

# 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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-361.9</b>	0.27	<b>0.782</b>	0.65	4	2
1	Tree-tw	-685.1	<b>0.294</b>	0.77	<b>0.4</b>	2	2
1	GS-tw	-449.6	0.27	0.78	0.64	2	2
2	GS-pruned	<b>-336.5</b>	0.28	0.76	0.62	3	2
2	Tree-tw	-595.59	0.22	0.77	<b>0.3</b>	2	2
2	GS-tw	-389.42	<b>0.345</b>	<b>0.794</b>	0.63	2	2
3	GS-pruned	<b>-298.8</b>	0.23	0.78	0.61	3	2
3	Tree-tw	-531.85	<b>0.345</b>	<b>0.804</b>	<b>0.4</b>	2	2
3	GS-tw	-355.2	0.29	0.79	0.61	2	2
4	GS-pruned	<b>-352.5</b>	<b>0.28</b>	0.76	0.65	3	2
4	Tree-tw	-600.43	0.24	<b>0.773</b>	<b>0.4</b>	2	2
4	GS-tw	-429.35	0.25	<b>0.773</b>	0.62	2	2
5	GS-pruned	<b>-338.7</b>	<b>0.322</b>	<b>0.797</b>	0.93	4	2
5	Tree-tw	-707.03	0.21	0.78	<b>0.4</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-348.9</b>	0.28	<b>0.782</b>	0.62	4	3
1	Tree-tw	-697.56	<b>0.294</b>	0.77	<b>0.4</b>	3	3
1	GS-tw	-357.54	0.29	<b>0.782</b>	0.75	3	3
2	GS-pruned	<b>-322.5</b>	0.2	0.76	0.64	4	3
2	Tree-tw	-596.03	0.22	<b>0.77</b>	<b>0.5</b>	3	3
2	GS-tw	-326.83	<b>0.269</b>	0.75	0.75	3	3
3	GS-pruned	-292.9	0.28	0.8	0.6	4	3
3	Tree-tw	-526.95	<b>0.345</b>	<b>0.8</b>	<b>0.4</b>	3	3
3	GS-tw	<b>-287.9</b>	0.3	<b>0.8</b>	0.73	3	3
4	GS-pruned	<b>-347.4</b>	<b>0.297</b>	<b>0.785</b>	0.58	4	3
4	Tree-tw	-598	0.26	0.78	<b>0.4</b>	3	3
4	GS-tw	-355.62	0.29	0.78	0.69	3	3
5	GS-pruned	<b>-333.8</b>	<b>0.314</b>	<b>0.802</b>	0.65	4	3
5	Tree-tw	-708.13	0.21	0.78	<b>0.4</b>	3	3
5	GS-tw	-348.01	<b>0.314</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-348.9</b>	0.28	<b>0.782</b>	0.65	4	3
1	Tree-tw	-697.56	<b>0.294</b>	0.77	<b>0.4</b>	3	3
1	GS-tw	<b>-348.9</b>	0.28	<b>0.782</b>	0.74	3	3
2	GS-pruned	<b>-322.5</b>	0.2	0.76	0.61	4	3
2	Tree-tw	-596.03	<b>0.218</b>	<b>0.77</b>	<b>0.4</b>	3	3
2	GS-tw	<b>-322.5</b>	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	<b>0.345</b>	0.8	<b>0.4</b>	3	3
3	GS-tw	<b>-286</b>	0.29	<b>0.801</b>	0.8	4	3
4	GS-pruned	<b>-347.4</b>	0.3	<b>0.785</b>	0.63	4	3
4	Tree-tw	-598	0.26	0.78	<b>0.4</b>	3	3
4	GS-tw	-348.21	<b>0.314</b>	0.78	0.75	3	3
5	GS-pruned	<b>-333.8</b>	<b>0.314</b>	<b>0.802</b>	0.65	4	3
5	Tree-tw	-708.13	0.21	0.78	<b>0.4</b>	3	3
5	GS-tw	-334.73	<b>0.314</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-348.9</b>	0.28	<b>0.782</b>	0.68	4	3
1	Tree-tw	-697.56	<b>0.294</b>	0.77	<b>0.4</b>	3	3
1	GS-tw	<b>-348.9</b>	0.28	<b>0.782</b>	0.79	3	3
2	GS-pruned	<b>-322.5</b>	0.2	0.76	0.66	4	3
2	Tree-tw	-596.03	<b>0.218</b>	<b>0.77</b>	<b>0.4</b>	3	3
2	GS-tw	<b>-322.5</b>	0.2	0.76	0.76	4	3
3	GS-pruned	<b>-292.9</b>	0.28	0.8	0.67	4	3
3	Tree-tw	-526.95	<b>0.345</b>	<b>0.8</b>	<b>0.4</b>	3	3
3	GS-tw	<b>-292.9</b>	0.28	0.8	0.76	4	3
4	GS-pruned	<b>-347.4</b>	<b>0.297</b>	<b>0.785</b>	0.63	4	3
4	Tree-tw	-598	0.26	0.78	<b>0.4</b>	3	3
4	GS-tw	<b>-347.4</b>	<b>0.297</b>	<b>0.785</b>	0.84	4	3
5	GS-pruned	<b>-333.8</b>	<b>0.314</b>	<b>0.802</b>	0.67	4	3
5	Tree-tw	-708.13	0.21	0.78	<b>0.4</b>	3	3
5	GS-tw	<b>-333.8</b>	<b>0.314</b>	<b>0.802</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-341.1	0.29	<b>0.846</b>	<b>0</b>	2	2
1	Tree-tw	<b>-338.6</b>	<b>0.317</b>	0.84	0.11	1	1
1	GS-tw	-341.1	0.29	<b>0.846</b>	0.06	2	2
2	GS-pruned	<b>-366</b>	<b>0.244</b>	0.84	<b>0</b>	2	2
2	Tree-tw	-368.19	0.22	<b>0.841</b>	0.1	1	1
2	GS-tw	<b>-366</b>	<b>0.244</b>	0.84	0.05	2	2
3	GS-pruned	-359.46	0.17	<b>0.845</b>	0.07	2	2
3	Tree-tw	<b>-357.9</b>	<b>0.185</b>	0.84	0.1	1	1
3	GS-tw	-359.46	0.17	<b>0.845</b>	<b>0</b>	2	2
4	GS-pruned	<b>-365</b>	<b>0.284</b>	<b>0.847</b>	0.06	2	2
4	Tree-tw	-370.26	0.21	0.84	0.11	1	1
4	GS-tw	<b>-365</b>	<b>0.284</b>	<b>0.847</b>	<b>0.1</b>	2	2
5	GS-pruned	-405.2	<b>0.21</b>	<b>0.818</b>	0.06	2	2
5	Tree-tw	<b>-403.6</b>	<b>0.21</b>	0.82	0.1	1	1
5	GS-tw	-405.2	<b>0.21</b>	<b>0.818</b>	<b>0.1</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-341.1	0.29	<b>0.846</b>	<b>0</b>	2	2
1	Tree-tw	<b>-338.6</b>	<b>0.317</b>	0.84	0.11	1	1
1	GS-tw	-341.1	0.29	<b>0.846</b>	0.06	2	2
2	GS-pruned	<b>-366</b>	<b>0.244</b>	0.84	0.06	2	2
2	Tree-tw	-368.19	0.22	<b>0.841</b>	0.1	1	1
2	GS-tw	<b>-366</b>	<b>0.244</b>	0.84	<b>0</b>	2	2
3	GS-pruned	-359.46	0.17	<b>0.845</b>	<b>0.1</b>	2	2
3	Tree-tw	<b>-357.9</b>	<b>0.185</b>	0.84	0.1	1	1
3	GS-tw	-359.46	0.17	<b>0.845</b>	0.05	2	2
4	GS-pruned	<b>-364</b>	<b>0.284</b>	<b>0.847</b>	<b>0.1</b>	3	3
4	Tree-tw	-370.26	0.21	0.84	0.12	1	1
4	GS-tw	<b>-364</b>	<b>0.284</b>	<b>0.847</b>	0.06	3	3
5	GS-pruned	-405.2	<b>0.21</b>	<b>0.818</b>	0.06	2	2
5	Tree-tw	<b>-403.6</b>	<b>0.21</b>	0.82	0.1	1	1
5	GS-tw	-405.2	<b>0.21</b>	<b>0.818</b>	<b>0.1</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-341.1	0.29	<b>0.846</b>	<b>0</b>	2	2
1	Tree-tw	<b>-338.6</b>	<b>0.317</b>	0.84	0.11	1	1
1	GS-tw	-341.1	0.29	<b>0.846</b>	0.05	2	2
2	GS-pruned	<b>-366</b>	<b>0.244</b>	0.84	0.05	2	2
2	Tree-tw	-368.19	0.22	<b>0.841</b>	0.1	1	1
2	GS-tw	<b>-366</b>	<b>0.244</b>	0.84	<b>0</b>	2	2
3	GS-pruned	-359.46	0.17	<b>0.845</b>	0.06	2	2
3	Tree-tw	<b>-357.9</b>	<b>0.185</b>	0.84	0.1	1	1
3	GS-tw	-359.46	0.17	<b>0.845</b>	<b>0</b>	2	2
4	GS-pruned	<b>-364</b>	<b>0.284</b>	<b>0.847</b>	0.07	3	3
4	Tree-tw	-370.26	0.21	0.84	0.1	1	1
4	GS-tw	<b>-364</b>	<b>0.284</b>	<b>0.847</b>	<b>0.1</b>	3	3
5	GS-pruned	-405.2	<b>0.21</b>	<b>0.818</b>	<b>0.1</b>	2	2
5	Tree-tw	<b>-403.6</b>	<b>0.21</b>	0.82	0.1	1	1
5	GS-tw	-405.2	<b>0.21</b>	<b>0.818</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-341.1	0.29	<b>0.846</b>	<b>0</b>	2	2
1	Tree-tw	<b>-338.6</b>	<b>0.317</b>	0.84	0.14	1	1
1	GS-tw	-341.1	0.29	<b>0.846</b>	0.06	2	2
2	GS-pruned	<b>-366</b>	<b>0.244</b>	0.84	0.05	2	2
2	Tree-tw	-368.19	0.22	<b>0.841</b>	0.1	1	1
