dual of signed network (\mathbf{G}, σ) is defined as a signed network (\mathbf{G}, σ') , on the same set of arcs as (\mathbf{G}, σ) , where the signs of all arcs have been reversed. Let $a_{ij} \in \mathcal{A}$. Whenever a_{ij} is mapped to +1 under σ in (\mathbf{G}, σ) it is mapped to -1 in (\mathbf{G}, σ') and whenever a_{ij} is mapped to -1 under σ in (\mathbf{G}, σ) it is mapped to +1 in (\mathbf{G}, σ') .

Theorem 5.

- (1) The signed dual network, (\mathbf{G}, σ') , of a relaxed balanced network, (\mathbf{G}, σ) , is also a relaxed signed network.
- (2) If (\mathbf{G}, σ) is balanced then its signed dual network, (\mathbf{G}, σ') is not balanced with the same partition.
- (3) If (\mathbf{G}, σ) is relaxed balanced with negative blocks on the diagonal and positive blocks off the diagonal, its signed dual, (\mathbf{G}, σ') is balanced.

The proof is trivial.

- (1) In a relaxed balanced (\mathbf{G}, σ) , every block in the blockmodel is a positive block, a negative block or a null block with the clusters remaining the same. Under the sign reversal each positive block becomes a negative block, each negative block becomes a positive block and null blocks are unchanged implying (\mathbf{G}, σ') is a relaxed balanced network.
- (2) With (\mathbf{G}, σ) balanced, the positive blocks are on the diagonal and the negative blocks are off the diagonal. Its dual, (\mathbf{G}, σ') , reverses these locations of block types and cannot be balanced.

- (3) The reversal of signs for (\mathbf{G}, σ) places the positive blocks on the diagonal and the negative blocks off the diagonal making (\mathbf{G}, σ') a balanced signed network.

One implication of Theorem 5 is that the term 'plus-set' does not apply for relaxed balanced networks. Even so, a balanced network in the traditional sense will be identified under a relaxed balanced specification for a blockmodel and use of the relocation method. In this sense, *relaxed balance* is a proper generalization of structural balance with balanced networks a special case of relaxed balanced networks.

4.2. Pre-specifying blockmodels for signed networks

Our proposal for relaxing structural balance blockmodels was made in the spirit of inductive uses of blockmodeling. Doreian et al. (2005, pp. 233–235) point out that network analysts often know more about the social processes generating structural data and the block structures for these data. This leads to a distinction between inductive and deductive blockmodels. As a result, it is possible to pre-specify blockmodels in terms of the locations of some or all of the block types in them. Blockmodels for signed networks within the traditional structural balance approach do have a pre-specified form with positive blocks on the main diagonal and negative blocks off the main diagonal of a blockmodel. Our proposal to relax structural balance, as stated, undid this. Pre-specification, together with deductive use of generalized blockmodeling, can be reinserted into relaxed balance blockmodels by specifying the locations of some, or all, the block types. An additional subtlety can be introduced in the form of null blocks.

In the relaxed balance approach, we can specify the number of null blocks as well as their locations on or off the main diagonal. We can also specify them by their exact location in a blockmodel. It is still necessary to specify how the criterion function is computed for null blocks given that they have neither positive nor negative ties in them. The contribution of the (i, j) block of a blockmodel to the value of the criterion function can be written as $\min[(1 - \alpha)\mathcal{P}, \alpha\mathcal{N}]$ for both structural balance and relaxed balance.³ The contribution for null blocks is defined as $(1 - \alpha)\mathcal{P} + \alpha\mathcal{N} + \beta(1 - c_i c_j / n^2)$ where c_i is the number of rows in the null block, c_j is the number of columns of the null block and n is the number of vertices for the whole network. The size of the null block is included and the β parameter weights the contribution of the null block inconsistency. If we want to have null blocks in a blockmodel, it makes sense to pre-specify their presence by location. If the block-specific contribution to the criterion function comes only from $\beta(1 - c_i c_j / n^2)$, then there are no ties in the block. If this holds over a range of values of β we can be confident that the null block is genuinely null. We argue that null blocks *must* be completely null as the requirement for including a null block in an established blockmodel. Using $(1 - c_i c_j / n^2)$ ensures that, other things equal, larger null blocks will be selected rather than smaller null blocks. If the empirical null block is specified incorrectly then the block specific contribution to the criterion function will include values due to the presence of positive and/or negative ties in the block. Such blocks will *not* be labeled as null blocks.⁴

³ Strictly, for structural balance $\alpha\mathcal{N}$ is calculated for diagonal blocks and $(1 - \alpha)\mathcal{P}$ is calculated for off-diagonal blocks.

