

Markov Blanket Discovery via Minimum Cut

Jonas Hallgren

Abstract

A Markov blanket is the minimal set of variables that renders a subsystem statistically independent from its environment. A minimum cut is the minimal set of edges that disconnects a graph. These are the same problem. We show that running the Stoer-Wagner algorithm on a graph weighted by mutual information directly discovers the natural statistical boundaries in complex systems.

1 The Core Idea

Consider a system of interacting variables. Some variables cluster together, sharing rich statistical dependencies, while communicating with the outside world through narrow information bottlenecks. These bottlenecks are Markov blankets—the minimal boundaries that separate inside from outside (Pearl, 1988; Friston, 2013).

The insight is simple: if we represent variables as nodes and weight edges by mutual information, then Markov blankets correspond exactly to minimum cuts. The cut that removes the least total information flow is precisely the minimal statistical boundary.

Definition 1 (Markov Blanket). *For a set of variables S in a system, the Markov blanket $\text{MB}(S)$ is the minimal set of variables such that S is conditionally independent of all other variables given $\text{MB}(S)$ (Pearl, 1988).*

Definition 2 (Minimum Cut). *For a weighted graph $G = (V, E, w)$, a minimum cut is a partition of V into two non-empty sets that minimizes the total weight of edges crossing the partition (Stoer and Wagner, 1997).*

Proposition 1. *Let G be a graph where nodes are random variables and edge weights are mutual information: $w(X, Y) = I(X; Y)$. Then the global minimum cut identifies the partition where the two resulting subsystems share minimal statistical dependence.*

The proof is immediate: mutual information quantifies shared information between variables (Cover and Thomas, 2006), so minimizing the sum of edge weights across a cut minimizes the total information flow between the resulting partitions.

2 The Stoer-Wagner Algorithm

Given a weighted graph, how do we find the minimum cut without knowing in advance which subsystems to separate? The Stoer-Wagner algorithm solves this elegantly (Stoer and Wagner, 1997).

The algorithm works by repeatedly finding a “minimum cut phase”—growing a cluster greedily by maximum adjacency, then recording the cut that separates the last-added node. After each

phase, it merges the final two nodes and repeats until the graph collapses to a single node. The smallest cut encountered is the global minimum.

Algorithm 1 Stoer-Wagner Minimum Cut (Stoer and Wagner, 1997)

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1: procedure GLOBALMINCUT( $G = (V, E, w)$ )
2:   best_cut  $\leftarrow \infty$ 
3:   while  $|V| > 1$  do
4:      $(s, t, \text{cut\_value}) \leftarrow \text{MINCUTPHASE}(G)$ 
5:     if cut_value < best_cut then
6:       best_cut  $\leftarrow$  cut_value
7:       Record the partition separating  $t$ 
8:     end if
9:     Merge nodes  $s$  and  $t$  in  $G$ 
10:  end while
11:  return best_cut and its partition
12: end procedure

