

All Supplemental Appendices will be available on the following website dedicated to this paper, http://discover.mc.vanderbilt.edu/discover/public/supplements/mmhcn-paper/mmhcn_index.html. In addition, the website has available code, scripts, the datasets used, the Bayesian Networks used, and the detailed results as Matlab datafiles.

B. Computational Efficiency Results

B.1. TIMING RESULTS

B.1.1. Median Timing Results

Table I. Median Normalized Time Results. Normalized time is the running time of each algorithm for a particular sample size and network divided by the corresponding running time of *MMHC*. The first term in the parentheses is the number of networks the algorithm terminated on (used in calculating the median for each algorithm) and the second is the number of networks the algorithm hit the 2 day time threshold and was stopped. Median normalized time values smaller than one correspond to an algorithm with faster running times than *MMHC*. The * reminds the reader that the *OR* algorithms running time was set to be 1 or 2 times that of *MMHC*. Also, recall the *GES* implementation did not contain all optimizations described by the original authors.

Algorithm	Median Normalized Times			Average Over SS
	500	1000	5000	
MMHC	1.00 (22/ 0)	1.00 (22/ 0)	1.00 (22/ 0)	1.00
OR1 k=5	1.18 (19/ 0)	1.15 (18/ 0)	1.12 (17/ 0)	1.15*
OR1 k=10	1.15 (19/ 0)	1.17 (18/ 0)	1.14 (16/ 0)	1.15*
OR1 k=20	1.18 (19/ 0)	1.18 (18/ 0)	1.13 (16/ 0)	1.16*
OR2 k=5	2.25 (19/ 0)	2.19 (18/ 0)	2.14 (16/ 0)	2.20*
OR2 k=10	2.32 (18/ 0)	2.17 (18/ 0)	2.13 (16/ 0)	2.21*
OR2 k=20	2.36 (18/ 0)	2.26 (18/ 0)	2.16 (16/ 0)	2.26*
SC k=5	5.99 (21/ 0)	6.51 (22/ 0)	4.68 (18/ 2)	5.73
SC k=10	9.37 (13/ 0)	11.69 (13/ 0)	7.82 (13/ 0)	9.63
GS	5.07 (20/ 2)	4.10 (20/ 2)	2.98 (20/ 2)	4.05
PC	1.87 (18/ 4)	1.69 (18/ 4)	1.29 (20/ 2)	1.62
TPDA	10.25 (21/ 1)	5.17 (21/ 1)	0.56 (22/ 0)	5.33
GES	341.20 (7/15)	135.65 (6/16)	33.46 (6/16)	170.10

B.1.2. Complete Timing Results

The complete results tables are given on the web as Matlab data files and text files. The Matlab files are 4-D matrices indexed by network (22), algorithm (13), sample size (3), and sampling (5). For each sample size there is a text document with the mean and standard deviation for all algorithms and networks.

The complete results are also visually shown in Figures 1 - 9. These figures are bar plots of the absolute timing results for each algorithm on a given network and sample size. The error bars plotted are at +/- standard deviation.

A red bar indicates that that particular algorithm hit the 2-day time limit. A bar with pink edging indicates it was an extreme value and exceeded the limits of the graph (the true value is given for comparison). Finally, a light green bar indicates the minimum time.

When a bar is missing for an algorithm, indicated with an X, the algorithm was unable to run on that particular network and sample size. Also, recall that the *OR* algorithm was set to run at one and two times the amount of time it took *MMHC* to finish.

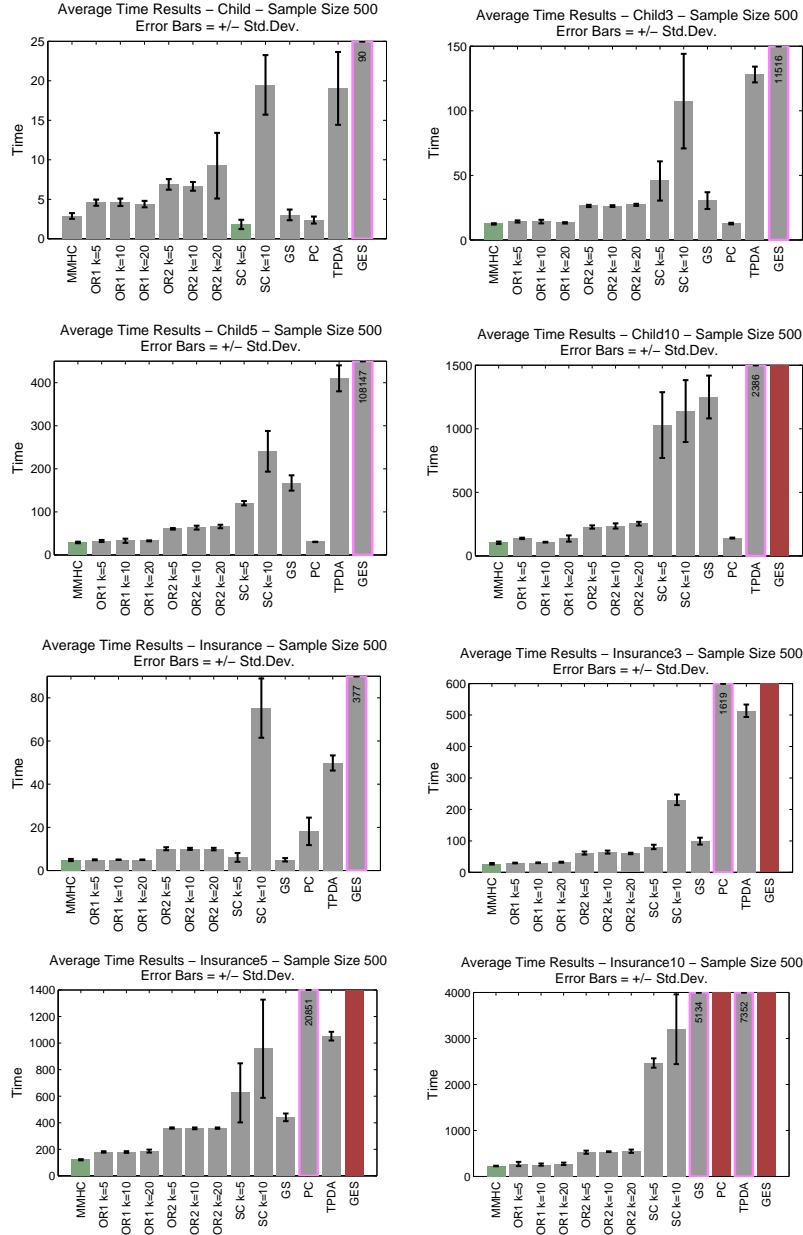


Figure 1. Time Results at Sample Size 500 for the CHILD, CHILD3, CHILD5, CHILD10, INSURANCE, INSURANCE3, INSURANCE5, and INSURANCE10 Networks.

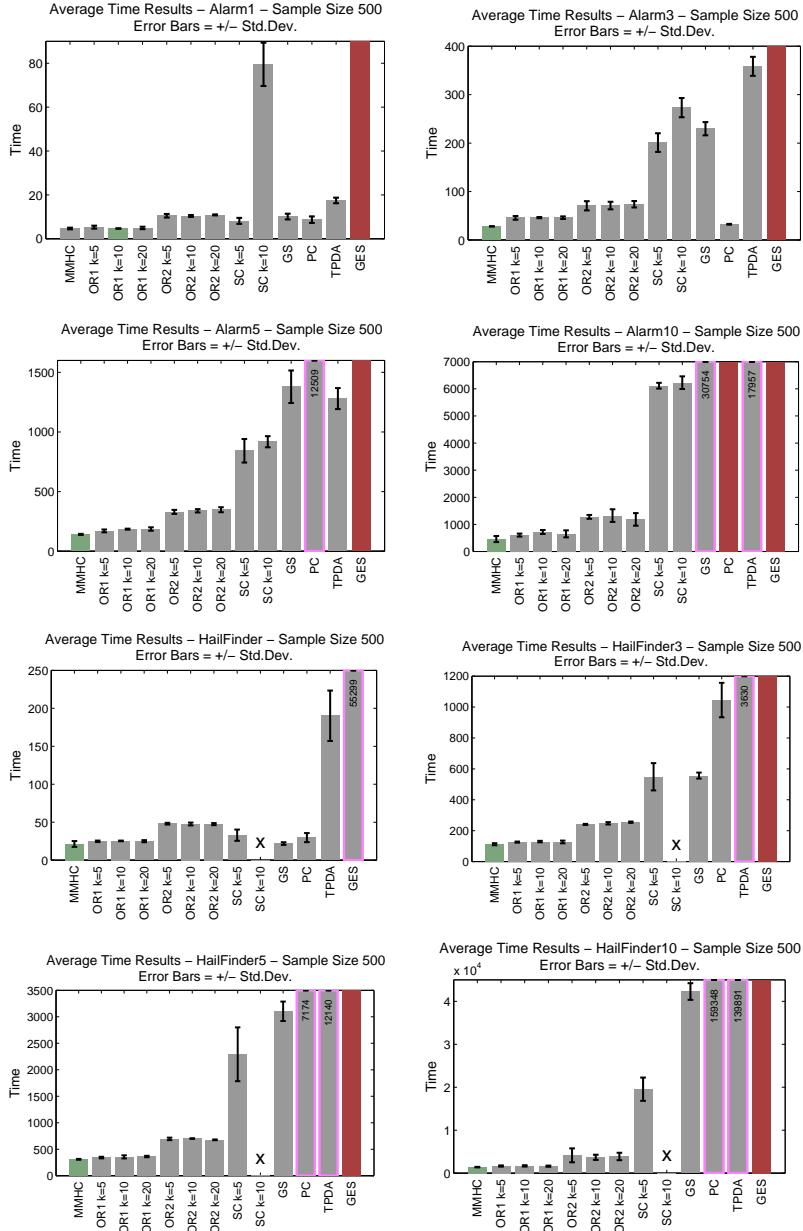


Figure 2. Time Results at Sample Size 500 for the ALARM, ALARM3, ALARM5, ALARM10, HAILFINDER, HAILFINDER3, HAILFINDER5, and HAILFINDER10 Networks.

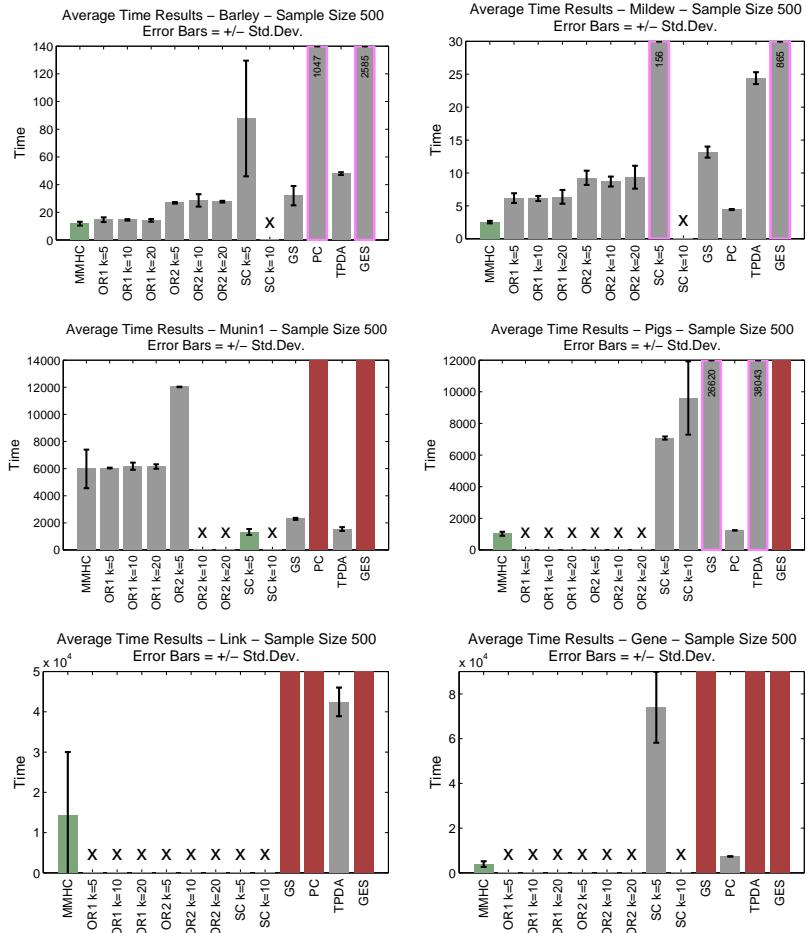


Figure 3. Time Results at Sample Size 500 for the BARLEY, MILDEW, MUNIN, PIGS, LINK, and GENE Networks.

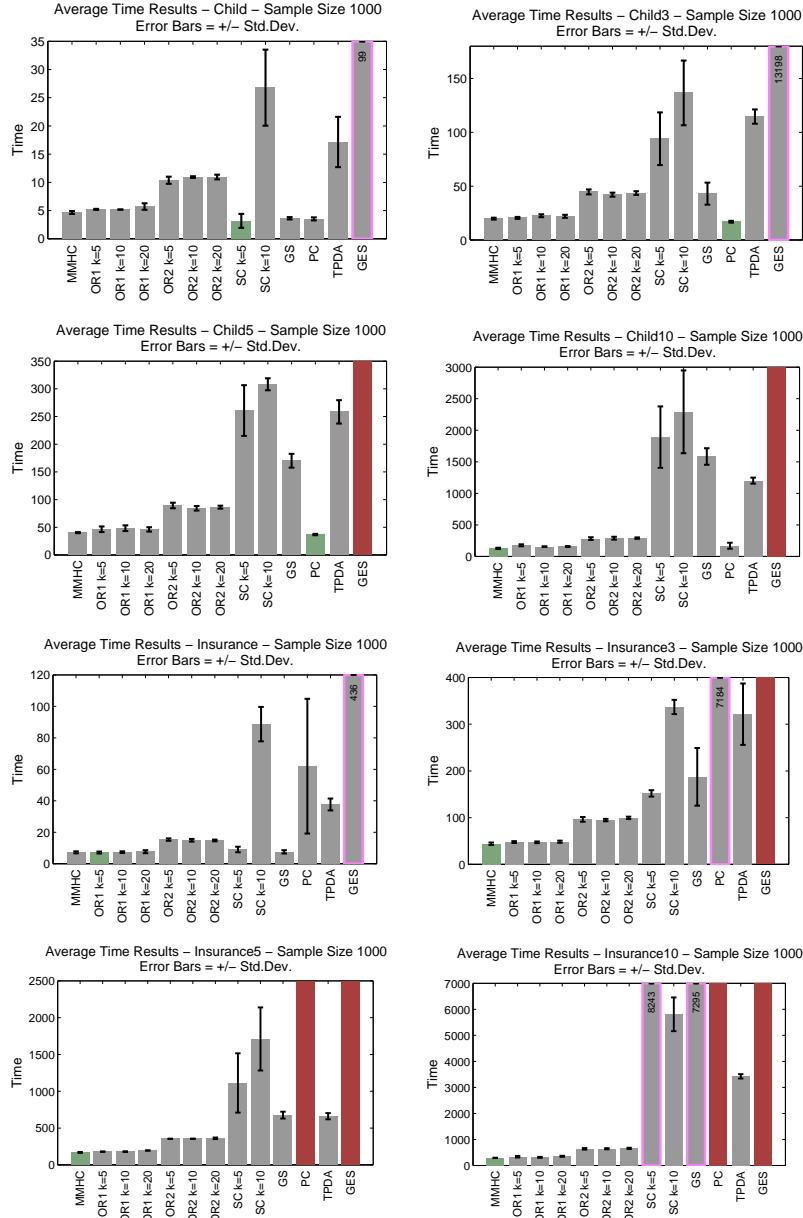


Figure 4. Time Results at Sample Size 1000 for the CHILD, CHILD3, CHILD5, CHILD10, INSURANCE, INSURANCE3, INSURANCE5, and INSURANCE10 Networks.

