Supplementary Material for Chapter 5: comparison of bounded treewidth methods

Table 1: Comparison of the methods in dataset emotions in 5-fold cross-validation, using a treewidth bound of 2. 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	**-361.9**	0.27	**0.782**	0.65	4	2
1	tree-tw	-685.1	**0.294**	0.77	**0.4**	2	2
1	GS-tw	-449.6	0.27	0.78	0.64	2	2
2	GS-pruned	**-336.5**	0.28	0.76	0.62	3	2
2	tree-tw	-595.59	0.22	0.77	**0.3**	2	2
2	GS-tw	-389.42	**0.345**	**0.794**	0.63	2	2
3	GS-pruned	**-298.8**	0.23	0.78	0.61	3	2
3	tree-tw	-531.85	**0.345**	**0.804**	**0.4**	2	2
3	GS-tw	-355.2	0.29	0.79	0.61	2	2
4	GS-pruned	**-352.5**	**0.28**	0.76	0.65	3	2
4	tree-tw	-600.43	0.24	**0.773**	**0.4**	2	2
4	GS-tw	-429.35	0.25	**0.773**	0.62	2	2
5	GS-pruned	**-338.7**	**0.322**	**0.797**	0.93	4	2
5	tree-tw	-707.03	0.21	0.78	**0.4**	2	2
5	GS-tw	-477.82	0.28	0.78	0.63	2	2

Table 2: Comparison of the methods in dataset emotions in 5-fold cross-validation, using a treewidth bound of 3. 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	**-348.9**	0.28	**0.782**	0.62	4	3
1	tree-tw	-697.56	**0.294**	0.77	**0.4**	3	3
1	GS-tw	-357.54	0.29	**0.782**	0.75	3	3
2	GS-pruned	**-322.5**	0.2	0.76	0.64	4	3
2	tree-tw	-596.03	0.22	**0.77**	**0.5**	3	3
2	GS-tw	-326.83	**0.269**	0.75	0.75	3	3
3	GS-pruned	-292.9	0.28	0.8	0.6	4	3
3	tree-tw	-526.95	**0.345**	**0.8**	**0.4**	3	3
3	GS-tw	**-287.9**	0.3	**0.8**	0.73	3	3
4	GS-pruned	**-347.4**	**0.297**	**0.785**	0.58	4	3
4	tree-tw	-598	0.26	0.78	**0.4**	3	3
4	GS-tw	-355.62	0.29	0.78	0.69	3	3
5	GS-pruned	**-333.8**	0.314	**0.802**	0.65	4	3
5	tree-tw	-708.13	0.21	0.78	**0.4**	3	3
5	GS-tw	-348.01	**0.314**	0.79	0.72	3	3

Table 3: Comparison of the methods in dataset emotions in 5-fold cross-validation, using a treewidth bound of 4. 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	**-348.9**	0.28	**0.782**	0.65	4	3
1	tree-tw	-697.56	**0.294**	0.77	**0.4**	3	3
1	GS-tw	**-348.9**	0.28	**0.782**	0.74	3	3
2	GS-pruned	**-322.5**	0.2	0.76	0.61	4	3
2	tree-tw	-596.03	**0.218**	**0.77**	**0.4**	3	3
2	GS-tw	**-322.5**	0.2	0.76	0.78	4	3
3	GS-pruned	-292.9	0.28	0.8	0.61	4	3
3	tree-tw	-526.95	**0.345**	0.8	**0.4**	3	3
3	GS-tw	**-286**	0.29	**0.801**	0.8	4	3
4	GS-pruned	**-347.4**	0.3	**0.785**	0.63	4	3
4	tree-tw	-598	0.26	0.78	**0.4**	3	3
4	GS-tw	-348.21	**0.314**	0.78	0.75	3	3
5	GS-pruned	**-333.8**	0.314	**0.802**	0.65	4	3
5	tree-tw	-708.13	0.21	0.78	**0.4**	3	3
5	GS-tw	-334.73	**0.314**	0.79	0.77	4	3

Table 4: Comparison of the methods in dataset emotions in 5-fold cross-validation, using a treewidth bound of 5. 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	**-348.9**	0.28	**0.782**	0.68	4	3
1	tree-tw	-697.56	**0.294**	0.77	**0.4**	3	3
1	GS-tw	**-348.9**	0.28	**0.782**	0.79	3	3
2	GS-pruned	**-322.5**	0.2	0.76	0.66	4	3
2	tree-tw	-596.03	**0.218**	**0.77**	**0.4**	3	3
2	GS-tw	**-322.5**	0.2	0.76	0.76	4	3
3	GS-pruned	**-292.9**	0.28	0.8	0.67	4	3
3	tree-tw	-526.95	**0.345**	**0.8**	**0.4**	3	3
3	GS-tw	**-292.9**	0.28	0.8	0.76	4	3
4	GS-pruned	**-347.4**	**0.297**	**0.785**	0.63	4	3
4	tree-tw	-598	0.26	0.78	**0.4**	3	3
4	GS-tw	**-347.4**	**0.297**	**0.785**	0.84	4	3
5	GS-pruned	**-333.8**	0.314	**0.802**	0.67	4	3
5	tree-tw	-708.13	0.21	0.78	**0.4**	3	3
5	GS-tw	**-333.8**	0.314	**0.802**	0.81	4	3

Table 5: Comparison of the methods in dataset foodtruck in 5-fold cross-validation, using a treewidth bound of 2. 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	**0.846**	**0**	2	2
1	tree-tw	**-338.6**	**0.317**	0.84	0.11	1	1
1	GS-tw	-341.1	0.29	**0.846**	0.06	2	2
2	GS-pruned	**-366**	**0.244**	0.84	**0**	2	2
2	tree-tw	-368.19	0.22	**0.841**	0.1	1	1
2	GS-tw	**-366**	**0.244**	0.84	0.05	2	2
3	GS-pruned	-359.46	0.17	**0.845**	0.07	2	2
3	tree-tw	**-357.9**	**0.185**	0.84	0.1	1	1
3	GS-tw	-359.46	0.17	**0.845**	**0**	2	2
4	GS-pruned	**-365**	**0.284**	**0.847**	0.06	2	2
4	tree-tw	-370.26	0.21	0.84	0.11	1	1
4	GS-tw	**-365**	**0.284**	**0.847**	**0.1**	2	2
5	GS-pruned	-405.2	**0.21**	**0.818**	0.06	2	2
5	tree-tw	**-403.6**	**0.21**	0.82	0.1	1	1
5	GS-tw	-405.2	**0.21**	**0.818**	**0.1**	2	2

Table 6: Comparison of the methods in dataset foodtruck in 5-fold cross-validation, using a treewidth bound of 3. 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	**0.846**	**0**	2	2
1	tree-tw	**-338.6**	**0.317**	0.84	0.11	1	1
1	GS-tw	-341.1	0.29	**0.846**	0.06	2	2
2	GS-pruned	**-366**	**0.244**	0.84	0.06	2	2
2	tree-tw	-368.19	0.22	**0.841**	0.1	1	1
2	GS-tw	**-366**	**0.244**	0.84	**0**	2	2
3	GS-pruned	-359.46	0.17	**0.845**	0.1	2	2
3	tree-tw	**-357.9**	**0.185**	0.84	0.1	1	1
3	GS-tw	-359.46	0.17	**0.845**	0.05	2	2
4	GS-pruned	**-364**	**0.284**	**0.847**	0.1	3	3
4	tree-tw	-370.26	0.21	0.84	0.12	1	1
4	GS-tw	**-364**	**0.284**	**0.847**	0.06	3	3
5	GS-pruned	-405.2	**0.21**	**0.818**	0.06	2	2
5	tree-tw	**-403.6**	**0.21**	0.82	0.1	1	1
5	GS-tw	-405.2	**0.21**	**0.818**	**0.1**	2	2

Table 7: Comparison of the methods in dataset foodtruck in 5-fold cross-validation, using a treewidth bound of 4. 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	**0.846**	**0**	2	2
1	tree-tw	**-338.6**	**0.317**	0.84	0.11	1	1
1	GS-tw	-341.1	0.29	**0.846**	0.05	2	2
2	GS-pruned	**-366**	**0.244**	0.84	0.05	2	2
2	tree-tw	-368.19	0.22	**0.841**	0.1	1	1
2	GS-tw	**-366**	**0.244**	0.84	**0**	2	2
3	GS-pruned	-359.46	0.17	**0.845**	0.06	2	2
3	tree-tw	**-357.9**	**0.185**	0.84	0.1	1	1
3	GS-tw	-359.46	0.17	**0.845**	**0**	2	2
4	GS-pruned	**-364**	**0.284**	**0.847**	0.07	3	3
4	tree-tw	-370.26	0.21	0.84	0.1	1	1
4	GS-tw	**-364**	**0.284**	**0.847**	**0.1**	3	3
5	GS-pruned	-405.2	**0.21**	**0.818**	**0.1**	2	2
5	tree-tw	**-403.6**	**0.21**	0.82	0.1	1	1
5	GS-tw	-405.2	**0.21**	**0.818**	0.07	2	2

Table 8: Comparison of the methods in dataset foodtruck in 5-fold cross-validation, using a treewidth bound of 5. 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	**0.846**	**0**	2	2
1	tree-tw	**-338.6**	**0.317**	0.84	0.14	1	1
1	GS-tw	-341.1	0.29	**0.846**	0.06	2	2
2	GS-pruned	**-366**	**0.244**	0.84	0.05	2	2
2	tree-tw	-368.19	0.22	**0.841**	0.1	1	1
2	GS-tw	**-366**	**0.244**	0.84	**0**	2	2
3	GS-pruned	-359.46	0.17	**0.845**	0.05	2	2
3	tree-tw	**-357.9**	**0.185**	0.84	0.11	1	1
3	GS-tw	-359.46	0.17	**0.845**	**0**	2	2
4	GS-pruned	**-364**	**0.284**	**0.847**	0.08	3	3
4	tree-tw	-370.26	0.21	0.84	0.1	1	1
4	GS-tw	**-364**	**0.284**	**0.847**	**0.1**	3	3
5	GS-pruned	-405.2	**0.21**	**0.818**	**0.1**	2	2
5	tree-tw	**-403.6**	**0.21**	0.82	0.11	1	1
5	GS-tw	-405.2	**0.21**	**0.818**	0.06	2	2

