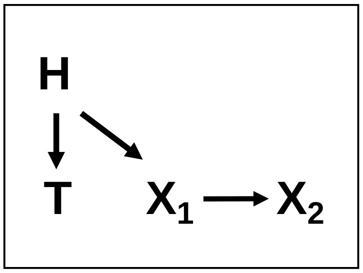
An example of signature multiplicity due to hidden variables

Consider a simplified pathway structure and parameterization shown in the figure below. It involves 3 genes (H, X_1, X_2) and a phenotypic response variable T. In the distribution with all variables observed, there is only one Markov boundary of T, which is $\{H\}$. Now consider that gene H is not observed in the data (i.e., it is hidden). Because H is not observed and genes X_1 and X_2 contain exactly the same information about T, two Markov boundaries $\{X_1\}$ and $\{X_2\}$ can be identified in this distribution. Notice that all these Markov boundaries have reproducible but suboptimal (relative to the original distribution with H observed) predictivity of the response variable T.



P(T | H)	$H = 0$	$H = 1$
$T = 0$	0.9	0.2
$T = 1$	0.1	0.8

P(X_1 | H)	$H = 0$	$H = 1$
$X_1 = 0$	0.9	0.1
$X_1 = 1$	0.1	0.9

P(X_2 | X_1)	$X_1 = 0$	$X_1 = 1$
$X_2 = 0$	1.0	0.0
$X_2 = 1$	0.0	1.0

Figure: Example pathway structure with 3 gene variables (H, X_1, X_2) and phenotypic response variable T. The structure is represented by a Bayesian network. The network parameterization is defined below the graph. All variables take values {0,1}.