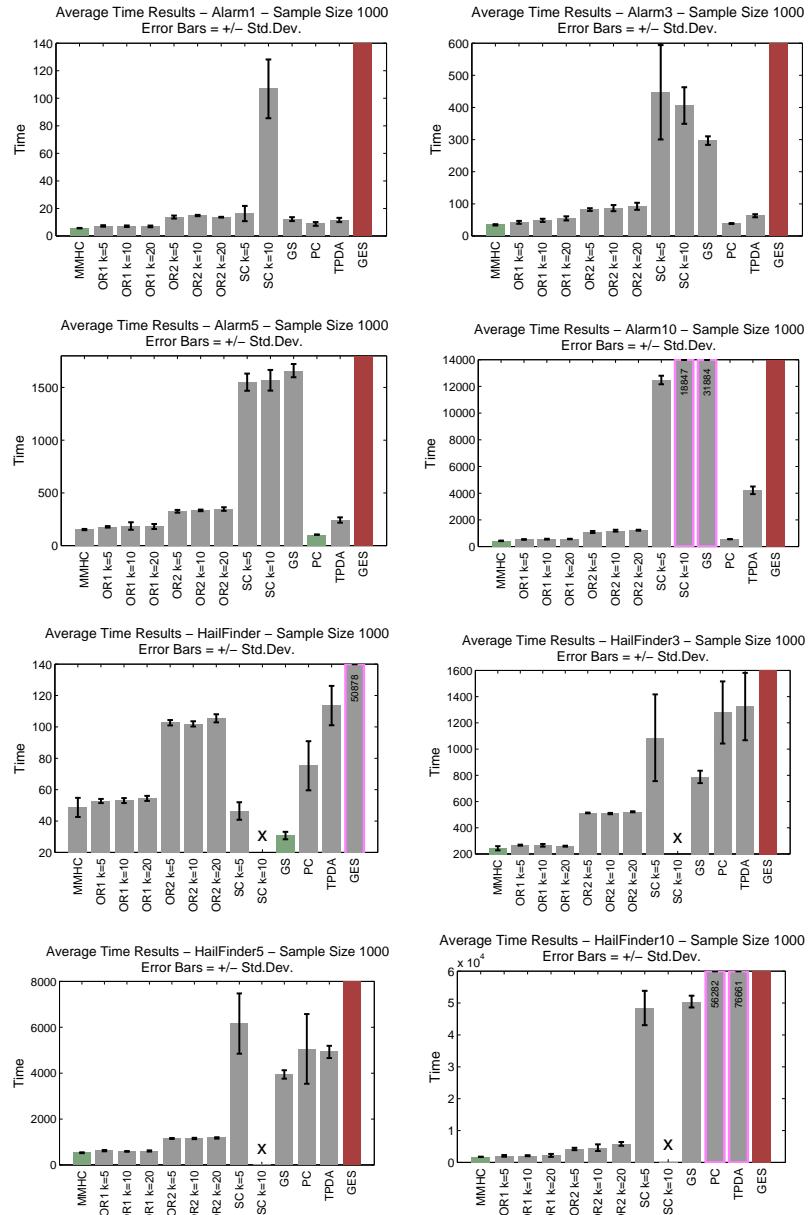


Figure 5. Time Results at Sample Size 1000 for the ALARM, ALARM3, ALARM5, ALARM10, HAILFINDER, HAILFINDER3, HAILFINDER5, and HAILFINDER10 Networks.

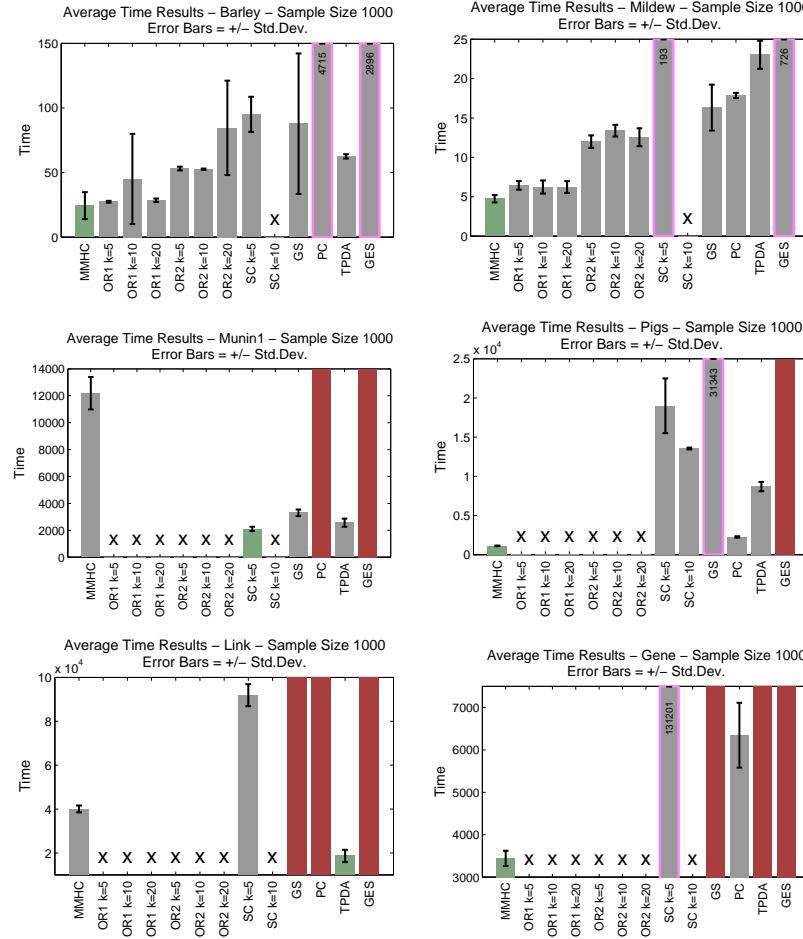


Figure 6. Time Results at Sample Size 1000 for the BARLEY, MILDEW, MUNIN, PIGS, LINK, and GENE Networks.

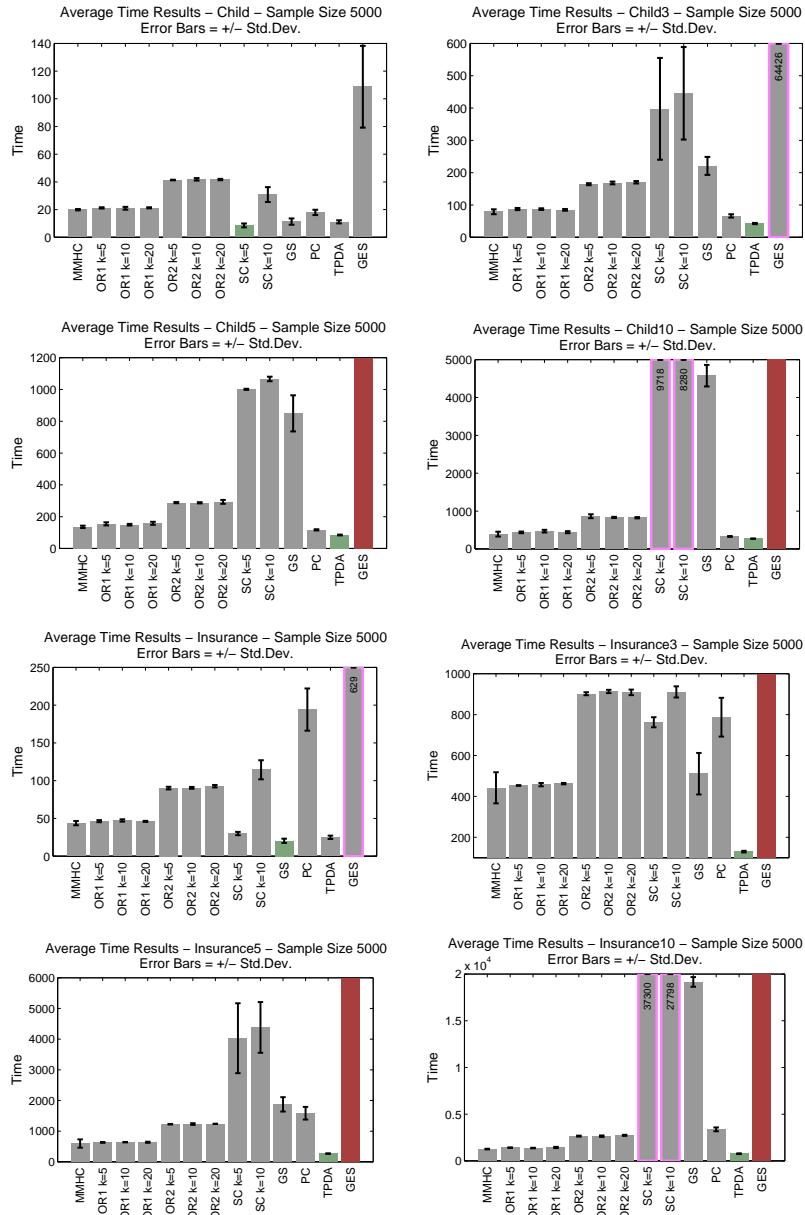


Figure 7. Time Results at Sample Size 5000 for the CHILD, CHILD3, CHILD5, CHILD10, INSURANCE, INSURANCE3, INSURANCE5, and INSURANCE10 Networks.

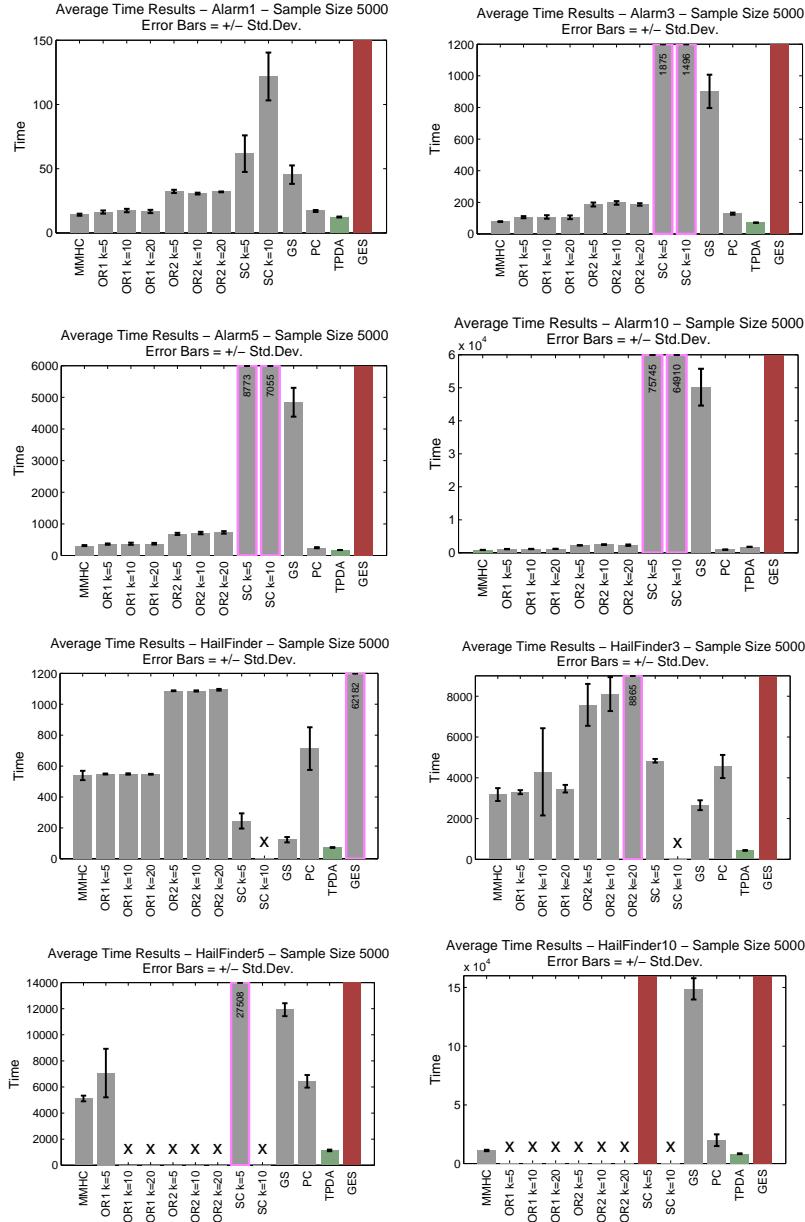


Figure 8. Time Results at Sample Size 5000 for the ALARM, ALARM3, ALARM5, ALARM10, HAILFINDER, HAILFINDER3, HAILFINDER5, and HAILFINDER10 Networks.

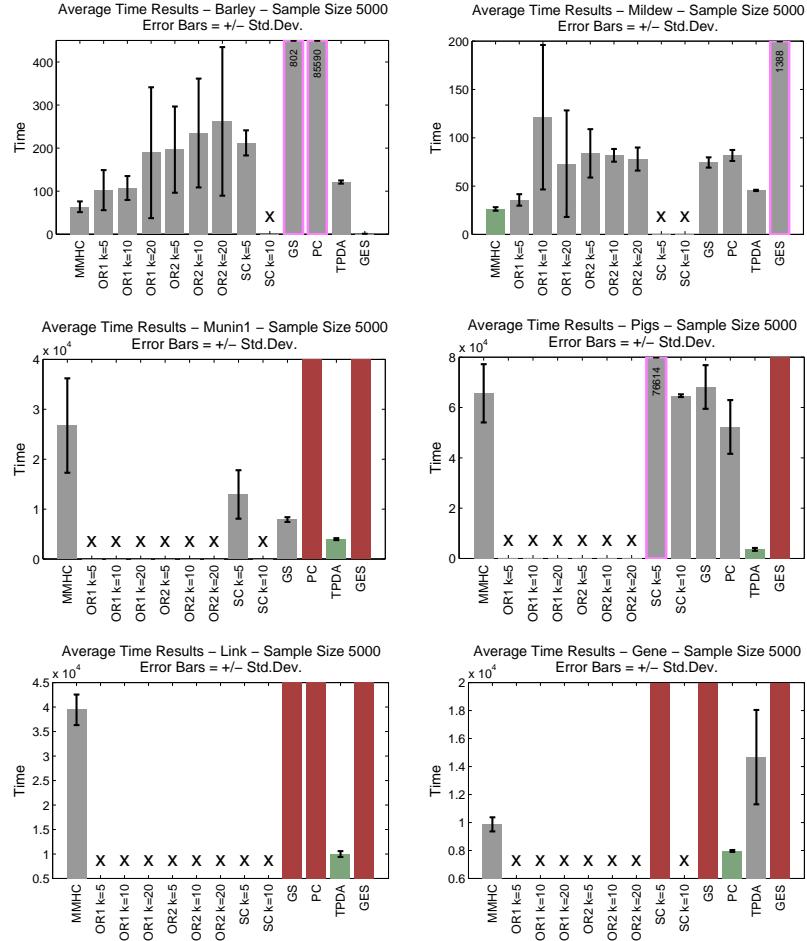


Figure 9. Time Results at Sample Size 5000 for the BARLEY, MILDEW, MUNIN, PIGS, LINK, and GENE Networks.

B.2. NUMBER OF STATISTICAL CALLS PERFORMED RESULTS

B.2.1. Median Statistical Calls Performed Results

Table II. Median Normalized Number of Statistics Calls Performed Results. Normalized number of statistics is the number of statistics completed by each algorithm (number of tests of conditional independence and/or number of calls to the scoring function) for a particular sample size and network divided by *MMHC*'s on the same sample size and network. The term in parentheses is the number of networks the algorithm was averaged across. Average normalized values greater than one correspond to an algorithm calling more statistical functions than *MMHC*.

Algorithm	Median Normalized Number of Statistics			Average Over SS
	500	1000	5000	
MMHC	1.00 (22)	1.00 (22)	1.00 (22)	1.00
GS	3.09 (20)	2.45 (20)	1.20 (20)	2.25
PC	0.80 (18)	0.79 (18)	1.06 (20)	0.88
TPDA	2.71 (21)	1.29 (21)	0.35 (22)	1.45

C. Quality of Reconstruction Results

C.1. BAYESIAN SCORE RESULTS

C.1.1. Median Bayesian Score Results

Table III. Median Normalized Bayesian Score Results. We normalize the scores reported by dividing by the corresponding score of *MMHC* on the same dataset. Normalized scores are positive numbers; *normalized scores less than one indicate a learned network that is more a posteriori probable (under the scoring assumptions) than that learned by MMHC on the same dataset*. The term in the parentheses is the number of networks for each algorithm was included in the median calculation (the algorithm finished within two days).