2	GS-tw	<b>-366</b>	<b>0.244</b>	0.84	<b>0</b>	2	2
3	GS-pruned	-359.46	0.17	<b>0.845</b>	0.05	2	2
3	Tree-tw	<b>-357.9</b>	<b>0.185</b>	0.84	0.11	1	1
3	GS-tw	-359.46	0.17	<b>0.845</b>	<b>0</b>	2	2
4	GS-pruned	<b>-364</b>	<b>0.284</b>	<b>0.847</b>	0.08	3	3
4	Tree-tw	-370.26	0.21	0.84	0.1	1	1
4	GS-tw	<b>-364</b>	<b>0.284</b>	<b>0.847</b>	<b>0.1</b>	3	3
5	GS-pruned	-405.2	<b>0.21</b>	<b>0.818</b>	<b>0.1</b>	2	2
5	Tree-tw	<b>-403.6</b>	<b>0.21</b>	0.82	0.11	1	1
5	GS-tw	-405.2	<b>0.21</b>	<b>0.818</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-483.2</b>	<b>0.403</b>	<b>0.937</b>	6.2	3	2
1	Tree-tw	-2173.52	0.35	0.91	<b>3</b>	2	2
1	GS-tw	-764.85	0.39	0.93	8.02	2	2
2	GS-pruned	<b>-451.6</b>	0.42	<b>0.946</b>	6.39	3	1
2	Tree-tw	-2418.07	0.31	0.92	<b>3</b>	2	2
2	GS-tw	-683.37	<b>0.457</b>	0.94	7.23	2	2
3	GS-pruned	<b>-456.7</b>	0.4	<b>0.941</b>	6.67	3	2
3	Tree-tw	-2262.8	0.31	0.92	<b>3.1</b>	2	2
3	GS-tw	-629.66	<b>0.442</b>	0.93	7.12	2	2
4	GS-pruned	<b>-396.3</b>	<b>0.527</b>	<b>0.956</b>	6.28	3	2
4	Tree-tw	-2318.8	0.4	0.93	<b>3</b>	2	2
4	GS-tw	-657.38	0.51	0.94	6.64	2	2
5	GS-pruned	<b>-394.9</b>	<b>0.488</b>	<b>0.95</b>	6.32	3	2
5	Tree-tw	-1815.12	0.4	0.93	<b>3</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-472.5</b>	<b>0.395</b>	<b>0.936</b>	6.5	3	3
1	Tree-tw	-2183.83	0.34	0.91	<b>3</b>	3	3
1	GS-tw	-493.39	0.36	0.94	7.81	3	3
2	GS-pruned	<b>-447.8</b>	0.44	<b>0.947</b>	8.09	3	3
2	Tree-tw	-2424.34	0.31	0.93	<b>3</b>	3	2
2	GS-tw	-473.13	<b>0.481</b>	0.94	7.82	3	2
3	GS-pruned	-434.36	0.44	<b>0.945</b>	7.69	3	2
3	Tree-tw	-2250.48	0.31	0.91	<b>3.1</b>	3	3
3	GS-tw	<b>-433.6</b>	<b>0.473</b>	0.94	8.36	3	2
4	GS-pruned	<b>-393.5</b>	<b>0.519</b>	<b>0.956</b>	6.83	4	2
4	Tree-tw	-2323.69	0.4	0.93	<b>3</b>	3	3
4	GS-tw	-422.26	<b>0.519</b>	0.95	9.38	3	2
5	GS-pruned	<b>-400.2</b>	0.52	<b>0.951</b>	6.49	4	2
5	Tree-tw	-1819.08	0.4	0.93	<b>3.1</b>	3	2
5	GS-tw	-426.54	<b>0.535</b>	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	<b>-472.5</b>	<b>0.395</b>	<b>0.936</b>	7.11	3	3
1	Tree-tw	-2183.83	0.34	0.91	<b>3</b>	3	3
1	GS-tw	<b>-472.5</b>	<b>0.395</b>	<b>0.936</b>	7.46	3	2
2	GS-pruned	-447.78	<b>0.442</b>	<b>0.947</b>	7.04	3	3
2	Tree-tw	-2424.34	0.31	0.93	<b>3</b>	3	2
2	GS-tw	<b>-443.9</b>	<b>0.442</b>	0.95	7.65	3	2
3	GS-pruned	<b>-434.4</b>	<b>0.442</b>	<b>0.945</b>	6.36	3	2
3	Tree-tw	-2250.48	0.31	0.91	<b>3</b>	3	3
3	GS-tw	-434.81	0.43	0.94	7.64	4	2
4	GS-pruned	<b>-393.5</b>	<b>0.519</b>	<b>0.956</b>	7.18	4	2
4	Tree-tw	-2323.69	0.4	0.93	<b>3</b>	3	3
4	GS-tw	<b>-393.5</b>	<b>0.519</b>	<b>0.956</b>	7.55	4	2
5	GS-pruned	<b>-400.2</b>	<b>0.519</b>	<b>0.951</b>	6.5	4	2
5	Tree-tw	-1819.08	0.4	0.93	<b>3</b>	3	2
5	GS-tw	<b>-400.2</b>	<b>0.519</b>	<b>0.951</b>	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	<b>-472.5</b>	<b>0.395</b>	<b>0.936</b>	6.73	3	3
1	Tree-tw	-2183.83	0.34	0.91	<b>3</b>	3	3
1	GS-tw	<b>-472.5</b>	<b>0.395</b>	<b>0.936</b>	7.47	3	2
2	GS-pruned	<b>-447.8</b>	<b>0.442</b>	<b>0.947</b>	6.53	3	3
2	Tree-tw	-2424.34	0.31	0.93	<b>3.1</b>	3	2
2	GS-tw	<b>-447.8</b>	<b>0.442</b>	<b>0.947</b>	7.78	3	2
3	GS-pruned	<b>-434.4</b>	<b>0.442</b>	<b>0.945</b>	6.81	3	2
3	Tree-tw	-2250.48	0.31	0.91	<b>3.1</b>	3	3
3	GS-tw	<b>-434.4</b>	<b>0.442</b>	<b>0.945</b>	7.89	4	2
4	GS-pruned	<b>-393.5</b>	<b>0.519</b>	<b>0.956</b>	6.26	4	2
4	Tree-tw	-2323.69	0.4	0.93	<b>3.4</b>	3	3
4	GS-tw	<b>-393.5</b>	<b>0.519</b>	<b>0.956</b>	7.7	4	2
5	GS-pruned	<b>-400.2</b>	<b>0.519</b>	<b>0.951</b>	6.58	4	2
5	Tree-tw	-1819.08	0.4	0.93	<b>3.1</b>	3	2
5	GS-tw	<b>-400.2</b>	<b>0.519</b>	<b>0.951</b>	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	<b>-799.9</b>	0.43	<b>0.875</b>	24.99	20	2
1	Tree-tw	-3761.44	0.47	0.86	14.31	2	2
1	GS-tw	-3190.74	<b>0.512</b>	0.86	<b>11.8</b>	2	2
2	GS-pruned	<b>-882.7</b>	0.45	0.86	21.39	17	2
2	Tree-tw	-3343.02	<b>0.5</b>	<b>0.865</b>	13.59	2	2
2	GS-tw	-2629.79	0.48	0.86	<b>11.8</b>	2	2
3	GS-pruned	<b>-866.8</b>	<b>0.447</b>	<b>0.859</b>	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	<b>12.2</b>	2	2
4	GS-pruned	<b>-815.4</b>	<b>0.472</b>	<b>0.872</b>	22.82	16	2
4	Tree-tw	-4479.17	0.46	0.85	<b>12.4</b>	2	2
4	GS-tw	-4030.28	0.41	0.84	12.44	2	2
5	GS-pruned	<b>-800.8</b>	0.41	<b>0.866</b>	27.73	20	2
5	Tree-tw	-3440.01	0.48	0.86	<b>12.3</b>	2	2
5	GS-tw	-3049.73	<b>0.482</b>	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	<b>-733.8</b>	0.49	0.88	22.92	21	3
1	Tree-tw	-3777.84	0.49	0.87	<b>13.7</b>	3	3
1	GS-tw	-1558.1	<b>0.508</b>	<b>0.88</b>	23.86	3	3
2	GS-pruned	<b>-842.9</b>	0.45	0.86	27.15	17	3
2	Tree-tw	-3283.9	<b>0.51</b>	0.87	<b>13.8</b>	3	3
2	GS-tw	-1356.8	0.51	<b>0.872</b>	24.01	3	3
3	GS-pruned	<b>-773.2</b>	0.49	<b>0.873</b>	25.7	22	3
3	Tree-tw	-3660.74	0.43	0.85	<b>14</b>	3	3
3	GS-tw	-1562.19	<b>0.493</b>	0.87	22.82	3	3
4	GS-pruned	<b>-727</b>	<b>0.545</b>	<b>0.883</b>	22.93	15	3
4	Tree-tw	-4105.95	0.48	0.86	<b>14.2</b>	3	3
4	GS-tw	-1395.93	0.5	0.87	24.01	3	3
5	GS-pruned	<b>-750.4</b>	0.46	0.86	23.8	21	3
5	Tree-tw	-3389.26	0.5	<b>0.87</b>	<b>13.5</b>	3	3
5	GS-tw	-1285.26	<b>0.505</b>	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	<b>16.2</b>	4	4
1	GS-tw	<b>-663.6</b>	<b>0.581</b>	<b>0.883</b>	27.42	4	4
2	GS-pruned	-762.25	0.46	0.85	29.05	18	4
2	Tree-tw	-3284.47	0.5	<b>0.867</b>	<b>14.7</b>	4	4
2	GS-tw	<b>-756.8</b>	<b>0.512</b>	0.86	26.66	4	4
3	GS-pruned	<b>-703.4</b>	<b>0.547</b>	<b>0.873</b>	24.96	17	4
3	Tree-tw	-3618.43	0.47	0.86	<b>14.1</b>	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	<b>13.6</b>	4	4
4	GS-tw	<b>-668</b>	<b>0.576</b>	<b>0.879</b>	25.65	4	4
5	GS-pruned	-708.94	<b>0.57</b>	0.87	26.72	22	4
5	Tree-tw	-3395.39	0.5	<b>0.869</b>	<b>13.5</b>	4	4
