

# Supplementary Material for Chapter 5: comparison with unbounded methods



Table 1: Comparison of the methods in dataset emotions in 5-fold cross-validation. For each fold and method, the conditional log-likelihood in the test dataset (CLL), the global accuracy (acc\_ $G$ ), the mean accuracy (acc\_ $M$ ), the learning time (time), the treewidth (tw) and the treewidth of the pruned graph (tw-pr) are shown. The optimal results are denoted in boldface.

Fold	Method	CLL	acc_ $G$	acc_ $M$	time	tw	tw-pr
1	GS-pruned	-342.02	0.28	0.78	0.68	3	3
1	Tree-tree	-412.81	<b>0.294</b>	<b>0.797</b>	10.55	5	3
1	Tree-tw	-697.56	<b>0.294</b>	0.77	<b>0.4</b>	3	3
1	GS	<b>-339.4</b>	0.29	0.78	0.6	3	3
1	GS-tw	-342.02	0.28	0.78	1.16	3	3
1	CDL2	–	0.18	0.67	51.47	–	–
1	SVM-struct	–	0.24	0.74	769.25	–	–
2	GS-pruned	<b>-322.5</b>	0.2	0.76	0.68	4	3
2	Tree-tree	-357.84	<b>0.345</b>	<b>0.803</b>	9.55	5	3
2	Tree-tw	-596.03	0.22	0.77	<b>0.4</b>	3	3
2	GS	<b>-322.5</b>	0.2	0.76	0.63	4	3
2	GS-tw	<b>-322.5</b>	0.2	0.76	1.36	4	3
2	CDL2	–	0.2	0.7	0.97	–	–
2	SVM-struct	–	0.24	0.74	575.85	–	–
3	GS-pruned	<b>-290.5</b>	0.29	0.79	0.63	4	3
3	Tree-tree	-341.76	<b>0.353</b>	<b>0.811</b>	8.61	5	3
3	Tree-tw	-526.95	0.34	0.8	<b>0.3</b>	3	3
3	GS	<b>-290.5</b>	0.29	0.79	0.59	4	3
3	GS-tw	<b>-290.5</b>	0.29	0.79	1.28	4	3
3	CDL2	–	0.24	0.71	0.91	–	–
3	SVM-struct	–	0.24	0.75	553.81	–	–
4	GS-pruned	<b>-344</b>	<b>0.297</b>	0.79	0.62	4	3
4	Tree-tree	-403.97	0.24	<b>0.792</b>	9.81	5	3
4	Tree-tw	-598	0.26	0.78	<b>0.4</b>	3	3
4	GS	<b>-344</b>	<b>0.297</b>	0.79	0.59	4	3
4	GS-tw	<b>-344</b>	<b>0.297</b>	0.79	0.97	4	3
4	CDL2	–	0.19	0.69	0.9	–	–
4	SVM-struct	–	0.18	0.73	567.53	–	–
5	GS-pruned	<b>-340.6</b>	<b>0.322</b>	<b>0.799</b>	0.76	4	2
5	Tree-tree	-409.62	0.26	0.78	9.21	5	3
5	Tree-tw	-708.13	0.21	0.78	<b>0.4</b>	3	3
5	GS	<b>-340.6</b>	<b>0.322</b>	<b>0.799</b>	0.67	4	2
5	GS-tw	<b>-340.6</b>	<b>0.322</b>	<b>0.799</b>	1.06	4	2
5	CDL2	–	0.19	0.73	0.89	–	–
5	SVM-struct	–	0.18	0.73	703	–	–

Table 2: Comparison of the methods in dataset foodtruck in 5-fold cross-validation. For each fold and method, the conditional log-likelihood in the test dataset (CLL), the global accuracy (acc\_ $G$ ), the mean accuracy (acc\_ $M$ ), the learning time (time), the treewidth (tw) and the treewidth of the pruned graph (tw-pr) are shown. The optimal results are denoted in boldface.