⁴ There is a subtle difference with the introduction of null blocks and the term $\beta(1 - c_i c_j / n^2)$. If the null block is genuinely null, there will be a non-zero contribution for this cell but there will be no contributions to \mathcal{P} nor \mathcal{N} . The true inconsistency count for the cell is 0 for there are no ties in a genuinely null block. For cases like this we report the true error count and the proof of Theorem 4 is not affected.

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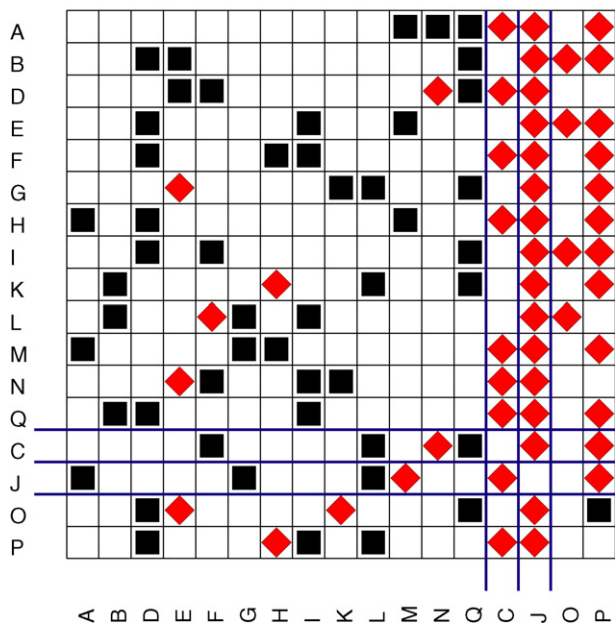


Fig. 4. The best balanced partition, $k = 4$: Newcomb last week data. (For interpretation of the references to color in the citation of this figure, the reader is referred to the web version of the article.)

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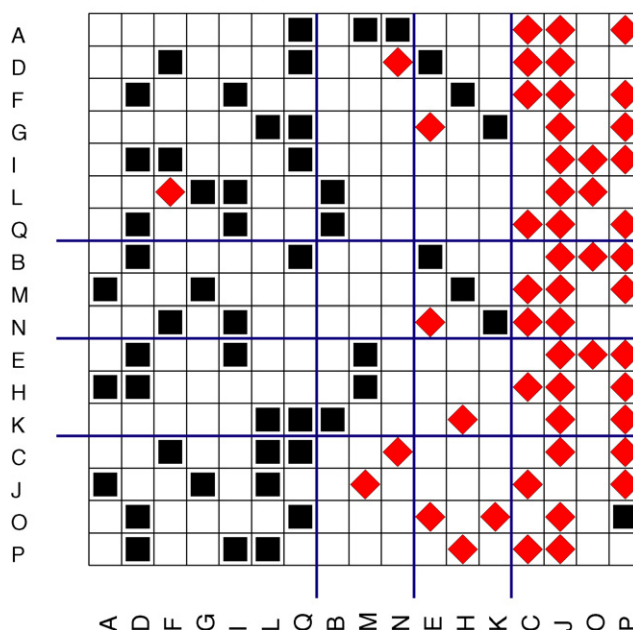


Fig. 5. The best relaxed balanced partition, $k = 4$: Newcomb last week data.

5. Applications

5.1. The newcomb data (last week)

The Newcomb data (see Nordlie, 1958; Newcomb, 1961) are well known and have been analyzed many times. Originally, the data were reported with rankings made by 17 men of each other while they lived in a pseudo-dormitory at a university. Previously unknown to each other, these men provided sociometric data that were used to study the evolution of network ties over time. Doreian et al. (2005) report the shift over time in the overall structure leading to a blockmodel of the signed relation at the last time point with one large cluster, one dyad and two singletons. We reconsider the Newcomb data with the top three ranks converted to positive choices and the bottom three ranks converted to negative choices.⁵ The best partition under structural balance still occurs for $k = 4$, with $P(C) = 8$, and is shown in Fig. 4 where the positive ties are shown as (black) squares and the negative ties are shown in (red) diamonds. Null ties are (white) blank in the display. This representation is a graphic version of the matrix of relations. The actual partition is identical to the one reported by Doreian et al. (2005) even though there is a change in the coding of negative ties.

