

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	3.1237
brm-correlation	4.4892
brm-cosine	4.2849
brm-manhattan	2.8656
gmm	3.3118
isof	5.2419
ocsvm	4.6828

Table 1: Average Rankings of the algorithms

Friedman statistic considering reduction performance (distributed according to chi-square with 6 degrees of freedom: 96.8053.
P-value computed by Friedman Test: 5.968114891174991E-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	brm-manhattan vs. isof	7.501229	0	0.002381
20	brm-original vs. isof	6.686616	0	0.0025
19	gmm vs. isof	6.092627	0	0.002632
18	brm-manhattan vs. ocsvm	5.736234	0	0.002778
17	brm-correlation vs. brm-manhattan	5.125274	0	0.002941
16	brm-original vs. ocsvm	4.921621	0.000001	0.003125
15	brm-cosine vs. brm-manhattan	4.480372	0.000007	0.003333
14	gmm vs. ocsvm	4.327632	0.000015	0.003571
13	brm-original vs. brm-correlation	4.310661	0.000016	0.003846
12	brm-correlation vs. gmm	3.716672	0.000202	0.004167
11	brm-original vs. brm-cosine	3.665759	0.000247	0.004545
10	brm-cosine vs. gmm	3.07177	0.002128	0.005
9	brm-cosine vs. isof	3.020857	0.002521	0.005556
8	brm-correlation vs. isof	2.375955	0.017504	0.00625
7	isof vs. ocsvm	1.764995	0.077565	0.007143
6	brm-manhattan vs. gmm	1.408602	0.158953	0.008333
5	brm-cosine vs. ocsvm	1.255862	0.209166	0.01
4	brm-original vs. brm-manhattan	0.814613	0.415294	0.0125
3	brm-correlation vs. brm-cosine	0.644902	0.518991	0.016667
2	brm-correlation vs. ocsvm	0.61096	0.541226	0.025
1	brm-original vs. gmm	0.593989	0.55252	0.05

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

Holm's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.00625 .

2.2 P-values for $\alpha = 0.10$

i	algorithms	$z = (R_0 - R_i)/SE$	p	Holm
21	brm-manhattan vs. isof	7.501229	0	0.004762
20	brm-original vs. isof	6.686616	0	0.005
19	gmm vs. isof	6.092627	0	0.005263
18	brm-manhattan vs. ocsvm	5.736234	0	0.005556
17	brm-correlation vs. brm-manhattan	5.125274	0	0.005882
16	brm-original vs. ocsvm	4.921621	0.000001	0.00625
15	brm-cosine vs. brm-manhattan	4.480372	0.000007	0.006667
14	gmm vs. ocsvm	4.327632	0.000015	0.007143
13	brm-original vs. brm-correlation	4.310661	0.000016	0.007692
12	brm-correlation vs. gmm	3.716672	0.000202	0.008333
11	brm-original vs. brm-cosine	3.665759	0.000247	0.009091
10	brm-cosine vs. gmm	3.07177	0.002128	0.01
9	brm-cosine vs. isof	3.020857	0.002521	0.011111
8	brm-correlation vs. isof	2.375955	0.017504	0.0125
7	isof vs. ocsvm	1.764995	0.077565	0.014286
6	brm-manhattan vs. gmm	1.408602	0.158953	0.016667
5	brm-cosine vs. ocsvm	1.255862	0.209166	0.02
4	brm-original vs. brm-manhattan	0.814613	0.415294	0.025
3	brm-correlation vs. brm-cosine	0.644902	0.518991	0.033333
2	brm-correlation vs. ocsvm	0.61096	0.541226	0.05
1	brm-original vs. gmm	0.593989	0.55252	0.1

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

Holm's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.0125 .

2.3 Adjusted p-values

i	hypothesis	unadjusted p	p_{Holm}
1	brm-manhattan vs .isof	0	0
2	brm-original vs .isof	0	0
3	gmm vs .isof	0	0
4	brm-manhattan vs .ocsvm	0	0
5	brm-correlation vs .brm-manhattan	0	0.000005
6	brm-original vs .ocsvm	0.000001	0.000014
7	brm-cosine vs .brm-manhattan	0.000007	0.000112
8	gmm vs .ocsvm	0.000015	0.000211
9	brm-original vs .brm-correlation	0.000016	0.000212
10	brm-correlation vs .gmm	0.000202	0.002422
11	brm-original vs .brm-cosine	0.000247	0.002713
12	brm-cosine vs .gmm	0.002128	0.021279
13	brm-cosine vs .isof	0.002521	0.022685
14	brm-correlation vs .isof	0.017504	0.140029
15	isof vs .ocsvm	0.077565	0.542952
16	brm-manhattan vs .gmm	0.158953	0.953718
17	brm-cosine vs .ocsvm	0.209166	1.04583
18	brm-original vs .brm-manhattan	0.415294	1.661175
19	brm-correlation vs .brm-cosine	0.518991	1.661175
20	brm-correlation vs .ocsvm	0.541226	1.661175
21	brm-original vs .gmm	0.55252	1.661175

Table 4: Adjusted p -values