Algorithm	Median Normalized Bayesian Scores			Average Over SS	
	Sample Size (SS)				
	500	1000	5000		
MMHC	1.000 (22)	1.000 (22)	1.000 (22)	1.000	
OR1 k=5	1.016 (19)	1.010 (18)	1.009 (17)	1.012	
OR1 k=10	1.012 (19)	1.011 (18)	1.008 (16)	1.010	
OR1 k=20	1.015 (19)	1.017 (18)	1.013 (16)	1.015	
OR2 k=5	1.003 (19)	1.011 (18)	1.008 (16)	1.007	
OR2 k=10	1.013 (18)	1.011 (18)	1.006 (16)	1.010	
OR2 k=20	1.009 (18)	1.011 (18)	1.008 (16)	1.009	
SC k=5	0.993 (21)	0.995 (22)	1.002 (18)	0.997	
SC k=10	0.987 (13)	0.996 (13)	0.995 (13)	0.993	
GS	0.986 (20)	0.991 (20)	0.997 (20)	0.991	
PC	1.203 (18)	1.157 (18)	1.184 (20)	1.181	
TPDA	1.394 (21)	1.335 (21)	1.139 (22)	1.289	
GES	1.051 (7)	1.020 (6)	1.032 (6)	1.034	
Empty Graph	1.395 (22)	1.411 (22)	1.446 (22)	1.411	
True Graph	0.981 (22)	0.987 (22)	0.994 (22)	0.987	

C.1.2. Complete Bayesian Score Results

The complete results tables are given on the web as Matlab data files and text files. The Matlab files are 4-D matrices indexed by network (22), algorithm (13), sample size (3), and sampling (5). For each sample size there is a text document with the mean and standard deviation for all algorithms and networks.

The complete Bayesian Score results are also visually shown in Figures 10 - 18. These figures are bar plots of the absolute timing results for each algorithm on a given network and sample size. The error bars plotted are at +/- standard deviation.

A red * indicates the algorithm hit a two-day time limit with the quality not-determined. A bar with pink edging indicates it was an extreme value and exceeded the limits of the plot; the value is given for comparison. The green bar indicates the minimum.

When a bar is missing for an algorithm, indicated by an X, the algorithm was unable to run on that particular network and sample size.

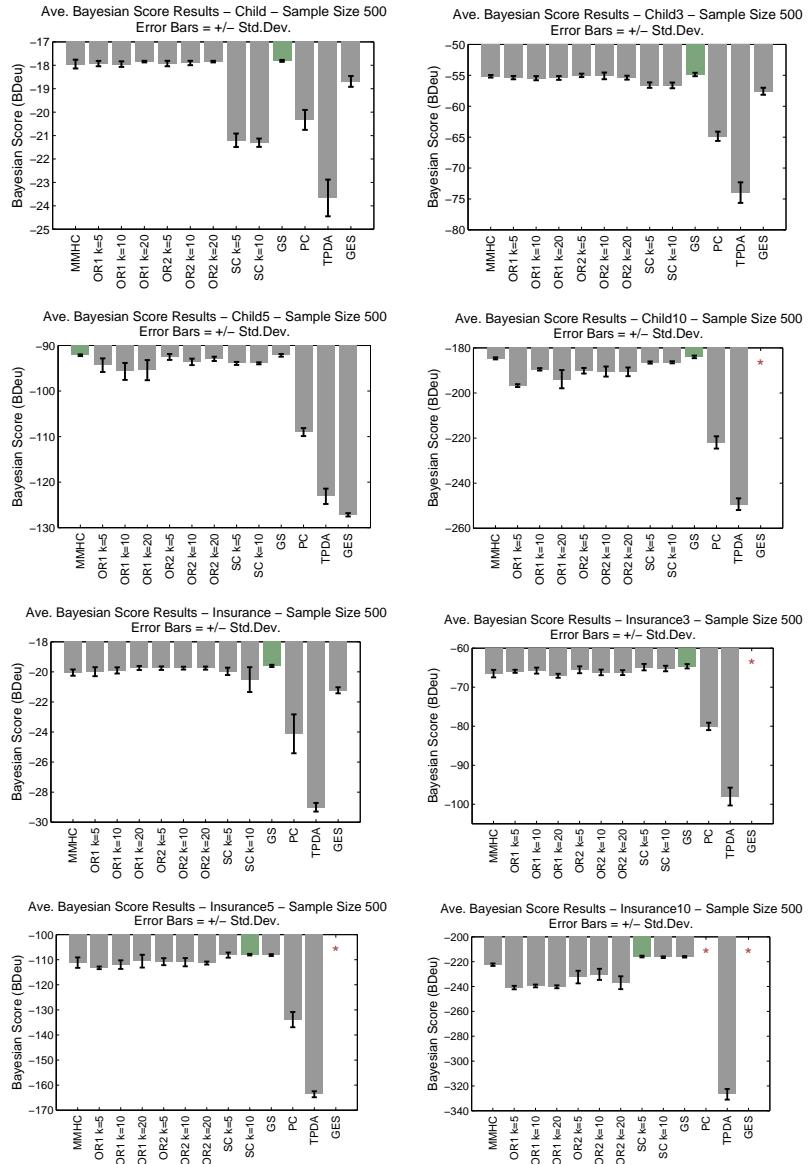


Figure 10. Bayesian Score Results at Sample Size 500 for the CHILD, CHILD3, CHILD5, CHILD10, INSURANCE, INSURANCE3, INSURANCE5, and INSURANCE10 Networks.

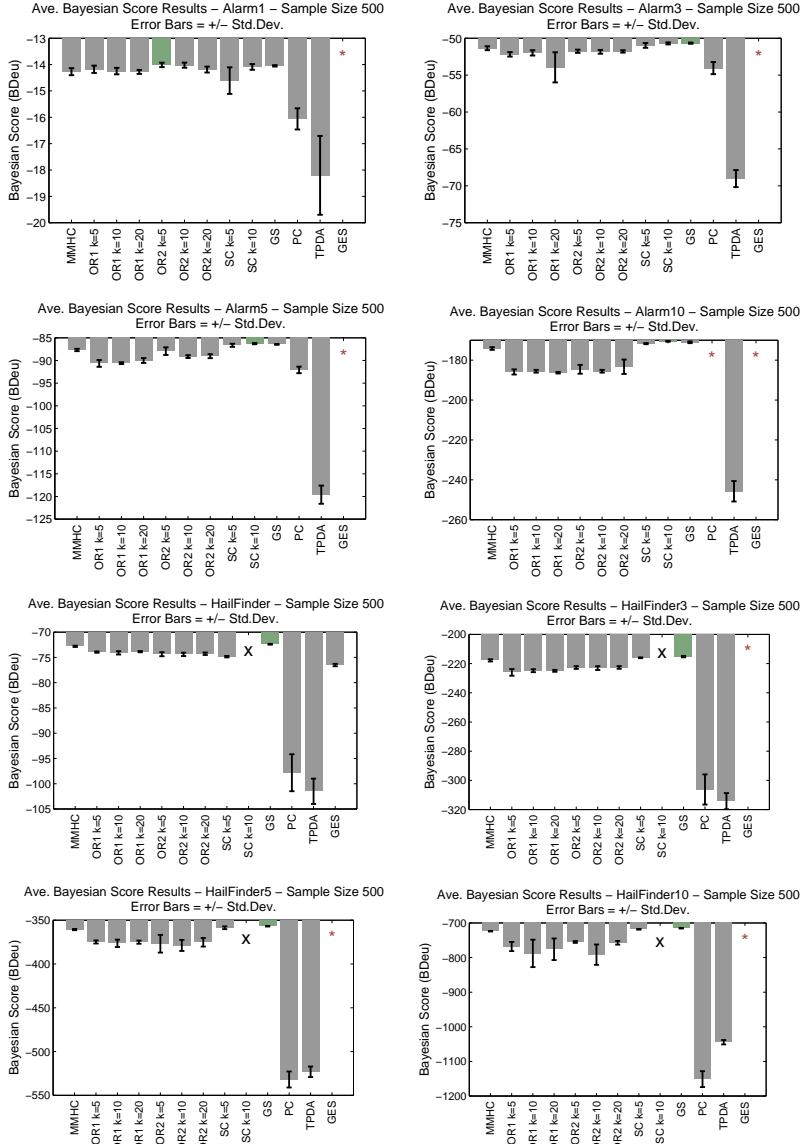


Figure 11. Bayesian Score Results at Sample Size 500 for the ALARM, ALARM3, ALARM5, ALARM10, HAILFINDER, HAILFINDER3, HAILFINDER5, and HAILFINDER10 Networks.

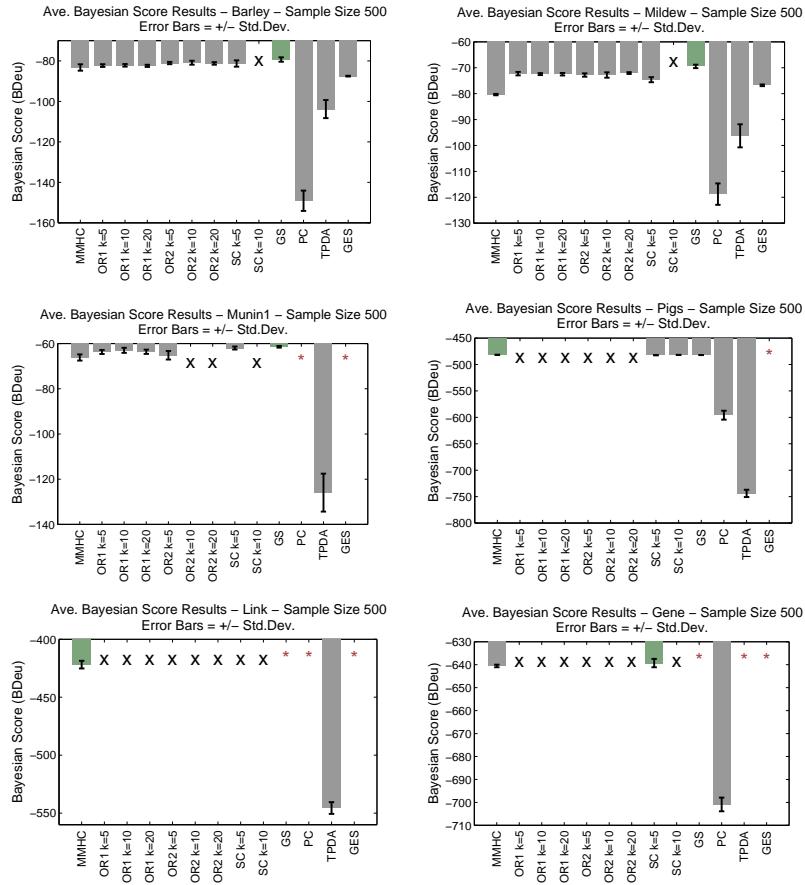


Figure 12. Bayesian Score Results at Sample Size 500 for the BARLEY, MILDEW, MUNIN, PIGS, LINK, and GENE Networks.

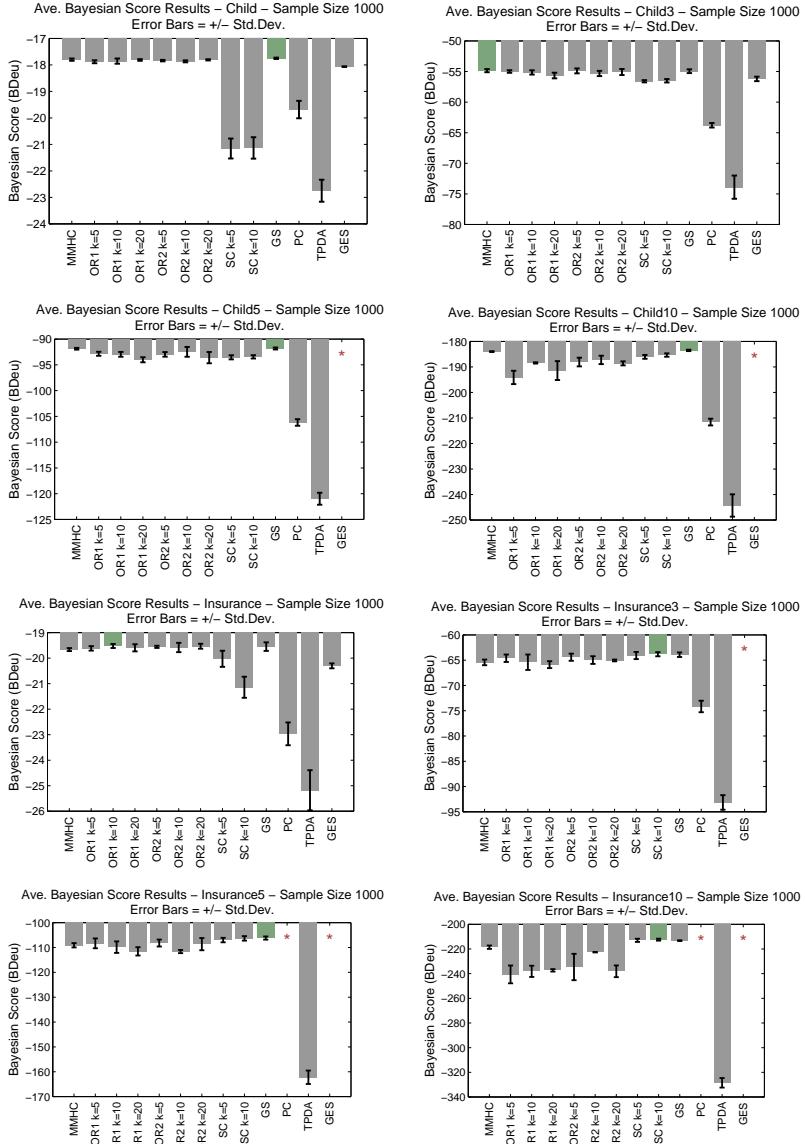


Figure 13. Bayesian Score Results at Sample Size 1000 for the CHILD, CHILD3, CHILD5, CHILD10, INSURANCE, INSURANCE3, INSURANCE5, and INSURANCE10 Networks.

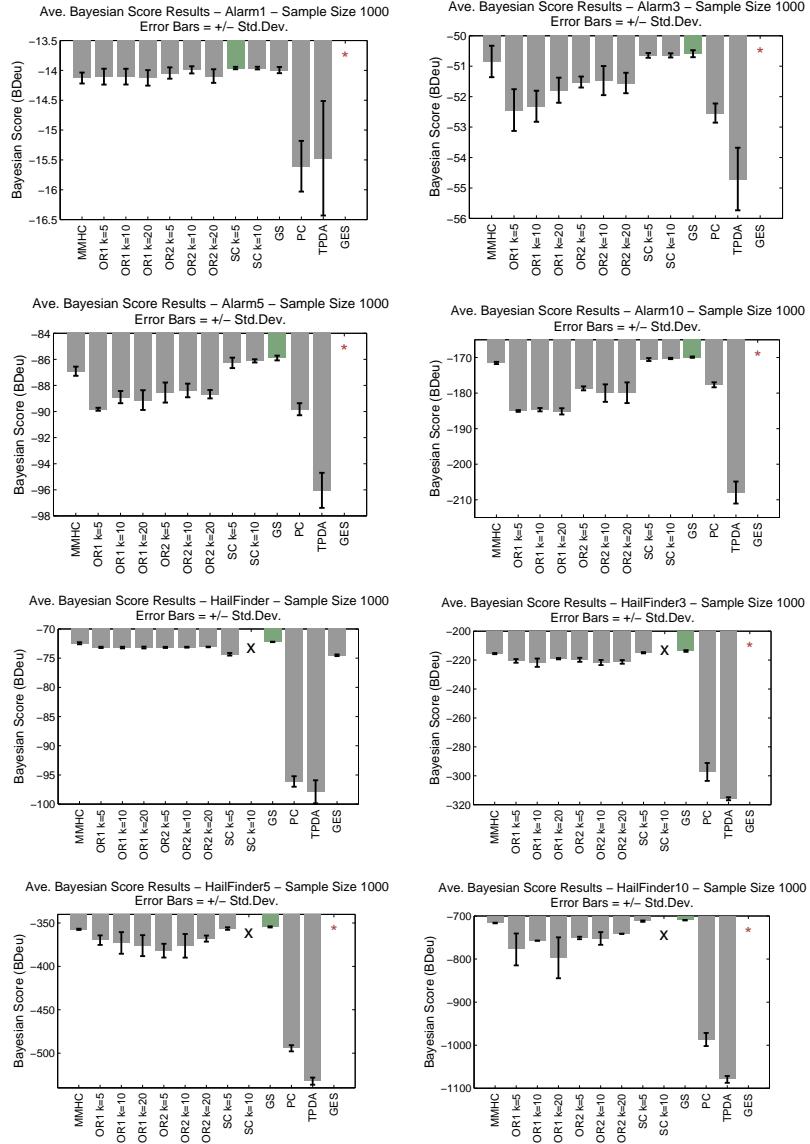


Figure 14. Bayesian Score Results at Sample Size 1000 for the ALARM, ALARM3, ALARM5, ALARM10, HAILFINDER, HAILFINDER3, HAILFINDER5, and HAILFINDER10 Networks.

