

Table 1: Comparison studies under Scenario 4 and Scenario 5 (new) under different sample sizes (n) and dimensions (p) with the Erdős-Reýi (ER) model. Methods are evaluated by FDR, TPR, SHD, and runtime (seconds), with standard errors (SE) reported for each metric, over 50 replications.

Scenario	Method	FDR±SE		TPR±SE		SHD±SE		Time±SE	
		n_1 (small)	n_2 (large)	n_1 (small)	n_2 (large)	n_1 (small)	n_2 (large)	n_1 (small)	n_2 (large)
S4	NSCSL-TE	0.11±0.02	0.00±0.01	1.00±0.00	1.00±0.00	0.86±0.24	0.04±0.01	10.8±0.3	56.2±1.1
$p = 20$	NSCSL-DE	0.11±0.02	0.00±0.01	0.69±0.01	0.67±0.00	1.34±0.08	1.00±0.01	12.4±0.8	54.5±1.3
$n_1 = 100$	NOTEARS	0.93±0.00	0.92±0.00	1.00±0.00	1.00±0.00	40.80±0.20	36.40±0.04	22.9±6.4	69.8±8.7
$n_2 = 1000$	PC	0.92±0.00	0.95±0.00	0.51±0.02	0.67±0.00	19.08±0.17	33.34±0.03	6.9±0.5	16.3±0.8
ER Model	ICA	0.92±0.00	0.93±0.00	0.99±0.01	1.00±0.00	33.00±0.20	37.10±0.02	8.1±0.5	24.6±0.6
Degree=5	DAGGNN	0.93±0.00	0.93±0.00	0.97±0.01	0.97±0.00	41.34±0.19	40.10±0.06	28.3 ² ±4.3	39.1 ² ±7.2
	GSGES	0.98±0.01	0.98±0.00	0.22±0.02	0.20±0.01	43.20±0.26	45.70±0.34	14.9 ² ±7.5	26.3 ² ±9.1
	FCI	0.98±0.01	0.99±0.00	0.10±0.02	0.06±0.01	22.70±0.17	32.90±0.02	6.6±0.3	12.7±0.2
	CAM	0.93±0.00	0.94±0.00	0.63±0.02	1.00±0.00	29.80±0.38	40.30±0.07	19.6 ² ±18.3	25.6 ² ±23.2
S5	NSCSL-TE	0.03±0.01	0.02±0.01	0.86±0.03	0.93±0.01	2.18±0.13	1.58±0.07	110.1±3.9	21.1 ² ±12.1
$p = 50$	NSCSL-DE	0.02±0.02	0.01±0.01	0.29±0.02	0.28±0.01	10.08±0.21	9.76±0.13	119.0±5.5	23.5 ² ±10.9
$n_1 = 1000$	NOTEARS	0.86±0.04	0.85±0.01	0.93±0.03	0.92±0.01	79.20±1.40	77.12±0.53	128.3±8.2	26.9 ² ±15.1
$n_2 = 3000$	PC	0.96±0.03	0.97±0.02	0.07±0.02	0.06±0.01	82.12±1.21	88.28±1.63	20.9±0.5	35.9±3.2
ER Model	ICA	0.86±0.02	0.86±0.01	0.97±0.02	0.99±0.01	86.12±1.20	85.70±0.84	43.1±6.3	145.3±7.9
Degree=5	DAGGNN	0.87±0.02	0.88±0.01	0.93±0.02	0.94±0.01	87.50±1.10	85.62±0.96	49.3 ² ±7.5	81.1 ² ±87.6
	GSGES	0.89±0.03	0.93±0.01	0.19±0.03	0.12±0.01	93.54±1.46	95.70±0.79	31.2 ² ±10.1	45.3 ² ±18.1
	FCI	0.96±0.02	0.97±0.01	0.08±0.01	0.07±0.01	84.00±0.80	88.50±0.60	14.3±0.8	17.7±0.5
	CAM	0.93±0.04	0.95±0.02	0.66±0.03	0.67±0.02	126.00±3.64	127.80±2.06	28.4 ² ±31.7	75.6 ² ±63.9

Table 2: Comparison studies under the nonlinear structural equation model with Scenario 4 and $\mathbf{D} = \{g(\mathbf{Z}), Y\}$ follows $D_i := \psi_i\{\text{PA}_{D_i}(\mathcal{G})\} + e_{D_i}$ and $\psi_i(x) = \lfloor 2\log(x+1) \rfloor$ where $\lfloor x \rfloor$ rounds to nearest integer for x , over 50 replications.

