## Algorithm HITON-PC (without “symmetry correction”)

**Input:** dataset with predictive variables (e.g., genes) \( V \), including a phenotypic response variable \( T \)

**Output:** a Markov boundary \( M \) of \( T \)

1. Initialize \( M \) with an empty set
2. Initialize the set of eligible variables \( E \leftarrow V \setminus \{T\} \)
3. Sort in descending order the variables in \( E \) according to their pairwise association with response variable \( T \)
4. Remove from \( E \) all variables \( X \) with zero association with \( T \), i.e. when \( T \perp X \)
5. Repeat
6. \( X \leftarrow \) first variable in \( E \)
7. \( \) Add \( X \) to \( M \) and remove it from \( E \)
8. If \( \exists Z \subseteq M \setminus \{X\} \), such that \( T \perp X | Z \), remove \( X \) from \( M \)
9. Until \( E \) is empty
10. For each \( X \in M \)
11. \( \) If \( \exists Z \subseteq M \setminus \{X\} \), such that \( T \perp X | Z \), remove \( X \) from \( M \)
12. Output \( M \)

**Figure S2:** HITON-PC algorithm. More details about the algorithm and characterization of distributions where it can correctly identify a Markov boundary are given in [1,2].

## References