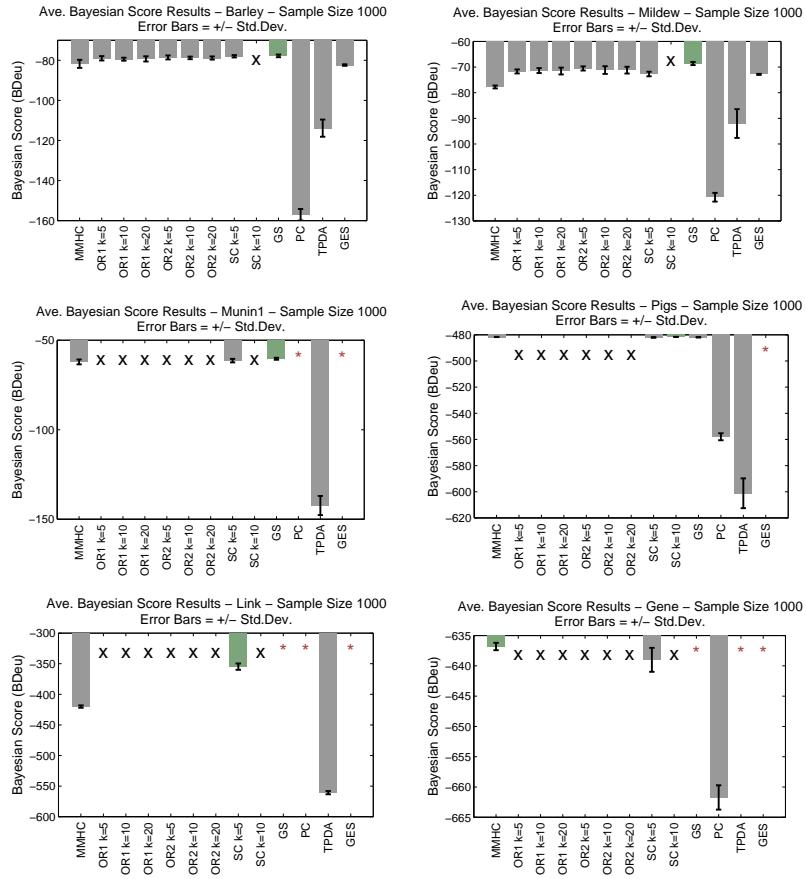


Figure 15. Bayesian Score Results at Sample Size 1000 for the BARLEY, MILDEW, MUNIN, PIGS, LINK, and GENE Networks.

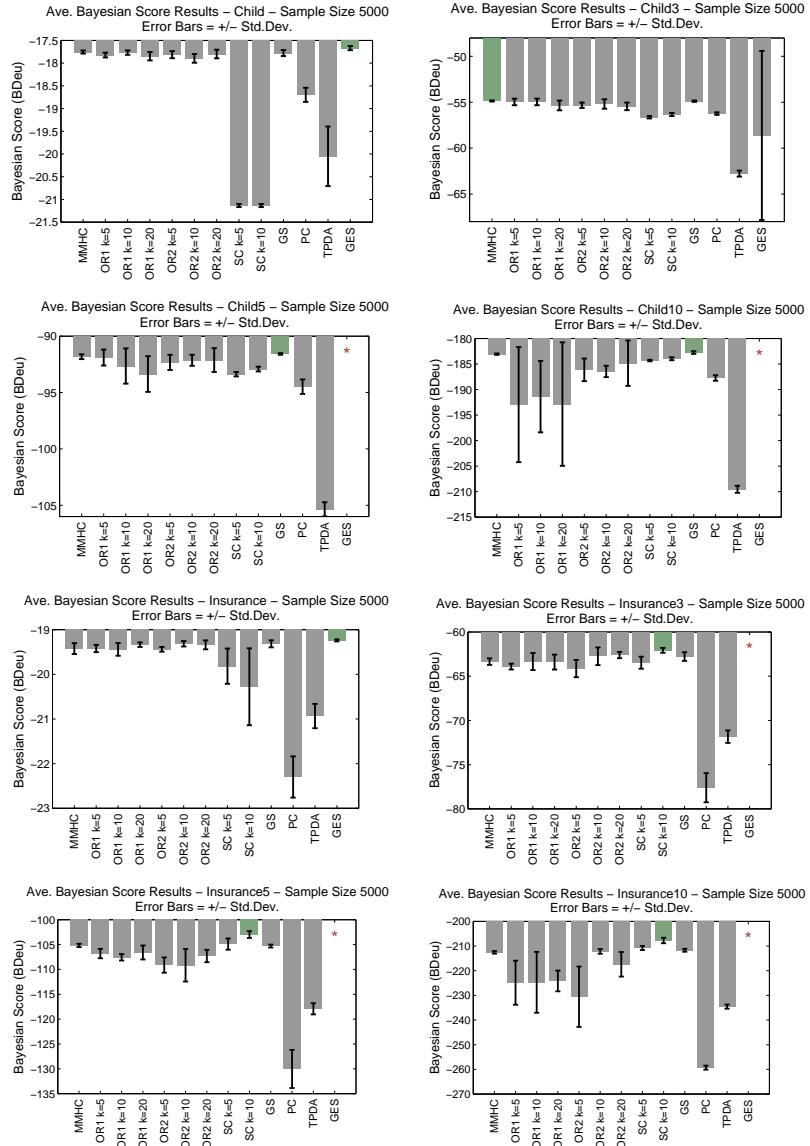


Figure 16. Bayesian Score Results at Sample Size 5000 for the CHILD, CHILD3, CHILD5, CHILD10, INSURANCE, INSURANCE3, INSURANCE5, and INSURANCE10 Networks.

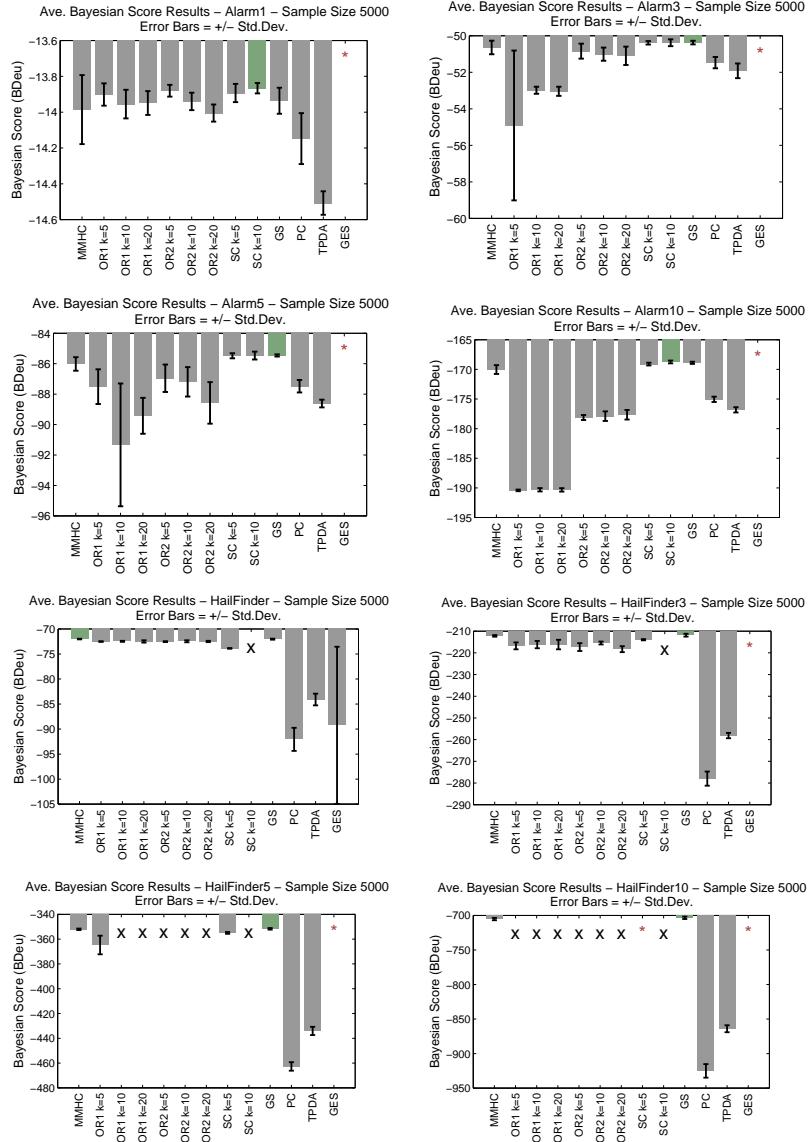


Figure 17. Bayesian Score Results at Sample Size 5000 for the ALARM, ALARM3, ALARM5, ALARM10, HAILFINDER, HAILFINDER3, HAILFINDER5, and HAILFINDER10 Networks.

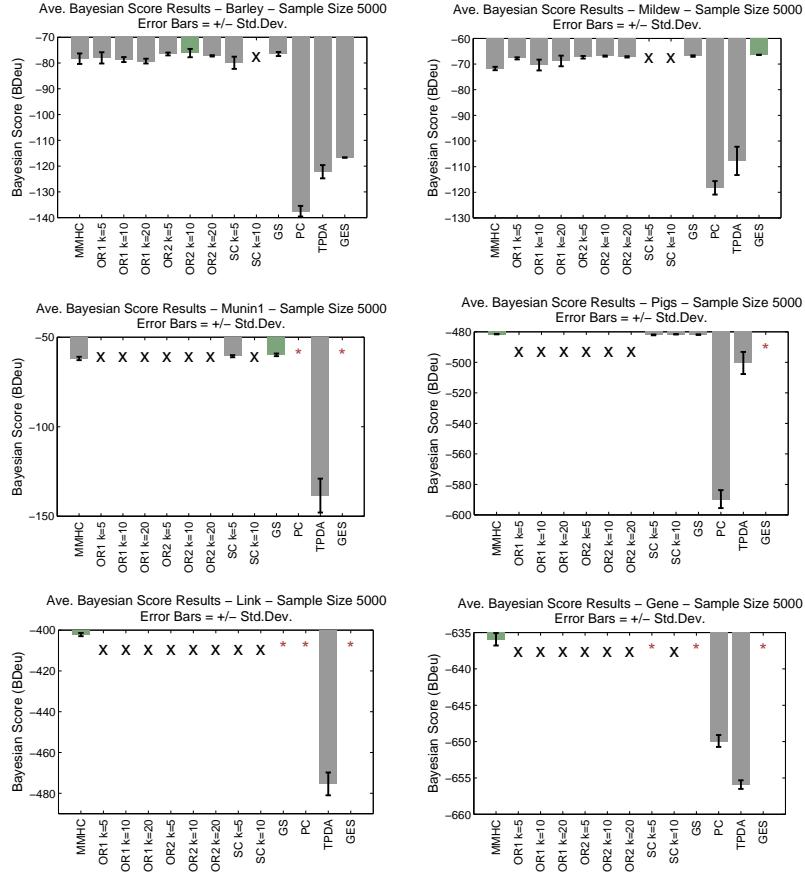


Figure 18. Bayesian Score Results at Sample Size 5000 for the BARLEY, MILDEW, MUNIN, PIGS, LINK, and GENE Networks.

C.2. STRUCTURAL HAMMING DISTANCE RESULTS

C.2.1. Median Structural Hamming Distance Result

Table IV. Median Normalized Structural Hamming Distance Results. Normalized Structural Hamming Distance (*SHD*) is the *SHD* of each algorithm for a particular sample size and network divided by *MMHC*'s *SHD* on the same sample size and network. The term in parentheses is the number of networks the algorithm in the median calculation. Median normalized *SHD* values greater than one correspond to an algorithm with more structural errors than *MMHC*.

Algorithm	Median Normalized Structural Hamming Distance			Average Over SS
	500	1000	5000	
MMHC	1.00 (22)	1.00 (22)	1.00 (22)	1.00
OR1 k=5	1.24 (19)	1.40 (18)	1.71 (17)	1.45
OR1 k=10	1.29 (19)	1.36 (18)	1.82 (16)	1.49
OR1 k=20	1.31 (19)	1.46 (18)	1.84 (16)	1.54
OR2 k=5	1.13 (19)	1.37 (18)	1.66 (16)	1.39
OR2 k=10	1.14 (18)	1.30 (18)	1.63 (16)	1.36
OR2 k=20	1.20 (18)	1.29 (18)	1.70 (16)	1.40
SC k=5	1.12 (21)	1.18 (22)	1.53 (18)	1.27
SC k=10	1.24 (13)	1.31 (13)	1.41 (13)	1.32
GS	1.20 (20)	1.36 (20)	1.51 (20)	1.35
PC	3.78 (18)	3.09 (18)	2.42 (20)	3.09
TPDA	2.99 (21)	2.71 (21)	1.61 (22)	2.44
GES	1.01 (7)	0.93 (6)	1.22 (6)	1.05

C.2.2. Complete Structural Hamming Distance Results

The complete results tables are given on the web as Matlab data files and text files. The 4-D matrices are indexed by network (22), algorithm (13), sample size (3), and sampling (5). Also, for each sample size there is a text document with the mean and standard deviation for all algorithms and networks.

The complete Structural Hamming Distance results are also visually shown in Figures 19 - 27. These figures are bar plots of the absolute timing results for each algorithm on a given network and sample size. The error bars plotted are at +/- standard deviation.

A red * indicates the algorithm hit a two-day time limit with the quality not-determined. A bar with pink edging indicates it was an extreme value and exceeded the limits of the plot; the value is given for comparison. The green bar indicates the minimum (for two cases CHILD and PIGS at sample size 5000 the minimum was *MMHC* with 0 errors in this case a green 0 is plotted instead).

When a bar is missing for an algorithm, denoted with an X, the algorithm was unable to run on that particular network and sample size.

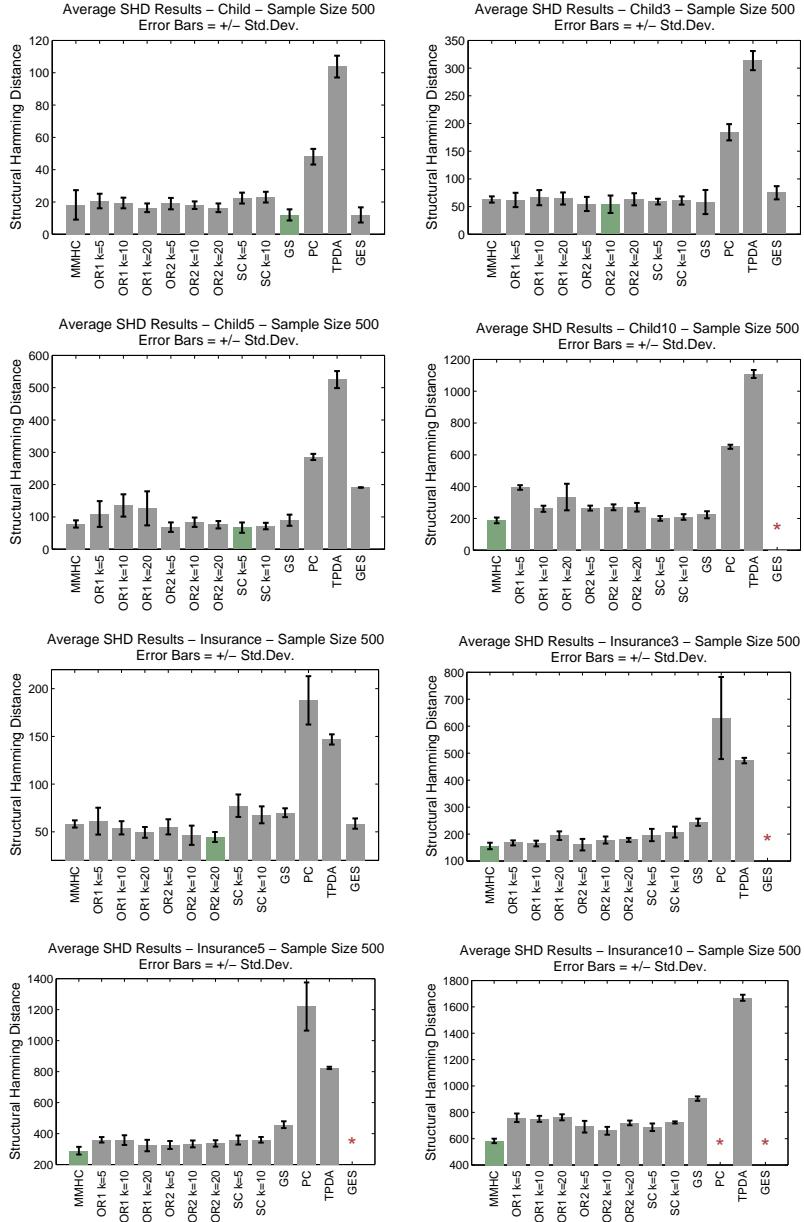


Figure 19. SHD Results at Sample Size 500 for the CHILD, CHILD3, CHILD5, CHILD10, INSURANCE, INSURANCE3, INSURANCE5, and INSURANCE10 Networks.