The structure of this partition has some obvious features that include: (i) C, J, O and P all pick up most of the negative ties, (ii) these four actors have dislike ties among themselves, (iii) there is evidence of a null diagonal block and (iv) in the rows for C, J, O and P there are negative ties that are alone in columns. This inspection suggest a blockmodel with the following block pattern

positive	positive	positive	negative
positive	null	positive	negative
positive	positive	negative	negative
positive	negative	negative	negative

⁵ This differs from the Doreian et al. (2005) coding where the bottom two choices were coded as negative.

Using this specification, with a wide range of values for β leads to the unique partition shown in Fig. 5.

The block structure, as a description of the structure, has appealing features. The cluster $\{A, D, F, G, I, L, Q\}$ is made up of actors whose ties with each other are positive (with one exception) and send positive ties to actors in two other clusters, $\{B, M, N\}$ and $\{E, H, K\}$. They also receive only positive ties from members of all of the remaining three clusters. The cluster made up of $\{C, J, O, P\}$ receives only negative ties from members of all of the other clusters, a feature consistent with the partition in Fig. 4. So one feature identified in this blockmodel has one cluster of actors receiving only positive ties from actors in other clusters. This is shown by three off-diagonal blocks in the first column and reflect differential popularity. Another feature is the cluster receiving only negative ties from actors not in that cluster. These off-diagonal negative blocks are consistent with structural balance but the corresponding off-diagonal positive blocks are not. The members of $\{C, J, O, P\}$, with one exception, send only negative ties to each other and this negative diagonal block is a real feature of the block structure. The members of $\{B, M, N\}$ form a null diagonal block. The pattern of inconsistencies expressed in terms of ties being present where they should not be present under a relaxed balance model is, by block, as follows:

1	1	1	0
0	0	1	0
0	0	0	0
0	0	0	1

There are only five inconsistencies with the specified model. Their contributions to the criterion function with $\alpha = 0.5$ amounts to 2.5, considerably less than the criterion function (8) for the best partition under traditional structural balance. The diagonal block with a single negative tie does satisfy the requirements for a negative block but it seems it is better described as a weak negative block. Apart from this, the relaxed balance blockmodel is much better than the blockmodel reached under structural balance and is readily interpreted.

Table 5
Nested relaxed balance partitions at T4

	1	7	2	12	14	15	16	3	13	17	18	4	6	8	10	11	5	9
1 John Bosco	0	-5	-1	5	2	0	-1	2	0	0	-3	0	0	3	-3	0	1	0
7 Mark	0	0	9	3	0	1	6	-4	0	-2	0	-7	-8	-5	0	0	0	0
2 Gregory	9	2	0	4	0	0	0	-2	-4	0	0	-9	0	0	0	0	1	0
12 Winfrid	9	2	6	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
14 Hugh	9	0	4	3	0	6	0	0	-6	-3	-2	-7	0	-2	0	-2	0	0
15 Boniface	1	2	9	2	4	0	0	-5	-5	-1	-1	-7	0	0	0	-1	0	0
16 Albert	0	6	9	1	0	4	0	-4	0	-4	-1	-9	0	0	0	-2	0	0
3 Basil	9	0	-4	0	0	0	-1	0	6	3	3	-9	-6	0	0	0	0	0
13 Amand	0	5	-8	-2	0	0	0	-1	0	0	3	0	-7	0	0	2	8	0
17 Elias	0	0	3	0	0	0	0	6	1	0	9	-5	-9	-4	0	0	0	0
18 Simplicius	0	0	6	0	0	0	0	7	0	5	0	-6	-3	-6	-3	-2	0	0
4 Peter	-6	0	-9	0	-3	0	0	0	0	0	0	0	3	0	4	8	3	0
6 Berthold	0	-8	0	0	0	0	0	-5	0	-6	-1	9	0	-1	0	2	1	4
8 Victor	2	0	-3	-1	-2	0	-3	-2	-2	-2	-3	9	4	0	0	2	1	2
10 Romuald	0	0	0	0	0	0	0	0	2	0	0	3	0	0	0	0	1	1
11 Louis	-2	-3	-6	0	1	0	-1	-4	0	-1	-2	1	0	3	0	0	7	5
5 Bonaventure	0	0	1	0	0	0	0	-2	0	-6	-4	9	0	0	0	6	0	2
9 Ambrose	4	0	2	1	0	0	0	-3	-1	-8	-5	4	0	5	0	0	1	0

