Output tables for the test of Multiple comparisons.

October 30, 2021

1 Average rankings of Friedman test

Average ranks obtained by applying the Friedman procedure

Algorithm	Ranking
brm-original	3.4301
brm-correlation	3.5484
brm-cosine	3.8441
brm-manhattan	3.5699
gmm	2.9301
isof	4.8763
ocsvm	5.8011

Table 1: Average Rankings of the algorithms

Friedman statistic considering reduction performance (distributed according to chi-square with 6 degrees of freedom: 117.470046.
P-value computed by Friedman Test: 5.644129608128878E-11.

2 Post hoc comparisons

Results achieved on post hoc comparisons for $\alpha = 0.05$, $\alpha = 0.10$ and adjusted p-values.

2.1 P-values for $\alpha = 0.05$

i	algorithms	$z = (R_0 - R_i)/SE$	p	Holm
21	gmm vs. ocsvm	9.062571	0	0.002381
20	brm-original vs. ocsvm	7.484258	0	0.0025
19	brm-correlation vs. ocsvm	7.110893	0	0.002632
18	brm-manhattan vs. ocsvm	7.043009	0	0.002778
17	brm-cosine vs. ocsvm	6.177483	0	0.002941
16	gmm vs. isof	6.14354	0	0.003125
15	brm-original vs. isof	4.565227	0.000005	0.003333
14	brm-correlation vs. isof	4.191863	0.000028	0.003571
13	brm-manhattan vs. isof	4.123979	0.000037	0.003846
12	brm-cosine vs. isof	3.258452	0.00112	0.004167
11	isof vs. ocsvm	2.91903	0.003511	0.004545
10	brm-cosine vs. gmm	2.885088	0.003913	0.005
9	brm-manhattan vs. gmm	2.019562	0.043429	0.005556
8	brm-correlation vs. gmm	1.951677	0.050977	0.00625
7	brm-original vs. gmm	1.578313	0.114494	0.007143
6	brm-original vs. brm-cosine	1.306775	0.191289	0.008333
5	brm-correlation vs. brm-cosine	0.933411	0.350608	0.01
4	brm-cosine vs. brm-manhattan	0.865526	0.38675	0.0125
3	brm-original vs. brm-manhattan	0.441249	0.659033	0.016667
2	brm-original vs. brm-correlation	0.373364	0.708877	0.025
1	brm-correlation vs. brm-manhattan	0.067884	0.945878	0.05

Table 2: P-values Table for $\alpha = 0.05$

Holm's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.005556.

2.2 P-values for $\alpha = 0.10$

i	algorithms	$z = (R_0 - R_i)/SE$	p	Holm
21	gmm vs. ocsvm	9.062571	0	0.004762
20	brm-original vs. ocsvm	7.484258	0	0.005
19	brm-correlation vs. ocsvm	7.110893	0	0.005263
18	brm-manhattan vs. ocsvm	7.043009	0	0.005556
17	brm-cosine vs. ocsvm	6.177483	0	0.005882
16	gmm vs. isof	6.14354	0	0.00625
15	brm-original vs. isof	4.565227	0.000005	0.006667
14	brm-correlation vs. isof	4.191863	0.000028	0.007143
13	brm-manhattan vs. isof	4.123979	0.000037	0.007692
12	brm-cosine vs. isof	3.258452	0.00112	0.008333
11	isof vs. ocsvm	2.91903	0.003511	0.009091
10	brm-cosine vs. gmm	2.885088	0.003913	0.01
9	brm-manhattan vs. gmm	2.019562	0.043429	0.011111
8	brm-correlation vs. gmm	1.951677	0.050977	0.0125
7	brm-original vs. gmm	1.578313	0.114494	0.014286
6	brm-original vs. brm-cosine	1.306775	0.191289	0.016667
5	brm-correlation vs. brm-cosine	0.933411	0.350608	0.02
4	brm-cosine vs. brm-manhattan	0.865526	0.38675	0.025
3	brm-original vs. brm-manhattan	0.441249	0.659033	0.033333
2	brm-original vs. brm-correlation	0.373364	0.708877	0.05
1	brm-correlation vs. brm-manhattan	0.067884	0.945878	0.1

Table 3: P-values Table for $\alpha = 0.10$

Holm's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.011111.

2.3 Adjusted p-values

i	hypothesis	unadjusted p	p_{Holm}
1	gmm vs .ocsvm	0	0
2	brm-original vs .ocsvm	0	0
3	brm-correlation vs .ocsvm	0	0
4	brm-manhattan vs .ocsvm	0	0
5	brm-cosine vs .ocsvm	0	0
6	gmm vs .isof	0	0
7	brm-original vs .isof	0.000005	0.000075
8	brm-correlation vs .isof	0.000028	0.000387
9	brm-manhattan vs .isof	0.000037	0.000484
10	brm-cosine vs .isof	0.00112	0.013443
11	isof vs .ocsvm	0.003511	0.038623
12	brm-cosine vs .gmm	0.003913	0.03913
13	brm-manhattan vs .gmm	0.043429	0.39086
14	brm-correlation vs .gmm	0.050977	0.407812
15	brm-original vs .gmm	0.114494	0.801456
16	brm-original vs .brm-cosine	0.191289	1.147735
17	brm-correlation vs .brm-cosine	0.350608	1.753039
18	brm-cosine vs .brm-manhattan	0.38675	1.753039
19	brm-original vs .brm-manhattan	0.659033	1.977099
20	brm-original vs .brm-correlation	0.708877	1.977099
21	brm-correlation vs .brm-manhattan	0.945878	1.977099

Table 4: Adjusted p-values