Table 9: Comparison of the methods in dataset birds in 5-fold cross-validation, using a treewidth bound of 2. 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	**-483.2**	**0.403**	**0.937**	6.2	3	2
1	tree-tw	-2173.52	0.35	0.91	**3**	2	2
1	GS-tw	-764.85	0.39	0.93	8.02	2	2
2	GS-pruned	**-451.6**	0.42	**0.946**	6.39	3	1
2	tree-tw	-2418.07	0.31	0.92	**3**	2	2
2	GS-tw	-683.37	**0.457**	0.94	7.23	2	2
3	GS-pruned	**-456.7**	0.4	**0.941**	6.67	3	2
3	tree-tw	-2262.8	0.31	0.92	**3.1**	2	2
3	GS-tw	-629.66	**0.442**	0.93	7.12	2	2
4	GS-pruned	**-396.3**	**0.527**	**0.956**	6.28	3	2
4	tree-tw	-2318.8	0.4	0.93	**3**	2	2
4	GS-tw	-657.38	0.51	0.94	6.64	2	2
5	GS-pruned	**-394.9**	**0.488**	**0.95**	6.32	3	2
5	tree-tw	-1815.12	0.4	0.93	**3**	2	2
5	GS-tw	-615.19	0.45	0.93	6.8	2	2

Table 10: Comparison of the methods in dataset birds in 5-fold cross-validation, using a treewidth bound of 3. 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	**-472.5**	**0.395**	**0.936**	6.5	3	3
1	tree-tw	-2183.83	0.34	0.91	**3**	3	3
1	GS-tw	-493.39	0.36	0.94	7.81	3	3
2	GS-pruned	**-447.8**	0.44	**0.947**	8.09	3	3
2	tree-tw	-2424.34	0.31	0.93	**3**	3	2
2	GS-tw	-473.13	**0.481**	0.94	7.82	3	2
3	GS-pruned	-434.36	0.44	**0.945**	7.69	3	2
3	tree-tw	-2250.48	0.31	0.91	**3.1**	3	3
3	GS-tw	**-433.6**	**0.473**	0.94	8.36	3	2
4	GS-pruned	**-393.5**	0.519	**0.956**	6.83	4	2
4	tree-tw	-2323.69	0.4	0.93	**3**	3	3
4	GS-tw	-422.26	**0.519**	0.95	9.38	3	2
5	GS-pruned	**-400.2**	0.52	**0.951**	6.49	4	2
5	tree-tw	-1819.08	0.4	0.93	**3.1**	3	2
5	GS-tw	-426.54	**0.535**	0.95	7.84	3	2

Table 11: Comparison of the methods in dataset birds in 5-fold cross-validation, using a treewidth bound of 4. 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	**-472.5**	**0.395**	**0.936**	7.11	3	3
1	tree-tw	-2183.83	0.34	0.91	**3**	3	3
1	GS-tw	**-472.5**	**0.395**	**0.936**	7.46	3	2
2	GS-pruned	-447.78	**0.442**	**0.947**	7.04	3	3
2	tree-tw	-2424.34	0.31	0.93	**3**	3	2
2	GS-tw	**-443.9**	**0.442**	0.95	7.65	3	2
3	GS-pruned	**-434.4**	**0.442**	**0.945**	6.36	3	2
3	tree-tw	-2250.48	0.31	0.91	**3**	3	3
3	GS-tw	-434.81	0.43	0.94	7.64	4	2
4	GS-pruned	**-393.5**	**0.519**	**0.956**	7.18	4	2
4	tree-tw	-2323.69	0.4	0.93	**3**	3	3
4	GS-tw	**-393.5**	**0.519**	**0.956**	7.55	4	2
5	GS-pruned	**-400.2**	**0.519**	**0.951**	6.5	4	2
5	tree-tw	-1819.08	0.4	0.93	**3**	3	2
5	GS-tw	**-400.2**	**0.519**	**0.951**	8.54	4	2

Table 12: Comparison of the methods in dataset birds in 5-fold cross-validation, using a treewidth bound of 5. 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	**-472.5**	**0.395**	**0.936**	6.73	3	3
1	tree-tw	-2183.83	0.34	0.91	**3**	3	3
1	GS-tw	**-472.5**	**0.395**	**0.936**	7.47	3	2
2	GS-pruned	**-447.8**	**0.442**	**0.947**	6.53	3	3
2	tree-tw	-2424.34	0.31	0.93	**3.1**	3	2
2	GS-tw	**-447.8**	**0.442**	**0.947**	7.78	3	2
3	GS-pruned	**-434.4**	**0.442**	**0.945**	6.81	3	2
3	tree-tw	-2250.48	0.31	0.91	**3.1**	3	3
3	GS-tw	**-434.4**	**0.442**	**0.945**	7.89	4	2
4	GS-pruned	**-393.5**	**0.519**	**0.956**	6.26	4	2
4	tree-tw	-2323.69	0.4	0.93	**3.4**	3	3
4	GS-tw	**-393.5**	**0.519**	**0.956**	7.7	4	2
5	GS-pruned	**-400.2**	**0.519**	**0.951**	6.58	4	2
5	tree-tw	-1819.08	0.4	0.93	**3.1**	3	2
5	GS-tw	**-400.2**	**0.519**	**0.951**	8.84	4	2

Table 13: Comparison of the methods in dataset scene in 5-fold cross-validation, using a treewidth bound of 2. 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	**-799.9**	0.43	**0.875**	24.99	20	2
1	tree-tw	-3761.44	0.47	0.86	14.31	2	2
1	GS-tw	-3190.74	**0.512**	0.86	**11.8**	2	2
2	GS-pruned	**-882.7**	0.45	0.86	21.39	17	2
2	tree-tw	-3343.02	**0.5**	**0.865**	13.59	2	2
2	GS-tw	-2629.79	0.48	0.86	**11.8**	2	2
3	GS-pruned	**-866.8**	**0.447**	**0.859**	25.96	13	2
3	tree-tw	-3638.37	0.39	0.85	12.73	2	2
3	GS-tw	-3140.02	0.42	0.85	**12.2**	2	2
4	GS-pruned	**-815.4**	**0.472**	**0.872**	22.82	16	2
4	tree-tw	-4479.17	0.46	0.85	**12.4**	2	2
4	GS-tw	-4030.28	0.41	0.84	12.44	2	2
5	GS-pruned	**-800.8**	0.41	**0.866**	27.73	20	2
5	tree-tw	-3440.01	0.48	0.86	**12.3**	2	2
5	GS-tw	-3049.73	**0.482**	0.86	12.36	2	2

Table 14: Comparison of the methods in dataset scene in 5-fold cross-validation, using a treewidth bound of 3. 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	**-733.8**	0.49	0.88	22.92	21	3
1	tree-tw	-3777.84	0.49	0.87	**13.7**	3	3
1	GS-tw	-1558.1	**0.508**	0.88	23.86	3	3
2	GS-pruned	**-842.9**	0.45	0.86	27.15	17	3
2	tree-tw	-3283.9	**0.51**	0.87	**13.8**	3	3
2	GS-tw	-1356.8	0.51	**0.872**	24.01	3	3
3	GS-pruned	**-773.2**	0.49	**0.873**	25.7	22	3
3	tree-tw	-3660.74	0.43	0.85	**14**	3	3
3	GS-tw	-1562.19	**0.493**	0.87	22.82	3	3
4	GS-pruned	**-727**	**0.545**	**0.883**	22.93	15	3
4	tree-tw	-4105.95	0.48	0.86	**14.2**	3	3
4	GS-tw	-1395.93	0.5	0.87	24.01	3	3
5	GS-pruned	**-750.4**	0.46	0.86	23.8	21	3
5	tree-tw	-3389.26	0.5	**0.87**	**13.5**	3	3
5	GS-tw	-1285.26	**0.505**	0.86	24.05	3	3

Table 15: Comparison of the methods in dataset scene in 5-fold cross-validation, using a treewidth bound of 4. 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	-678.54	0.53	0.88	24.42	20	4
1	tree-tw	-3782.24	0.49	0.86	**16.2**	4	4
1	GS-tw	**-663.6**	**0.581**	**0.883**	27.42	4	4
2	GS-pruned	-762.25	0.46	0.85	29.05	18	4
2	tree-tw	-3284.47	0.5	**0.867**	**14.7**	4	4
2	GS-tw	**-756.8**	**0.512**	0.86	26.66	4	4
3	GS-pruned	**-703.4**	**0.547**	**0.873**	24.96	17	4
3	tree-tw	-3618.43	0.47	0.86	**14.1**	4	4
3	GS-tw	-730.73	0.53	0.87	27.49	4	4
4	GS-pruned	-705.44	0.51	0.87	23.34	16	4
4	tree-tw	-4102	0.48	0.86	**13.6**	4	4
4	GS-tw	**-668**	**0.576**	**0.879**	25.65	4	4
5	GS-pruned	-708.94	**0.57**	0.87	26.72	22	4
5	tree-tw	-3395.39	0.5	**0.869**	**13.5**	4	4
5	GS-tw	**-690.4**	0.56	0.87	26.56	4	4