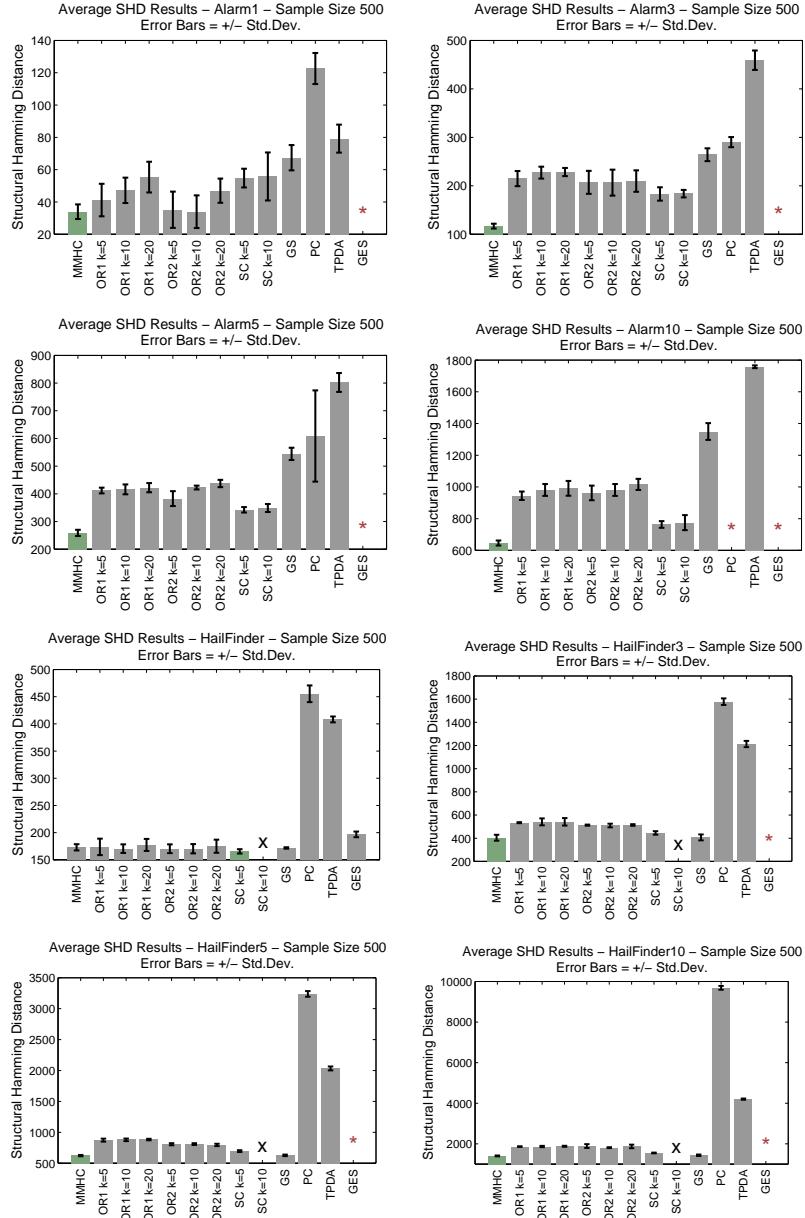


Figure 20. SHD Results at Sample Size 500 for the ALARM, ALARM3, ALARM5, ALARM10, HAILFINDER, HAILFINDER3, HAILFINDER5, and HAILFINDER10 Networks.

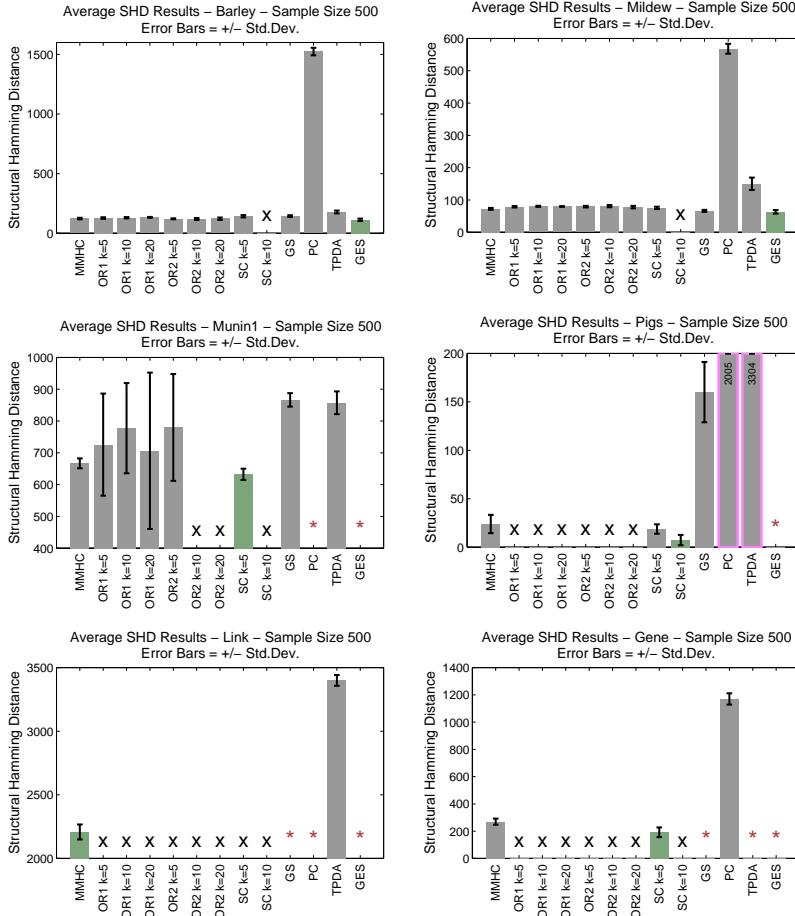


Figure 21. SHD Results at Sample Size 500 for the BARLEY, MILDEW, MUNIN, PIGS, LINK, and GENE Networks.

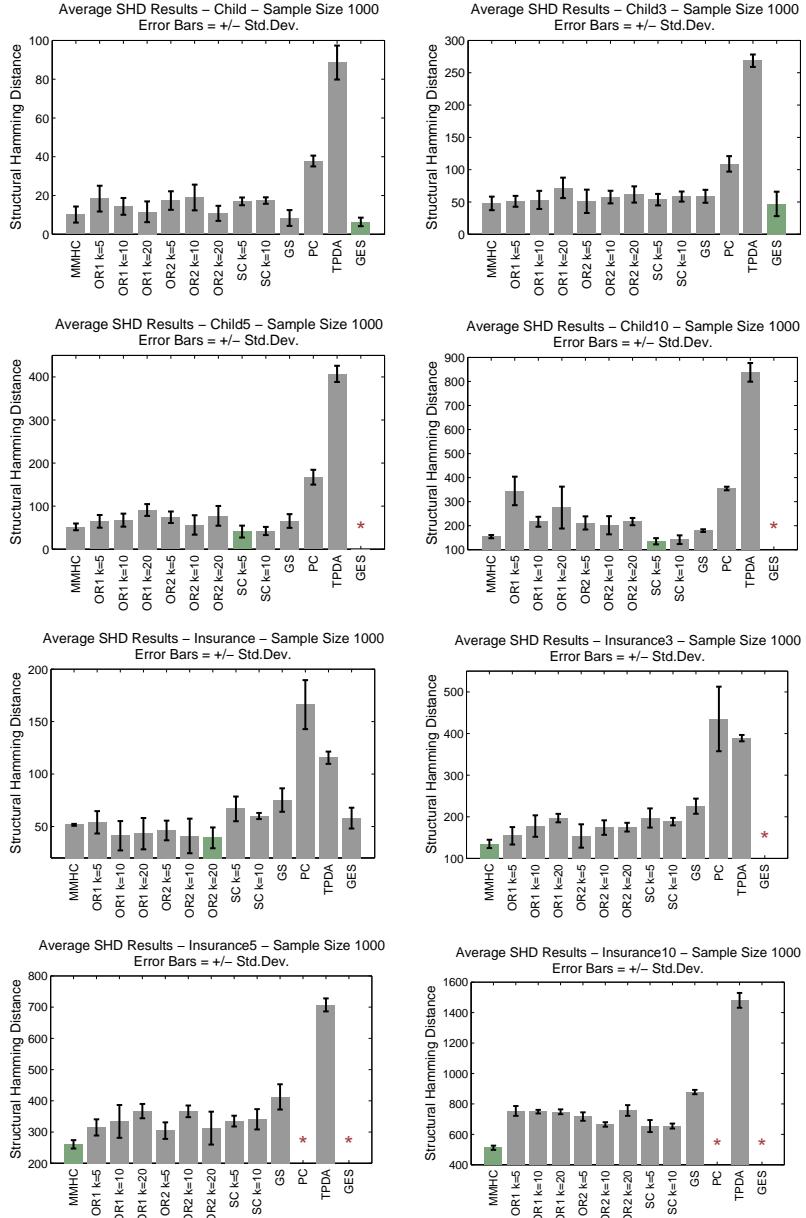


Figure 22. SHD Results at Sample Size 1000 for the CHILD, CHILD3, CHILD5, CHILD10, INSURANCE, INSURANCE3, INSURANCE5, and INSURANCE10 Networks.

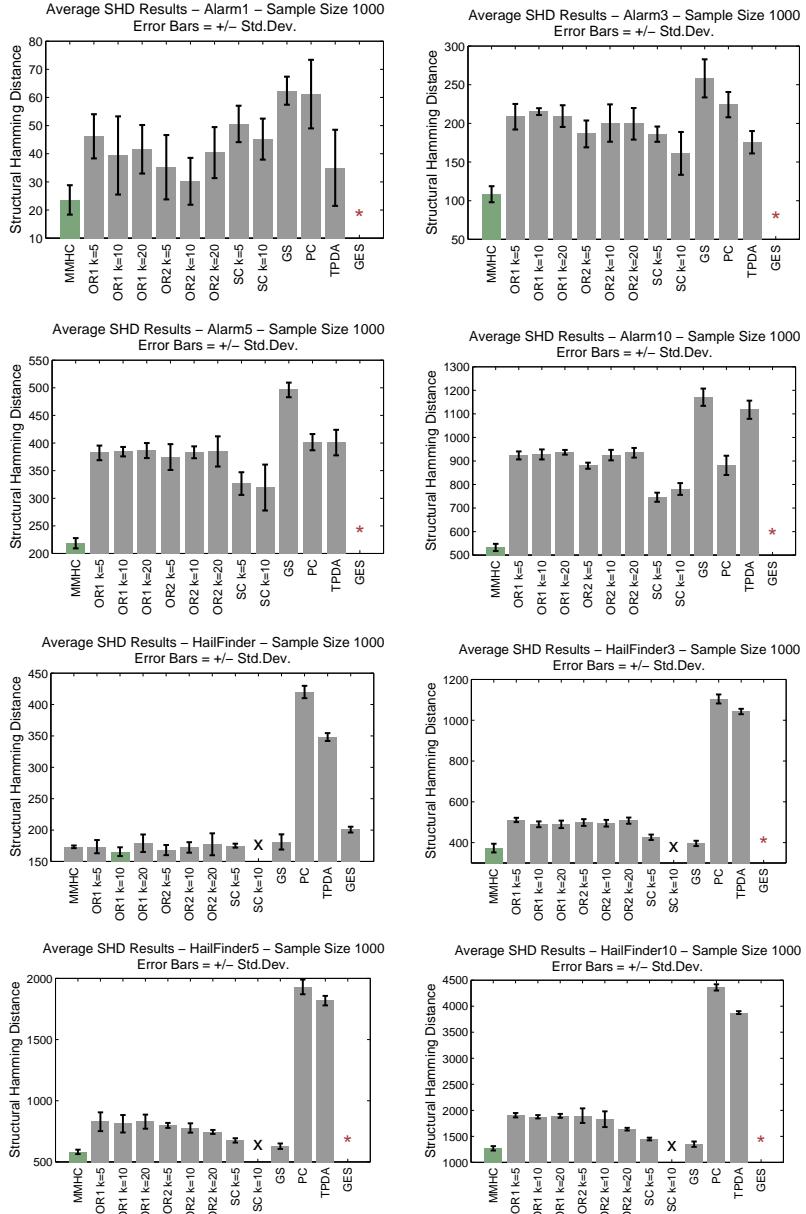


Figure 23. SHD Results at Sample Size 1000 for the ALARM, ALARM3, ALARM5, ALARM10, HAILFINDER, HAILFINDER3, HAILFINDER5, and HAILFINDER10 Networks.

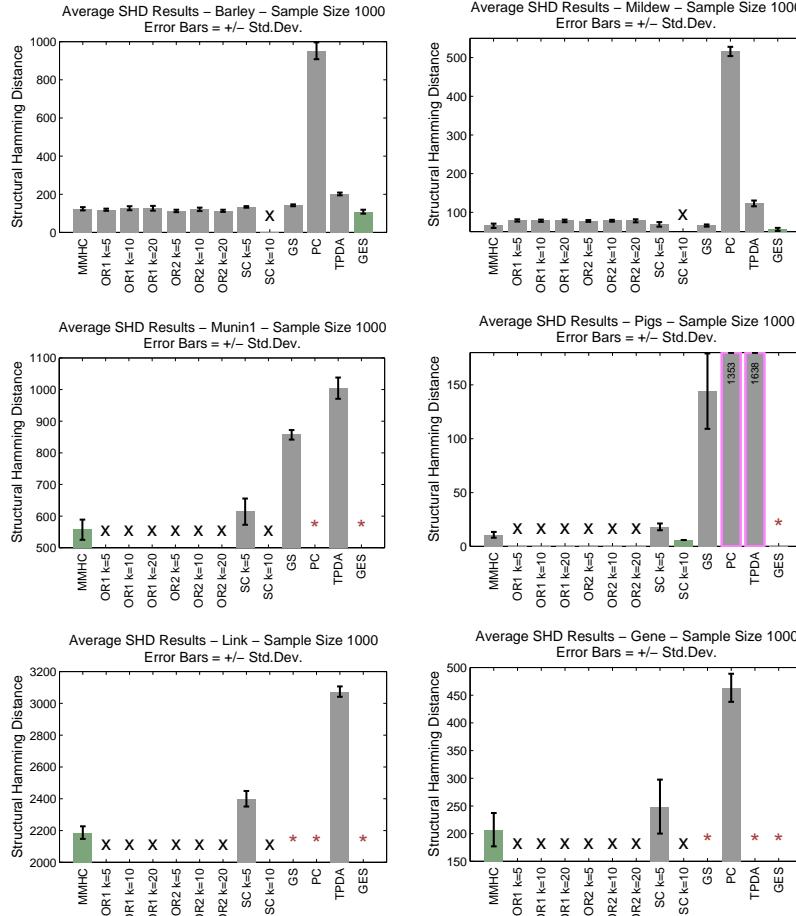


Figure 24. SHD Results at Sample Size 1000 for the BARLEY, MILDEW, MUNIN, PIGS, LINK, and GENE Networks.