13: procedure MINCUTPHASE( $G$ )
14:   Pick arbitrary starting node  $a$ 
15:    $A \leftarrow \{a\}$ 
16:   while  $A \neq V$  do
17:     Add to  $A$  the node  $v \notin A$  maximizing  $\sum_{u \in A} w(u, v)$ 
18:   end while
19:   Let  $s$  be second-to-last added,  $t$  the last
20:   return  $(s, t, \sum_{v \neq t} w(v, t))$ 
21: end procedure

```

The complexity is $O(VE + V^2 \log V)$, making it tractable for moderately sized systems.

3 Example: A Biological Cell

Consider a simplified cell with eight variables representing molecular processes:

- **Internal metabolites:** X_1, X_2, X_3 (core biochemistry)
- **Membrane components:** X_4, X_5 (transporters and receptors)
- **External signals:** X_6, X_7, X_8 (nutrients and signaling molecules)

From time-series data, we estimate pairwise mutual information:

3.1 The Information-Weighted Graph

3.2 Applying the Algorithm

Running Stoer-Wagner, we evaluate possible cuts:

Cut A — separating $\{X_1, X_2, X_3, X_4, X_5\}$ from $\{X_6, X_7, X_8\}$:

$$\text{cap}_A = w(X_4, X_6) + w(X_4, X_7) + w(X_5, X_7) + w(X_5, X_8) = 0.5 + 0.3 + 0.4 + 0.6 = 1.8 \quad (1)$$

$I(X_i; X_j)$	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8
X_1	—	2.1	1.8	0.4	0.3	0.0	0.0	0.0
X_2	2.1	—	1.9	0.5	0.2	0.0	0.0	0.0
X_3	1.8	1.9	—	0.6	0.4	0.0	0.0	0.0
X_4	0.4	0.5	0.6	—	0.8	0.5	0.3	0.0
X_5	0.3	0.2	0.4	0.8	—	0.2	0.4	0.6
X_6	0.0	0.0	0.0	0.5	0.2	—	1.5	1.2
X_7	0.0	0.0	0.0	0.3	0.4	1.5	—	1.8
X_8	0.0	0.0	0.0	0.0	0.6	1.2	1.8	—

Table 1: Mutual information matrix (in bits). Note the block structure: strong coupling within internal variables (X_1 – X_3), strong coupling within external variables (X_6 – X_8), and weak coupling through membrane nodes (X_4 – X_5).

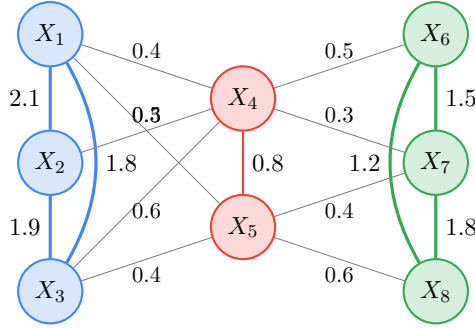


Figure 1: Information-weighted graph. Edge thickness indicates mutual information. The three clusters are visible: internal (blue), membrane (red), external (green).

Cut B — separating $\{X_1, X_2, X_3\}$ from $\{X_4, X_5, X_6, X_7, X_8\}$:

$$\text{cap}_B = 0.4 + 0.5 + 0.6 + 0.3 + 0.4 = 2.2 \quad (2)$$

Cut A has lower capacity. The algorithm identifies $\{X_4, X_5\}$ as the Markov blanket—the membrane components through which the cell interior communicates with the external environment.

3.3 Result

The algorithm recovers the known biological architecture—nucleus, cytoplasm, membrane—purely from statistical dependencies. The cut capacity of 1.8 bits represents the information bandwidth through which the agent senses and acts upon its environment, substantially lower than internal coupling (~ 6 bits) or external coupling (~ 4.5 bits).

4 Discussion

The identification of Markov blankets with minimum cuts provides an efficient algorithm for discovering natural boundaries in complex systems. Where conditional independence testing requires exponential search over variable subsets, minimum cut runs in polynomial time.

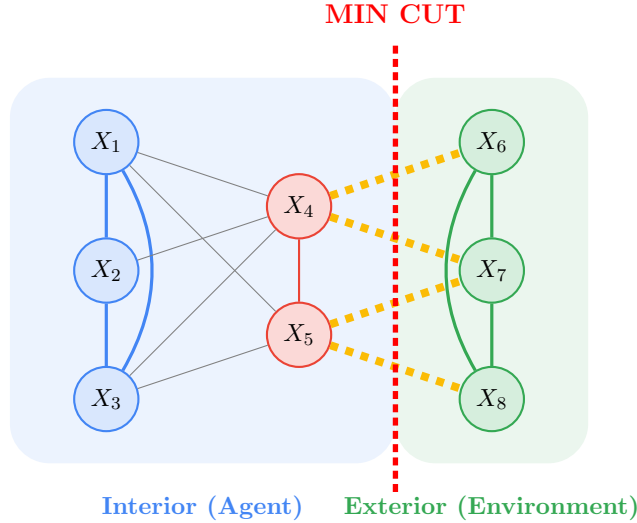


Figure 2: The minimum cut (dashed yellow edges, capacity 1.8 bits) identifies the statistical boundary. Nodes X_4 and X_5 form the Markov blanket.

This approach finds application wherever systems exhibit modular structure: biological networks (Friston, 2013), neural circuits (Sporns, 2016), social organizations, and distributed computing systems. The minimum cut reveals where information flows constrict—the natural joints along which complex systems decompose into quasi-independent parts.

The connection to active inference is direct: in the free energy principle, Markov blankets define the boundary across which agents minimize surprise about their environment (Friston, 2013; Parr et al., 2022). The min-cut formulation provides a data-driven method for identifying these boundaries without assuming the graphical structure in advance.

The simplicity is the point. Markov blankets are about minimal statistical separation. Minimum cuts find minimal separation. The mutual information weighting makes these the same thing.

References

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