Table 16: Comparison of the methods in dataset scene in 5-fold cross-validation, using a treewidth bound of 5. 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	-590.17	0.62	0.88	25.07	20	5
1	tree-tw	-3782.24	0.49	0.86	**14.9**	4	4
1	GS-tw	**-566.4**	**0.639**	**0.886**	39.26	5	5
2	GS-pruned	-681.04	0.57	0.87	25.49	16	5
2	tree-tw	-3284.47	0.5	0.87	**14.9**	4	4
2	GS-tw	**-645.7**	**0.577**	**0.872**	29.56	5	5
3	GS-pruned	-670.17	0.58	0.87	25.43	18	5
3	tree-tw	-3618.43	0.47	0.86	**16**	4	4
3	GS-tw	**-659.3**	**0.599**	**0.878**	28.57	5	5
4	GS-pruned	-634.36	0.57	0.87	25.62	14	5
4	tree-tw	-4102	0.48	0.86	**14.7**	4	4
4	GS-tw	**-587.1**	**0.632**	**0.888**	32.9	5	5
5	GS-pruned	-623.14	**0.58**	0.87	27.33	22	5
5	tree-tw	-3395.39	0.5	0.87	**14.8**	4	4
5	GS-tw	**-602.4**	0.58	**0.875**	29.17	5	5

Table 17: Comparison of the methods in dataset genbase in 5-fold cross-validation, using a treewidth bound of 2. 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	-20.18	**0.985**	**0.999**	17.8	4	2
1	tree-tw	**-14.4**	**0.985**	**0.999**	**15**	2	2
1	GS-tw	-19.79	**0.985**	**0.999**	17.48	2	2
2	GS-pruned	**-21.7**	**0.97**	0.999	18.28	4	2
2	tree-tw	-22.93	0.96	1	**14.1**	2	2
2	GS-tw	-21.69	**0.97**	0.999	17.75	2	2
3	GS-pruned	-50.25	**0.955**	**0.998**	17.43	5	2
3	tree-tw	-50.63	**0.955**	**0.998**	**14.7**	2	2
3	GS-tw	**-49.9**	**0.955**	**0.998**	17.13	2	2
4	GS-pruned	-20.1	**0.962**	**0.999**	17.05	5	2
4	tree-tw	-20.44	0.95	1	**14.1**	2	2
4	GS-tw	**-19.5**	**0.962**	**0.999**	16.68	2	2
5	GS-pruned	-12.15	0.98	**1**	18.04	4	2
5	tree-tw	**-12**	**0.992**	**1**	**14.7**	2	2
5	GS-tw	-12.11	0.98	**1**	17.25	2	2

Table 18: Comparison of the methods in dataset genbase in 5-fold cross-validation, using a treewidth bound of 3. 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	-19.79	**0.985**	**0.999**	18.4	3	3
1	tree-tw	**-14.9**	**0.985**	**0.999**	**15.7**	3	3
1	GS-tw	-19.79	**0.985**	**0.999**	18.87	3	3
2	GS-pruned	-23.25	**0.97**	**0.999**	18.63	4	3
2	tree-tw	-24.48	0.96	1	**14.6**	3	2
2	GS-tw	**-23.2**	**0.97**	**0.999**	20.86	3	3
3	GS-pruned	-50.21	**0.955**	**0.998**	18.06	5	3
3	tree-tw	-50.72	**0.955**	**0.998**	**14.6**	3	3
3	GS-tw	**-50.2**	**0.955**	**0.998**	18.3	3	3
4	GS-pruned	**-20**	**0.962**	**0.999**	17.59	4	3
4	tree-tw	-20.43	0.95	1	**14.4**	3	3
4	GS-tw	-20.04	**0.962**	**0.999**	17.53	3	3
5	GS-pruned	-12.09	0.98	**1**	18.12	4	3
5	tree-tw	-12.15	**0.992**	**1**	**15.1**	3	3
5	GS-tw	**-12**	0.98	**1**	18.14	3	3

Table 19: Comparison of the methods in dataset genbase in 5-fold cross-validation, using a treewidth bound of 4. 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	**0.985**	**0.999**	18.81	4	4
1	tree-tw	**-14.9**	**0.985**	**0.999**	**15.5**	3	3
1	GS-tw	-19.86	**0.985**	**0.999**	18.87	4	4
2	GS-pruned	**-23.3**	**0.97**	0.999	18.75	4	3
2	tree-tw	-24.48	0.96	1	**14.6**	3	2
2	GS-tw	**-23.3**	**0.97**	0.999	19.09	4	3
3	GS-pruned	**-49.3**	**0.955**	**0.998**	18.44	5	3
3	tree-tw	-50.72	**0.955**	**0.998**	**14.6**	3	3
3	GS-tw	-49.29	**0.955**	**0.998**	18.24	4	3
4	GS-pruned	**-20**	**0.962**	**0.999**	18.02	5	4
4	tree-tw	-20.43	0.95	1	**14.2**	3	3
4	GS-tw	-20.02	**0.962**	**0.999**	17.52	4	4
5	GS-pruned	**-12.1**	0.98	**1**	18.43	4	3
5	tree-tw	-12.15	**0.992**	**1**	**15**	3	3
5	GS-tw	**-12.1**	0.98	**1**	18.53	4	3

Table 20: Comparison of the methods in dataset genbase in 5-fold cross-validation, using a treewidth bound of 5. 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	**0.985**	**0.999**	18.71	4	4
1	tree-tw	**-14.9**	**0.985**	**0.999**	**15.4**	3	3
1	GS-tw	-19.86	**0.985**	**0.999**	18.64	4	4
2	GS-pruned	**-23.3**	**0.97**	0.999	18.67	4	3
2	tree-tw	-24.48	0.96	1	**14.6**	3	2
2	GS-tw	**-23.3**	**0.97**	0.999	18.83	4	3
3	GS-pruned	**-49.3**	**0.955**	**0.998**	18.48	5	3
3	tree-tw	-50.72	**0.955**	**0.998**	**14.7**	3	3
3	GS-tw	**-49.3**	**0.955**	**0.998**	18.46	5	3
4	GS-pruned	**-20**	**0.962**	**0.999**	17.9	5	4
4	tree-tw	-20.43	0.95	1	**14.3**	3	3
4	GS-tw	**-20**	**0.962**	**0.999**	17.95	5	4
5	GS-pruned	**-12.1**	0.98	**1**	18.2	4	3
5	tree-tw	-12.15	**0.992**	**1**	**15.1**	3	3
5	GS-tw	**-12.1**	0.98	**1**	18.16	4	3

Table 21: Comparison of the methods in dataset yeast in 5-fold cross-validation, using a treewidth bound of 2. 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	**-2260.5**	0.12	**0.776**	2.4	5	2
1	tree-tw	-3250.68	0.13	0.76	**1.2**	2	2
1	GS-tw	-2660.47	**0.143**	0.77	1.87	2	2
2	GS-pruned	**-2185.6**	**0.174**	0.79	2.43	6	2
2	tree-tw	-3324.72	0.13	0.77	**1.2**	2	2
2	GS-tw	-2642.62	0.16	**0.791**	1.75	2	2
3	GS-pruned	**-2182.2**	0.12	0.78	2.3	4	2
3	tree-tw	-3495.99	0.12	0.77	**1.2**	2	2
3	GS-tw	-2816.39	**0.157**	**0.79**	1.7	2	2
4	GS-pruned	**-2270.9**	0.09	**0.773**	2.36	5	2
4	tree-tw	-3198.38	**0.13**	0.76	**1.2**	2	2
4	GS-tw	-2740.16	0.11	0.77	2	2	2
5	GS-pruned	**-2115.9**	**0.18**	**0.787**	2.5	6	2
5	tree-tw	-3095.34	0.13	0.77	**1.1**	2	2
5	GS-tw	-2489.37	0.18	0.78	1.56	2	2

Table 22: Comparison of the methods in dataset yeast in 5-fold cross-validation, using a treewidth bound of 3. 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	**-2109.8**	0.17	0.77	2.26	6	3
1	tree-tw	-3330.72	0.13	0.76	**1.2**	3	3
1	GS-tw	-2116.96	**0.182**	**0.776**	2.81	3	3
2	GS-pruned	**-2036**	0.18	0.78	2.47	5	3
2	tree-tw	-3325.05	0.12	0.77	**1.2**	3	3
2	GS-tw	-2039.12	**0.184**	**0.789**	2.6	3	3
3	GS-pruned	**-2058.6**	0.17	0.78	2.38	5	3
3	tree-tw	-3507.93	0.13	0.77	**1.2**	3	3
3	GS-tw	-2120.75	**0.19**	**0.787**	2.31	3	3
4	GS-pruned	-2066.41	0.15	**0.778**	2.55	6	3
4	tree-tw	-3255.1	0.13	0.76	**1.1**	3	3
4	GS-tw	**-2031.3**	**0.157**	0.78	2.32	3	3
5	GS-pruned	**-1964.7**	0.2	0.79	2.42	6	3
5	tree-tw	-3115.3	0.14	0.77	**1.1**	3	3
5	GS-tw	-1982.61	**0.207**	**0.795**	2.55	3	3

Table 23: Comparison of the methods in dataset yeast in 5-fold cross-validation, using a treewidth bound of 4. 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	**-2030.4**	0.19	**0.776**	2.56	6	4
1	tree-tw	-3351.42	0.13	0.76	**1.3**	4	4
1	GS-tw	-2038.22	**0.19**	0.78	2.87	4	4
2	GS-pruned	-2015.46	**0.178**	0.78	2.47	5	4
2	tree-tw	-3313.69	0.12	0.77	**1.1**	3	3
2	GS-tw	**-2012.2**	0.17	**0.786**	2.66	4	4
3	GS-pruned	-2023.37	0.18	0.78	2.58	5	4
3	tree-tw	-3506.54	0.12	0.77	**1.2**	4	4
3	GS-tw	**-2017.8**	**0.18**	**0.788**	2.94	4	4
4	GS-pruned	-2038.18	**0.151**	0.77	2.45	5	4
4	tree-tw	-3265.65	0.13	0.76	**1.3**	4	4
4	GS-tw	**-2002.3**	**0.151**	**0.778**	2.86	4	4
5	GS-pruned	-1934.79	0.2	**0.79**	2.56	6	4
5	tree-tw	-3113.29	0.14	0.77	**1.2**	4	4
5	GS-tw	**-1933.3**	**0.209**	0.79	3.06	4	4

