Supplementary Material for Chapter 5: comparison with unbounded methods

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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