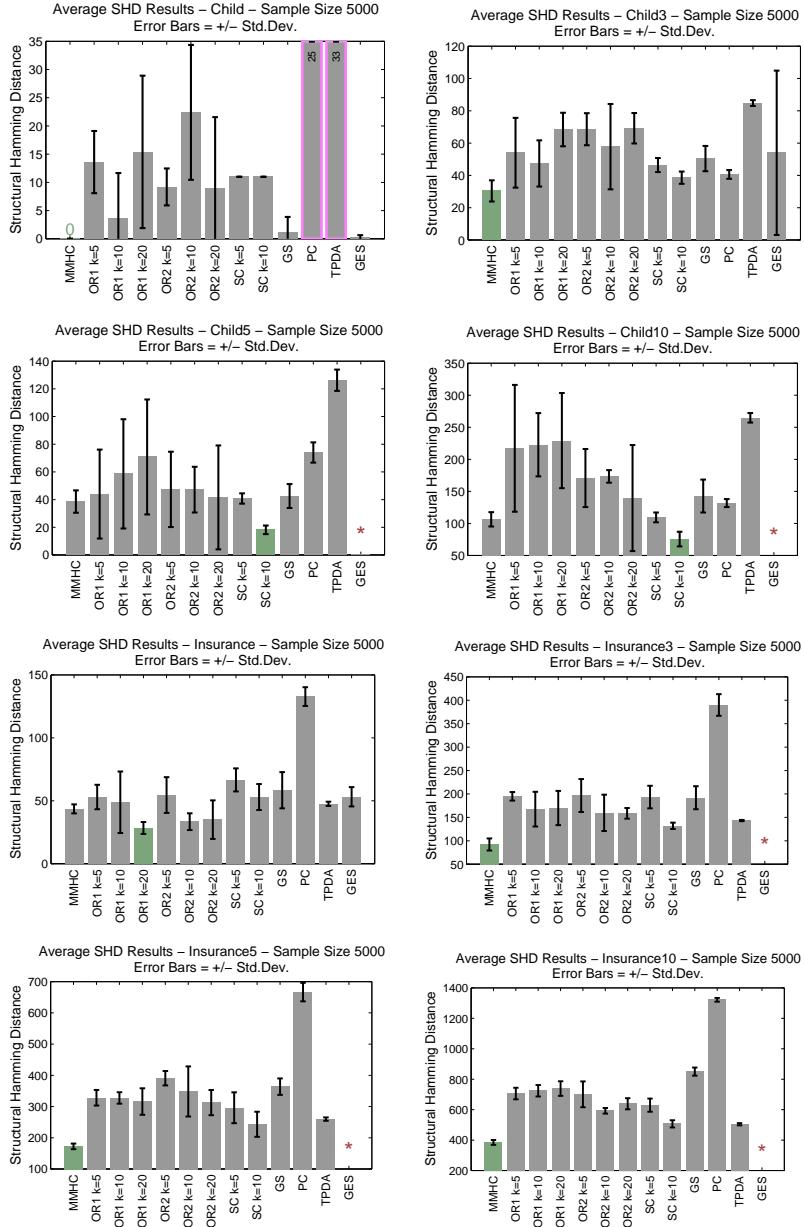


Figure 25. SHD Results at Sample Size 5000 for the CHILD, CHILD3, CHILD5, CHILD10, INSURANCE, INSURANCE3, INSURANCE5, and INSURANCE10 Networks.

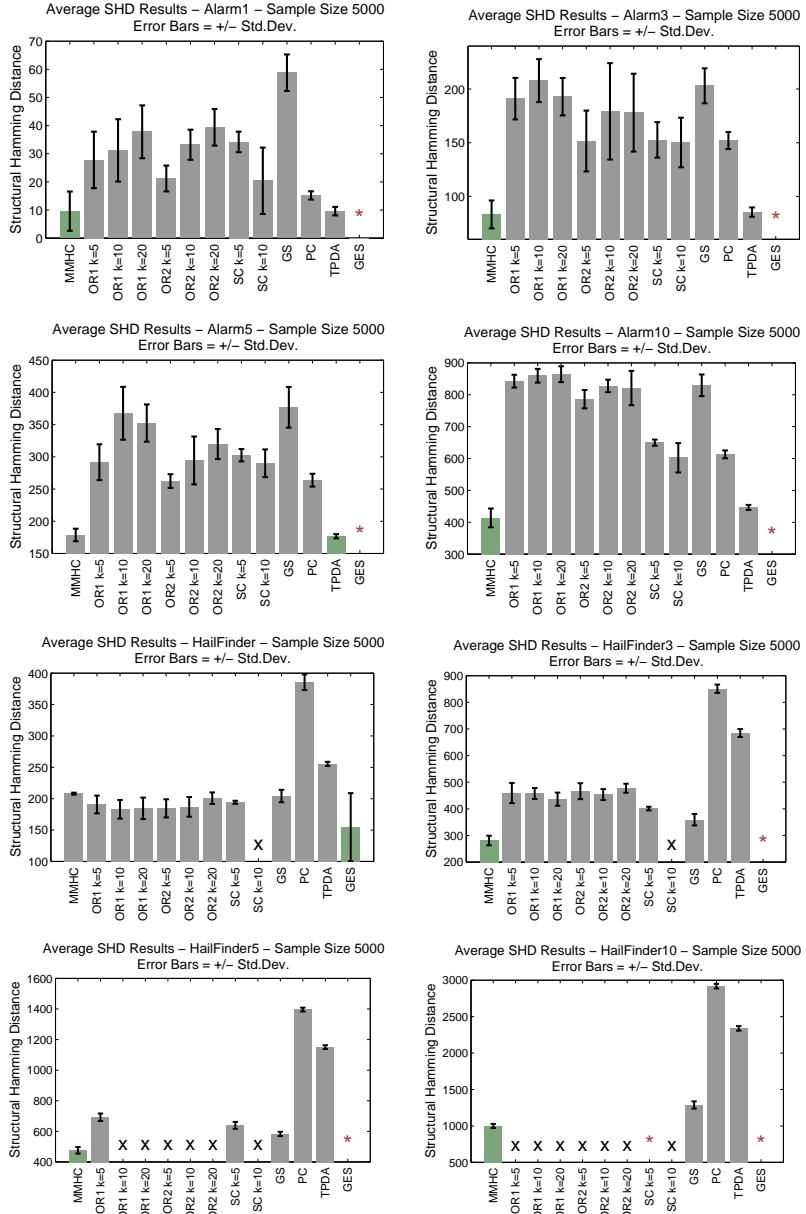


Figure 26. SHD Results at Sample Size 5000 for the ALARM, ALARM3, ALARM5, ALARM10, HAILFINDER, HAILFINDER3, HAILFINDER5, and HAILFINDER10 Networks.

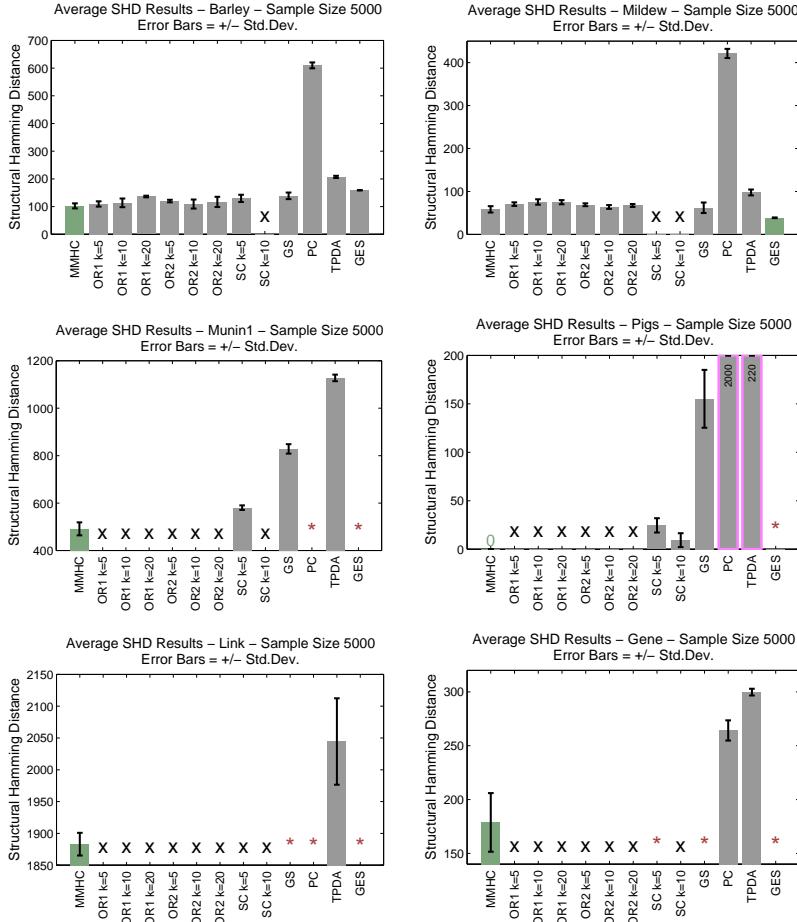


Figure 27. SHD Results at Sample Size 5000 for the BARLEY, MILDEW, MUNIN, PIGS, LINK, and GENE Networks.

C.3. KULLBACK-LEIBLER DIVERGENCE RESULTS

Table V. Average Normalized Kullback-Leibler Divergence Results. We have calculated a monotonic linear transformation of the KL-divergence as described in Section 9.1.4 of the paper that we call KL-div. Normalized KL-div is the KL-div of each algorithm for a particular sample size and network divided by *MMHC*'s KL-div on the same sample size and network. The term in parentheses is the number of networks the algorithm in the average calculation. Average normalized KL-div values greater than one correspond to an algorithm learning the distribution closer to the original distribution of the network than *MMHC*.

Algorithm	Sample Size (SS)			Average Over SS
	500	1000	5000	
MMHC	1.00 (22)	1.00 (22)	1.00 (22)	1.00
OR1 k=5	0.99 (19)	0.98 (18)	0.96 (17)	0.98
OR1 k=10	0.99 (19)	0.98 (18)	0.96 (16)	0.98
OR1 k=20	0.99 (19)	0.97 (18)	0.96 (16)	0.97
OR2 k=5	1.01 (19)	1.00 (18)	0.99 (16)	1.00
OR2 k=10	1.00 (18)	1.00 (18)	1.01 (16)	1.00
OR2 k=20	1.01 (18)	1.00 (18)	1.00 (16)	1.00
SC k=5	1.01 (21)	1.02 (22)	0.96 (17)	1.00
SC k=10	0.97 (13)	0.96 (13)	0.96 (13)	0.96
GS	1.09 (20)	1.06 (20)	1.03 (20)	1.06
PC	1.49 (18)	1.28 (18)	1.11 (20)	1.29
TPDA	1.03 (21)	1.05 (21)	0.97 (22)	1.02
GES	1.07 (7)	1.18 (6)	0.76 (6)	1.00

Table VI. Median Normalized Kullback-Leibler Divergence Results. We have calculated a monotonic linear transformation of the KL-divergence as described in Section 9.1.4 of the paper that we call KL-div. Normalized KL-div is the KL-div of each algorithm for a particular sample size and network divided by *MMHC*'s KL-div on the same sample size and network. The term in parentheses is the number of networks the algorithm in the median calculation. Median normalized KL-div values greater than one correspond to an algorithm learning the distribution closer to the original distribution of the network than *MMHC*.

Algorithm	Median Normalized Kullback-Leibler Divergence			Average Over SS	
	Sample Size (SS)				
	500	1000	5000		
MMHC	1.00 (22)	1.00 (22)	1.00 (22)	1.00	
OR1 k=5	0.96 (19)	0.97 (18)	0.98 (17)	0.97	
OR1 k=10	0.98 (19)	0.97 (18)	0.98 (16)	0.98	
OR1 k=20	0.96 (19)	0.96 (18)	0.98 (16)	0.96	
OR2 k=5	1.00 (19)	0.98 (18)	0.98 (16)	0.98	
OR2 k=10	0.98 (18)	0.97 (18)	0.99 (16)	0.98	
OR2 k=20	0.98 (18)	0.98 (18)	0.98 (16)	0.98	
SC k=5	1.02 (21)	1.01 (22)	1.00 (17)	1.01	
SC k=10	1.01 (13)	1.01 (13)	1.01 (13)	1.01	
GS	1.03 (20)	1.02 (20)	1.01 (20)	1.02	
PC	1.05 (18)	0.98 (18)	0.99 (20)	1.01	
TPDA	0.96 (21)	0.98 (21)	0.94 (22)	0.96	
GES	1.03 (7)	1.02 (6)	0.91 (6)	0.98	

D. Results Across Common Datasets

In order to compare all algorithms to each other, the metrics are evaluated across common networks. In order to keep the number of common networks high we exclude *GES* from this analysis. Every algorithm (except for *GES*) runs across 10 networks at sample size 500 and 1000 and 12 networks at sample size 5000. With this analysis comparisons may be made between all algorithms and not just with *MMHC*.

D.1. COMPUTATIONAL EFFICIENCY RESULTS

D.1.1. Time Results

Normalized time is the running time of each algorithm for a particular sample size and network divided by the corresponding running time of *MMHC*. A normalized time value smaller than one corresponds to an algorithm with faster running times than *MMHC*. The average normalized timing results and median normalized timing results are presented over the common networks in Tables VII and VIII. The term in parenthesis is the number of networks taken in the average (median) calculation; here those networks are common across all algorithms.

Table VII. Average Normalized Time Results Over Common Networks.

Algorithm	Average Normalized Times			Average Over SS
	500	1000	5000	
MMHC	1.00 (10)	1.00 (10)	1.00 (12)	1.00
OR1 k=5	1.27 (10)	1.17 (10)	1.14 (12)	1.19
OR1 k=10	1.25 (10)	1.19 (10)	1.15 (12)	1.20
OR1 k=20	1.28 (10)	1.22 (10)	1.15 (12)	1.22
OR2 k=5	2.31 (10)	2.26 (10)	2.18 (12)	2.25
OR2 k=10	2.34 (10)	2.31 (10)	2.21 (12)	2.28
OR2 k=20	2.47 (10)	2.34 (10)	2.21 (12)	2.34
SC k=5	4.25 (10)	8.61 (10)	18.31 (12)	10.39
SC k=10	9.93 (10)	14.23 (10)	16.25 (12)	13.47
GS	4.96 (10)	12.04 (10)	10.76 (12)	9.26
PC	33.07 (10)	17.98 (10)	1.64 (12)	17.56
TPDA	11.70 (10)	5.29 (10)	0.73 (12)	5.90

Table VIII. Median Normalized Time Results Over Common Networks.

Algorithm	Median Normalized Times			Average Over SS
	500	1000	5000	
MMHC	1.00 (10)	1.00 (10)	1.00 (12)	1.00
OR1 k=5	1.18 (10)	1.16 (10)	1.12 (12)	1.15
OR1 k=10	1.14 (10)	1.21 (10)	1.10 (12)	1.15
OR1 k=20	1.25 (10)	1.21 (10)	1.13 (12)	1.20
OR2 k=5	2.24 (10)	2.22 (10)	2.10 (12)	2.19
OR2 k=10	2.28 (10)	2.22 (10)	2.12 (12)	2.21
OR2 k=20	2.38 (10)	2.27 (10)	2.15 (12)	2.27
SC k=5	3.90 (10)	5.59 (10)	7.04 (12)	5.51
SC k=10	8.51 (10)	10.99 (10)	8.19 (12)	9.23
GS	3.63 (10)	4.23 (10)	4.71 (12)	4.19
PC	1.60 (10)	1.21 (10)	1.15 (12)	1.32
TPDA	10.20 (10)	5.47 (10)	0.59 (12)	5.42

D.1.2. Number of Statistical Calls Performed Results

Normalized number of statistical calls performed is the number of statistical calls completed by each algorithm (number of tests of conditional independence, measures of association, and/or number of calls to the scoring function) for a dataset divided by *MMHC*'s on the same dataset. Normalized values greater than one correspond to an algorithm performing a greater number of statistical functions than *MMHC*. The average and median normalized number of statistical calls performed are presented in Tables IX and X. The term in parentheses indicate the number of common networks included in the average (median) calculation.

Table IX. Average Normalized Number of Statistical Calls Performed Over Common Networks.