Table 24: Comparison of the methods in dataset yeast in 5-fold cross-validation, using a treewidth bound of 5. 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	-2023.76	**0.176**	**0.773**	2.53	6	5
1	tree-tw	-3351.42	0.13	0.76	**1.2**	4	4
1	GS-tw	**-2007.4**	0.17	0.77	3.07	5	5
2	GS-pruned	**-2023.4**	0.18	0.78	2.26	5	5
2	tree-tw	-3313.69	0.12	0.77	**1.2**	3	3
2	GS-tw	-2023.42	**0.182**	**0.782**	2.79	5	5
3	GS-pruned	**-2031.6**	0.18	0.78	2.72	5	5
3	tree-tw	-3506.54	0.12	0.77	**1.3**	4	4
3	GS-tw	-2034.29	**0.19**	**0.788**	2.82	5	5
4	GS-pruned	-2018.41	**0.153**	0.77	2.48	6	5
4	tree-tw	-3265.65	0.13	0.76	**1.2**	4	4
4	GS-tw	**-1991.6**	0.15	**0.779**	2.89	5	5
5	GS-pruned	-1930.62	**0.203**	**0.79**	2.31	6	5
5	tree-tw	-3113.29	0.14	0.77	**1.2**	4	4
5	GS-tw	**-1924.6**	0.2	0.79	2.9	5	5

Table 25: Comparison of the methods in dataset medical in 5-fold cross-validation, using a treewidth bound of 2. 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	**-365.4**	**0.628**	**0.988**	221.29	20	2
1	tree-tw	-514.14	0.51	0.98	**119.2**	2	2
1	GS-tw	-459.99	0.55	0.99	182.41	2	2
2	GS-pruned	**-343.1**	**0.607**	**0.988**	203.29	18	2
2	tree-tw	-498.74	0.59	0.99	**111.5**	2	2
2	GS-tw	-478.11	0.6	0.99	170.01	2	2
3	GS-pruned	**-295.6**	**0.622**	**0.99**	224.87	20	2
3	tree-tw	-403.25	0.57	0.99	**120.4**	2	2
3	GS-tw	-376.55	0.6	0.99	188.42	2	2
4	GS-pruned	**-377.7**	**0.621**	**0.988**	237.23	19	2
4	tree-tw	-475.83	0.59	0.99	**116.6**	3	3
4	GS-tw	-452.76	0.58	0.99	185.87	2	2
5	GS-pruned	**-322.5**	**0.656**	**0.989**	231.24	16	2
5	tree-tw	-429.71	0.63	0.99	**116.4**	2	2
5	GS-tw	-378.15	0.62	0.99	181.93	2	2

Table 26: Comparison of the methods in dataset medical in 5-fold cross-validation, using a treewidth bound of 3. 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	**-361.6**	**0.607**	**0.988**	241.87	20	3
1	tree-tw	-510.76	0.54	0.98	**122.3**	3	3
1	GS-tw	-396.33	0.57	0.99	223.35	3	3
2	GS-pruned	**-341.4**	**0.628**	**0.988**	221.57	20	3
2	tree-tw	-508.89	0.58	0.98	**112.6**	3	3
2	GS-tw	-384	0.62	0.99	212	3	3
3	GS-pruned	**-298.8**	**0.653**	**0.991**	245.04	22	3
3	tree-tw	-397.78	0.61	0.99	**133.3**	3	3
3	GS-tw	-300.24	0.64	0.99	232.62	3	3
4	GS-pruned	**-390.2**	**0.6**	**0.987**	235.87	19	3
4	tree-tw	-476.62	0.58	0.99	**119.2**	3	3
4	GS-tw	-432.17	0.57	0.99	231.52	3	3
5	GS-pruned	**-329.7**	0.63	0.99	231.44	16	3
5	tree-tw	-425.83	0.59	0.99	**120.2**	3	3
5	GS-tw	-331.65	**0.641**	**0.988**	218.36	3	3

Table 27: Comparison of the methods in dataset medical in 5-fold cross-validation, using a treewidth bound of 4. 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	**-361.6**	**0.607**	**0.988**	227.32	20	3
1	tree-tw	-510.76	0.54	0.98	**122.3**	3	3
1	GS-tw	-386.58	0.58	0.99	220.73	4	3
2	GS-pruned	**-342.1**	**0.628**	**0.988**	209.79	20	4
2	tree-tw	-508.89	0.58	0.98	**116.6**	3	3
2	GS-tw	-359.65	**0.628**	0.99	214.23	4	4
3	GS-pruned	**-298.8**	**0.653**	**0.991**	229.07	22	3
3	tree-tw	-397.78	0.61	0.99	**130.8**	3	3
3	GS-tw	-302.69	0.65	0.99	226.99	4	3
4	GS-pruned	**-394.9**	**0.6**	**0.988**	227.9	19	4
4	tree-tw	-477.73	0.58	0.99	**120.5**	4	4
4	GS-tw	-408.62	0.59	0.99	218.29	4	4
5	GS-pruned	-329.74	0.63	0.99	219.21	16	3
5	tree-tw	-425.83	0.59	0.99	**122.9**	3	3
5	GS-tw	**-324.5**	**0.631**	**0.988**	213.73	4	3

Table 28: Comparison of the methods in dataset medical in 5-fold cross-validation, using a treewidth bound of 5. 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	**-361.6**	**0.607**	**0.988**	230.65	20	3
1	tree-tw	-510.76	0.54	0.98	**120.1**	3	3
1	GS-tw	-380.44	0.58	0.99	221.47	5	3
2	GS-pruned	**-342.1**	0.63	**0.988**	211.38	20	4
2	tree-tw	-508.89	0.58	0.98	**112.5**	3	3
2	GS-tw	-352.29	**0.633**	0.99	216.3	5	4
3	GS-pruned	-298.75	**0.653**	**0.991**	230.21	22	3
3	tree-tw	-397.78	0.61	0.99	**125.8**	3	3
3	GS-tw	**-295**	0.64	0.99	234.83	5	3
4	GS-pruned	**-394.9**	**0.6**	**0.988**	226.14	19	4
4	tree-tw	-477.73	0.58	0.99	**118.9**	4	4
4	GS-tw	-405.3	0.59	0.99	223.41	5	3
5	GS-pruned	-329.74	0.63	0.99	217.13	16	3
5	tree-tw	-425.83	0.59	0.99	**120.1**	3	3
5	GS-tw	**-318.9**	**0.631**	**0.988**	230.34	5	3

Table 29: Comparison of the methods in dataset enron in 5-fold cross-validation, using a treewidth bound of 2. 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	**-2540.5**	**0.185**	**0.952**	879.31	301	2
1	tree-tw	-5009.29	0.1	0.95	**360.3**	2	2
1	GS-tw	-4945.07	0.16	0.95	465.16	2	2
2	GS-pruned	**-2601.8**	**0.138**	0.95	865.86	290	2
2	tree-tw	-7062.66	0.13	**0.949**	**330.4**	2	2
2	GS-tw	-6225.88	0.12	0.95	499.77	2	2
3	GS-pruned	**-2955.4**	**0.147**	**0.947**	832.53	285	2
3	tree-tw	-7081.91	0.11	0.94	**389.7**	2	2
3	GS-tw	-6974.26	0.12	0.95	466.29	2	2
4	GS-pruned	**-2640.2**	**0.138**	**0.95**	852.39	321	2
4	tree-tw	-5636.98	0.08	0.95	**401.6**	2	2
4	GS-tw	-5536.03	0.13	0.95	502.06	2	2
5	GS-pruned	**-3112.4**	**0.135**	**0.95**	817.18	280	2
5	tree-tw	-6935.54	0.11	0.95	**353.1**	3	3
5	GS-tw	-6744.56	0.12	0.95	470.56	2	2

Table 30: Comparison of the methods in dataset enron in 5-fold cross-validation, using a treewidth bound of 3. 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	**-2487.7**	**0.188**	**0.952**	861.36	278	3
1	tree-tw	-5119.83	0.16	0.95	**368.4**	3	3
1	GS-tw	-3546.09	0.18	0.95	737.09	3	3
2	GS-pruned	**-2668.5**	0.13	0.95	892.97	306	3
2	tree-tw	-6745.59	0.13	0.95	**391**	3	3
2	GS-tw	-3954.07	**0.138**	0.95	694.1	3	3
3	GS-pruned	**-2976.5**	**0.147**	**0.948**	858.14	295	3
3	tree-tw	-7168.74	0.11	0.94	**405.1**	3	3
3	GS-tw	-4502.73	0.13	0.95	649.7	3	3
4	GS-pruned	**-2669.7**	0.15	**0.949**	868.05	302	3
4	tree-tw	-5783.54	0.14	0.94	**401.3**	3	3
4	GS-tw	-3371.59	**0.162**	0.95	687.44	3	3
5	GS-pruned	**-3085.8**	0.129	**0.95**	830.34	286	3
5	tree-tw	-7102.64	0.11	0.95	**365**	4	4
5	GS-tw	-5049.49	0.12	0.95	629.29	3	3