5.2. Reconsidering the Sampson network data

The **Sampson (1968)** data are among the most studied signed network data sets (see, for example, **Breiger et al., 1975; White et al., 1976; Faust, 1988; Doreian and Mrvar, 1996**). Sampson collected data on four signed relations – affect, esteem, influence and sanction – at a first time point (T1) before some members departed having finished their studies. Some of the T1 members remained in the monastery for three subsequent time points (T2, T3, and T4). They were joined by a new group of trainee monks prior to T2, the time of the second round of sociometric data collection. The consensual view of these data, for T2 through T4, is that the trainee monks in this monastery formed three broad groups: the Young Turks (who wanted to see liberalizing changes take place in the monastery), the Outcasts and the Loyal Opposition (who opposed the Young Turks in doctrinal and organizational matters). We have taken the T4 data and summed the affect, esteem and respect relations to create a valued signed network⁶. There is some doubt concerning the sanctioning relational data due to some monks not sanctioning other monks—or not reporting doing so. When these signed data, shown in **Table 5**, are partitioned using *both* the structural balance model or the relaxed balance model with $k = 3$, the same partition into three subgroups results. **Table 5** is formatted to show the three groups between the double lines. The Young Turks (YT) are made up of John Bosco, Mark, Gregory, Winfrid, Hugh, Boniface and Albert. Basil, Amand, Elias and Simplicius make up the Outcasts.⁷ Finally, Peter, Berthold, Victor, Romuald, Louis, Bonaventure and Ambrose make up the Loyal Opposition (LO).

There is one interesting difference between the analyses using the balance and relaxed balance procedures even though the clusters returned are identical. For structural balance, $P(C_3) = 31$ while for relaxed structural balance, $P(C_3) = 27$, a better fit. At face value, this may seem odd given the identical partitions. The ambiguity is

resolved by looking closely at the ties from the Outcasts to members of the Young Turks. The sum of the negative ties is 15 while the sum of the positive ties is 23. Under relaxed balance, this block is a positive block making the total of 15 contribute to $P(C_3)$, while, for structural balance it *must* be a negative block so that the sum of 23 contributes to $P(C_3)$. The difference in these counts is 8 and with $\alpha = 0.5$, this accounts for the difference in the values of the criterion function. If the ties were binarized, then both the count of the negative ties and positive ties would be 4. Such mixed blocks are problematic.

Using structural balance, this partition into three plus-sets is the best that is possible with a criterion function value of 31. From **Theorem 4**, using the relaxed balance partitioning will create finer grained partitions with a monotonically declining criterion function. For $k=4$, $P(C^{min})=18$, for a unique partition with John Bosco and Mark separated from the remaining Young Turks. The rest of the partitioning unchanged. When k is increased to 5, Bonaventure and Ambrose are separated from the others in the Loyal Opposition, again with the remaining partitioning unchanged. For five clusters, $P(C^{min}) = 12.5$. The block structure for the nested partitioning of the data in **Table 5** is given in **Table 6** where these nested partitions are shown by using single bars. (The meaning of the parentheses is given below.)

The use of the relaxed balanced partitioning has allowed some discrimination among members within Young Turks (YT1 and YT2 in **Table 6**) and within the Loyal Opposition (LO1 and LO2 in **Table 6**). For the Loyal Opposition, all of the internal refined blocks are

Table 6
Nested relaxed balance partition structure for T4

	YT1	YT2	Out	LO1	LO2
YT1	(Negative)	Positive	Negative	Negative	(Positive)
YT2	Positive	Positive	Negative	Negative	(Positive)
Out	Positive	Negative	Positive	Negative	(Positive)
LO1	Negative	Negative	Negative	Positive	Positive
LO2	(Positive)	Positive	Negative	Positive	Positive

⁶ **Doreian (2008)** presents evidence supporting such a multiple indicator approach for signed networks.