Fold	Method	CLL	acc_ $G$	acc_ $M$	time	tw	tw-pr
1	GS-pruned	-341.1	0.29	0.85	0.05	2	2
1	Tree-tree	-340.91	0.3	0.85	0.53	3	1
1	Tree-tw	<b>-338.6</b>	<b>0.317</b>	0.84	0.11	1	1
1	GS	-341.1	0.29	0.85	<b>0</b>	2	2
1	GS-tw	-341.1	0.29	0.85	0.05	2	2
1	CDL2	–	0.11	0.79	0.6	–	–
1	SVM-struct	–	0.2	<b>0.853</b>	505.33	–	–
2	GS-pruned	-366.04	0.24	0.84	0.06	2	2
2	Tree-tree	<b>-366</b>	0.23	0.84	0.4	3	1
2	Tree-tw	-368.19	0.22	0.84	0.1	1	1
2	GS	-366.04	0.24	0.84	<b>0</b>	2	2
2	GS-tw	-366.04	0.24	0.84	0.07	2	2
2	CDL2	–	0.13	0.79	0.6	–	–
2	SVM-struct	–	<b>0.256</b>	<b>0.855</b>	417.96	–	–
3	GS-pruned	-361.89	0.19	0.84	0.09	2	2
3	Tree-tree	-362.01	0.25	0.84	0.41	3	1
3	Tree-tw	<b>-357.9</b>	0.19	0.84	0.12	1	1
3	GS	-361.89	0.19	0.84	0.05	2	2
3	GS-tw	-361.89	0.19	0.84	<b>0</b>	2	2
3	CDL2	–	0.07	0.78	0.61	–	–
3	SVM-struct	–	<b>0.296</b>	<b>0.856</b>	365.62	–	–
4	GS-pruned	<b>-367.5</b>	0.25	0.85	0.06	2	2
4	Tree-tree	-368.37	<b>0.259</b>	0.85	0.4	3	1
4	Tree-tw	-370.26	0.21	0.84	0.1	1	1
4	GS	<b>-367.5</b>	0.25	0.85	0.06	2	2
4	GS-tw	<b>-367.5</b>	0.25	0.85	<b>0.1</b>	2	2
4	CDL2	–	0.1	0.8	0.6	–	–
4	SVM-struct	–	0.21	<b>0.85</b>	473.76	–	–
5	GS-pruned	-405.79	0.21	0.82	0.07	2	2
5	Tree-tree	-407.36	<b>0.247</b>	0.82	0.49	2	1
5	Tree-tw	<b>-403.6</b>	0.21	0.82	0.11	1	1
5	GS	-405.79	0.21	0.82	<b>0</b>	2	2
5	GS-tw	-405.79	0.21	0.82	0.09	2	2
5	CDL2	–	0.09	0.78	0.6	–	–
5	SVM-struct	–	0.19	<b>0.821</b>	407.19	–	–

Table 3: Comparison of the methods in dataset birds in 5-fold cross-validation. For each fold and method, the conditional log-likelihood in the test dataset (CLL), the global accuracy (acc\_ $G$ ), the mean accuracy (acc\_ $M$ ), the learning time (time), the treewidth (tw) and the treewidth of the pruned graph (tw-pr) are shown. The optimal results are denoted in boldface.

Fold	Method	CLL	acc_ $G$	acc_ $M$	time	tw	tw-pr
1	GS-pruned	<b>-480.5</b>	<b>0.411</b>	0.94	4.52	3	3
1	Tree-tree	-653.2	0.4	<b>0.94</b>	89.41	6	3
1	Tree-tw	-2183.83	0.34	0.91	<b>2.3</b>	3	3
1	GS	<b>-480.5</b>	<b>0.411</b>	0.94	4.06	3	2
1	GS-tw	<b>-480.5</b>	<b>0.411</b>	0.94	5.56	3	2
1	CDL2	–	0.25	0.89	2.45	–	–
1	SVM-struct	–	0.27	0.9	917.6	–	–
2	GS-pruned	<b>-446.9</b>	0.45	0.95	4.61	3	3
2	Tree-tree	-568.3	<b>0.465</b>	<b>0.95</b>	89.79	5	2
2	Tree-tw	-2424.34	0.31	0.93	<b>2.4</b>	3	2
2	GS	<b>-446.9</b>	0.45	0.95	4.12	3	2
2	GS-tw	<b>-446.9</b>	0.45	0.95	5.75	4	2
2	CDL2	–	0.29	0.91	2.45	–	–
2	SVM-struct	–	0.35	0.92	922.17	–	–
3	GS-pruned	<b>-443.3</b>	0.45	<b>0.945</b>	4.52	3	2
3	Tree-tree	-589.25	<b>0.457</b>	0.94	98.93	7	3
3	Tree-tw	-2250.48	0.31	0.91	2.47	3	3
3	GS	<b>-443.3</b>	0.45	<b>0.945</b>	4.05	3	2
3	GS-tw	<b>-443.3</b>	0.45	<b>0.945</b>	5.63	4	2
3	CDL2	–	0.28	0.89	<b>2.4</b>	–	–
3	SVM-struct	–	0.38	0.91	907.02	–	–
4	GS-pruned	<b>-393.5</b>	0.52	0.96	4.47	4	2
4	Tree-tree	-512.66	<b>0.543</b>	<b>0.958</b>	93.33	6	3
4	Tree-tw	-2323.69	0.4	0.93	<b>2.4</b>	3	3
4	GS	<b>-393.5</b>	0.52	0.96	4.11	4	2
4	GS-tw	<b>-393.5</b>	0.52	0.96	5.64	4	2
4	CDL2	–	0.34	0.9	2.45	–	–
4	SVM-struct	–	0.37	0.93	765.05	–	–
5	GS-pruned	<b>-399.4</b>	0.52	0.95	4.41	4	2
5	Tree-tree	-498.38	<b>0.527</b>	<b>0.954</b>	96.04	5	2
5	Tree-tw	-1819.08	0.4	0.93	<b>2.4</b>	3	2
5	GS	<b>-399.4</b>	0.52	0.95	4.12	4	2
5	GS-tw	<b>-399.4</b>	0.52	0.95	5.71	4	2
5	CDL2	–	0.36	0.92	2.49	–	–
5	SVM-struct	–	0.36	0.92	982.48	–	–

