

Results

June 18, 2010

1 Tables of Friedman, Aligned Friedman, Bonferroni-Dunn, Holm, Hochberg and Hommel Tests

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Table 1: Average Rankings of the algorithms (Friedman)

Algorithm	Ranking
DE	3.368421052631578
CHC	1.368421052631579
G-CMA-ES	2.026315789473684
VXQR1	3.2368421052631575

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 31.94210526315776. P-value computed by Friedman Test: 5.383031408401351E-7.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 22.945179584120762. P-value computed by Iman and Davenport Test: 1.0403653494250875E-9.

Table 2: Average Rankings of the algorithms (Aligned Friedman)

Algorithm	Ranking
DE	48.42105263157895
CHC	20.52631578947368
G-CMA-ES	35.13157894736842
VXQR1	49.92105263157896

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.241162499160188. P-value computed by Aligned Friedman Test: 0.0025946072003562026.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.26578947368421
CHC	1.3684210526315788
G-CMA-ES	2.021052631578947
VXQR1	3.344736842105263

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 25.492408367528714. P-value computed by Quade Test: 2.0828894164992562E-10.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-54.75	-32.02	-3.225
CHC	54.75	0.000	22.73	51.53
G-CMA-ES	32.02	-22.73	0.000	28.80
VXQR1	3.225	-51.53	-28.80	0.000

Table 5: Holm / Hochberg / Holland / Rom / Finner / Li Table for $\alpha = 0.05$ (FRIEDMAN)

i	algorithm	$z = (R_0 - R_i)/SE$	p	Holm/Hochberg/Hommel	Holland	Rom	Finner	Li
3	DE	4.774934554525326	1.7976570566877927E-6	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.0465130606235343
2	VXQR1	4.460794123306556	8.165650609903694E-6	0.025	0.025320565519103866	0.025	0.033361747021845407	0.0465130606235343
1	G-CMA-ES	1.5707021560938577	0.11625184815284836	0.05	0.050000000000000044	0.05	0.050000000000000044	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

Holm's procedure rejects those hypotheses that have a p-value ≤ 0.05 .

Hochberg's procedure rejects those hypotheses that have a p-value ≤ 0.025 .

Hommel's procedure rejects those hypotheses that have a p-value ≤ 0.05 .

Holland's procedure rejects those hypotheses that have a p-value $\leq 0.050000000000000044$.

Rom's procedure rejects those hypotheses that have a p-value ≤ 0.025 .

Finner's procedure rejects those hypotheses that have a p-value $\leq 0.050000000000000044$.

Li's procedure rejects those hypotheses that have a p-value ≤ 0.0465130606235343 .

Table 6: Holm / Hochberg / Holland / Rom / Finner / Li Table for $\alpha = 0.05$ (ALIGNED FRIEDMAN)

i	algorithm	$z = (R_0 - R_i)/SE$	p	Holm/Hochberg/Hommel	Holland	Rom	Finner	Li
3	VXQR1	4.102700775059575	4.083552273908021E-5	0.016952427508441503	0.016952427508441503	0.016952427508441503	0.016952427508441503	0.05044734458272409
2	DE	3.8933418277199188	9.88726779596866E-5	0.025	0.025320565519103666	0.025	0.03361747021845407	0.05044734458272409
1	G-CMA-ES	2.038495013570334	0.041500452928242317	0.05	0.050000000000000044	0.05	0.050000000000000044	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

Hochberg's procedure rejects those hypotheses that have a p-value ≤ 0.05 .

Hommel's procedure rejects all hypotheses.

Rom's procedure rejects those hypotheses that have a p-value ≤ 0.05 .

Li's procedure rejects those hypotheses that have a p-value ≤ 0.05 .

Table 7: Holm / Hochberg / Holland / Rom / Finner / Li Table for $\alpha = 0.05$ (QUADE)

i	algorithm	$z = (R_0 - R_i)/SE$	p	Holm/Hochberg/Hommel	Holland	Rom	Finner	Li
3	VXQR1	3.378908742700515	7.277416083453931E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.03871022528434968
2	DE	3.24393236150076	0.001178917376647768	0.025	0.025320565519103666	0.025	0.03361747021845407	0.03871022528434968
1	G-CMA-ES	1.1158047512513016	0.26450571959735625	0.05	0.0500000000000000044	0.05	0.0500000000000000044	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

Holm's procedure rejects those hypotheses that have a p-value ≤ 0.05 .

Hochberg's procedure rejects those hypotheses that have a p-value ≤ 0.025 .

Hommel's procedure rejects those hypotheses that have a p-value ≤ 0.05 .

Holland's procedure rejects those hypotheses that have a p-value $\leq 0.0500000000000000044$.

Rom's procedure rejects those hypotheses that have a p-value ≤ 0.025 .

Finner's procedure rejects those hypotheses that have a p-value $\leq 0.0500000000000000044$.

Li's procedure rejects those hypotheses that have a p-value ≤ 0.03871022528434968 .

Table 8: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	DE	1.7976570566877927E-6	5.3929711700633785E-6	5.3929711700633785E-6	5.3929711700633785E-6	5.3929711700633785E-6
2	VXQR1	8.165650609903694E-6	2.449695182971108E-5	1.6331301219807388E-5	1.6331301219807388E-5	1.6331301219807388E-5
3	G-CMA-ES	0.11625184815284836	0.34875554445854506	0.11625184815284836	0.11625184815284836	0.11625184815284836

Table 9: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Hol}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	1.7976570566877927E-6	5.392961475281233E-6	5.3929711700633785E-6	5.392961475281233E-6	2.0341240841895315E-6
2	VXQR1	8.165650609903694E-6	1.633123454192198E-5	1.6331301219807388E-5	1.2248450910634645E-5	9.23970833161753E-6
3	G-CMA-ES	0.11625184815284836	0.11625184815284839	0.11625184815284836	0.11625184815284839	0.11625184815284836

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hom}
1	VXQR1	4.083552273908021E-5	1.2250656821724063E-4	1.2250656821724063E-4	1.2250656821724063E-4	1.2250656821724063E-4
2	DE	9.88726779596866E-5	2.966180338790598E-4	1.977453559193732E-4	1.977453559193732E-4	1.977453559193732E-4
3	G-CMA-ES	0.041500452928242317	0.12450135878472696	0.041500452928242317	0.041500452928242317	0.041500452928242317

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	VXQR1	4.083552273908021E-5	1.225015656654005E-4	1.225015656654005E-4	1.225015656654005E-4	4.260177607598549E-5
2	DE	9.88726779596866E-5	1.9773558011293435E-4	1.977453559193732E-4	1.4830535095178288E-4	1.0314295947358385E-4
3	G-CMA-ES	0.041500452928242317	0.04150045292824234	0.04150045292824234	0.04150045292824234	0.041500452928242317

Table 12: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	VXQR1	7.277416083453931E-4	0.0021832248250361792	0.0021832248250361792	0.0021832248250361792	0.0017683760649716519
2	DE	0.001178917376647768	0.0035367521299433037	0.002357834753295536	0.002357834753295536	0.002357834753295536
3	G-CMA-ES	0.26450571959735625	0.7935171587920687	0.26450571959735625	0.26450571959735625	0.26450571959735625

Table 13: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	VXQR1	7.277416083453931E-4	0.002181636386908381	0.0021832248250361792	0.002181636386908381	9.884811735970194E-4
2	DE	0.001178917376647768	0.0023564449071146187	0.002357834753295536	0.002181636386908381	0.0016003261421775978
3	G-CMA-ES	0.26450571959735625	0.26450571959735625	0.26450571959735625	0.26450571959735625	0.26450571959735625