⁷ See **White et al. (1976); Doreian and Mrvar (1996)** and Sampson's ethnographic descriptions for solid reasons for including Amand among the Outcasts.

positive suggesting considerable and consistent internal positive sentiment among all members. While most of the ties within the YT block are positive, there are some negative ties, all of which involve John Bosco. Both refined blocks from the Loyal Opposition and the Young Turks to the Outcasts (Table 6) are negative. Bonaventure and Ambrose differ from the other LO members only by having some positive ties with members of the Young Turks. This can be viewed as an element of mediation as far as the finer grained clusters are concerned. Bonaventure and Ambrose send positive ties to some members of the YT and to members of the LO. They also receive only positive ties from both the YT and the LO, also consistent with mediation. Inside the Young Turks, however, there is a negative refined block on the main diagonal stemming from the strong negative tie from John Bosco to Mark. In the main, the Young Turks joined the monastery after T1 while most of the Loyal Opposition were holdovers from T1. Mark, present before T1, ranked very low at T1 and switched allegiance to the new group of trainee monks but was not received positively by John Bosco, one of the leaders of the Young Turks. Allowing negative blocks on the diagonal permitted the detection of this internal difference (although this data set is small enough that this can be done visually in Table 5). Structurally, members of the Outcasts could have played a mediating role because positive ties are sent to YT1 and LO2 but, given their Outcast status as described by Sampson and reconfirmed here, their chances of successful mediation were near zero.

There are some blocks in Table 6 that have a single tie. It would seem that these blocks are close to being null blocks. As such, they can be seen as quite ‘fragile’ as blocks with a sign. We did check this with some supplementary analyses by specifying, in turn, each of these blocks as null while keeping the rest of the blockmodel. In each case, the null specification was *not* confirmed. Recognizing the single ties in these blocks leads us to enclose the labels in parentheses in Table 6.

Trainee monks within clusters are not identical in sending ties but while further discrimination within blocks is possible the resulting clusters will be small and the resulting refined blockmodel would be too fine grained given this is a small network.

5.3. Another binary signed network

Doreian et al. (2005, Chapter 10) report some results for partitions of a signed network obtained by Bales (1970) and re-analyzed by Schwartz and Sprinzen (1984). After 13 weeks of interaction, the group members provided data on three social relations, two of which were positive affect (liking), negative affect (disliking). These data are provided in permuted form in Fig. 6. The primary intent of Doreian et al. (2005) was a comparison of partitions made in terms of structural balance and structural equivalence, but they did report an optimal partition based on structural balance for $k = 4$ with $P(C_4) = 7.0$ with $\alpha = 0.5$. This had one huge plus-set, {A, B, C, E, G, H, I, J, K, L, N, O, P, Q, S, T}, two individuals in plus-set, {D, R}, and two singletons in their own plus-sets, {M} and {F}. This partition seems unsatisfactory for two reasons. First, the description of the network delineates limited structure. Second, the large plus-set contains most of the inconsistencies with balance in the form of negative ties within the plus-set. Using the relaxed balanced approach for the Sampson data suggests that it could provide some finer grain description of the overall structure of this binary network. For $k = 6$ there exists a unique partition, with null blocks specified, with $P(C_6) = 0.5$ (with $\alpha = 0.5$). It is reported in Fig. 6.

Even though this is another sparse network there is some interesting structural features that were obscured by the traditional balance partition. Members of the cluster {J, S, T} receive only positive ties and these ties come from individuals in all of the other clusters. Being viewed in such a positive fashion is captured by the

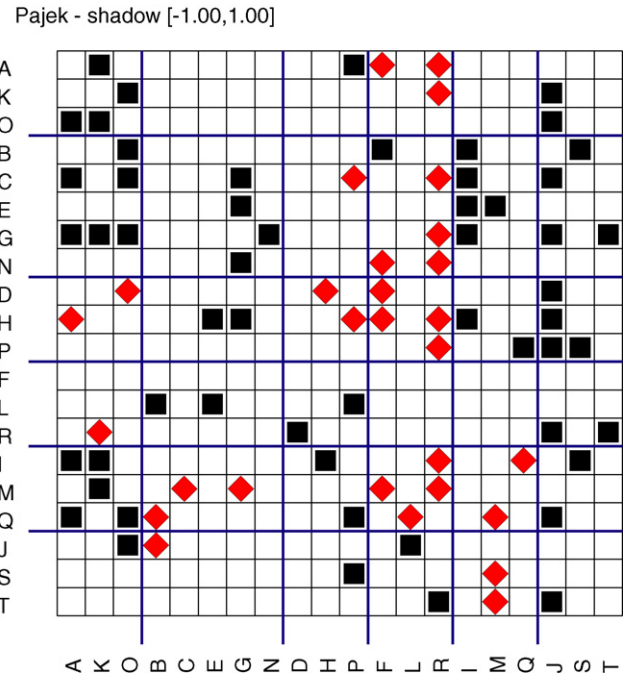


Fig. 6. A relaxed balance partitions for the Bales Group.