Table 4: Comparison of the methods in dataset scene in 5-fold cross-validation. For each fold and method, the conditional log-likelihood in the test dataset (CLL), the global accuracy (acc\_ $G$ ), the mean accuracy (acc\_ $M$ ), the learning time (time), the treewidth (tw) and the treewidth of the pruned graph (tw-pr) are shown. The optimal results are denoted in boldface.

Fold	Method	CLL	acc_ $G$	acc_ $M$	time	tw	tw-pr
1	GS-pruned	<b>-588.9</b>	0.61	0.88	11.2	9	5
1	Tree-tree	-974.69	0.45	<b>0.886</b>	295.38	6	3
1	Tree-tw	-3233.11	0.43	0.86	5.49	3	3
1	GS	-645.27	0.59	0.87	9.62	9	5
1	GS-tw	-596.97	<b>0.616</b>	0.88	12.94	5	5
1	CDL2	–	0.3	0.77	<b>5.3</b>	–	–
1	SVM-struct	–	0.51	0.87	3535.07	–	–
2	GS-pruned	<b>-656.6</b>	0.57	0.87	10.82	9	5
2	Tree-tree	-960.74	0.44	0.87	274.32	6	3
2	Tree-tw	-2768.98	0.41	0.84	<b>5.6</b>	3	3
2	GS	-667.91	<b>0.587</b>	<b>0.871</b>	10.13	10	5
2	GS-tw	-656.63	0.57	0.87	14.84	5	5
2	CDL2	–	0.29	0.77	5.74	–	–
2	SVM-struct	–	0.49	0.87	5159.37	–	–
3	GS-pruned	-668.67	0.55	0.87	11.21	9	5
3	Tree-tree	-952.27	0.46	<b>0.887</b>	261.49	5	3
3	Tree-tw	-2937.92	0.37	0.85	6.06	3	3
3	GS	<b>-659.9</b>	<b>0.576</b>	0.88	14.38	9	5
3	GS-tw	-672.1	0.55	0.87	13.23	5	5
3	CDL2	–	0.28	0.77	<b>6</b>	–	–
3	SVM-struct	–	0.47	0.87	3640.36	–	–
4	GS-pruned	-612	0.59	0.88	10.63	8	5
4	Tree-tree	-1029.26	0.47	0.88	268.06	5	3
4	Tree-tw	-3398.61	0.42	0.85	<b>5.3</b>	3	3
4	GS	<b>-596.5</b>	<b>0.617</b>	<b>0.883</b>	9.32	7	5
4	GS-tw	-612	0.59	0.88	14.19	5	5
4	CDL2	–	0.33	0.78	5.66	–	–
4	SVM-struct	–	0.55	0.88	4809.72	–	–
5	GS-pruned	<b>-601.2</b>	0.56	0.87	10.74	10	5
5	Tree-tree	-929.8	0.44	<b>0.881</b>	291.35	6	3
5	Tree-tw	-2833.7	0.42	0.86	<b>5.8</b>	3	3
5	GS	-613.24	<b>0.576</b>	0.87	9.12	9	5
5	GS-tw	-601.83	0.57	0.87	15.61	5	5
5	CDL2	–	0.33	0.79	6.1	–	–
5	SVM-struct	–	0.52	0.88	4454.02	–	–