Table 31: Comparison of the methods in dataset enron in 5-fold cross-validation, using a treewidth bound of 4. 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	**-2436.2**	**0.199**	0.95	889.45	287	4
1	tree-tw	-5111.45	0.16	0.95	**379.5**	4	4
1	GS-tw	-3171.39	0.19	**0.953**	680.08	4	4
2	GS-pruned	**-2660.4**	0.13	0.95	888.34	312	4
2	tree-tw	-6843.61	0.11	0.95	**411.6**	4	4
2	GS-tw	-3709.44	**0.141**	**0.95**	680.87	4	4
3	GS-pruned	**-2941.4**	**0.147**	0.948	867.92	288	4
3	tree-tw	-7169.95	0.11	0.94	**423**	4	4
3	GS-tw	-4157.39	0.13	0.95	631.33	4	4
4	GS-pruned	**-2646**	**0.15**	0.951	903.22	299	4
4	tree-tw	-5850.63	0.13	0.94	**427.3**	4	4
4	GS-tw	-3008.88	0.14	0.95	687.45	4	4
5	GS-pruned	**-3075.9**	**0.138**	0.95	849.94	272	4
5	tree-tw	-7107.92	0.1	0.95	**370.5**	4	4
5	GS-tw	-4523.7	0.13	0.95	627.91	4	4

Table 32: Comparison of the methods in dataset enron in 5-fold cross-validation, using a treewidth bound of 5. 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	**-2472**	0.18	0.95	914.53	298	5
1	tree-tw	-5098	0.15	0.95	**389.6**	5	5
1	GS-tw	-3075.4	**0.191**	**0.952**	729.43	5	5
2	GS-pruned	**-2655.3**	**0.129**	0.95	888.46	303	4
2	tree-tw	-6900.13	0.11	0.95	**405.2**	5	5
2	GS-tw	-3450.06	**0.129**	**0.949**	693.06	5	5
3	GS-pruned	**-2970.1**	**0.147**	0.948	898.75	286	4
3	tree-tw	-7182.7	0.11	0.94	**421.4**	5	5
3	GS-tw	-3944.27	0.14	0.94	669.04	5	5
4	GS-pruned	**-2642.6**	0.15	0.95	931.31	310	4
4	tree-tw	-5833.88	0.14	0.94	**417.5**	5	5
4	GS-tw	-3002.33	**0.156**	**0.95**	759.91	5	5
5	GS-pruned	**-3072.8**	0.12	**0.949**	872.62	282	5
5	tree-tw	-7092.11	0.1	0.95	**376.1**	5	5
5	GS-tw	-4351.29	**0.126**	0.95	655.88	5	5

Table 33: Comparison of the methods in dataset ohsumed in 5-fold cross-validation, using a treewidth bound of 2. 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	**-10745.5**	**0.233**	**0.945**	473.26	177	2
1	tree-tw	-14423.6	0.19	0.94	**142.3**	2	2
1	GS-tw	-13210.81	0.2	0.94	233.52	2	2
2	GS-pruned	**-10738.3**	**0.237**	**0.943**	482.9	172	2
2	tree-tw	-14168.27	0.19	0.94	**136.9**	2	2
2	GS-tw	-13114.68	0.2	0.94	239.59	2	2
3	GS-pruned	**-10794.8**	**0.242**	**0.944**	468.76	171	2
3	tree-tw	-14510.94	0.2	0.94	**142.4**	2	2
3	GS-tw	-13287.28	0.21	0.94	234.06	2	2
4	GS-pruned	**-10879.4**	**0.239**	**0.943**	487.51	173	2
4	tree-tw	-14242.26	0.2	0.94	**136.5**	2	2
4	GS-tw	-13091.09	0.21	0.94	239.87	2	2
5	GS-pruned	**-10925.1**	**0.239**	**0.944**	467.16	170	2
5	tree-tw	-14668.35	0.19	0.94	**138.4**	2	2
5	GS-tw	-13430.92	0.21	0.94	237.99	2	2

Table 34: Comparison of the methods in dataset ohsumed in 5-fold cross-validation, using a treewidth bound of 3. 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	**-10663.2**	**0.238**	**0.945**	499.53	175	3
1	tree-tw	-14360.51	0.2	0.94	**153.7**	3	3
1	GS-tw	-11908.4	0.22	0.94	314.67	3	3
2	GS-pruned	**-10663.9**	**0.246**	**0.944**	491.28	169	3
2	tree-tw	-14336.67	0.2	0.94	**149.4**	3	3
2	GS-tw	-11638.21	0.23	0.94	320.45	3	3
3	GS-pruned	**-10779.5**	**0.247**	**0.945**	488.49	175	3
3	tree-tw	-14606.71	0.2	0.94	**152.6**	3	3
3	GS-tw	-11994.52	0.22	0.94	323.4	3	3
4	GS-pruned	**-10846.2**	**0.242**	**0.943**	496.2	167	3
4	tree-tw	-14424.57	0.2	0.94	**151.2**	3	3
4	GS-tw	-11902.49	0.23	0.94	326.17	3	3
5	GS-pruned	**-10896.1**	**0.244**	**0.943**	469.98	180	3
5	tree-tw	-14766.92	0.2	0.94	**152.7**	3	3
5	GS-tw	-12153.04	0.22	0.94	319.2	3	3

Table 35: Comparison of the methods in dataset ohsumed in 5-fold cross-validation, using a treewidth bound of 4. 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	**-10645.1**	**0.243**	**0.945**	525.42	176	4
1	tree-tw	-14376.37	0.2	0.94	**163.8**	4	4
1	GS-tw	-11508.74	0.23	0.94	356.62	4	4
2	GS-pruned	**-10681.2**	**0.247**	**0.944**	504.34	175	4
2	tree-tw	-14285.79	0.2	0.94	**157.1**	4	4
2	GS-tw	-11495.26	0.24	0.94	353.66	4	4
3	GS-pruned	**-10737.4**	**0.251**	**0.945**	520.56	173	4
3	tree-tw	-14592.54	0.2	0.94	**158.4**	4	4
3	GS-tw	-11634.14	0.23	0.94	364.44	4	4
4	GS-pruned	**-10786.4**	**0.254**	**0.943**	510.39	176	4
4	tree-tw	-14436.21	0.21	0.94	**160.8**	4	4
4	GS-tw	-11554.26	0.24	0.94	363.35	4	4
5	GS-pruned	**-10835.5**	**0.252**	**0.944**	496.44	170	4
5	tree-tw	-14840.67	0.2	0.94	**158.6**	4	4
5	GS-tw	-11673.81	0.24	0.94	384.26	4	4

Table 36: Comparison of the methods in dataset ohsumed in 5-fold cross-validation, using a treewidth bound of 5. 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	**-10558.6**	**0.245**	**0.946**	533.56	163	5
1	tree-tw	-14323.58	0.2	0.94	**166.5**	5	5
1	GS-tw	-11287.85	0.23	0.94	400.53	5	5
2	GS-pruned	**-10652.3**	**0.252**	**0.944**	508	175	5
2	tree-tw	-14369.98	0.2	0.94	**159.1**	5	5
2	GS-tw	-11265.4	0.24	0.94	386.13	5	5
3	GS-pruned	**-10683.4**	**0.251**	**0.944**	514.42	175	5
3	tree-tw	-14587.71	0.2	0.94	**163.2**	5	5
3	GS-tw	-11471.09	0.23	0.94	421.57	5	5
4	GS-pruned	**-10715.4**	**0.254**	**0.943**	516.16	169	5
4	tree-tw	-14449.06	0.21	0.94	**162**	5	5
4	GS-tw	-11437.73	0.24	0.94	398.48	5	5
5	GS-pruned	**-10806.9**	**0.25**	**0.943**	491.91	174	5
5	tree-tw	-14867.97	0.19	0.94	**162.7**	5	5
5	GS-tw	-11597.13	0.24	0.94	406.84	5	5

Table 37: Comparison of the methods in dataset reutersk500 in 5-fold cross-validation, using a treewidth bound of 2. 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	**-7003.8**	**0.061**	**0.986**	8.05	3	2
1	tree-tw	-7078.18	0.03	0.99	11.36	2	2
1	GS-tw	-7011.71	0.03	0.99	**8.1**	2	2
2	GS-pruned	-6862.44	**0.044**	**0.986**	8.07	4	2
2	tree-tw	-6936.03	0.03	0.99	11.66	2	2
2	GS-tw	**-6857.9**	0.03	0.99	**8**	2	2
3	GS-pruned	-6947.91	0.01	0.99	8.09	3	2
3	tree-tw	-7004.4	**0.022**	**0.986**	11.55	2	2
3	GS-tw	**-6946.7**	**0.022**	**0.986**	**8**	2	2
4	GS-pruned	-6990.22	**0.047**	**0.986**	7.84	4	2
4	tree-tw	-7043.22	0.03	0.99	11.64	2	2
4	GS-tw	**-6989.6**	0.03	0.99	**7.8**	2	2
5	GS-pruned	**-7054.9**	0.02	0.99	8.71	4	2
5	tree-tw	-7125.45	**0.02**	**0.986**	11.68	2	2
5	GS-tw	-7064.29	**0.02**	**0.986**	**8.5**	2	2

Table 38: Comparison of the methods in dataset reutersk500 in 5-fold cross-validation, using a treewidth bound of 3. 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	**-6876.6**	**0.066**	0.99	8.62	4	3
1	tree-tw	-6996.27	0.04	**0.986**	11.55	3	3
1	GS-tw	-6898.37	0.05	**0.986**	**8.5**	3	3
2	GS-pruned	**-6767.4**	**0.062**	0.99	8.78	4	3
2	tree-tw	-6872.25	0.04	**0.986**	11.95	3	3
2	GS-tw	-6776.23	0.05	**0.986**	**8.6**	3	3
3	GS-pruned	**-6840.5**	**0.054**	0.99	8.71	4	3
3	tree-tw	-6938.32	0.03	**0.986**	11.78	3	3
3	GS-tw	-6852.63	0.04	**0.986**	**8.7**	3	3
4	GS-pruned	**-6927.5**	0.05	**0.986**	8.19	5	3
4	tree-tw	-6979.31	0.04	0.99	11.77	3	3
4	GS-tw	-6928.91	**0.057**	0.99	**8**	3	3
5	GS-pruned	**-6936.3**	0.045	0.99	**8.9**	5	3
5	tree-tw	-7035.78	0.03	**0.986**	11.8	3	3
5	GS-tw	-6959.44	0.03	**0.986**	8.94	3	3