Table 7
Relaxed balance partition structure for the Bales Group

Positive	Null	(Positive)	Negative	Null	Positive
Positive	Positive	(Negative)	Negative	Positive	Positive
Negative	Positive	Negative	Negative	Positive	Positive
(Negative)	Positive	Positive	Null	Null	Positive
Positive	Negative	Positive	Negative	Negative	Positive
(Positive)	(Negative)	(Positive)	Positive	Negative	(Positive)

off-diagonal blocks of received ties. Members of the cluster {A, K, O} receive mainly positive ties from each other and members of the second and fifth clusters in Fig. 6. Their mutual positive ties has the further implication that the positive ties they receive from members of both {B, C, E, G, N} and {I, M, Q} are not reciprocated leading to two null blocks in the top panel of Fig. 6. The cluster {F, L, R} receives primarily negative ties (in three negative blocks) and receives only positive ties from {J, S, T} for another off-diagonal positive block. Also, {F, L, R} has a genuine diagonal null block with no ties among themselves. The block from {F, L, R} to {I, M, O} is the fourth genuine null block. For $k = 7$ there are 14 equally well fitting partitions that fit with zero inconsistencies that are not considered further given their high number.

Fig. 6 shows a lot more discrimination in terms of structure than did the original partition based on structural balance. The block structure is given in Table 7 where the parentheses are used to indicate blocks containing just one tie of the specified sign. These seem perilously close to being null blocks suggesting one potential modification to include null blocks if their presence is anticipated. However they are not null blocks because pre-specifying them as null is not confirmed with a null block in the fitted blockmodel.⁸ So three of null blocks were established inductively while the fourth was established deductively. If there is a series of signed networks in time, a null block having a sign appear in it from one time point

⁸ In earlier analyses, a blockmodel was obtained where the (1, 2) block had a single tie. On specifying that block as null, the specification was confirmed and the blockmodel of Fig. 6 was established.

Table 8
Relaxed balance partition for the Supreme Court, 2006–2007

Justice		JS1	JG	JS2	JB	JK	JA	JR	JS3	JT
Stevens	JS1	46	30	16	21	-7	-18	-17	-26	-31
Ginsburg	JG	30	46	28	29	1	-10	-11	-18	-21
Souter	JS2	16	28	46	29	7	-4	-1	-16	-19
Breyer	JB	21	29	29	45	10	-5	-6	-21	-24
Kennedy	JK	-7	1	7	10	45	29	24	9	8
Alito	JA	-18	-10	-4	-5	29	46	33	22	19
Roberts	JR	-17	-11	-1	-6	24	33	45	29	24
Scalia	JS3	-26	-18	-16	-21	9	22	29	46	37
Thomas	JT	-31	-21	-19	-24	8	19	24	37	45

to another could be an indication of change starting in the overall block structure. One feature of the partition structure of this Bales group is that positive blocks appear off the main diagonal and two negative blocks appear on the main diagonal. Their presence implies that structural balance is unlikely to detect them, given their location in the blockmodel, but the relaxed balance partitioning can identify them when they are present.

5.4. *The U.S. supreme court justices: 2006–2007 term*

Our final example is taken from the voting behavior of the nine justices on the U.S. Supreme Court for the 2006–2007 term. In discussions about the splits in the Supreme Court, the unanimous (9–0) decisions are often ignored yet there were 28 of them in the 2006–2007 term.⁹ This tells there are numerous cases where laws and lower court decisions, in relation to the U.S. Constitution, where the legal issues appear clear. When justices disagree it is reasonable to ask if there are any systematic patterns in their differences. Accordingly, we focus on the remaining 46 *non-unanimous* decisions. The elements in the main diagonal of this data matrix give the number of votes made by the justices in these decisions. As noted, justices recuse themselves from particular cases so not all elements in the diagonal are 46. The off diagonal elements are net counts of the number of times justices votes together (if positive) or the number of times they vote against each other (if negative). These count data are shown in Table 8 where the partition shown comes from the relaxed balance procedure. The value of $P(\mathbf{C}_3)$ is 7, and with $\alpha = 0.5$, consists of the net seven times Justices Kennedy and Stevens voted against each other. This partition is the oft-noted divide of the court into a liberal wing and a conservative wing with Justice Kennedy aligned between them.