Table 5: Comparison of the methods in dataset genbase in 5-fold cross-validation. For each fold and method, the conditional log-likelihood in the test dataset (CLL), the global accuracy (acc\_ $G$ ), the mean accuracy (acc\_ $M$ ), the learning time (time), the treewidth (tw) and the treewidth of the pruned graph (tw-pr) are shown. The optimal results are denoted in boldface.

Fold	Method	CLL	acc_ $G$	acc_ $M$	time	tw	tw-pr
1	GS-pruned	-19.86	<b>0.985</b>	1	1.98	4	4
1	Tree-tree	-15.34	<b>0.985</b>	1	15.92	12	3
1	Tree-tw	<b>-14.9</b>	<b>0.985</b>	1	<b>1.4</b>	3	3
1	GS	-19.86	<b>0.985</b>	1	1.5	4	4
1	GS-tw	-19.86	<b>0.985</b>	1	1.77	4	4
1	CDL2	–	0.95	1	1.89	–	–
1	SVM-struct	–	<b>0.985</b>	<b>0.999</b>	176.2	–	–
2	GS-pruned	<b>-23.3</b>	<b>0.97</b>	<b>0.999</b>	1.8	4	3
2	Tree-tree	-29.58	0.96	1	15.09	11	2
2	Tree-tw	-24.48	0.96	1	<b>1.4</b>	3	2
2	GS	<b>-23.3</b>	<b>0.97</b>	<b>0.999</b>	1.57	4	3
2	GS-tw	<b>-23.3</b>	<b>0.97</b>	<b>0.999</b>	1.93	4	3
2	CDL2	–	0.95	1	1.71	–	–
2	SVM-struct	–	<b>0.97</b>	1	125.24	–	–
3	GS-pruned	<b>-49.2</b>	<b>0.955</b>	<b>0.998</b>	2.13	5	3
3	Tree-tree	-55.09	<b>0.955</b>	1	12.31	8	3
3	Tree-tw	-50.72	<b>0.955</b>	<b>0.998</b>	<b>1.4</b>	3	3
3	GS	<b>-49.2</b>	<b>0.955</b>	<b>0.998</b>	1.62	5	3
3	GS-tw	<b>-49.2</b>	<b>0.955</b>	<b>0.998</b>	2.04	5	3
3	CDL2	–	0.92	1	1.65	–	–
3	SVM-struct	–	0.95	1	226.38	–	–
4	GS-pruned	<b>-19.1</b>	<b>0.962</b>	<b>0.999</b>	1.99	5	4
4	Tree-tree	-24.76	0.95	1	11	10	3
4	Tree-tw	-20.43	0.95	1	<b>1.4</b>	3	3
4	GS	<b>-19.1</b>	<b>0.962</b>	<b>0.999</b>	1.4	5	4
4	GS-tw	<b>-19.1</b>	<b>0.962</b>	<b>0.999</b>	1.85	5	4
4	CDL2	–	0.9	1	1.72	–	–
4	SVM-struct	–	<b>0.962</b>	<b>0.999</b>	171.99	–	–
5	GS-pruned	<b>-12.1</b>	0.98	<b>1</b>	1.96	4	3
5	Tree-tree	-19.39	0.98	1	12.91	10	3
5	Tree-tw	-12.15	<b>0.992</b>	<b>1</b>	1.5	3	3
5	GS	<b>-12.1</b>	0.98	<b>1</b>	<b>1.4</b>	4	3
5	GS-tw	<b>-12.1</b>	0.98	<b>1</b>	1.88	4	3
5	CDL2	–	0.96	1	1.78	–	–
5	SVM-struct	–	0.98	1	209.97	–	–

Table 6: Comparison of the methods in dataset yeast in 5-fold cross-validation. For each fold and method, the conditional log-likelihood in the test dataset (CLL), the global accuracy (acc\_ $G$ ), the mean accuracy (acc\_ $M$ ), the learning time (time), the treewidth (tw) and the treewidth of the pruned graph (tw-pr) are shown. The optimal results are denoted in boldface.