5	GS-tw	<b>-690.4</b>	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	<b>14.9</b>	4	4
1	GS-tw	<b>-566.4</b>	<b>0.639</b>	<b>0.886</b>	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	<b>14.9</b>	4	4
2	GS-tw	<b>-645.7</b>	<b>0.577</b>	<b>0.872</b>	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	<b>16</b>	4	4
3	GS-tw	<b>-659.3</b>	<b>0.599</b>	<b>0.878</b>	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	<b>14.7</b>	4	4
4	GS-tw	<b>-587.1</b>	<b>0.632</b>	<b>0.888</b>	32.9	5	5
5	GS-pruned	-623.14	<b>0.58</b>	0.87	27.33	22	5
5	Tree-tw	-3395.39	0.5	0.87	<b>14.8</b>	4	4
5	GS-tw	<b>-602.4</b>	0.58	<b>0.875</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-20.18	<b>0.985</b>	<b>0.999</b>	17.8	4	2
1	Tree-tw	<b>-14.4</b>	<b>0.985</b>	<b>0.999</b>	<b>15</b>	2	2
1	GS-tw	-19.79	<b>0.985</b>	<b>0.999</b>	17.48	2	2
2	GS-pruned	<b>-21.7</b>	<b>0.97</b>	<b>0.999</b>	18.28	4	2
2	Tree-tw	-22.93	0.96	1	<b>14.1</b>	2	2
2	GS-tw	-21.69	<b>0.97</b>	<b>0.999</b>	17.75	2	2
3	GS-pruned	-50.25	<b>0.955</b>	<b>0.998</b>	17.43	5	2
3	Tree-tw	-50.63	<b>0.955</b>	<b>0.998</b>	<b>14.7</b>	2	2
3	GS-tw	<b>-49.9</b>	<b>0.955</b>	<b>0.998</b>	17.13	2	2
4	GS-pruned	-20.1	<b>0.962</b>	<b>0.999</b>	17.05	5	2
4	Tree-tw	-20.44	0.95	1	<b>14.1</b>	2	2
4	GS-tw	<b>-19.5</b>	<b>0.962</b>	<b>0.999</b>	16.68	2	2
5	GS-pruned	-12.15	0.98	<b>1</b>	18.04	4	2
5	Tree-tw	<b>-12</b>	<b>0.992</b>	<b>1</b>	<b>14.7</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-19.79	<b>0.985</b>	<b>0.999</b>	18.4	3	3
1	Tree-tw	<b>-14.9</b>	<b>0.985</b>	<b>0.999</b>	<b>15.7</b>	3	3
1	GS-tw	-19.79	<b>0.985</b>	<b>0.999</b>	18.87	3	3
2	GS-pruned	-23.25	<b>0.97</b>	<b>0.999</b>	18.63	4	3
2	Tree-tw	-24.48	0.96	1	<b>14.6</b>	3	2
2	GS-tw	<b>-23.2</b>	<b>0.97</b>	<b>0.999</b>	20.86	3	3
3	GS-pruned	-50.21	<b>0.955</b>	<b>0.998</b>	18.06	5	3
3	Tree-tw	-50.72	<b>0.955</b>	<b>0.998</b>	<b>14.6</b>	3	3
3	GS-tw	<b>-50.2</b>	<b>0.955</b>	<b>0.998</b>	18.3	3	3
4	GS-pruned	<b>-20</b>	<b>0.962</b>	<b>0.999</b>	17.59	4	3
4	Tree-tw	-20.43	0.95	1	<b>14.4</b>	3	3
4	GS-tw	-20.04	<b>0.962</b>	<b>0.999</b>	17.53	3	3
5	GS-pruned	-12.09	0.98	<b>1</b>	18.12	4	3
5	Tree-tw	-12.15	<b>0.992</b>	<b>1</b>	<b>15.1</b>	3	3
5	GS-tw	<b>-12</b>	0.98	<b>1</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-19.86	<b>0.985</b>	<b>0.999</b>	18.81	4	4
1	Tree-tw	<b>-14.9</b>	<b>0.985</b>	<b>0.999</b>	<b>15.5</b>	3	3
1	GS-tw	-19.86	<b>0.985</b>	<b>0.999</b>	18.87	4	4
2	GS-pruned	<b>-23.3</b>	<b>0.97</b>	<b>0.999</b>	18.75	4	3
2	Tree-tw	-24.48	0.96	1	<b>14.6</b>	3	2
2	GS-tw	<b>-23.3</b>	<b>0.97</b>	<b>0.999</b>	19.09	4	3
3	GS-pruned	<b>-49.3</b>	<b>0.955</b>	<b>0.998</b>	18.44	5	3
3	Tree-tw	-50.72	<b>0.955</b>	<b>0.998</b>	<b>14.6</b>	3	3
3	GS-tw	-49.29	<b>0.955</b>	<b>0.998</b>	18.24	4	3
4	GS-pruned	<b>-20</b>	<b>0.962</b>	<b>0.999</b>	18.02	5	4
4	Tree-tw	-20.43	0.95	1	<b>14.2</b>	3	3
4	GS-tw	-20.02	<b>0.962</b>	<b>0.999</b>	17.52	4	4
5	GS-pruned	<b>-12.1</b>	0.98	<b>1</b>	18.43	4	3
5	Tree-tw	-12.15	<b>0.992</b>	<b>1</b>	<b>15</b>	3	3
5	GS-tw	<b>-12.1</b>	0.98	<b>1</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-19.86	<b>0.985</b>	<b>0.999</b>	18.71	4	4
1	Tree-tw	<b>-14.9</b>	<b>0.985</b>	<b>0.999</b>	<b>15.4</b>	3	3
1	GS-tw	-19.86	<b>0.985</b>	<b>0.999</b>	18.64	4	4
2	GS-pruned	<b>-23.3</b>	<b>0.97</b>	<b>0.999</b>	18.67	4	3
2	Tree-tw	-24.48	0.96	1	<b>14.6</b>	3	2
2	GS-tw	<b>-23.3</b>	<b>0.97</b>	<b>0.999</b>	18.83	4	3
3	GS-pruned	<b>-49.3</b>	<b>0.955</b>	<b>0.998</b>	18.48	5	3
3	Tree-tw	-50.72	<b>0.955</b>	<b>0.998</b>	<b>14.7</b>	3	3
3	GS-tw	<b>-49.3</b>	<b>0.955</b>	<b>0.998</b>	18.46	5	3
4	GS-pruned	<b>-20</b>	<b>0.962</b>	<b>0.999</b>	17.9	5	4
4	Tree-tw	-20.43	0.95	1	<b>14.3</b>	3	3
4	GS-tw	<b>-20</b>	<b>0.962</b>	<b>0.999</b>	17.95	5	4
5	GS-pruned	<b>-12.1</b>	0.98	<b>1</b>	18.2	4	3
5	Tree-tw	-12.15	<b>0.992</b>	<b>1</b>	<b>15.1</b>	3	3
5	GS-tw	<b>-12.1</b>	0.98	<b>1</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-2260.5</b>	0.12	<b>0.776</b>	2.4	5	2
1	Tree-tw	-3250.68	0.13	0.76	<b>1.2</b>	2	2
1	GS-tw	-2660.47	<b>0.143</b>	0.77	1.87	2	2
2	GS-pruned	<b>-2185.6</b>	<b>0.174</b>	0.79	2.43	6	2
2	Tree-tw	-3324.72	0.13	0.77	<b>1.2</b>	2	2
2	GS-tw	-2642.62	0.16	<b>0.791</b>	1.75	2	2
3	GS-pruned	<b>-2182.2</b>	0.12	0.78	2.3	4	2
3	Tree-tw	-3495.99	0.12	0.77	<b>1.2</b>	2	2
3	GS-tw	-2816.39	<b>0.157</b>	<b>0.79</b>	1.7	2	2
4	GS-pruned	<b>-2270.9</b>	0.09	<b>0.773</b>	2.36	5	2
4	Tree-tw	-3198.38	<b>0.13</b>	0.76	<b>1.2</b>	2	2
4	GS-tw	-2740.16	0.11	0.77	2	2	2
5	GS-pruned	<b>-2115.9</b>	<b>0.18</b>	<b>0.787</b>	2.5	6	2
5	Tree-tw	-3095.34	0.13	0.77	<b>1.1</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-2109.8</b>	0.17	0.77	2.26	6	3
1	Tree-tw	-3330.72	0.13	0.76	<b>1.2</b>	3	3
1	GS-tw	-2116.96	<b>0.182</b>	<b>0.776</b>	2.81	3	3
2	GS-pruned	<b>-2036</b>	0.18	0.78	2.47	5	3
2	Tree-tw	-3325.05	0.12	0.77	<b>1.2</b>	3	3
2	GS-tw	-2039.12	<b>0.184</b>	<b>0.789</b>	2.6	3	3
3	GS-pruned	<b>-2058.6</b>	0.17	0.78	2.38	5	3
3	Tree-tw	-3507.93	0.13	0.77	<b>1.2</b>	3	3
3	GS-tw	-2120.75	<b>0.19</b>	<b>0.787</b>	2.31	3	3
4	GS-pruned	-2066.41	0.15	<b>0.778</b>	2.55	6	3
4	Tree-tw	-3255.1	0.13	0.76	<b>1.1</b>	3	3
4	GS-tw	<b>-2031.3</b>	<b>0.157</b>	0.78	2.32	3	3
5	GS-pruned	<b>-1964.7</b>	0.2	0.79	2.42	6	3
5	Tree-tw	-3115.3	0.14	0.77	<b>1.1</b>	3	3
5	GS-tw	-1982.61	<b>0.207</b>	<b>0.795</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-2030.4</b>	0.19	<b>0.776</b>	2.56	6	4
1	Tree-tw	-3351.42	0.13	0.76	<b>1.3</b>	4	4
1	GS-tw	-2038.22	<b>0.19</b>	0.78	2.87	4	4
2	GS-pruned	-2015.46	<b>0.178</b>	0.78	2.47	5	4
2	Tree-tw	-3313.69	0.12	0.77	<b>1.1</b>	3	3
2	GS-tw	<b>-2012.2</b>	0.17	<b>0.786</b>	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	<b>1.2</b>	4	4