When these data are partitioned using structural balance, the unique optimal partition occurs for $k = 2$ with $P(\mathbf{C}_3) = 18$. (The relaxed balance partition performs in exactly the same fashion.) When $k = 3$ the optimal value of $P(\mathbf{C}_3)$ is 85 for traditional structural balance indicating an extremely poor fit where Justice Stevens a singleton and Justice Kennedy is clustered with the conservative wing. From Theorem 3, using the relaxed balance method with $k = 3$ provides the best partition of the joint voting data for the non-unanimous decisions. The partition into two clusters is shown in Table 9. With $\alpha = 0.5$, this count represents the times Justice Kennedy votes with members of the liberal wing of the Supreme Court. This partition, even though it is consistent with an argument that Justice Kennedy belongs to the conservative wing of the court, is an inferior partition to the one obtained via the relaxed balance partitioning procedure. It does not take into account the one time he voted with Justice Ginsberg, the seven time he voted with Justice

Table 9
Structural balance partition for the Supreme Court, 2006–2007

Justice		JS1	JG	JS2	JB	JK	JA	JR	JS3	JT
Stevens	JS1	46	30	16	21	-7	-18	-17	-26	-31
Ginsburg	JG	30	46	28	29	1	-10	-11	-18	-21
Souter	JS2	16	28	46	29	7	-4	-1	-16	-19
Breyer	JB	21	29	29	45	10	-5	-6	-21	-24
Kennedy	JK	-7	1	7	10	45	29	24	9	8
Alito	JA	-18	-10	-4	-5	29	46	33	22	19
Roberts	JR	-17	-11	-1	-6	24	33	45	29	24
Scalia	JS3	-26	-18	-16	-21	9	22	29	46	37
Thomas	JT	-31	-21	-19	-24	8	19	24	37	45

Souter and the 10 times he voted with Justice Breyer (all in cases that were not decided on a unanimous basis).

6. Discussion

Partitioning based on structural balance has proven useful for delineating the structure of signed social networks. While most observed signed social networks have not been balanced, in the sense of having a line index of balance that is non-zero, the delineated structures have been interpretable. For the few signed networks where data have been available over time, a tendency towards balance has been observed, notably in the Sampson (1968) data (Doreian and Mrvar, 1996) where the measure of imbalance declined over time. When balance has not been observed, implicitly, the assumption has been made that these structures are not balanced due to a process towards balance not being complete. Doreian and Krackhardt (2001) by considering the Newcomb (1961) data over time examined a set of pre-transitive triples, at one time point, to see if they were completed at the next time point in a way that was consistent with balance. While some did get completed in this way others did not. Even more puzzling was the presence of balanced types of triples that decreased in frequency over time and some imbalanced types of triples that increased in frequency—all in the context of an overall movement towards balance in these data. They speculated that ‘the structural balance process’ is actually a set of processes that may compete with each other.

In this paper we have suggested that the balance process – or a set of such processes – may have more rival processes. They include mediation between mutually hostile plus-sets, differential popularity and subgroups with internal mutual hostility. These are all inconsistent with traditional structural balance. This led us to formulate a relaxed structural balance model as a proper generalization of the structural balance model. The reformulation kept the presence of positive and negative blocks but allowed them to appear anywhere in the blockmodel. This amounts to relaxing the restriction that only positive blocks appear on the main diagonal and negative blocks are only off the main diagonal of the blockmodel. This was modified further by allowing prespecification, especially for null blocks. The same relocation fitting algorithm and criterion function as for structural balance were retained. Four real data sets were then re-analyzed using this new type of blockmodel.

Interesting structure was found in the Newcomb data considered here that could not be identified with traditional structural balance. There was a cluster of actors who received most of the negative ties. The negative off-diagonal blocks are consistent with balance but the diagonal negative block is not. For other actors there are two columns of positive blocks as these individuals are viewed positively by the other actors with very few exceptions. These columns of off-diagonal positive blocks are a real part of the signed structure but inconsistent with traditional balance. There is

⁹ Some were 8–0 or 7–0 when justices recuse themselves on specific decisions.

