

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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	-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	–	–