3	GS-tw	<b>-2017.8</b>	<b>0.18</b>	<b>0.788</b>	2.94	4	4
4	GS-pruned	-2038.18	<b>0.151</b>	0.77	2.45	5	4
4	Tree-tw	-3265.65	0.13	0.76	<b>1.3</b>	4	4
4	GS-tw	<b>-2002.3</b>	<b>0.151</b>	<b>0.778</b>	2.86	4	4
5	GS-pruned	-1934.79	0.2	<b>0.79</b>	2.56	6	4
5	Tree-tw	-3113.29	0.14	0.77	<b>1.2</b>	4	4
5	GS-tw	<b>-1933.3</b>	<b>0.209</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-2023.76	<b>0.176</b>	<b>0.773</b>	2.53	6	5
1	Tree-tw	-3351.42	0.13	0.76	<b>1.2</b>	4	4
1	GS-tw	<b>-2007.4</b>	0.17	0.77	3.07	5	5
2	GS-pruned	<b>-2023.4</b>	0.18	0.78	2.26	5	5
2	Tree-tw	-3313.69	0.12	0.77	<b>1.2</b>	3	3
2	GS-tw	-2023.42	<b>0.182</b>	<b>0.782</b>	2.79	5	5
3	GS-pruned	<b>-2031.6</b>	0.18	0.78	2.72	5	5
3	Tree-tw	-3506.54	0.12	0.77	<b>1.3</b>	4	4
3	GS-tw	-2034.29	<b>0.19</b>	<b>0.788</b>	2.82	5	5
4	GS-pruned	-2018.41	<b>0.153</b>	0.77	2.48	6	5
4	Tree-tw	-3265.65	0.13	0.76	<b>1.2</b>	4	4
4	GS-tw	<b>-1991.6</b>	0.15	<b>0.779</b>	2.89	5	5
5	GS-pruned	-1930.62	<b>0.203</b>	<b>0.79</b>	2.31	6	5
5	Tree-tw	-3113.29	0.14	0.77	<b>1.2</b>	4	4
5	GS-tw	<b>-1924.6</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-365.4</b>	<b>0.628</b>	<b>0.988</b>	221.29	20	2
1	Tree-tw	-514.14	0.51	0.98	<b>119.2</b>	2	2
1	GS-tw	-459.99	0.55	0.99	182.41	2	2
2	GS-pruned	<b>-343.1</b>	<b>0.607</b>	<b>0.988</b>	203.29	18	2
2	Tree-tw	-498.74	0.59	0.99	<b>111.5</b>	2	2
2	GS-tw	-478.11	0.6	0.99	170.01	2	2
3	GS-pruned	<b>-295.6</b>	<b>0.622</b>	<b>0.99</b>	224.87	20	2
3	Tree-tw	-403.25	0.57	0.99	<b>120.4</b>	2	2
3	GS-tw	-376.55	0.6	0.99	188.42	2	2
4	GS-pruned	<b>-377.7</b>	<b>0.621</b>	<b>0.988</b>	237.23	19	2
4	Tree-tw	-475.83	0.59	0.99	<b>116.6</b>	3	3
4	GS-tw	-452.76	0.58	0.99	185.87	2	2
5	GS-pruned	<b>-322.5</b>	<b>0.656</b>	<b>0.989</b>	231.24	16	2
5	Tree-tw	-429.71	0.63	0.99	<b>116.4</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-361.6</b>	<b>0.607</b>	<b>0.988</b>	241.87	20	3
1	Tree-tw	-510.76	0.54	0.98	<b>122.3</b>	3	3
1	GS-tw	-396.33	0.57	0.99	223.35	3	3
2	GS-pruned	<b>-341.4</b>	<b>0.628</b>	<b>0.988</b>	221.57	20	3
2	Tree-tw	-508.89	0.58	0.98	<b>112.6</b>	3	3
2	GS-tw	-384	0.62	0.99	212	3	3
3	GS-pruned	<b>-298.8</b>	<b>0.653</b>	<b>0.991</b>	245.04	22	3
3	Tree-tw	-397.78	0.61	0.99	<b>133.3</b>	3	3
3	GS-tw	-300.24	0.64	0.99	232.62	3	3
4	GS-pruned	<b>-390.2</b>	<b>0.6</b>	<b>0.987</b>	235.87	19	3
4	Tree-tw	-476.62	0.58	0.99	<b>119.2</b>	3	3
4	GS-tw	-432.17	0.57	0.99	231.52	3	3
5	GS-pruned	<b>-329.7</b>	0.63	0.99	231.44	16	3
5	Tree-tw	-425.83	0.59	0.99	<b>120.2</b>	3	3
5	GS-tw	-331.65	<b>0.641</b>	<b>0.988</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-361.6</b>	<b>0.607</b>	<b>0.988</b>	227.32	20	3
1	Tree-tw	-510.76	0.54	0.98	<b>122.3</b>	3	3
1	GS-tw	-386.58	0.58	0.99	220.73	4	3
2	GS-pruned	<b>-342.1</b>	<b>0.628</b>	<b>0.988</b>	209.79	20	4
2	Tree-tw	-508.89	0.58	0.98	<b>116.6</b>	3	3
2	GS-tw	-359.65	<b>0.628</b>	0.99	214.23	4	4
3	GS-pruned	<b>-298.8</b>	<b>0.653</b>	<b>0.991</b>	229.07	22	3
3	Tree-tw	-397.78	0.61	0.99	<b>130.8</b>	3	3
3	GS-tw	-302.69	0.65	0.99	226.99	4	3
4	GS-pruned	<b>-394.9</b>	<b>0.6</b>	<b>0.988</b>	227.9	19	4
4	Tree-tw	-477.73	0.58	0.99	<b>120.5</b>	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	<b>122.9</b>	3	3
5	GS-tw	<b>-324.5</b>	<b>0.631</b>	<b>0.988</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-361.6</b>	<b>0.607</b>	<b>0.988</b>	230.65	20	3
1	Tree-tw	-510.76	0.54	0.98	<b>120.1</b>	3	3
1	GS-tw	-380.44	0.58	0.99	221.47	5	3
2	GS-pruned	<b>-342.1</b>	0.63	<b>0.988</b>	211.38	20	4
2	Tree-tw	-508.89	0.58	0.98	<b>112.5</b>	3	3
2	GS-tw	-352.29	<b>0.633</b>	0.99	216.3	5	4
3	GS-pruned	-298.75	<b>0.653</b>	<b>0.991</b>	230.21	22	3
3	Tree-tw	-397.78	0.61	0.99	<b>125.8</b>	3	3
3	GS-tw	<b>-295</b>	0.64	0.99	234.83	5	3
4	GS-pruned	<b>-394.9</b>	<b>0.6</b>	<b>0.988</b>	226.14	19	4
4	Tree-tw	-477.73	0.58	0.99	<b>118.9</b>	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	<b>120.1</b>	3	3
5	GS-tw	<b>-318.9</b>	<b>0.631</b>	<b>0.988</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-2540.5</b>	<b>0.185</b>	<b>0.952</b>	879.31	301	2
1	Tree-tw	-5009.29	0.1	0.95	<b>360.3</b>	2	2
1	GS-tw	-4945.07	0.16	0.95	465.16	2	2
2	GS-pruned	<b>-2601.8</b>	<b>0.138</b>	0.95	865.86	290	2
2	Tree-tw	-7062.66	0.13	<b>0.949</b>	<b>330.4</b>	2	2
2	GS-tw	-6225.88	0.12	0.95	499.77	2	2
3	GS-pruned	<b>-2955.4</b>	<b>0.147</b>	<b>0.947</b>	832.53	285	2
3	Tree-tw	-7081.91	0.11	0.94	<b>389.7</b>	2	2
3	GS-tw	-6974.26	0.12	0.95	466.29	2	2
4	GS-pruned	<b>-2640.2</b>	<b>0.138</b>	<b>0.95</b>	852.39	321	2
4	Tree-tw	-5636.98	0.08	0.95	<b>401.6</b>	2	2
4	GS-tw	-5536.03	0.13	0.95	502.06	2	2
5	GS-pruned	<b>-3112.4</b>	<b>0.135</b>	<b>0.95</b>	817.18	280	2
5	Tree-tw	-6935.54	0.11	0.95	<b>353.1</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-2487.7</b>	<b>0.188</b>	<b>0.952</b>	861.36	278	3
1	Tree-tw	-5119.83	0.16	0.95	<b>368.4</b>	3	3
1	GS-tw	-3546.09	0.18	0.95	737.09	3	3
2	GS-pruned	<b>-2668.5</b>	0.13	0.95	892.97	306	3
2	Tree-tw	-6745.59	0.13	0.95	<b>391</b>	3	3
2	GS-tw	-3954.07	<b>0.138</b>	<b>0.95</b>	694.1	3	3
3	GS-pruned	<b>-2976.5</b>	<b>0.147</b>	<b>0.948</b>	858.14	295	3
3	Tree-tw	-7168.74	0.11	0.94	<b>405.1</b>	3	3
3	GS-tw	-4502.73	0.13	0.95	649.7	3	3
4	GS-pruned	<b>-2669.7</b>	0.15	<b>0.949</b>	868.05	302	3
4	Tree-tw	-5783.54	0.14	0.94	<b>401.3</b>	3	3
4	GS-tw	-3371.59	<b>0.162</b>	0.95	687.44	3	3
5	GS-pruned	<b>-3085.8</b>	<b>0.129</b>	<b>0.95</b>	830.34	286	3
5	Tree-tw	-7102.64	0.11	0.95	<b>365</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-2436.2</b>	<b>0.199</b>	0.95	889.45	287	4
1	Tree-tw	-5111.45	0.16	0.95	<b>379.5</b>	4	4