Table 39: Comparison of the methods in dataset reutersk500 in 5-fold cross-validation, using a treewidth bound of 4. 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	**-6818.5**	**0.072**	**0.986**	8.88	5	4
1	tree-tw	-6925.95	0.05	0.99	11.71	4	4
1	GS-tw	-6829.82	0.05	**0.986**	**8.8**	4	4
2	GS-pruned	**-6703.8**	0.06	**0.986**	8.96	5	4
2	tree-tw	-6807.34	0.06	**0.986**	12.01	4	4
2	GS-tw	-6708.65	**0.084**	**0.986**	**8.7**	4	4
3	GS-pruned	**-6757.3**	0.06	0.99	9.01	5	4
3	tree-tw	-6882.8	0.03	**0.986**	12	4	4
3	GS-tw	-6780.41	**0.081**	**0.986**	**8.8**	4	4
4	GS-pruned	**-6844.6**	0.06	0.99	8.63	5	4
4	tree-tw	-6921.99	0.04	0.99	12.02	4	4
4	GS-tw	-6845.49	**0.073**	**0.986**	**8.5**	4	4
5	GS-pruned	**-6854.4**	0.06	**0.986**	9.37	5	4
5	tree-tw	-6960.79	0.03	0.99	11.99	4	4
5	GS-tw	-6864.08	**0.062**	**0.986**	**9.2**	4	4

Table 40: Comparison of the methods in dataset reutersk500 in 5-fold cross-validation, using a treewidth bound of 5. 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	**-6801.8**	**0.078**	0.99	9.13	5	5
1	tree-tw	-6902.36	0.05	**0.986**	11.67	5	4
1	GS-tw	**-6801.8**	**0.078**	0.99	**9.1**	5	5
2	GS-pruned	-6655.26	**0.071**	0.99	8.94	6	5
2	tree-tw	-6763.59	0.06	**0.986**	12.11	5	5
2	GS-tw	**-6649.6**	**0.071**	**0.986**	**8.9**	5	5
3	GS-pruned	**-6740**	**0.061**	0.99	**9.2**	5	5
3	tree-tw	-6845.16	0.03	**0.986**	11.91	5	5
3	GS-tw	**-6740**	**0.061**	0.99	9.21	5	5
4	GS-pruned	-6812.67	0.06	**0.986**	8.85	6	5
4	tree-tw	-6890.58	0.06	0.99	12.02	5	4
4	GS-tw	**-6807**	**0.074**	**0.986**	**8.7**	5	5
5	GS-pruned	**-6827.5**	**0.049**	**0.986**	9.72	5	5
5	tree-tw	-6940.02	0.02	**0.986**	12.16	5	5
5	GS-tw	**-6827.5**	**0.049**	**0.986**	**9.7**	5	5

Table 41: Comparison of the methods in dataset mediamill in 5-fold cross-validation, using a treewidth bound of 2. 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	**-65127.5**	**0.072**	**0.966**	23.72	35	2
1	tree-tw	-236278.88	0.04	0.96	31.2	2	2
1	GS-tw	-230702.76	0.04	0.96	**13.5**	2	2
2	GS-pruned	**-64141.2**	**0.078**	**0.967**	23.48	42	2
2	tree-tw	-232738.26	0.04	0.96	30.59	2	2
2	GS-tw	-225868.26	0.04	0.96	**13.7**	2	2
3	GS-pruned	**-64703.4**	**0.068**	**0.967**	23.59	45	2
3	tree-tw	-237048.99	0.04	0.96	30.53	2	2
3	GS-tw	-230041.11	0.04	0.96	**13.6**	2	2
4	GS-pruned	**-65069.5**	**0.068**	**0.966**	23.54	42	2
4	tree-tw	-241465.27	0.04	0.96	30.84	2	2
4	GS-tw	-230803.25	0.03	0.96	**13.8**	2	2
5	GS-pruned	**-65745.2**	**0.072**	**0.966**	23.69	37	2
5	tree-tw	-237165.72	0.04	0.96	30.68	2	2
5	GS-tw	-230562.66	0.04	0.96	**14.2**	2	2

Table 42: Comparison of the methods in dataset mediamill in 5-fold cross-validation, using a treewidth bound of 3. 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	**-62980.4**	**0.078**	**0.967**	28.95	38	3
1	tree-tw	-268879.68	0.03	0.96	34.48	3	3
1	GS-tw	-260184.35	0.03	0.96	**17.7**	3	3
2	GS-pruned	**-62804**	**0.068**	**0.967**	29.8	37	3
2	tree-tw	-263579.14	0.04	0.96	34.41	3	3
2	GS-tw	-260044.28	0.04	0.96	**17.4**	3	3
3	GS-pruned	**-62681.3**	**0.068**	**0.967**	29.62	40	3
3	tree-tw	-279179.17	0.03	0.95	34.58	3	3
3	GS-tw	-268497.53	0.03	0.96	**17.3**	3	3
4	GS-pruned	**-62464.5**	**0.077**	**0.967**	28.71	42	3
4	tree-tw	-269312.16	0.04	0.96	34.33	4	4
4	GS-tw	-262699.9	0.04	0.96	**16.9**	3	3
5	GS-pruned	**-62650.4**	**0.075**	**0.967**	28.88	34	3
5	tree-tw	-269217.65	0.04	0.96	34.13	3	3
5	GS-tw	-262344.27	0.04	0.96	**17.4**	3	3

Table 43: Comparison of the methods in dataset mediamill in 5-fold cross-validation, using a treewidth bound of 4. 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	**-61661.6**	**0.077**	**0.966**	33.84	40	4
1	tree-tw	-283821.18	0.04	0.96	35.45	4	4
1	GS-tw	-261727.4	0.04	0.96	**20.9**	4	4
2	GS-pruned	**-61737.6**	**0.081**	**0.967**	33.92	36	4
2	tree-tw	-279996.01	0.03	0.95	35.44	4	4
2	GS-tw	-258541.44	0.04	0.96	**21.3**	4	4
3	GS-pruned	**-61631.9**	**0.085**	**0.967**	33.8	40	4
3	tree-tw	-294084.46	0.04	0.96	35.13	4	4
3	GS-tw	-264572.27	0.04	0.96	**21**	4	4
4	GS-pruned	**-61270.8**	**0.081**	**0.967**	33.8	37	4
4	tree-tw	-287693.22	0.03	0.95	36.05	4	4
4	GS-tw	-272078.14	0.04	0.96	**20.8**	4	4
5	GS-pruned	**-61992.1**	**0.076**	**0.967**	33.41	42	4
5	tree-tw	-284277.99	0.04	0.96	35.6	4	4
5	GS-tw	-262981.07	0.04	0.96	**20.7**	4	4

Table 44: Comparison of the methods in dataset mediamill in 5-fold cross-validation, using a treewidth bound of 5. 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	**-61429.4**	**0.072**	**0.966**	34.45	44	5
1	tree-tw	-289018.81	0.04	0.96	37.67	5	5
1	GS-tw	-90368.71	0.06	0.96	**30**	5	5
2	GS-pruned	**-61258.6**	**0.081**	**0.967**	33.61	41	5
2	tree-tw	-287415.38	0.03	0.96	37.22	5	5
2	GS-tw	-102520.34	0.06	0.96	**29.3**	5	5
3	GS-pruned	**-61086.4**	**0.073**	**0.967**	35.33	41	5
3	tree-tw	-299053.86	0.03	0.96	37.7	5	5
3	GS-tw	-95421.69	0.07	0.96	**30.2**	5	5
4	GS-pruned	**-61700.1**	**0.076**	**0.967**	33.92	43	5
4	tree-tw	-295901.94	0.03	0.96	37.38	5	5
4	GS-tw	-93889.54	0.06	0.96	**29.3**	5	5
5	GS-pruned	**-61922.5**	**0.076**	**0.966**	33.61	40	5
5	tree-tw	-291824.78	0.04	0.96	37.2	5	5
5	GS-tw	-92636.48	0.07	0.96	**29.7**	5	5

Table 45: Comparison of the methods in dataset corel5k in 5-fold cross-validation, using a treewidth bound of 2. 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	**-12970.1**	0	0.99	119.03	42	2
1	tree-tw	-13191.68	**0.008**	0.99	138.97	3	3
1	GS-tw	-12982.03	0.01	**0.99**	**98.5**	2	2
2	GS-pruned	**-12934.1**	0.01	**0.99**	119.27	58	2
2	tree-tw	-13215.49	**0.013**	0.99	133.1	3	3
2	GS-tw	-12961.6	0.01	0.99	**97.7**	2	2
3	GS-pruned	**-12890.3**	0.01	**0.99**	119.93	45	2
3	tree-tw	-13157.82	0.01	0.99	139.29	3	3
3	GS-tw	-12899.4	**0.014**	0.99	**100.1**	2	2
4	GS-pruned	**-13014.8**	0.01	**0.99**	120.77	40	2
4	tree-tw	-13189.21	**0.014**	0.99	135.79	3	3
4	GS-tw	-13030.36	0.01	0.99	**97.3**	2	2
5	GS-pruned	**-12950.2**	0.02	**0.99**	127.47	51	2
5	tree-tw	-13204.27	0.02	0.99	135.91	3	3
5	GS-tw	-12972.62	**0.02**	0.99	**98.7**	2	2