Fold	Method	CLL	acc_ $G$	acc_ $M$	time	tw	tw-pr
1	GS-pruned	<b>-1998.8</b>	0.18	<b>0.772</b>	2.64	6	5
1	Tree-tree	-2654.28	0.15	0.77	34.63	8	4
1	Tree-tw	-3351.42	0.13	0.76	<b>1.2</b>	4	4
1	GS	-2016.63	0.17	0.77	2.04	6	6
1	GS-tw	-2013.88	<b>0.184</b>	0.77	2.93	5	5
1	CDL2	–	0.03	0.64	6.68	–	–
1	SVM-struct	–	0.1	0.77	1543.07	–	–
2	GS-pruned	-2004.35	<b>0.178</b>	0.78	2.4	5	5
2	Tree-tree	-2581.22	0.18	<b>0.788</b>	32.41	7	3
2	Tree-tw	-3313.69	0.12	0.77	<b>1.1</b>	3	3
2	GS	<b>-1989.1</b>	<b>0.178</b>	0.78	1.9	5	5
2	GS-tw	-2006.09	0.17	0.78	3.62	5	5
2	CDL2	–	0.01	0.64	22.75	–	–
2	SVM-struct	–	0.13	0.78	1561.43	–	–
3	GS-pruned	-2025.88	<b>0.182</b>	0.79	2.53	7	5
3	Tree-tree	-2771.64	0.16	<b>0.786</b>	32.59	8	4
3	Tree-tw	-3506.54	0.12	0.77	<b>1.2</b>	4	4
3	GS	<b>-2020.4</b>	0.18	0.78	2	7	6
3	GS-tw	-2031.66	0.17	0.79	3.88	5	5
3	CDL2	–	0.02	0.63	49.42	–	–
3	SVM-struct	–	0.12	0.78	1461.21	–	–
4	GS-pruned	-2011.83	<b>0.159</b>	0.77	2.38	6	5
4	Tree-tree	-2629.21	0.15	<b>0.782</b>	35	8	4
4	Tree-tw	-3265.65	0.13	0.76	<b>1.2</b>	4	4
4	GS	<b>-2001.6</b>	0.15	0.78	2.15	6	5
4	GS-tw	-2003.42	0.15	0.78	2.87	5	4
4	CDL2	–	0.02	0.63	609.58	–	–
4	SVM-struct	–	0.1	0.78	1535.1	–	–
5	GS-pruned	-1931.96	<b>0.209</b>	0.79	3.09	6	5
5	Tree-tree	-2576.03	0.18	<b>0.794</b>	33.46	8	4
5	Tree-tw	-3113.29	0.14	0.77	<b>1.1</b>	4	4
5	GS	<b>-1918.9</b>	0.2	0.79	2.43	6	6
5	GS-tw	-1947.22	0.2	0.79	3.73	5	5
5	CDL2	–	0.01	0.64	7.51	–	–
5	SVM-struct	–	0.13	0.79	1697.14	–	–

Table 7: Comparison of the methods in dataset medical in 5-fold cross-validation. For each fold and method, the conditional log-likelihood in the test dataset (CLL), the global accuracy (acc\_ $G$ ), the mean accuracy (acc\_ $M$ ), the learning time (time), the treewidth (tw) and the treewidth of the pruned graph (tw-pr) are shown. The optimal results are denoted in boldface.