1	GS-tw	-3171.39	0.19	<b>0.953</b>	680.08	4	4
2	GS-pruned	<b>-2660.4</b>	0.13	0.95	888.34	312	4
2	Tree-tw	-6843.61	0.11	0.95	<b>411.6</b>	4	4
2	GS-tw	-3709.44	<b>0.141</b>	<b>0.95</b>	680.87	4	4
3	GS-pruned	<b>-2941.4</b>	<b>0.147</b>	<b>0.948</b>	867.92	288	4
3	Tree-tw	-7169.95	0.11	0.94	<b>423</b>	4	4
3	GS-tw	-4157.39	0.13	0.95	631.33	4	4
4	GS-pruned	<b>-2646</b>	<b>0.15</b>	<b>0.951</b>	903.22	299	4
4	Tree-tw	-5850.63	0.13	0.94	<b>427.3</b>	4	4
4	GS-tw	-3008.88	0.14	0.95	687.45	4	4
5	GS-pruned	<b>-3075.9</b>	<b>0.138</b>	<b>0.95</b>	849.94	272	4
5	Tree-tw	-7107.92	0.1	0.95	<b>370.5</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-2472</b>	0.18	0.95	914.53	298	5
1	Tree-tw	-5098	0.15	0.95	<b>389.6</b>	5	5
1	GS-tw	-3075.4	<b>0.191</b>	<b>0.952</b>	729.43	5	5
2	GS-pruned	<b>-2655.3</b>	<b>0.129</b>	0.95	888.46	303	4
2	Tree-tw	-6900.13	0.11	0.95	<b>405.2</b>	5	5
2	GS-tw	-3450.06	<b>0.129</b>	<b>0.949</b>	693.06	5	5
3	GS-pruned	<b>-2970.1</b>	<b>0.147</b>	<b>0.948</b>	898.75	286	4
3	Tree-tw	-7182.7	0.11	0.94	<b>421.4</b>	5	5
3	GS-tw	-3944.27	0.14	0.94	669.04	5	5
4	GS-pruned	<b>-2642.6</b>	0.15	0.95	931.31	310	4
4	Tree-tw	-5833.88	0.14	0.94	<b>417.5</b>	5	5
4	GS-tw	-3002.33	<b>0.156</b>	<b>0.95</b>	759.91	5	5
5	GS-pruned	<b>-3072.8</b>	0.12	<b>0.949</b>	872.62	282	5
5	Tree-tw	-7092.11	0.1	0.95	<b>376.1</b>	5	5
5	GS-tw	-4351.29	<b>0.126</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-10745.5</b>	<b>0.233</b>	<b>0.945</b>	473.26	177	2
1	Tree-tw	-14423.6	0.19	0.94	<b>142.3</b>	2	2
1	GS-tw	-13210.81	0.2	0.94	233.52	2	2
2	GS-pruned	<b>-10738.3</b>	<b>0.237</b>	<b>0.943</b>	482.9	172	2
2	Tree-tw	-14168.27	0.19	0.94	<b>136.9</b>	2	2
2	GS-tw	-13114.68	0.2	0.94	239.59	2	2
3	GS-pruned	<b>-10794.8</b>	<b>0.242</b>	<b>0.944</b>	468.76	171	2
3	Tree-tw	-14510.94	0.2	0.94	<b>142.4</b>	2	2
3	GS-tw	-13287.28	0.21	0.94	234.06	2	2
4	GS-pruned	<b>-10879.4</b>	<b>0.239</b>	<b>0.943</b>	487.51	173	2
4	Tree-tw	-14242.26	0.2	0.94	<b>136.5</b>	2	2
4	GS-tw	-13091.09	0.21	0.94	239.87	2	2
5	GS-pruned	<b>-10925.1</b>	<b>0.239</b>	<b>0.944</b>	467.16	170	2
5	Tree-tw	-14668.35	0.19	0.94	<b>138.4</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-10663.2</b>	<b>0.238</b>	<b>0.945</b>	499.53	175	3
1	Tree-tw	-14360.51	0.2	0.94	<b>153.7</b>	3	3
1	GS-tw	-11908.4	0.22	0.94	314.67	3	3
2	GS-pruned	<b>-10663.9</b>	<b>0.246</b>	<b>0.944</b>	491.28	169	3
2	Tree-tw	-14336.67	0.2	0.94	<b>149.4</b>	3	3
2	GS-tw	-11638.21	0.23	0.94	320.45	3	3
3	GS-pruned	<b>-10779.5</b>	<b>0.247</b>	<b>0.945</b>	488.49	175	3
3	Tree-tw	-14606.71	0.2	0.94	<b>152.6</b>	3	3
3	GS-tw	-11994.52	0.22	0.94	323.4	3	3
4	GS-pruned	<b>-10846.2</b>	<b>0.242</b>	<b>0.943</b>	496.2	167	3
4	Tree-tw	-14424.57	0.2	0.94	<b>151.2</b>	3	3
4	GS-tw	-11902.49	0.23	0.94	326.17	3	3
5	GS-pruned	<b>-10896.1</b>	<b>0.244</b>	<b>0.943</b>	469.98	180	3
5	Tree-tw	-14766.92	0.2	0.94	<b>152.7</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-10645.1</b>	<b>0.243</b>	<b>0.945</b>	525.42	176	4
1	Tree-tw	-14376.37	0.2	0.94	<b>163.8</b>	4	4
1	GS-tw	-11508.74	0.23	0.94	356.62	4	4
2	GS-pruned	<b>-10681.2</b>	<b>0.247</b>	<b>0.944</b>	504.34	175	4
2	Tree-tw	-14285.79	0.2	0.94	<b>157.1</b>	4	4
2	GS-tw	-11495.26	0.24	0.94	353.66	4	4
3	GS-pruned	<b>-10737.4</b>	<b>0.251</b>	<b>0.945</b>	520.56	173	4
3	Tree-tw	-14592.54	0.2	0.94	<b>158.4</b>	4	4
3	GS-tw	-11634.14	0.23	0.94	364.44	4	4
4	GS-pruned	<b>-10786.4</b>	<b>0.254</b>	<b>0.943</b>	510.39	176	4
4	Tree-tw	-14436.21	0.21	0.94	<b>160.8</b>	4	4
4	GS-tw	-11554.26	0.24	0.94	363.35	4	4
5	GS-pruned	<b>-10835.5</b>	<b>0.252</b>	<b>0.944</b>	496.44	170	4
5	Tree-tw	-14840.67	0.2	0.94	<b>158.6</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-10558.6</b>	<b>0.245</b>	<b>0.946</b>	533.56	163	5
1	Tree-tw	-14323.58	0.2	0.94	<b>166.5</b>	5	5
1	GS-tw	-11287.85	0.23	0.94	400.53	5	5
2	GS-pruned	<b>-10652.3</b>	<b>0.252</b>	<b>0.944</b>	508	175	5
2	Tree-tw	-14369.98	0.2	0.94	<b>159.1</b>	5	5
2	GS-tw	-11265.4	0.24	0.94	386.13	5	5
3	GS-pruned	<b>-10683.4</b>	<b>0.251</b>	<b>0.944</b>	514.42	175	5
3	Tree-tw	-14587.71	0.2	0.94	<b>163.2</b>	5	5
3	GS-tw	-11471.09	0.23	0.94	421.57	5	5
4	GS-pruned	<b>-10715.4</b>	<b>0.254</b>	<b>0.943</b>	516.16	169	5
4	Tree-tw	-14449.06	0.21	0.94	<b>162</b>	5	5
4	GS-tw	-11437.73	0.24	0.94	398.48	5	5
5	GS-pruned	<b>-10806.9</b>	<b>0.25</b>	<b>0.943</b>	491.91	174	5
5	Tree-tw	-14867.97	0.19	0.94	<b>162.7</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-7003.8</b>	<b>0.061</b>	<b>0.986</b>	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	<b>8.1</b>	2	2
2	GS-pruned	-6862.44	<b>0.044</b>	<b>0.986</b>	8.07	4	2
2	Tree-tw	-6936.03	0.03	0.99	11.66	2	2
2	GS-tw	<b>-6857.9</b>	0.03	0.99	<b>8</b>	2	2
3	GS-pruned	-6947.91	0.01	0.99	8.09	3	2
3	Tree-tw	-7004.4	<b>0.022</b>	<b>0.986</b>	11.55	2	2
3	GS-tw	<b>-6946.7</b>	<b>0.022</b>	<b>0.986</b>	<b>8</b>	2	2
4	GS-pruned	-6990.22	<b>0.047</b>	<b>0.986</b>	7.84	4	2
4	Tree-tw	-7043.22	0.03	0.99	11.64	2	2
4	GS-tw	<b>-6989.6</b>	0.03	0.99	<b>7.8</b>	2	2
5	GS-pruned	<b>-7054.9</b>	0.02	0.99	8.71	4	2
5	Tree-tw	-7125.45	<b>0.02</b>	<b>0.986</b>	11.68	2	2
5	GS-tw	-7064.29	<b>0.02</b>	<b>0.986</b>	<b>8.5</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-6876.6</b>	<b>0.066</b>	0.99	8.62	4	3
1	Tree-tw	-6996.27	0.04	<b>0.986</b>	11.55	3	3
1	GS-tw	-6898.37	0.05	<b>0.986</b>	<b>8.5</b>	3	3
2	GS-pruned	<b>-6767.4</b>	<b>0.062</b>	0.99	8.78	4	3
2	Tree-tw	-6872.25	0.04	<b>0.986</b>	11.95	3	3
2	GS-tw	-6776.23	0.05	<b>0.986</b>	<b>8.6</b>	3	3
3	GS-pruned	<b>-6840.5</b>	<b>0.054</b>	0.99	8.71	4	3
3	Tree-tw	-6938.32	0.03	<b>0.986</b>	11.78	3	3
3	GS-tw	-6852.63	0.04	<b>0.986</b>	<b>8.7</b>	3	3