Table 46: Comparison of the methods in dataset corel5k in 5-fold cross-validation, using a treewidth bound of 3. 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	-12837.21	0.01	**0.99**	124.83	44	3
1	tree-tw	-13216.03	**0.008**	0.99	135.65	3	3
1	GS-tw	**-12831.4**	0.01	0.99	**113.4**	3	3
2	GS-pruned	-12832.62	0.01	**0.99**	133.28	52	3
2	tree-tw	-13238.52	**0.013**	0.99	134.69	4	4
2	GS-tw	**-12827.1**	0.01	0.99	**111.1**	3	3
3	GS-pruned	-12795.29	0.01	0.99	128.75	51	3
3	tree-tw	-13186.44	0.01	0.99	137.77	3	3
3	GS-tw	**-12760.2**	**0.016**	**0.99**	**111.2**	3	3
4	GS-pruned	-12934.33	0.01	**0.99**	127.05	48	3
4	tree-tw	-13212.92	**0.013**	0.99	136.93	3	3
4	GS-tw	**-12904**	0.01	0.99	**107.7**	3	3
5	GS-pruned	**-12817.6**	0.02	**0.99**	124.77	55	3
5	tree-tw	-13201.23	0.01	0.99	143.75	3	3
5	GS-tw	-12832.31	**0.021**	0.99	**108.6**	3	3

Table 47: Comparison of the methods in dataset corel5k in 5-fold cross-validation, using a treewidth bound of 4. 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	-12830.52	**0.008**	**0.99**	131.04	46	4
1	tree-tw	-13218.71	0.01	0.99	137.29	4	4
1	GS-tw	**-12801**	0.01	0.99	**113.8**	4	4
2	GS-pruned	**-12778.2**	0.01	**0.99**	130.39	56	4
2	tree-tw	-13248.09	**0.013**	0.99	142.18	4	4
2	GS-tw	-12779.1	0.01	0.99	**112.2**	4	4
3	GS-pruned	-12706.9	0.01	0.99	130.27	53	4
3	tree-tw	-13181.28	0.01	0.99	137.5	4	4
3	GS-tw	**-12674**	**0.016**	**0.99**	**113.3**	4	4
4	GS-pruned	-12836.54	0.01	**0.99**	128.42	47	4
4	tree-tw	-13215.57	**0.012**	0.99	137.07	5	5
4	GS-tw	**-12809.5**	0.01	0.99	**110.4**	4	4
5	GS-pruned	**-12785.6**	0.02	**0.99**	129	56	4
5	tree-tw	-13207.97	0.02	0.99	136.38	4	4
5	GS-tw	-12793.31	**0.022**	0.99	**109.5**	4	4

Table 48: Comparison of the methods in dataset corel5k in 5-fold cross-validation, using a treewidth bound of 5. 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	-12832.04	**0.008**	**0.99**	139.98	51	5
1	tree-tw	-13223.6	0.01	0.99	134.62	5	5
1	GS-tw	**-12824.5**	0.01	0.99	**115.2**	5	5
2	GS-pruned	-12783.79	**0.012**	0.99	143.67	52	5
2	tree-tw	-13237.96	**0.012**	0.99	135.21	5	5
2	GS-tw	**-12774**	0.01	**0.99**	**114.4**	5	5
3	GS-pruned	-12685.71	0.01	0.99	145.14	47	5
3	tree-tw	-13187.51	0.01	0.99	135.97	5	5
3	GS-tw	**-12649.9**	**0.019**	**0.99**	**121**	5	5
4	GS-pruned	-12835.98	0.01	**0.99**	143.36	44	5
4	tree-tw	-13212.17	**0.012**	0.99	134.87	5	5
4	GS-tw	**-12806.1**	0.01	0.99	**123**	5	5
5	GS-pruned	**-12776.7**	**0.021**	**0.99**	159.4	54	5
5	tree-tw	-13207.24	0.02	0.99	135.55	5	5
5	GS-tw	-12803.46	0.02	0.99	**121.2**	5	5

Table 49: Comparison of the methods in dataset tmc2007_500 in 5-fold cross-validation, using a treewidth bound of 2. 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	**-21116.3**	**0.264**	**0.934**	102.67	74	2
1	tree-tw	-28622.25	0.22	0.93	**40.5**	2	2
1	GS-tw	-28030.39	0.24	0.93	55.68	2	2
2	GS-pruned	**-20496.3**	**0.266**	**0.935**	101.32	62	2
2	tree-tw	-27816.83	0.24	0.93	**38.9**	2	2
2	GS-tw	-27084.77	0.24	0.93	54	2	2
3	GS-pruned	**-20218.9**	**0.27**	**0.936**	103.64	66	2
3	tree-tw	-27134.19	0.23	0.93	**40.4**	2	2
3	GS-tw	-26223.62	0.25	0.93	54.47	2	2
4	GS-pruned	**-21134.4**	**0.26**	**0.934**	101.45	62	2
4	tree-tw	-28776.73	0.22	0.93	**40.5**	2	2
4	GS-tw	-28104.55	0.24	0.93	54.41	2	2
5	GS-pruned	**-20851.2**	**0.238**	**0.933**	106.29	64	2
5	tree-tw	-28193.69	0.22	0.93	**39.9**	2	2
5	GS-tw	-27389.33	0.22	0.93	54.52	2	2

Table 50: Comparison of the methods in dataset tmc2007_500 in 5-fold cross-validation, using a treewidth bound of 3. 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	**-20768.9**	**0.272**	**0.936**	110.03	59	3
1	tree-tw	-28656.97	0.23	0.93	**49**	3	3
1	GS-tw	-26100.14	0.24	0.93	75.11	3	3
2	GS-pruned	**-20455.3**	**0.293**	**0.938**	112.16	54	3
2	tree-tw	-28068.07	0.24	0.93	**47.9**	3	3
2	GS-tw	-25537.51	0.27	0.93	74.14	3	3
3	GS-pruned	**-20002.2**	**0.284**	**0.938**	112.05	59	3
3	tree-tw	-26975.48	0.24	0.93	**48**	3	3
3	GS-tw	-24578.89	0.26	0.93	74.29	3	3
4	GS-pruned	**-21013.6**	**0.272**	**0.936**	109.68	56	3
4	tree-tw	-28668.23	0.23	0.93	**49.6**	3	3
4	GS-tw	-26518.1	0.26	0.93	74.19	3	3
5	GS-pruned	**-20521.6**	**0.273**	**0.936**	110.38	61	3
5	tree-tw	-28214.71	0.22	0.93	**48.4**	3	3
5	GS-tw	-25099.09	0.25	0.93	76.04	3	3

Table 51: Comparison of the methods in dataset tmc2007_500 in 5-fold cross-validation, using a treewidth bound of 4. 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	**-21042.1**	**0.274**	**0.936**	112.29	63	4
1	tree-tw	-28742.16	0.23	0.93	**52.4**	4	4
1	GS-tw	-24785.8	0.25	0.93	87.92	4	4
2	GS-pruned	**-20619.9**	**0.287**	**0.937**	112.54	51	4
2	tree-tw	-27885.11	0.25	0.93	**50.6**	4	4
2	GS-tw	-24063.92	0.27	0.93	88.15	4	4
3	GS-pruned	**-20042.4**	**0.293**	**0.939**	114.89	60	4
3	tree-tw	-26893.2	0.24	0.93	**51.7**	4	4
3	GS-tw	-23033.78	0.28	0.94	89.1	4	4
4	GS-pruned	**-21046.4**	**0.277**	**0.936**	111.19	62	4
4	tree-tw	-28738.6	0.23	0.93	**53.4**	4	4
4	GS-tw	-24891.71	0.26	0.93	87.34	4	4
5	GS-pruned	**-20602.7**	**0.276**	**0.936**	112.8	60	4
5	tree-tw	-28316.49	0.23	0.93	**51.9**	4	4
5	GS-tw	-23842.49	0.26	0.93	88.74	4	4

Table 52: Comparison of the methods in dataset tmc2007_500 in 5-fold cross-validation, using a treewidth bound of 5. 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	**-20993.2**	**0.274**	**0.936**	113.26	62	5
1	tree-tw	-28576.28	0.24	0.93	**54.1**	5	5
1	GS-tw	-23431.19	0.27	0.93	95.04	5	5
2	GS-pruned	**-20984.6**	**0.274**	**0.936**	111.53	50	5
2	tree-tw	-28068.07	0.24	0.93	**52.6**	5	5
2	GS-tw	-23068.58	0.27	0.94	93.9	5	5
3	GS-pruned	**-20419.9**	**0.289**	**0.938**	114.15	61	5
3	tree-tw	-26886.13	0.24	0.93	**54.2**	5	5
3	GS-tw	-22342.69	0.28	0.94	95.79	5	5
4	GS-pruned	**-21111.9**	**0.289**	**0.937**	112	53	5
4	tree-tw	-28776.6	0.23	0.93	**54**	5	5
4	GS-tw	-23616.57	0.28	0.93	94.18	5	5
5	GS-pruned	**-20877**	**0.275**	**0.936**	114.3	58	5
5	tree-tw	-28270.12	0.23	0.93	**54.8**	5	5
5	GS-tw	-22894.14	0.27	0.93	96.93	5	5

Table 53: Comparison of the methods in dataset bibtex in 5-fold cross-validation, using a treewidth bound of 2. 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	**-11299.4**	**0.162**	**0.987**	2227.37	157	2
1	tree-tw	-14148.48	0.14	0.98	**945.8**	3	3
1	GS-tw	-13425.81	0.15	0.98	1298.65	2	2
2	GS-pruned	**-11240.6**	**0.176**	**0.987**	2222.64	157	2
2	tree-tw	-13898.17	0.16	0.98	**910.4**	3	3
2	GS-tw	-12858.09	0.16	0.99	1413.93	2	2
3	GS-pruned	**-11108.5**	**0.17**	**0.987**	2112.64	168	2
3	tree-tw	-14264.92	0.14	0.98	**942.2**	3	3
3	GS-tw	-13169.12	0.15	0.99	1401.55	2	2
4	GS-pruned	**-10871.4**	**0.183**	**0.987**	2108.82	170	2
4	tree-tw	-13702.97	0.16	0.98	**973.9**	3	3
4	GS-tw	-12769.65	0.17	0.99	1437.57	2	2
5	GS-pruned	**-11352.1**	**0.147**	**0.986**	2165.53	173	2
5	tree-tw	-14392.87	0.14	0.98	**934.1**	3	3
5	GS-tw	-13374.59	0.14	0.98	1454.01	2	2