Algorithm	Average Normalized Number of Statistics			Average Over SS
	500	1000	5000	
MMHC	1.00 (10)	1.00 (10)	1.00 (12)	1.00
GS	2.84 (10)	2.70 (10)	2.04 (12)	2.52
PC	37.91 (10)	8.22 (10)	1.62 (12)	15.92
TPDA	2.91 (10)	1.40 (10)	0.43 (12)	1.58

Table X. Median Normalized Number of Statistical Calls Performed Over Common Networks.

Algorithm	Median Normalized Number of Statistics			Average Over SS
	500	1000	5000	
MMHC	1.00 (10)	1.00 (10)	1.00 (12)	1.00
GS	2.80 (10)	2.70 (10)	1.99 (12)	2.50
PC	1.10 (10)	8.22 (10)	1.31 (12)	3.54
TPDA	2.97 (10)	1.40 (10)	0.44 (12)	1.60

D.2. QUALITY OF RECONSTRUCTION RESULTS

D.2.1. Bayesian Score Results

Normalized scores are positive numbers, created by dividing a score by the corresponding score of *MMHC* on the same dataset. A normalized score less than one indicates a learned network that is more a posteriori probable than that learned by *MMHC* on the same dataset. The average and median normalized Bayesian score results are presented in Tables XI and XII. The term in parenthesis is the number of common networks included in the average (median) calculation.

Table XI. Average Normalized Bayesian Score Results Over Common Networks.

Algorithm	Average Normalized Bayesian Scores			Average Over SS
	500	1000	5000	
MMHC	1.000 (10)	1.000 (10)	1.000 (12)	1.000
OR1 k=5	1.014 (10)	1.020 (10)	1.030 (12)	1.021
OR1 k=10	1.010 (10)	1.016 (10)	1.030 (12)	1.019
OR1 k=20	1.015 (10)	1.021 (10)	1.029 (12)	1.022
OR2 k=5	0.999 (10)	1.008 (10)	1.019 (12)	1.009
OR2 k=10	1.003 (10)	1.009 (10)	1.010 (12)	1.008
OR2 k=20	1.004 (10)	1.012 (10)	1.012 (12)	1.009
SC k=5	1.019 (10)	1.022 (10)	1.020 (12)	1.020
SC k=10	1.018 (10)	1.026 (10)	1.016 (12)	1.020
GS	0.986 (10)	0.993 (10)	0.996 (12)	0.992
PC	1.153 (10)	1.108 (10)	1.086 (12)	1.116
TPDA	1.372 (10)	1.246 (10)	1.095 (12)	1.238
Empty Graph	1.544 (10)	1.573 (10)	1.584 (12)	1.521
True Graph	0.969 (10)	0.982 (10)	0.988 (12)	0.991

Table XII. Median Normalized Bayesian Score Results Over Common Networks.

Algorithm	Median Normalized Bayesian Score			Average Over SS	
	Sample Size (SS)				
	500	1000	5000		
MMHC	1.000 (10)	1.000 (10)	1.000 (12)	1.000	
OR1 k=5	1.010 (10)	1.008 (10)	1.012 (12)	1.010	
OR1 k=10	1.006 (10)	1.008 (10)	1.016 (12)	1.010	
OR1 k=20	1.007 (10)	1.016 (10)	1.015 (12)	1.013	
OR2 k=5	0.998 (10)	1.007 (10)	1.010 (12)	1.005	
OR2 k=10	0.999 (10)	1.007 (10)	1.007 (12)	1.004	
OR2 k=20	1.003 (10)	1.009 (10)	1.009 (12)	1.007	
SC k=5	1.003 (10)	1.004 (10)	1.000 (12)	1.002	
SC k=10	0.998 (10)	1.002 (10)	0.994 (12)	0.998	
GS	0.986 (10)	0.995 (10)	0.996 (12)	0.992	
PC	1.180 (10)	1.120 (10)	1.029 (12)	1.109	
TPDA	1.347 (10)	1.279 (10)	1.112 (12)	1.246	
Empty Graph	1.497 (10)	1.553 (10)	1.577 (12)	1.411	
True Graph	0.973 (10)	0.985 (10)	0.989 (12)	0.987	

D.2.2. Structural Hamming Distance Results

Normalized Structural Hamming Distance (*SHD*) is the *SHD* of each algorithm for a particular sample size and network divided by *MMHC*'s *SHD* on the same sample size and network. A normalized *SHD* value greater than one corresponds to an algorithm with more structural errors than *MMHC*. The average and median normalized Structural Hamming Distance results over common networks are presented in Tables XIII and XIV. The term in parenthesis is the number of common networks included in the average (median) calculation.

Table XIII. Average Normalized Structural Hamming Distance Results Over Common Networks.

Algorithm	Average Normalized Structural Hamming Distance			Average Over SS
	500	1000	5000	
MMHC	1.00 (10)	1.00 (10)	1.00 (12)	1.00
OR1 k=5	1.36 (10)	1.59 (10)	1.90 (12)	1.62
OR1 k=10	1.34 (10)	1.45 (10)	1.98 (12)	1.59
OR1 k=20	1.38 (10)	1.57 (10)	2.07 (12)	1.67
OR2 k=5	1.16 (10)	1.42 (10)	1.81 (12)	1.46
OR2 k=10	1.18 (10)	1.42 (10)	1.82 (12)	1.48
OR2 k=20	1.23 (10)	1.44 (10)	1.88 (12)	1.51
SC k=5	1.24 (10)	1.40 (10)	1.75 (12)	1.46
SC k=10	1.26 (10)	1.35 (10)	1.35 (12)	1.32
GS	1.46 (10)	1.71 (10)	2.23 (12)	1.80
PC	3.26 (10)	2.61 (10)	2.31 (12)	2.73
TPDA	4.11 (10)	3.97 (10)	1.65 (12)	3.24

Table XIV. Median Normalized Structural Hamming Distance Results Over Common Networks.

Algorithm	Median Normalized Structural Hamming Distance			Average Over SS
	500	1000	5000	
MMHC	1.00 (10)	1.00 (10)	1.00 (12)	1.00
OR1 k=5	1.23 (10)	1.74 (10)	1.90 (12)	1.62
OR1 k=10	1.31 (10)	1.41 (10)	1.90 (12)	1.54
OR1 k=20	1.43 (10)	1.75 (10)	1.97 (12)	1.72
OR2 k=5	1.04 (10)	1.46 (10)	1.82 (12)	1.44
OR2 k=10	1.11 (10)	1.30 (10)	1.73 (12)	1.38
OR2 k=20	1.15 (10)	1.45 (10)	1.79 (12)	1.46
SC k=5	1.25 (10)	1.43 (10)	1.64 (12)	1.44
SC k=10	1.25 (10)	1.43 (10)	1.41 (12)	1.36
GS	1.38 (10)	1.56 (10)	2.08 (12)	1.68
PC	3.35 (10)	2.44 (10)	1.83 (12)	2.54
TPDA	3.51 (10)	2.56 (10)	1.31 (12)	2.46

E. Effects On Time and Quality of Learning with Increasing the Number of Variables

E.1. EFFECT ON GREEDY SEARCH OF INCREASING THE NUMBER OF VARIABLES

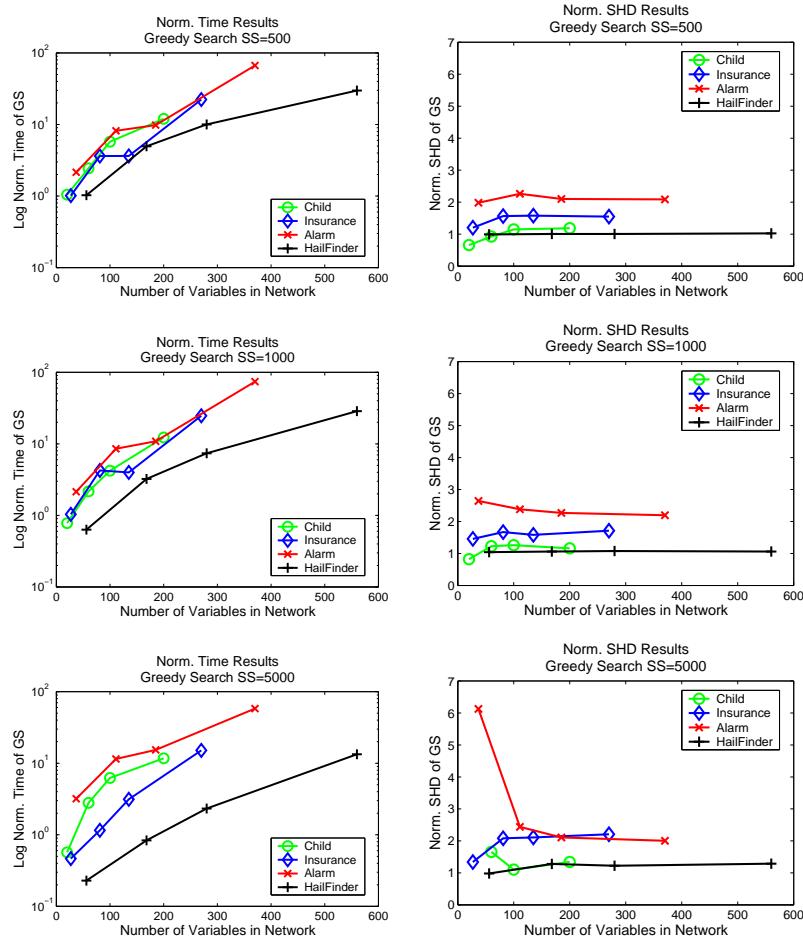


Figure 28. Normalized Time and Normalized SHD vs. number of variables in the network for the Greedy Search algorithm on the CHILD, INSURANCE, ALARM, HAILFINDER tiled networks.

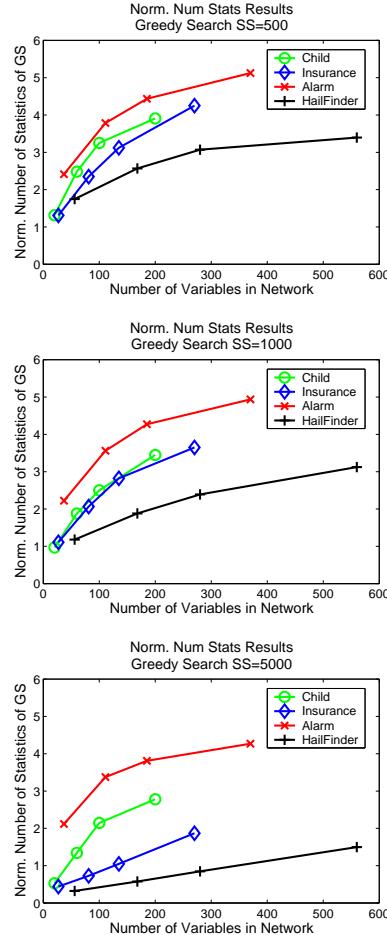


Figure 29. Normalized Number of Statistics vs. number of variables in the network for the Greedy Search algorithm on the CHILD, INSURANCE, ALARM, HAILFINDER tiled networks.

E.2. EFFECT ON PC OF INCREASING THE NUMBER OF VARIABLES.

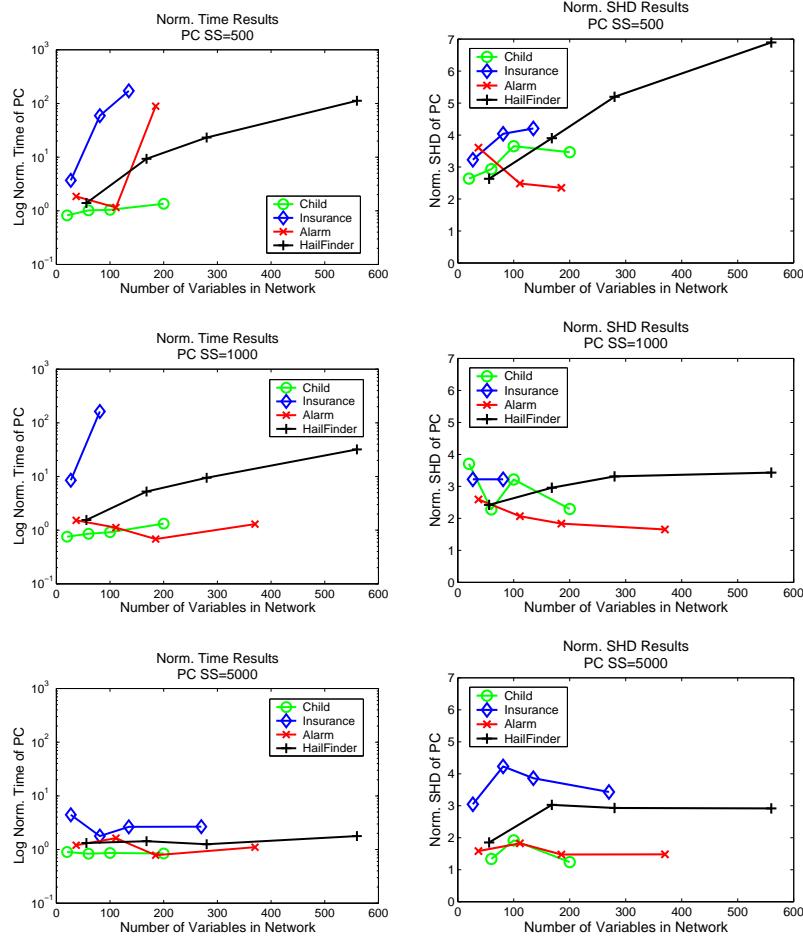


Figure 30. Normalized Time and Normalized SHD vs. number of variables in the network for the PC algorithm on the CHILD, INSURANCE, ALARM, HAILFINDER tiled networks.

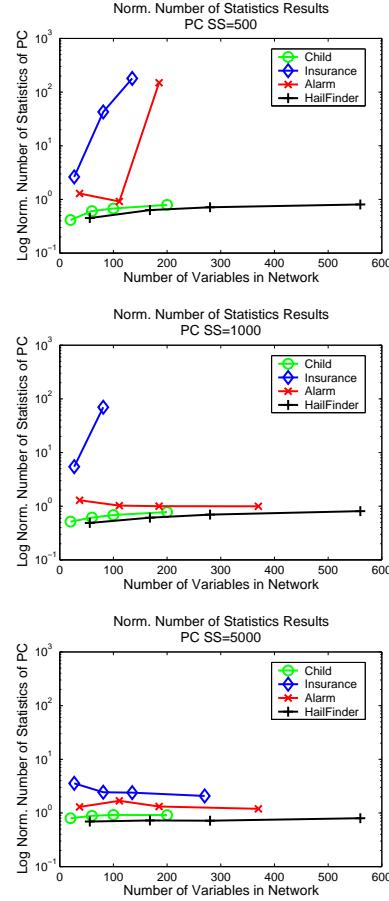


Figure 31. Normalized Number of Statistics vs. number of variables in the network for the PC algorithm on the CHILD, INSURANCE, ALARM, HAILFINDER tiled networks.

E.3. EFFECT ON TPDA OF INCREASING THE NUMBER OF VARIABLES.