Fold	Method	CLL	acc_ $G$	acc_ $M$	time	tw	tw-pr
1	GS-pruned	<b>-296.8</b>	<b>0.658</b>	<b>0.989</b>	5.95	11	3
1	Tree-tree	-298.14	0.6	0.99	201.94	19	3
1	Tree-tw	-436.09	0.6	0.99	<b>4.6</b>	3	3
1	GS	<b>-296.8</b>	<b>0.658</b>	<b>0.989</b>	5.5	11	3
1	GS-tw	-307.01	0.62	0.99	6.59	5	3
1	CDL2	–	0.45	0.97	6.6	–	–
1	SVM-struct	–	0.64	0.99	340.23	–	–
2	GS-pruned	-333.13	0.63	0.99	8.17	12	4
2	Tree-tree	<b>-305.6</b>	<b>0.689</b>	<b>0.99</b>	188.58	18	3
2	Tree-tw	-462.7	0.58	0.98	<b>5.4</b>	3	3
2	GS	-333.13	0.63	0.99	5.39	12	4
2	GS-tw	-324.62	0.64	0.99	10.23	5	4
2	CDL2	–	0.44	0.98	7.01	–	–
2	SVM-struct	–	0.63	0.99	222.1	–	–
3	GS-pruned	-266.28	<b>0.714</b>	<b>0.992</b>	5.69	9	3
3	Tree-tree	<b>-259.2</b>	0.67	0.99	214.86	18	3
3	Tree-tw	-356.51	0.58	0.99	<b>4.6</b>	3	3
3	GS	-266.28	<b>0.714</b>	<b>0.992</b>	5.43	9	3
3	GS-tw	-267.69	0.7	0.99	6.88	5	3
3	CDL2	–	0.48	0.98	6.81	–	–
3	SVM-struct	–	0.69	0.99	282.68	–	–
4	GS-pruned	-345.34	<b>0.626</b>	0.99	5.91	12	3
4	Tree-tree	<b>-315.8</b>	0.58	0.99	193.59	17	4
4	Tree-tw	-413.3	0.59	0.99	<b>4.7</b>	4	4
4	GS	-345.34	<b>0.626</b>	0.99	8.8	12	3
4	GS-tw	-353.99	0.62	0.99	6.54	5	3
4	CDL2	–	0.47	0.98	6.84	–	–
4	SVM-struct	–	0.59	<b>0.988</b>	237.36	–	–
5	GS-pruned	-286.08	<b>0.672</b>	0.99	6.32	10	3
5	Tree-tree	-294.75	<b>0.672</b>	<b>0.99</b>	187.73	18	3
5	Tree-tw	-380.58	0.61	0.99	<b>4.5</b>	3	3
5	GS	-286.08	<b>0.672</b>	0.99	6.1	10	3
5	GS-tw	<b>-272.2</b>	0.67	0.99	6.27	5	3
5	CDL2	–	0.44	0.97	6.61	–	–
5	SVM-struct	–	0.65	0.99	225.1	–	–



Table 8: Comparison of the methods in dataset enron in 5-fold cross-validation. For each fold and method, the conditional log-likelihood in the test dataset (CLL), the global accuracy (acc\_ $G$ ), the mean accuracy (acc\_ $M$ ), the learning time (time), the treewidth (tw) and the treewidth of the pruned graph (tw-pr) are shown. The optimal results are denoted in boldface.

Fold	Method	CLL	acc_ $G$	acc_ $M$	time	tw	tw-pr
1	GS-pruned	<b>-2350.3</b>	<b>0.191</b>	<b>0.95</b>	18.18	62	5
1	Tree-tree	-2794.99	0.17	0.95	255.43	8	4
1	Tree-tw	-3314.49	0.15	0.95	<b>11</b>	4	4
1	GS	<b>-2350.3</b>	<b>0.191</b>	<b>0.95</b>	24.95	62	4
1	GS-tw	-2441.65	0.18	0.95	24.94	5	4
1	CDL2	–	0.01	0.89	62.51	–	–
1	SVM-struct	–	0.13	0.94	10556.4	–	–
2	GS-pruned	<b>-2540.6</b>	<b>0.117</b>	0.95	17.31	56	4
2	Tree-tree	-3046.92	0.1	0.95	255	7	4
2	Tree-tw	-4239.91	0.1	0.94	<b>13.9</b>	4	4
2	GS	-2543.5	<b>0.117</b>	0.95	25.8	60	4
2	GS-tw	-2663.5	0.11	<b>0.946</b>	19.34	5	4
2	CDL2	–	0.01	0.89	57.89	–	–
2	SVM-struct	–	0.09	0.94	14445.1	–	–
3	GS-pruned	<b>-2721.9</b>	<b>0.141</b>	<b>0.944</b>	18.34	58	5
3	Tree-tree	-3498.1	<b>0.141</b>	0.94	253.35	7	4
3	Tree-tw	-5802.86	<b>0.141</b>	0.94	<b>11.8</b>	4	4
3	GS	-2733.72	<b>0.141</b>	0.94	38.56	48	5
3	GS-tw	-3029.32	0.14	0.94	28.78	5	5
3	CDL2	–	0.01	0.89	52.37	–	–
3	SVM-struct	–	0.1	0.94	8694.95	–	–
4	GS-pruned	<b>-2469.9</b>	<b>0.156</b>	<b>0.947</b>	18.53	54	5
4	Tree-tree	-2891.81	0.13	0.95	254.53	7	4
4	Tree-tw	-3381.6	0.13	0.94	<b>12.6</b>	4	4
4	GS	-2476.57	<b>0.156</b>	0.95	26.17	58	4
4	GS-tw	-2603.69	0.15	0.95	19.47	5	5
4	CDL2	–	0	0.9	44.25	–	–
4	SVM-struct	–	0.09	0.94	7641.37	–	–
5	GS-pruned	<b>-2629.4</b>	<b>0.126</b>	<b>0.948</b>	18.28	67	4
5	Tree-tree	-3252.28	0.12	0.95	253.74	8	4
5	Tree-tw	-5202.88	0.12	0.94	<b>10.4</b>	4	4
5	GS	-2657.38	<b>0.126</b>	0.95	30.84	59	4
5	GS-tw	-2923.77	0.12	0.95	16.61	5	5
5	CDL2	–	0	0.9	87.61	–	–
5	SVM-struct	–	0.08	0.94	9373.92	–	–