4	GS-pruned	<b>-6927.5</b>	0.05	<b>0.986</b>	8.19	5	3
4	Tree-tw	-6979.31	0.04	0.99	11.77	3	3
4	GS-tw	-6928.91	<b>0.057</b>	0.99	<b>8</b>	3	3
5	GS-pruned	<b>-6936.3</b>	<b>0.045</b>	0.99	<b>8.9</b>	5	3
5	Tree-tw	-7035.78	0.03	<b>0.986</b>	11.8	3	3
5	GS-tw	-6959.44	0.03	<b>0.986</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-6818.5</b>	<b>0.072</b>	<b>0.986</b>	8.88	5	4
1	Tree-tw	-6925.95	0.05	0.99	11.71	4	4
1	GS-tw	-6829.82	0.05	<b>0.986</b>	<b>8.8</b>	4	4
2	GS-pruned	<b>-6703.8</b>	0.06	<b>0.986</b>	8.96	5	4
2	Tree-tw	-6807.34	0.06	<b>0.986</b>	12.01	4	4
2	GS-tw	-6708.65	<b>0.084</b>	<b>0.986</b>	<b>8.7</b>	4	4
3	GS-pruned	<b>-6757.3</b>	0.06	0.99	9.01	5	4
3	Tree-tw	-6882.8	0.03	<b>0.986</b>	12	4	4
3	GS-tw	-6780.41	<b>0.081</b>	<b>0.986</b>	<b>8.8</b>	4	4
4	GS-pruned	<b>-6844.6</b>	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	<b>0.073</b>	<b>0.986</b>	<b>8.5</b>	4	4
5	GS-pruned	<b>-6854.4</b>	0.06	<b>0.986</b>	9.37	5	4
5	Tree-tw	-6960.79	0.03	0.99	11.99	4	4
5	GS-tw	-6864.08	<b>0.062</b>	<b>0.986</b>	<b>9.2</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-6801.8</b>	<b>0.078</b>	0.99	9.13	5	5
1	Tree-tw	-6902.36	0.05	<b>0.986</b>	11.67	5	4
1	GS-tw	<b>-6801.8</b>	<b>0.078</b>	0.99	<b>9.1</b>	5	5
2	GS-pruned	-6655.26	<b>0.071</b>	0.99	8.94	6	5
2	Tree-tw	-6763.59	0.06	<b>0.986</b>	12.11	5	5
2	GS-tw	<b>-6649.6</b>	<b>0.071</b>	<b>0.986</b>	<b>8.9</b>	5	5
3	GS-pruned	<b>-6740</b>	<b>0.061</b>	0.99	<b>9.2</b>	5	5
3	Tree-tw	-6845.16	0.03	<b>0.986</b>	11.91	5	5
3	GS-tw	<b>-6740</b>	<b>0.061</b>	0.99	9.21	5	5
4	GS-pruned	-6812.67	0.06	<b>0.986</b>	8.85	6	5
4	Tree-tw	-6890.58	0.06	0.99	12.02	5	4
4	GS-tw	<b>-6807</b>	<b>0.074</b>	<b>0.986</b>	<b>8.7</b>	5	5
5	GS-pruned	<b>-6827.5</b>	<b>0.049</b>	<b>0.986</b>	9.72	5	5
5	Tree-tw	-6940.02	0.02	<b>0.986</b>	12.16	5	5
5	GS-tw	<b>-6827.5</b>	<b>0.049</b>	<b>0.986</b>	<b>9.7</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-65127.5</b>	<b>0.072</b>	<b>0.966</b>	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	<b>13.5</b>	2	2
2	GS-pruned	<b>-64141.2</b>	<b>0.078</b>	<b>0.967</b>	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	<b>13.7</b>	2	2
3	GS-pruned	<b>-64703.4</b>	<b>0.068</b>	<b>0.967</b>	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	<b>13.6</b>	2	2
4	GS-pruned	<b>-65069.5</b>	<b>0.068</b>	<b>0.966</b>	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	<b>13.8</b>	2	2
5	GS-pruned	<b>-65745.2</b>	<b>0.072</b>	<b>0.966</b>	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	<b>14.2</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-62980.4</b>	<b>0.078</b>	<b>0.967</b>	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	<b>17.7</b>	3	3
2	GS-pruned	<b>-62804</b>	<b>0.068</b>	<b>0.967</b>	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	<b>17.4</b>	3	3
3	GS-pruned	<b>-62681.3</b>	<b>0.068</b>	<b>0.967</b>	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	<b>17.3</b>	3	3
4	GS-pruned	<b>-62464.5</b>	<b>0.077</b>	<b>0.967</b>	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	<b>16.9</b>	3	3
5	GS-pruned	<b>-62650.4</b>	<b>0.075</b>	<b>0.967</b>	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	<b>17.4</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-61661.6</b>	<b>0.077</b>	<b>0.966</b>	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	<b>20.9</b>	4	4
2	GS-pruned	<b>-61737.6</b>	<b>0.081</b>	<b>0.967</b>	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	<b>21.3</b>	4	4
3	GS-pruned	<b>-61631.9</b>	<b>0.085</b>	<b>0.967</b>	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	<b>21</b>	4	4
4	GS-pruned	<b>-61270.8</b>	<b>0.081</b>	<b>0.967</b>	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	<b>20.8</b>	4	4
5	GS-pruned	<b>-61992.1</b>	<b>0.076</b>	<b>0.967</b>	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	<b>20.7</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-61429.4</b>	<b>0.072</b>	<b>0.966</b>	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	<b>30</b>	5	5
2	GS-pruned	<b>-61258.6</b>	<b>0.081</b>	<b>0.967</b>	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	<b>29.3</b>	5	5
3	GS-pruned	<b>-61086.4</b>	<b>0.073</b>	<b>0.967</b>	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	<b>30.2</b>	5	5
4	GS-pruned	<b>-61700.1</b>	<b>0.076</b>	<b>0.967</b>	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	<b>29.3</b>	5	5
5	GS-pruned	<b>-61922.5</b>	<b>0.076</b>	<b>0.966</b>	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	<b>29.7</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-12970.1</b>	0	0.99	119.03	42	2
1	Tree-tw	-13191.68	<b>0.008</b>	0.99	138.97	3	3
1	GS-tw	-12982.03	0.01	<b>0.99</b>	<b>98.5</b>	2	2
2	GS-pruned	<b>-12934.1</b>	0.01	<b>0.99</b>	119.27	58	2
2	Tree-tw	-13215.49	<b>0.013</b>	0.99	133.1	3	3
2	GS-tw	-12961.6	0.01	0.99	<b>97.7</b>	2	2
3	GS-pruned	<b>-12890.3</b>	0.01	<b>0.99</b>	119.93	45	2
3	Tree-tw	-13157.82	0.01	0.99	139.29	3	3
3	GS-tw	-12899.4	<b>0.014</b>	0.99	<b>100.1</b>	2	2
4	GS-pruned	<b>-13014.8</b>	0.01	<b>0.99</b>	120.77	40	2
4	Tree-tw	-13189.21	<b>0.014</b>	0.99	135.79	3	3
4	GS-tw	-13030.36	0.01	0.99	<b>97.3</b>	2	2
5	GS-pruned	<b>-12950.2</b>	0.02	<b>0.99</b>	127.47	51	2
5	Tree-tw	-13204.27	0.02	0.99	135.91	3	3
5	GS-tw	-12972.62	<b>0.02</b>	0.99	<b>98.7</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-12837.21	0.01	<b>0.99</b>	124.83	44	3
1	Tree-tw	-13216.03	<b>0.008</b>	0.99	135.65	3	3
1	GS-tw	<b>-12831.4</b>	0.01	0.99	<b>113.4</b>	3	3
2	GS-pruned	-12832.62	0.01	<b>0.99</b>	133.28	52	3
2	Tree-tw	-13238.52	<b>0.013</b>	0.99	134.69	4	4
2	GS-tw	<b>-12827.1</b>	0.01	0.99	<b>111.1</b>	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	<b>-12760.2</b>	<b>0.016</b>	<b>0.99</b>	<b>111.2</b>	3	3