Table 54: Comparison of the methods in dataset bibtex in 5-fold cross-validation, using a treewidth bound of 3. 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	**-11090.4**	**0.17**	**0.987**	2252.57	161	3
1	tree-tw	-14596.16	0.14	0.98	**1068.7**	4	4
1	GS-tw	-13031.31	0.15	0.98	1659.8	3	3
2	GS-pruned	**-11093.1**	**0.181**	**0.987**	2209.16	168	3
2	tree-tw	-13996.01	0.16	0.98	**1071.2**	4	4
2	GS-tw	-12384.95	0.16	0.99	1695.27	3	3
3	GS-pruned	**-11098.8**	**0.169**	**0.987**	2166	161	3
3	tree-tw	-14469.91	0.14	0.98	**1071.1**	4	4
3	GS-tw	-12785.68	0.16	0.99	1612.76	3	3
4	GS-pruned	**-10869.4**	**0.184**	**0.987**	2264.55	153	3
4	tree-tw	-13974.8	0.15	0.98	**1085.5**	4	4
4	GS-tw	-12406.06	0.16	0.99	1730.51	3	3
5	GS-pruned	**-11343.9**	0.16	**0.987**	2241.75	163	3
5	tree-tw	-14519.54	0.15	0.98	**1080.6**	4	4
5	GS-tw	-12640.94	**0.16**	0.99	1724.08	3	3

Table 55: Comparison of the methods in dataset bibtex in 5-fold cross-validation, using a treewidth bound of 4. 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	**-11163.7**	0.17	**0.987**	2344.13	154	4
1	tree-tw	-14797.66	0.14	0.98	**1153.8**	5	5
1	GS-tw	-12030.82	**0.17**	0.99	1795.47	4	4
2	GS-pruned	**-11044.3**	**0.185**	**0.987**	2403.38	158	4
2	tree-tw	-14148.77	0.16	0.98	**1111.8**	5	5
2	GS-tw	-11615.69	0.17	0.99	1913.45	4	4
3	GS-pruned	**-11112.8**	**0.17**	**0.987**	2351.94	183	4
3	tree-tw	-14592.64	0.14	0.98	**1119.5**	5	5
3	GS-tw	-11871.06	0.17	0.99	1872.99	4	4
4	GS-pruned	**-10837.9**	0.18	**0.987**	2199.8	153	4
4	tree-tw	-14098.97	0.17	0.98	**1144.9**	5	5
4	GS-tw	-11594.91	**0.185**	0.99	1863.18	4	4
5	GS-pruned	**-11335.9**	0.16	**0.987**	2360.88	171	4
5	tree-tw	-14632.12	0.15	0.98	**1109.1**	5	5
5	GS-tw	-12038.81	**0.171**	0.99	1868.77	4	4

Table 56: Comparison of the methods in dataset bibtex in 5-fold cross-validation, using a treewidth bound of 5. 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	**-11179.9**	0.17	**0.987**	2349.92	167	5
1	tree-tw	-14877.27	0.14	0.98	**1078.5**	6	6
1	GS-tw	-11909.28	**0.171**	0.99	1886.92	5	5
2	GS-pruned	**-11029.7**	**0.182**	**0.987**	2359.26	172	5
2	tree-tw	-14149.64	0.16	0.98	**1105.7**	6	6
2	GS-tw	-11584.34	0.18	0.99	1910.93	5	5
3	GS-pruned	**-11107.6**	0.17	**0.987**	2376.38	184	5
3	tree-tw	-14620.07	0.15	0.98	**1094.9**	6	6
3	GS-tw	-11680.54	**0.168**	0.99	1979.93	5	5
4	GS-pruned	**-10837.5**	**0.185**	**0.987**	2319.04	172	5
4	tree-tw	-14217.4	0.16	0.98	**1131.1**	6	6
4	GS-tw	-11392.62	0.17	0.99	1936.27	5	5
5	GS-pruned	**-11437.4**	0.16	**0.987**	2284.55	172	5
5	tree-tw	-14647.96	0.15	0.98	**1119.1**	6	6
5	GS-tw	-11974.16	**0.169**	0.99	1995.67	5	5

Table 57: Comparison of the methods in dataset imdb in 5-fold cross-validation, using a treewidth bound of 2. 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	**-130185.5**	**0.118**	**0.929**	824.91	147	2
1	tree-tw	-137613.32	0.06	0.92	**164**	2	2
1	GS-tw	-131700.79	0.09	0.93	383.86	2	2
2	GS-pruned	**-130733**	**0.118**	**0.928**	803.65	133	2
2	tree-tw	-138083.66	0.06	0.92	**161.3**	2	2
2	GS-tw	-132110.88	0.11	0.93	394.84	2	2
3	GS-pruned	**-129653.5**	**0.118**	**0.929**	820.19	144	2
3	tree-tw	-136872.97	0.06	0.92	**160.9**	2	2
3	GS-tw	-131500.83	0.08	0.93	390.94	2	2
4	GS-pruned	**-131302.5**	**0.109**	**0.928**	846.24	152	2
4	tree-tw	-138596.89	0.06	0.92	**160.4**	2	2
4	GS-tw	-133351.94	0.09	0.93	398.97	2	2
5	GS-pruned	**-130542.7**	**0.114**	**0.929**	833.14	141	2
5	tree-tw	-137963.96	0.06	0.92	**159.7**	2	2
5	GS-tw	-132272.68	0.08	0.93	396.28	2	2

Table 58: Comparison of the methods in dataset imdb in 5-fold cross-validation, using a treewidth bound of 3. 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	**-128035.7**	0.12	**0.929**	848.91	160	3
1	tree-tw	-137282.38	0.06	0.92	**164.1**	3	3
1	GS-tw	-128290.35	**0.116**	0.93	535.42	3	3
2	GS-pruned	**-128606.6**	**0.123**	**0.928**	812.61	128	3
2	tree-tw	-137876.92	0.06	0.92	**164.2**	3	3
2	GS-tw	-128794.85	0.12	0.93	552.8	3	3
3	GS-pruned	**-127059.6**	**0.126**	**0.929**	832.76	134	3
3	tree-tw	-136503.3	0.06	0.92	**163.4**	3	3
3	GS-tw	-127440.46	0.12	0.93	564.84	3	3
4	GS-pruned	**-128954.4**	0.11	**0.928**	860.87	154	3
4	tree-tw	-138493.99	0.06	0.92	**167.7**	3	3
4	GS-tw	-129254.32	**0.11**	0.93	531.42	3	3
5	GS-pruned	**-128508.7**	**0.117**	**0.929**	840.93	137	3
5	tree-tw	-137748.32	0.06	0.92	**165**	3	3
5	GS-tw	-128661.81	0.11	0.93	534.69	3	3

Table 59: Comparison of the methods in dataset imdb in 5-fold cross-validation, using a treewidth bound of 4. 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	-126716.17	0.12	**0.929**	846.6	139	4
1	tree-tw	-137396.97	0.06	0.92	**168.7**	4	4
1	GS-tw	**-126695.8**	**0.123**	0.93	591.17	4	4
2	GS-pruned	-127860.67	0.12	**0.928**	816.94	142	4
2	tree-tw	-137955.81	0.06	0.92	**174.2**	4	4
2	GS-tw	**-127781.8**	**0.122**	0.93	591.4	4	4
3	GS-pruned	**-125959.5**	0.12	**0.929**	848.1	147	4
3	tree-tw	-136686.82	0.06	0.92	**169.3**	4	4
3	GS-tw	-126046.37	**0.122**	0.93	605.3	4	4
4	GS-pruned	**-127236.8**	0.12	**0.928**	859.36	137	4
4	tree-tw	-138526.54	0.06	0.92	**176.7**	5	5
4	GS-tw	-127299.75	**0.118**	0.93	606.52	4	4
5	GS-pruned	**-127246.2**	**0.117**	**0.929**	857.86	153	4
5	tree-tw	-137864.78	0.06	0.92	**181.1**	4	4
5	GS-tw	-127398.88	0.12	0.93	598.75	4	4

Table 60: Comparison of the methods in dataset imdb in 5-fold cross-validation, using a treewidth bound of 5. 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	**-126097**	**0.124**	**0.929**	879.83	141	5
1	tree-tw	-137533.27	0.06	0.92	**173.2**	6	6
1	GS-tw	-126132.06	0.12	0.93	658.52	5	5
2	GS-pruned	-126820.89	**0.12**	**0.928**	835.69	134	5
2	tree-tw	-137978.12	0.06	0.92	**171.3**	5	5
2	GS-tw	**-126770.5**	0.12	0.93	638.11	5	5
3	GS-pruned	-124662.1	0.12	**0.929**	854.26	152	5
3	tree-tw	-136727.17	0.06	0.92	**172.5**	5	5
3	GS-tw	**-124590.4**	**0.126**	0.93	673.49	5	5
4	GS-pruned	-126195.54	0.12	**0.928**	887.45	148	5
4	tree-tw	-138692.29	0.06	0.92	**176.1**	5	5
4	GS-tw	**-126162.8**	**0.121**	0.93	669.09	5	5
5	GS-pruned	-126091.93	**0.121**	**0.929**	876.82	138	5
5	tree-tw	-137928.05	0.06	0.92	**174.4**	5	5
5	GS-tw	**-125914.8**	0.12	0.93	658.17	5	5