Table 9: Comparison of the methods in dataset ohsumed in 5-fold cross-validation. For each fold and method, the conditional log-likelihood in the test dataset (CLL), the global accuracy (acc\_ $G$ ), the mean accuracy (acc\_ $M$ ), the learning time (time), the treewidth (tw) and the treewidth of the pruned graph (tw-pr) are shown. The optimal results are denoted in boldface.

Fold	Method	CLL	acc_ $G$	acc_ $M$	time	tw	tw-pr
1	GS-pruned	-10431.23	<b>0.25</b>	0.94	14.35	25	5
1	Tree-tree	-10721.18	0.23	0.94	701.3	18	8
1	Tree-tw	-12013.61	0.21	0.94	<b>8.9</b>	5	5
1	GS	<b>-10415.3</b>	0.25	0.94	16.28	27	8
1	GS-tw	-10684.21	0.25	0.94	14.37	5	5
1	CDL2	–	0.21	0.94	186.85	–	–
1	SVM-struct	–	0.24	<b>0.946</b>	14315.04	–	–
2	GS-pruned	-10478	<b>0.253</b>	0.95	17.01	32	5
2	Tree-tree	-10711.78	0.23	0.94	689.99	17	8
2	Tree-tw	-11963.32	0.22	0.94	<b>7.2</b>	5	5
2	GS	<b>-10445.4</b>	0.25	0.95	15.76	28	8
2	GS-tw	-10682.71	0.25	0.94	15.29	5	5
2	CDL2	–	0.22	0.94	189.33	–	–
2	SVM-struct	–	0.25	<b>0.947</b>	10083.66	–	–
3	GS-pruned	-10569.64	<b>0.256</b>	0.94	15.75	32	5
3	Tree-tree	-10851.95	0.24	0.94	690.33	17	7
3	Tree-tw	-12043.44	0.23	0.94	<b>7.6</b>	5	5
3	GS	<b>-10550.9</b>	<b>0.256</b>	0.94	15.73	29	7
3	GS-tw	-10841.38	0.24	0.94	15.65	5	5
3	CDL2	–	0.21	0.94	194.95	–	–
3	SVM-struct	–	0.24	<b>0.945</b>	10097.59	–	–
4	GS-pruned	-10680.53	0.24	0.94	13.54	31	5
4	Tree-tree	-10950.69	0.24	0.94	717.65	19	8
4	Tree-tw	-12170.59	0.21	0.94	<b>7.5</b>	5	5
4	GS	<b>-10624.9</b>	<b>0.247</b>	0.94	15.95	32	7
4	GS-tw	-10928.12	<b>0.247</b>	0.94	13.86	5	5
4	CDL2	–	0.21	0.94	195.7	–	–
4	SVM-struct	–	0.24	<b>0.944</b>	11213.44	–	–
5	GS-pruned	-10739.03	0.24	0.94	13.4	32	5
5	Tree-tree	-11093.44	0.22	0.94	673.97	17	8
5	Tree-tw	-12428.24	0.2	0.94	<b>8.8</b>	5	5
5	GS	<b>-10701.2</b>	<b>0.246</b>	<b>0.944</b>	15.74	29	8
5	GS-tw	-11067.44	0.24	0.94	12.98	5	5
5	CDL2	–	0.22	0.94	167.96	–	–
5	SVM-struct	–	0.23	0.94	16703.34	–	–