4	GS-pruned	-12934.33	0.01	<b>0.99</b>	127.05	48	3
4	Tree-tw	-13212.92	<b>0.013</b>	0.99	136.93	3	3
4	GS-tw	<b>-12904</b>	0.01	0.99	<b>107.7</b>	3	3
5	GS-pruned	<b>-12817.6</b>	0.02	<b>0.99</b>	124.77	55	3
5	Tree-tw	-13201.23	0.01	0.99	143.75	3	3
5	GS-tw	-12832.31	<b>0.021</b>	0.99	<b>108.6</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-12830.52	<b>0.008</b>	<b>0.99</b>	131.04	46	4
1	Tree-tw	-13218.71	0.01	0.99	137.29	4	4
1	GS-tw	<b>-12801</b>	0.01	0.99	<b>113.8</b>	4	4
2	GS-pruned	<b>-12778.2</b>	0.01	<b>0.99</b>	130.39	56	4
2	Tree-tw	-13248.09	<b>0.013</b>	0.99	142.18	4	4
2	GS-tw	-12779.1	0.01	0.99	<b>112.2</b>	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	<b>-12674</b>	<b>0.016</b>	<b>0.99</b>	<b>113.3</b>	4	4
4	GS-pruned	-12836.54	0.01	<b>0.99</b>	128.42	47	4
4	Tree-tw	-13215.57	<b>0.012</b>	0.99	137.07	5	5
4	GS-tw	<b>-12809.5</b>	0.01	0.99	<b>110.4</b>	4	4
5	GS-pruned	<b>-12785.6</b>	0.02	<b>0.99</b>	129	56	4
5	Tree-tw	-13207.97	0.02	0.99	136.38	4	4
5	GS-tw	-12793.31	<b>0.022</b>	0.99	<b>109.5</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-12832.04	<b>0.008</b>	<b>0.99</b>	139.98	51	5
1	Tree-tw	-13223.6	0.01	0.99	134.62	5	5
1	GS-tw	<b>-12824.5</b>	0.01	0.99	<b>115.2</b>	5	5
2	GS-pruned	-12783.79	<b>0.012</b>	0.99	143.67	52	5
2	Tree-tw	-13237.96	<b>0.012</b>	0.99	135.21	5	5
2	GS-tw	<b>-12774</b>	0.01	<b>0.99</b>	<b>114.4</b>	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	<b>-12649.9</b>	<b>0.019</b>	<b>0.99</b>	<b>121</b>	5	5
4	GS-pruned	-12835.98	0.01	<b>0.99</b>	143.36	44	5
4	Tree-tw	-13212.17	<b>0.012</b>	0.99	134.87	5	5
4	GS-tw	<b>-12806.1</b>	0.01	0.99	<b>123</b>	5	5
5	GS-pruned	<b>-12776.7</b>	<b>0.021</b>	<b>0.99</b>	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	<b>121.2</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-21116.3</b>	<b>0.264</b>	<b>0.934</b>	102.67	74	2
1	Tree-tw	-28622.25	0.22	0.93	<b>40.5</b>	2	2
1	GS-tw	-28030.39	0.24	0.93	55.68	2	2
2	GS-pruned	<b>-20496.3</b>	<b>0.266</b>	<b>0.935</b>	101.32	62	2
2	Tree-tw	-27816.83	0.24	0.93	<b>38.9</b>	2	2
2	GS-tw	-27084.77	0.24	0.93	54	2	2
3	GS-pruned	<b>-20218.9</b>	<b>0.27</b>	<b>0.936</b>	103.64	66	2
3	Tree-tw	-27134.19	0.23	0.93	<b>40.4</b>	2	2
3	GS-tw	-26223.62	0.25	0.93	54.47	2	2
4	GS-pruned	<b>-21134.4</b>	<b>0.26</b>	<b>0.934</b>	101.45	62	2
4	Tree-tw	-28776.73	0.22	0.93	<b>40.5</b>	2	2
4	GS-tw	-28104.55	0.24	0.93	54.41	2	2
5	GS-pruned	<b>-20851.2</b>	<b>0.238</b>	<b>0.933</b>	106.29	64	2
5	Tree-tw	-28193.69	0.22	0.93	<b>39.9</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-20768.9</b>	<b>0.272</b>	<b>0.936</b>	110.03	59	3
1	Tree-tw	-28656.97	0.23	0.93	<b>49</b>	3	3
1	GS-tw	-26100.14	0.24	0.93	75.11	3	3
2	GS-pruned	<b>-20455.3</b>	<b>0.293</b>	<b>0.938</b>	112.16	54	3
2	Tree-tw	-28068.07	0.24	0.93	<b>47.9</b>	3	3
2	GS-tw	-25537.51	0.27	0.93	74.14	3	3
3	GS-pruned	<b>-20002.2</b>	<b>0.284</b>	<b>0.938</b>	112.05	59	3
3	Tree-tw	-26975.48	0.24	0.93	<b>48</b>	3	3
3	GS-tw	-24578.89	0.26	0.93	74.29	3	3
4	GS-pruned	<b>-21013.6</b>	<b>0.272</b>	<b>0.936</b>	109.68	56	3
4	Tree-tw	-28668.23	0.23	0.93	<b>49.6</b>	3	3
4	GS-tw	-26518.1	0.26	0.93	74.19	3	3
5	GS-pruned	<b>-20521.6</b>	<b>0.273</b>	<b>0.936</b>	110.38	61	3
5	Tree-tw	-28214.71	0.22	0.93	<b>48.4</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-21042.1</b>	<b>0.274</b>	<b>0.936</b>	112.29	63	4
1	Tree-tw	-28742.16	0.23	0.93	<b>52.4</b>	4	4
1	GS-tw	-24785.8	0.25	0.93	87.92	4	4
2	GS-pruned	<b>-20619.9</b>	<b>0.287</b>	<b>0.937</b>	112.54	51	4
2	Tree-tw	-27885.11	0.25	0.93	<b>50.6</b>	4	4
2	GS-tw	-24063.92	0.27	0.93	88.15	4	4
3	GS-pruned	<b>-20042.4</b>	<b>0.293</b>	<b>0.939</b>	114.89	60	4
3	Tree-tw	-26893.2	0.24	0.93	<b>51.7</b>	4	4
3	GS-tw	-23033.78	0.28	0.94	89.1	4	4
4	GS-pruned	<b>-21046.4</b>	<b>0.277</b>	<b>0.936</b>	111.19	62	4
4	Tree-tw	-28738.6	0.23	0.93	<b>53.4</b>	4	4
4	GS-tw	-24891.71	0.26	0.93	87.34	4	4
5	GS-pruned	<b>-20602.7</b>	<b>0.276</b>	<b>0.936</b>	112.8	60	4
5	Tree-tw	-28316.49	0.23	0.93	<b>51.9</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-20993.2</b>	<b>0.274</b>	<b>0.936</b>	113.26	62	5
1	Tree-tw	-28576.28	0.24	0.93	<b>54.1</b>	5	5
1	GS-tw	-23431.19	0.27	0.93	95.04	5	5
2	GS-pruned	<b>-20984.6</b>	<b>0.274</b>	<b>0.936</b>	111.53	50	5
2	Tree-tw	-28068.07	0.24	0.93	<b>52.6</b>	5	5
2	GS-tw	-23068.58	0.27	0.94	93.9	5	5
3	GS-pruned	<b>-20419.9</b>	<b>0.289</b>	<b>0.938</b>	114.15	61	5
3	Tree-tw	-26886.13	0.24	0.93	<b>54.2</b>	5	5
3	GS-tw	-22342.69	0.28	0.94	95.79	5	5
4	GS-pruned	<b>-21111.9</b>	<b>0.289</b>	<b>0.937</b>	112	53	5
4	Tree-tw	-28776.6	0.23	0.93	<b>54</b>	5	5
4	GS-tw	-23616.57	0.28	0.93	94.18	5	5
5	GS-pruned	<b>-20877</b>	<b>0.275</b>	<b>0.936</b>	114.3	58	5
5	Tree-tw	-28270.12	0.23	0.93	<b>54.8</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-11299.4</b>	<b>0.162</b>	<b>0.987</b>	2227.37	157	2
1	Tree-tw	-14148.48	0.14	0.98	<b>945.8</b>	3	3
1	GS-tw	-13425.81	0.15	0.98	1298.65	2	2
2	GS-pruned	<b>-11240.6</b>	<b>0.176</b>	<b>0.987</b>	2222.64	157	2
2	Tree-tw	-13898.17	0.16	0.98	<b>910.4</b>	3	3
2	GS-tw	-12858.09	0.16	0.99	1413.93	2	2
3	GS-pruned	<b>-11108.5</b>	<b>0.17</b>	<b>0.987</b>	2112.64	168	2
3	Tree-tw	-14264.92	0.14	0.98	<b>942.2</b>	3	3
3	GS-tw	-13169.12	0.15	0.99	1401.55	2	2
4	GS-pruned	<b>-10871.4</b>	<b>0.183</b>	<b>0.987</b>	2108.82	170	2
4	Tree-tw	-13702.97	0.16	0.98	<b>973.9</b>	3	3
4	GS-tw	-12769.65	0.17	0.99	1437.57	2	2
5	GS-pruned	<b>-11352.1</b>	<b>0.147</b>	<b>0.986</b>	2165.53	173	2
5	Tree-tw	-14392.87	0.14	0.98	<b>934.1</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-11090.4</b>	<b>0.17</b>	<b>0.987</b>	2252.57	161	3