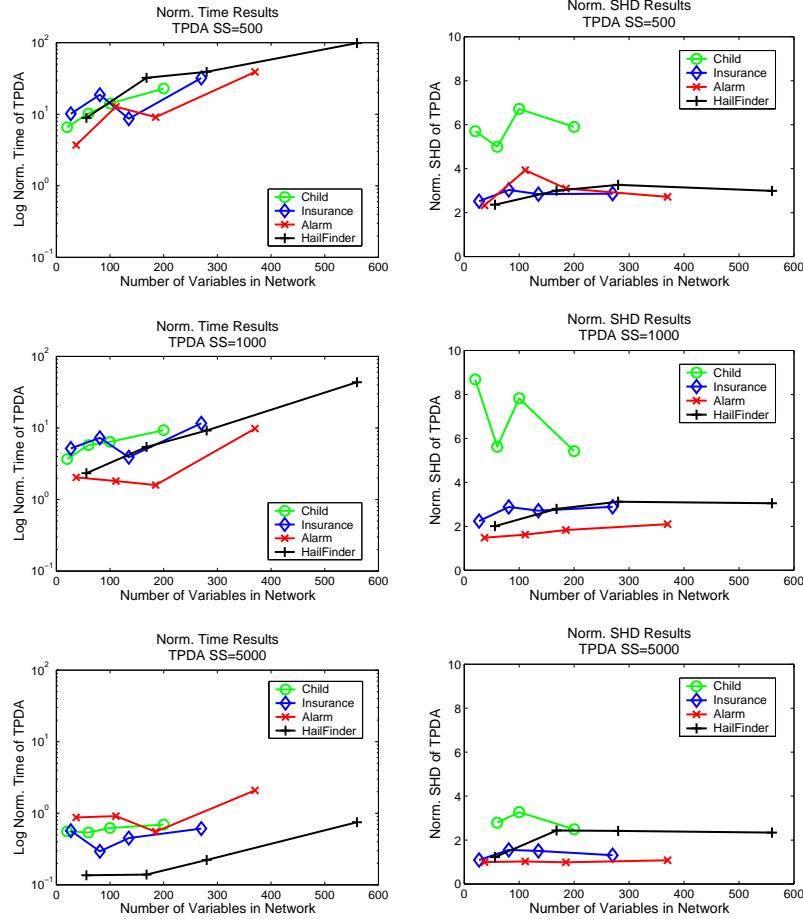


Figure 32. Normalized Time and Normalized SHD vs. number of variables in the network for the TPDA algorithm on the CHILD, INSURANCE, ALARM, HAILFINDER tiled networks.

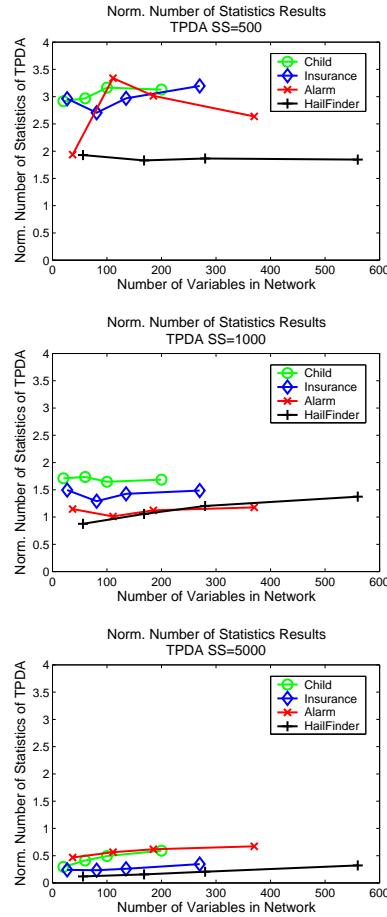


Figure 33. Normalized Number of Statistics vs. number of variables in the network for the TPDA algorithm on the CHILD, INSURANCE, ALARM, HAILFINDER tiled networks.

E.4. EFFECT ON SPARSE CANDIDATE $k=5$ OF INCREASING THE NUMBER OF VARIABLES.

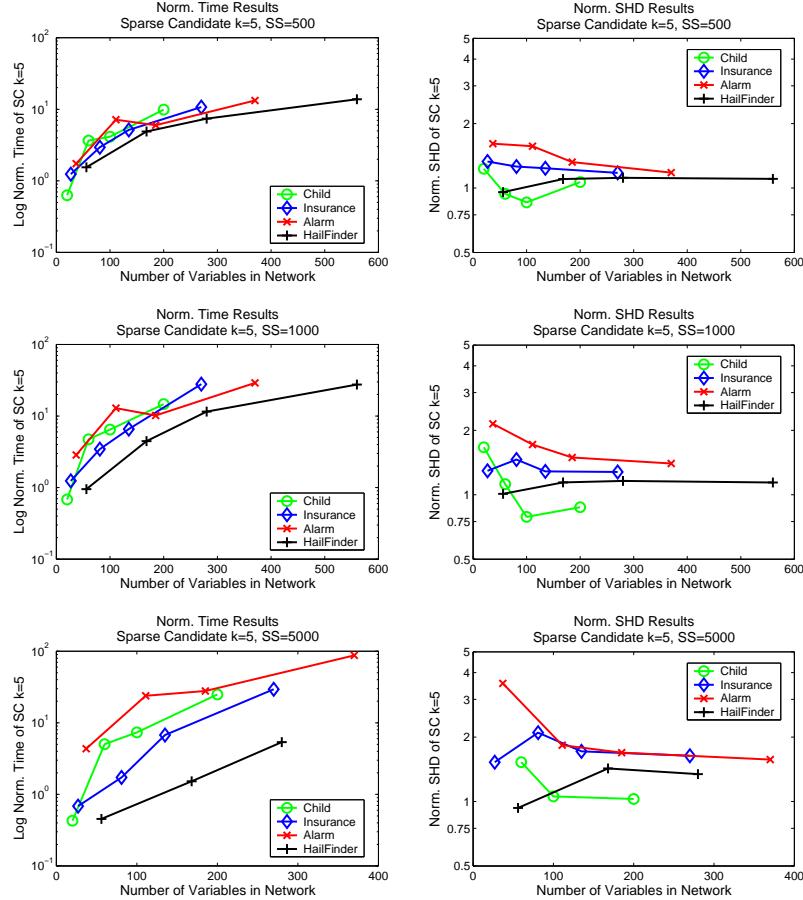


Figure 34. Normalized Time and Normalized SHD vs. number of variables in the network for the Sparse Candidate algorithm with $k = 5$ on the CHILD, INSURANCE, ALARM, HAILFINDER tiled networks.

E.5. EFFECT ON SPARSE CANDIDATE $k=10$ OF INCREASING THE NUMBER OF VARIABLES.

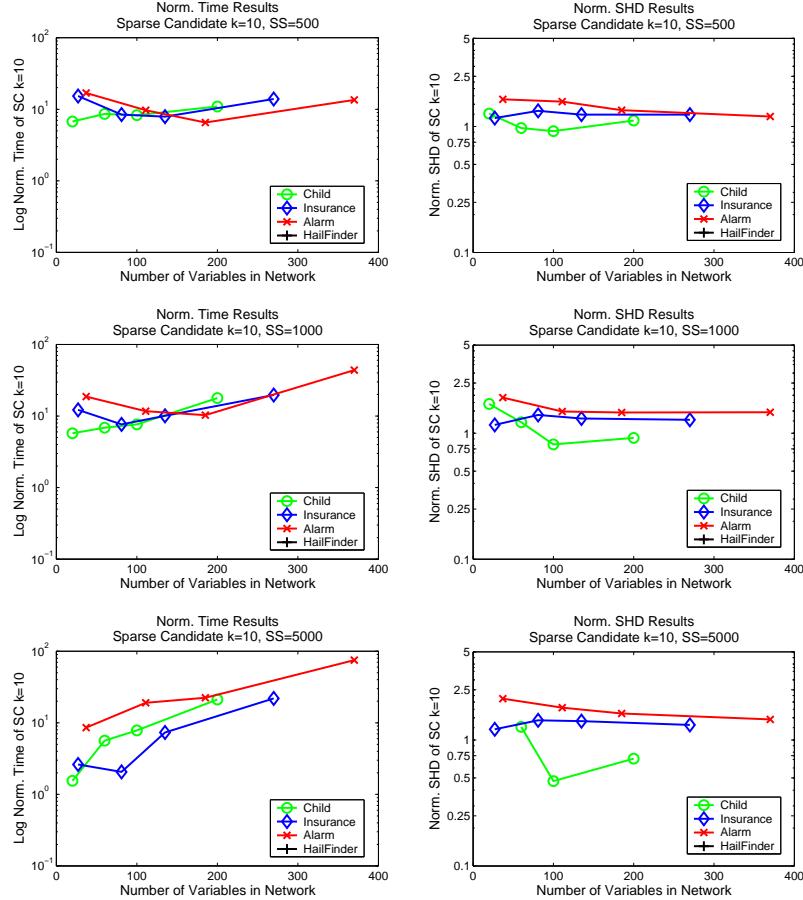


Figure 35. Normalized Time and Normalized SHD vs. number of variables in the network for the Sparse Candidate algorithm with $k = 10$ on the CHILD, INSURANCE, ALARM, HAILFINDER tiled networks.

E.6. EFFECT ON OPTIMAL REINSERTION 1 & 2 $k=5$ OF INCREASING THE NUMBER OF VARIABLES.

Recall that the timing results for Optimal Reinsertion are based upon that of *MMHC* therefore we have excluded the plots of the Normalized Time here for Optimal Reinsertion.

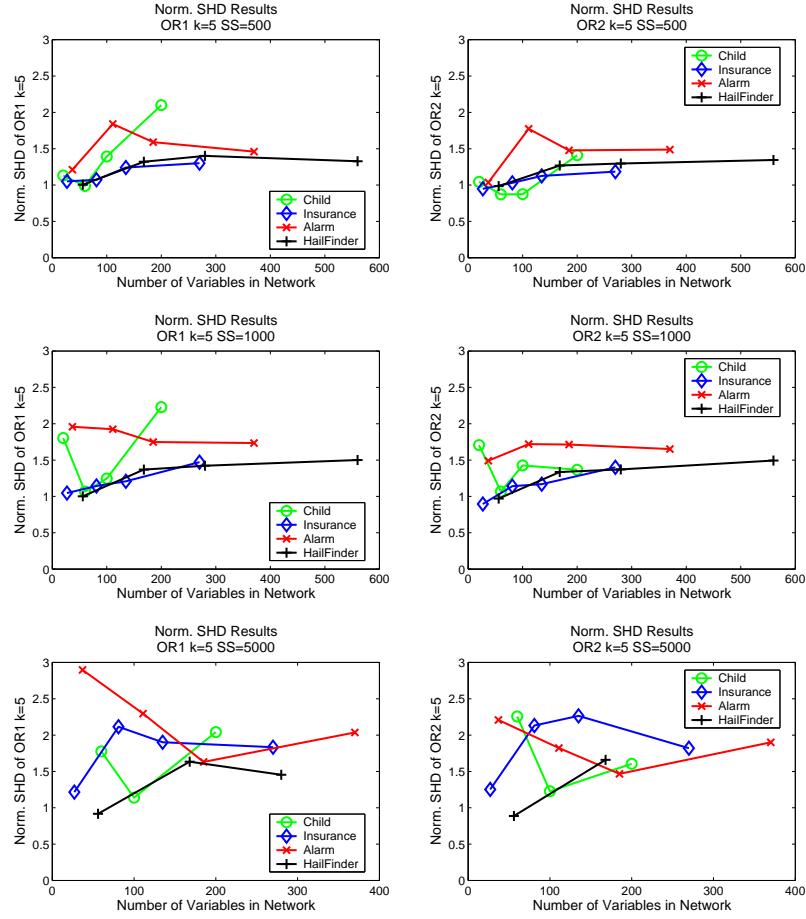


Figure 36. Normalized SHD vs. number of variables in the network for the Optimal Reinsertion 1 & 2 algorithm with $k = 5$ on the CHILD, INSURANCE, ALARM, HAILFINDER tiled networks.

E.7. EFFECT ON OPTIMAL REINSERTION 1 & 2 $k=10$ OF
INCREASING THE NUMBER OF VARIABLES.

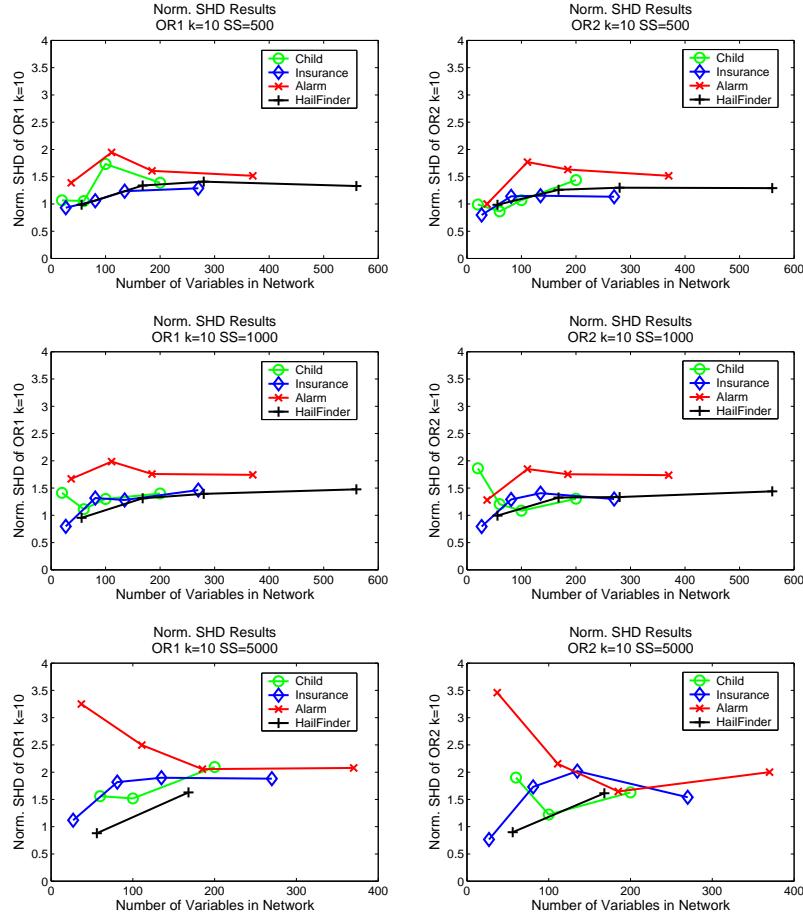


Figure 37. Normalized SHD vs. number of variables in the network for the Optimal Reinsertion 1 & 2 algorithm with $k = 10$ on the CHILD, INSURANCE, ALARM, HAILFINDER tiled networks.

E.8. EFFECT ON OPTIMAL REINSERTION 1 & 2 $k=20$ OF
INCREASING THE NUMBER OF VARIABLES.

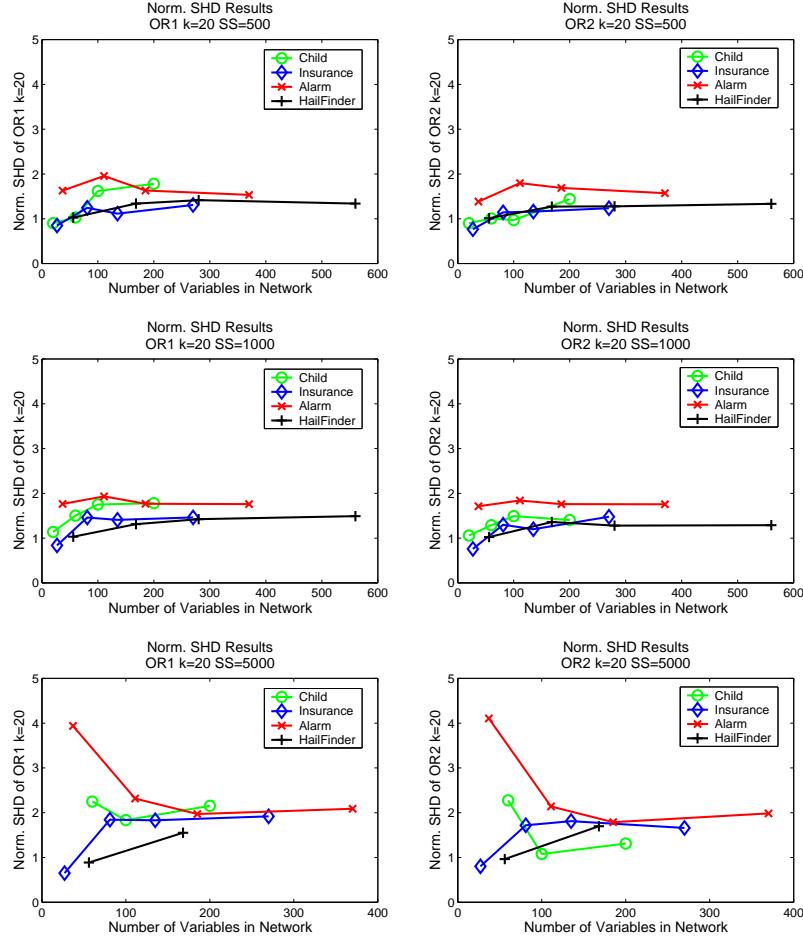


Figure 38. Normalized SHD vs. number of variables in the network for the Optimal Reinsertion 1 & 2 algorithm with $k = 20$ on the CHILD, INSURANCE, ALARM, HAILFINDER tiled networks.