also a genuine diagonal null block, something that is not considered under structural balance. For the Sampson data, the well known partition into the Young Turks, the Loyal Opposition and the Outcasts was obtained, consistent with structural balance. However, the relaxed balance model permitted an interpretable refined partition that was nested within the structural balance partition. The two rival subgroups are not monolithic and contain subtle variations regarding the ties between the members of the rival groups. Some of these take the form of positive blocks off the main diagonal and can be interpreted in terms of mediation. There are no null blocks in the Sampson data. Viewing the Bales data in terms of structural balance led to an unsatisfactory partition with all but four actors in a single large plus-set. However, this plus-set has a number of negative ties within it that are inconsistencies with structural balance. Using the relaxed balance type of blockmodel permitted a much finer grained partition that focused on positive ties and negative ties appearing in separate blocks. Finally, the Supreme Court data, for the *non-unanimous* decisions of the 2006–2007 term were examined using both the structural balance blockmodel and the relaxed structural balance blockmodel. The latter provided a better partition of these data. In all four empirical examples that were considered here, the relaxed structural balance model had the better fits compared to the structural balance model.¹⁰ The pattern of the locations of the positive and negative blocks showed why the former model performed better than the latter. Of course, if there are empirical data conforming solely with structural balance, both models would perform in the same fashion. One is simply a generalization of the other and is more flexible as a result. If an analyst has reason to believe that structural balance alone is operative, then the structural balance blockmodel assumes a pre-specified form (Doreian et al., 2005, Chapter 12) compared to the relaxed balance blockmodel and is preferred. The traditional structural balance model can always be pre-specified within the relaxed balance model.

There are other approaches to clustering signed network data. Two (Yang et al., 2004; Bansal et al., 2004) seem of particular relevance. Yang et al. (2004) use a block diagonalization approach with a random walk based heuristic while Bansal et al. (2004) sought communities in signed networks. While the origins of their data structures have nothing to do with structural balance as a theoretical idea, the partitions that they seek are fully consistent with structural balance. However, our generalization of structural balance has created different possible block configurations of which the block structure consistent with structural balance is a special case. The presence of off-diagonal positive blocks and on-diagonal negative blocks are not compatible with these other approaches. Nor do they consider null blocks. Further, Yang et al. (2004) specify and require dense positive diagonal blocks¹¹ while we do not. The data structures considered in these alternative approaches are much more dense than the signed data considered here. A final distinction is that the other approaches are designed to be *atheoretic* and are (deliberately) *based on ignorance* about the data and the processes generating them.¹² As we note here, social network analysts often know more about data than ignorance would suggest. Further, they often have substantive reasons for analyzing network data and it seems odd to suspend that knowledge and understanding. One

virtue claimed for the Yang et al. (2004) approach is that it works for very large networks where appeals to ignorance have utility in terms of computational efficiency. However, for most social science signed data in social networks the data sets are small. Finally, with the relaxed balance model, specific hypotheses about the block structure can be tested through use of the criterion function that we use.

Having the relaxed structural balance blockmodel as a generalization of the structural balance model provides a way of delineating the structure of signed social networks that permits better fits to the data when there is evidence of polarization, mediation, differential popularity and subgroup internal hostility processes. Having such better fits also provides some commentary on the majority of observed cases when structural balance does not hold: there are another processes that can be accommodated with a framework based on a consistency theory for the distribution of signed social relations. Differential popularity can be represented by off-diagonal positive blocks and is the outcome of a different process, as can clusters of actors with mutually negative ties. Some problems remain. The number of clusters (k) has to be specified or determined and it would be useful to have a better way of determining k . In the context of structural equivalence, null blocks are important (see Arabie et al., 1978 and White et al., 1976 regarding null blocks and 'lean fit'). In a similar fashion, the presence of null blocks in two of the empirical examples considered here suggests that formally pre-specifying them in this new type of blockmodel merits further attention in studying the structure and dynamics of signed networks.

7. Conclusion

We have proposed a generalization of structural balance where the notion of positive and negative blocks has been retained but with the modification that they can appear anywhere in the blockmodel of a signed network. Assuming that structural processes leave traces found in the network structure, as delineated by blocks, it is now possible to identify structural features additional to those implied by the operation of structural balance processes. Differential popularity, differential receipt of negative ties, mediation blocks and actors with mutual negative ties can all be identified. Because the measure of imbalance remains the same, as does the local optimization fitting process, the richer identified structure is due to the more general conception of the permitted blockmodels. However, if a signed network is close to that implied by structural balance, it will be identified as such. The relaxed structural balance model is a genuine generalization of structural balance permitting the identification of more complex structures.

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¹⁰ For both models, the same criterion function was used so differences in performance are not due to a changes in the criterion function.

¹¹ It is of some interest that when they consider the data sets considered by Doreian and Mrvar (1996) they reach the same partitions.

¹² Bansal et al. (2004) make this explicit: "Suppose that you are given a set of n documents to cluster into topics. Unfortunately, you have no idea what the 'topic' is."

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