Scenario	Method	FDR±SE	TPR±SE	SHD±SE	Time±SE
S4	NSCSL-TE	0.03±0.01	0.83±0.01	0.60±0.02	55.8±0.3
$p = 20$	NSCSL-DE	0.03±0.01	0.50±0.01	1.60±0.02	56.8±0.2
$n = 1000$	NOTEARS	0.91±0.01	0.83±0.01	35.90±0.04	56.5±0.7
ER Model	PC	0.99±0.01	0.12±0.01	44.12±0.03	15.7±0.2
Degree=5	ICA	0.93±0.01	0.70±0.00	37.30±0.03	11.6±0.1
	DAGGNN	0.94±0.01	0.86±0.01	34.80±0.06	41.3 ² ±9.8
	GSGES	0.98±0.01	0.23±0.01	52.40±0.38	22.1 ² ±7.5
	FCI	0.97±0.01	0.13±0.01	33.80±0.06	12.6±0.3
	CAM	0.95±0.01	1.00±0.01	31.60±0.08	27.9 ² ±33.7

Table 3: Comparison studies under the scale-free (SF) model using Scenario 5. Methods are evaluated by FDR, TPR, SHD, and runtime, over 50 replications.

Scenario	Method	FDR±SE	TPR±SE	SHD±SE	Time±SE
S5	NSCSL-TE	0.02±0.02	0.78±0.03	5.08±0.11	135.7±5.6
$p = 50$	NSCSL-DE	0.02±0.02	0.51±0.02	17.20±0.35	147.0±6.3
$n = 1000$	NOTEARS	0.88±0.04	0.75±0.03	123.10±1.50	160.5±8.1
SF Model	PC	0.97±0.03	0.06±0.02	79.34±1.17	32.1±0.8
Degree=5	ICA	0.91±0.02	0.98±0.01	212.00±5.12	117.7±6.3
	DAGGNN	0.92±0.02	0.85±0.02	203.50±7.80	57.3 ² ±13.6
	GSGES	0.96±0.03	0.10±0.03	98.34±2.15	35.9 ² ±13.5
	FCI	0.97±0.02	0.07±0.01	81.70±1.40	15.7±1.1
	CAM	0.98±0.04	0.24±0.03	218.00±8.15	37.1 ² ±53.6

Table 4: Real data results for the single-cell data by Sachs et al. (2005) under the proposed NSCSL with TE and 7 baseline methods, evaluated by total edges, correct edges, and SHD, based on the true NSCG with respect to the protein Akt.

Method	NSCSL	NOTEARS	PC	ICA	DAGGNN	GSGES	FCI	CAM
Total Edges	8	20	25	6	33	28	24	7
Correct Edges	4	2	2	1	4	2	2	1
SHD	8	21	28	11	30	32	27	10

Table 5: Real data results for the yeast gene data under the proposed NSCSL with TE and 7 baseline methods, evaluated by total edges, the identified parents/ancestors of the variant YER124C, and the edges towards YER124C.

Method	NSCSL-TE	NOTEARS	PC	ICA	DAGGNN	GSGES	FCI	CAM
Total Edges	11	25	22	15	35	27	22	33
# Parents/Ancestors of YER124C	8	8	6	4	8	7	5	7
# Edges towards YER124C	11	9	8	6	10	9	8	10

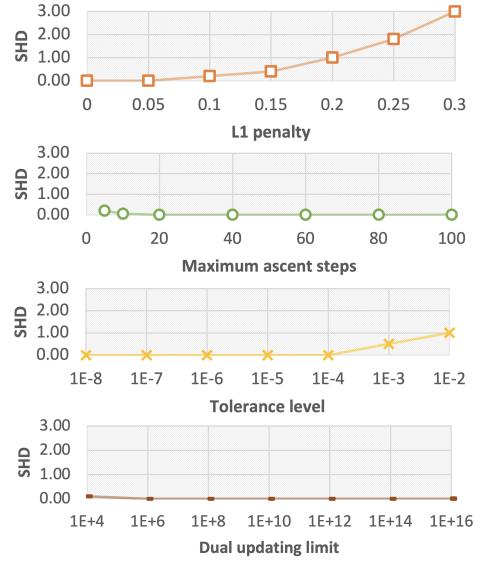


Figure 1: Sensitivity analyses.

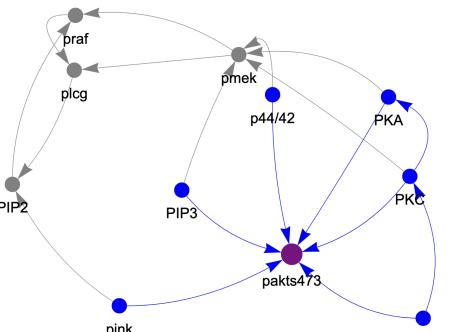


Figure 2: The Sachs causal signaling network, where the blue-colored sub-graph is the true NSCG for protein Akt (purple).