



P(A)	
A = 0	0.5
A = 1	0.3
A = 2	0.2

P(T A)	A = 0	A = 1	A = 2
T = 0	1	1	0
T = 1	0	0	0.3
T = 2	0	0	0.7

P(B A)	A = 0	A = 1	A = 2
B = 0	0.2	0.9	0
B = 1	0.8	0.1	0
B = 2	0	0	1

P(C T)	T = 0	T = 1	T = 2
C = 0	0.2	0.9	0.3
C = 1	0.8	0.1	0.7

Figure S1: Example pathway structure with 3 gene variables (A , B , C) and phenotypic response variable T . The structure is represented by a Bayesian network (defined as a set of variables \mathbf{V} , a directed acyclic graph G with one-to-one correspondence of nodes to the variables in \mathbf{V} , and a probability distribution P over \mathbf{V} such that every variable W in \mathbf{V} is independent of all non-descendants of W given the parents of W). The network parameterization is defined below the graph. All variables take values $\{0,1,2\}$ except for C that takes values $\{0,1\}$. Genes A and B contain exactly the same information about T and are highlighted with the same color.