1	Tree-tw	-14596.16	0.14	0.98	<b>1068.7</b>	4	4
1	GS-tw	-13031.31	0.15	0.98	1659.8	3	3
2	GS-pruned	<b>-11093.1</b>	<b>0.181</b>	<b>0.987</b>	2209.16	168	3
2	Tree-tw	-13996.01	0.16	0.98	<b>1071.2</b>	4	4
2	GS-tw	-12384.95	0.16	0.99	1695.27	3	3
3	GS-pruned	<b>-11098.8</b>	<b>0.169</b>	<b>0.987</b>	2166	161	3
3	Tree-tw	-14469.91	0.14	0.98	<b>1071.1</b>	4	4
3	GS-tw	-12785.68	0.16	0.99	1612.76	3	3
4	GS-pruned	<b>-10869.4</b>	<b>0.184</b>	<b>0.987</b>	2264.55	153	3
4	Tree-tw	-13974.8	0.15	0.98	<b>1085.5</b>	4	4
4	GS-tw	-12406.06	0.16	0.99	1730.51	3	3
5	GS-pruned	<b>-11343.9</b>	0.16	<b>0.987</b>	2241.75	163	3
5	Tree-tw	-14519.54	0.15	0.98	<b>1080.6</b>	4	4
5	GS-tw	-12640.94	<b>0.16</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-11163.7</b>	0.17	<b>0.987</b>	2344.13	154	4
1	Tree-tw	-14797.66	0.14	0.98	<b>1153.8</b>	5	5
1	GS-tw	-12030.82	<b>0.17</b>	0.99	1795.47	4	4
2	GS-pruned	<b>-11044.3</b>	<b>0.185</b>	<b>0.987</b>	2403.38	158	4
2	Tree-tw	-14148.77	0.16	0.98	<b>1111.8</b>	5	5
2	GS-tw	-11615.69	0.17	0.99	1913.45	4	4
3	GS-pruned	<b>-11112.8</b>	<b>0.17</b>	<b>0.987</b>	2351.94	183	4
3	Tree-tw	-14592.64	0.14	0.98	<b>1119.5</b>	5	5
3	GS-tw	-11871.06	0.17	0.99	1872.99	4	4
4	GS-pruned	<b>-10837.9</b>	0.18	<b>0.987</b>	2199.8	153	4
4	Tree-tw	-14098.97	0.17	0.98	<b>1144.9</b>	5	5
4	GS-tw	-11594.91	<b>0.185</b>	0.99	1863.18	4	4
5	GS-pruned	<b>-11335.9</b>	0.16	<b>0.987</b>	2360.88	171	4
5	Tree-tw	-14632.12	0.15	0.98	<b>1109.1</b>	5	5
5	GS-tw	-12038.81	<b>0.171</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-11179.9</b>	0.17	<b>0.987</b>	2349.92	167	5
1	Tree-tw	-14877.27	0.14	0.98	<b>1078.5</b>	6	6
1	GS-tw	-11909.28	<b>0.171</b>	0.99	1886.92	5	5
2	GS-pruned	<b>-11029.7</b>	<b>0.182</b>	<b>0.987</b>	2359.26	172	5
2	Tree-tw	-14149.64	0.16	0.98	<b>1105.7</b>	6	6
2	GS-tw	-11584.34	0.18	0.99	1910.93	5	5
3	GS-pruned	<b>-11107.6</b>	0.17	<b>0.987</b>	2376.38	184	5
3	Tree-tw	-14620.07	0.15	0.98	<b>1094.9</b>	6	6
3	GS-tw	-11680.54	<b>0.168</b>	0.99	1979.93	5	5
4	GS-pruned	<b>-10837.5</b>	<b>0.185</b>	<b>0.987</b>	2319.04	172	5
4	Tree-tw	-14217.4	0.16	0.98	<b>1131.1</b>	6	6
4	GS-tw	-11392.62	0.17	0.99	1936.27	5	5
5	GS-pruned	<b>-11437.4</b>	0.16	<b>0.987</b>	2284.55	172	5
5	Tree-tw	-14647.96	0.15	0.98	<b>1119.1</b>	6	6
5	GS-tw	-11974.16	<b>0.169</b>	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	<b>-130185.5</b>	<b>0.118</b>	<b>0.929</b>	824.91	147	2
1	Tree-tw	-137613.32	0.06	0.92	<b>164</b>	2	2
1	GS-tw	-131700.79	0.09	0.93	383.86	2	2
2	GS-pruned	<b>-130733</b>	<b>0.118</b>	<b>0.928</b>	803.65	133	2
2	Tree-tw	-138083.66	0.06	0.92	<b>161.3</b>	2	2
2	GS-tw	-132110.88	0.11	0.93	394.84	2	2
3	GS-pruned	<b>-129653.5</b>	<b>0.118</b>	<b>0.929</b>	820.19	144	2
3	Tree-tw	-136872.97	0.06	0.92	<b>160.9</b>	2	2
3	GS-tw	-131500.83	0.08	0.93	390.94	2	2
4	GS-pruned	<b>-131302.5</b>	<b>0.109</b>	<b>0.928</b>	846.24	152	2
4	Tree-tw	-138596.89	0.06	0.92	<b>160.4</b>	2	2
4	GS-tw	-133351.94	0.09	0.93	398.97	2	2
5	GS-pruned	<b>-130542.7</b>	<b>0.114</b>	<b>0.929</b>	833.14	141	2
5	Tree-tw	-137963.96	0.06	0.92	<b>159.7</b>	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	<b>-128035.7</b>	0.12	<b>0.929</b>	848.91	160	3
1	Tree-tw	-137282.38	0.06	0.92	<b>164.1</b>	3	3
1	GS-tw	-128290.35	<b>0.116</b>	0.93	535.42	3	3
2	GS-pruned	<b>-128606.6</b>	<b>0.123</b>	<b>0.928</b>	812.61	128	3
2	Tree-tw	-137876.92	0.06	0.92	<b>164.2</b>	3	3
2	GS-tw	-128794.85	0.12	0.93	552.8	3	3
3	GS-pruned	<b>-127059.6</b>	<b>0.126</b>	<b>0.929</b>	832.76	134	3
3	Tree-tw	-136503.3	0.06	0.92	<b>163.4</b>	3	3
3	GS-tw	-127440.46	0.12	0.93	564.84	3	3
4	GS-pruned	<b>-128954.4</b>	0.11	<b>0.928</b>	860.87	154	3
4	Tree-tw	-138493.99	0.06	0.92	<b>167.7</b>	3	3
4	GS-tw	-129254.32	<b>0.11</b>	0.93	531.42	3	3
5	GS-pruned	<b>-128508.7</b>	<b>0.117</b>	<b>0.929</b>	840.93	137	3
5	Tree-tw	-137748.32	0.06	0.92	<b>165</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	-126716.17	0.12	<b>0.929</b>	846.6	139	4
1	Tree-tw	-137396.97	0.06	0.92	<b>168.7</b>	4	4
1	GS-tw	<b>-126695.8</b>	<b>0.123</b>	0.93	591.17	4	4
2	GS-pruned	-127860.67	0.12	<b>0.928</b>	816.94	142	4
2	Tree-tw	-137955.81	0.06	0.92	<b>174.2</b>	4	4
2	GS-tw	<b>-127781.8</b>	<b>0.122</b>	0.93	591.4	4	4
3	GS-pruned	<b>-125959.5</b>	0.12	<b>0.929</b>	848.1	147	4
3	Tree-tw	-136686.82	0.06	0.92	<b>169.3</b>	4	4
3	GS-tw	-126046.37	<b>0.122</b>	0.93	605.3	4	4
4	GS-pruned	<b>-127236.8</b>	0.12	<b>0.928</b>	859.36	137	4
4	Tree-tw	-138526.54	0.06	0.92	<b>176.7</b>	5	5
4	GS-tw	-127299.75	<b>0.118</b>	0.93	606.52	4	4
5	GS-pruned	<b>-127246.2</b>	<b>0.117</b>	<b>0.929</b>	857.86	153	4
5	Tree-tw	-137864.78	0.06	0.92	<b>181.1</b>	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 ( $\text{acc}_G$ ), the mean accuracy ( $\text{acc}_M$ ), 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	$\text{acc}_G$	$\text{acc}_M$	time	tw	tw-pr
1	GS-pruned	<b>-126097</b>	<b>0.124</b>	<b>0.929</b>	879.83	141	5
1	Tree-tw	-137533.27	0.06	0.92	<b>173.2</b>	6	6
1	GS-tw	-126132.06	0.12	0.93	658.52	5	5
2	GS-pruned	-126820.89	<b>0.12</b>	<b>0.928</b>	835.69	134	5
2	Tree-tw	-137978.12	0.06	0.92	<b>171.3</b>	5	5
2	GS-tw	<b>-126770.5</b>	0.12	0.93	638.11	5	5
3	GS-pruned	-124662.1	0.12	<b>0.929</b>	854.26	152	5
3	Tree-tw	-136727.17	0.06	0.92	<b>172.5</b>	5	5
3	GS-tw	<b>-124590.4</b>	<b>0.126</b>	0.93	673.49	5	5
4	GS-pruned	-126195.54	0.12	<b>0.928</b>	887.45	148	5
4	Tree-tw	-138692.29	0.06	0.92	<b>176.1</b>	5	5
4	GS-tw	<b>-126162.8</b>	<b>0.121</b>	0.93	669.09	5	5
5	GS-pruned	-126091.93	<b>0.121</b>	<b>0.929</b>	876.82	138	5
5	Tree-tw	-137928.05	0.06	0.92	<b>174.4</b>	5	5
5	GS-tw	<b>-125914.8</b>	0.12	0.93	658.17	5	5