

Results

June 18, 2010

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

1

Table 1: Average Rankings of the algorithms (Friedman)

Algorithm	Ranking
DE	3.394736842105262
CHC	1.368421052631579
G-CMA-ES	2.0526315789473686
VXQR1	3.1842105263157894

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 31.342105263157823. P-value computed by Friedman Test: 7.201353263708299E-7.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 21.987692307692196. P-value computed by Iman and Davenport Test: 1.9533780148961455E-9.

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

Algorithm	Ranking
DE	47.55263157894736
CHC	21.210526315789473
G-CMA-ES	33.68421052631579
VXQR1	51.55263157894737

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.54580344769467. P-value computed by Aligned Friedman Test: 0.002248957980650612.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.276315789473684
CHC	1.3578947368421055
G-CMA-ES	2.0342105263157886
VXQR1	3.331578947368421

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 25.58441210007378. P-value computed by Quade Test: 1.9687562691217408E-10.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-152.2	-149.3	77.20
CHC	152.2	0.000	2.822	229.4
G-CMA-ES	149.3	-2.822	0.000	226.5
VXQR1	-77.20	-229.4	-226.5	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	4.837762640769081	1.3130881465534958E-6	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.04724434075935377
2	VXQR1	4.335137950819048	1.4566874163845129E-5	0.025	0.025320565519103866	0.025	0.033361747021845407	0.04724434075935377
1	G-CMA-ES	1.6335302423376128	0.10235752557227855	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 ≤ 0.04724434075935377 .

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	4.234927478642515	2.2862547728578336E-5	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.048332304208441784
2	DE	3.676636952403431	2.363290034745086E-4	0.025	0.025320565519103866	0.025	0.033361747021845407	0.048332304208441784
1	G-CMA-ES	1.7409849305087177	0.08168622003960622	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 $\leq 0.048332304208441784$.

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	3.374409529993856	7.397422685537693E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.03960213563867472
2	DE	3.279926063154028	0.00103883429465063584	0.025	0.025320565519103866	0.025	0.033361747021845407	0.03960213563867472
1	G-CMA-ES	1.1562976656112263	0.2475594228651804	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 ≤ 0.03960213563867472 .

Table 8: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	DE	1.3130881465534958E-6	3.9392644396604875E-6	3.9392644396604875E-6	3.9392644396604875E-6	3.9392644396604875E-6
2	VXQR1	1.4566874163845129E-5	4.3700622491535539E-5	2.9133748327690257E-5	2.9133748327690257E-5	2.9133748327690257E-5
3	G-CMA-ES	0.10235752557227855	0.30707257671683563	0.10235752557227855	0.10235752557227855	0.10235752557227855

Table 9: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Hol}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	1.3130881465534958E-6	3.939259267005113E-6	3.9392644396604875E-6	3.939259267005113E-6	1.4628165034008923E-6
2	VXQR1	1.4566874163845129E-5	2.9133536133763016E-5	2.9133748327690257E-5	2.1850231672781995E-5	1.622766100371538E-5
3	G-CMA-ES	0.10235752557227855	0.10235752557227851	0.10235752557227855	0.10235752557227851	0.10235752557227855

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	VXQR1	2.2862547728578336E-5	6.8587643185735E-5	6.8587643185735E-5	6.8587643185735E-5	6.8587643185735E-5
2	DE	2.363290034745086E-4	7.089870104235258E-4	4.726580069490172E-4	4.726580069490172E-4	4.726580069490172E-4
3	G-CMA-ES	0.08168622003960622	0.24505866011881866	0.08168622003960622	0.08168622003960622	0.08168622003960622

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	VXQR1	2.2862547728578336E-5	6.858607510928927E-5	6.8587643185735E-5	6.858607510928927E-5	2.4895606545914482E-5
2	DE	2.363290034745086E-4	4.726021555511162E-4	4.726580069490172E-4	3.54472560112451E-4	2.572848243859984E-4
3	G-CMA-ES	0.08168622003960622	0.08168622003960624	0.08168622003960622	0.08168622003960624	0.08168622003960622

Table 12: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	VXQR1	7.397422685537693E-4	0.002219226805661308	0.002219226805661308	0.0020766858930127167	0.0015575144197595375
2	DE	0.0010383429465063584	0.003115028839519075	0.002219226805661308	0.0020766858930127167	0.0020766858930127167
3	G-CMA-ES	0.2475594228651804	0.7426782685955412	0.2475594228651804	0.2475594228651804	0.2475594228651804

Table 13: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	VXQR1	7.397422685537693E-4	0.0022175855545903955	0.0020766858930127167	0.0022175855545903955	9.82158255462319E-4
2	DE	0.0010383429465063584	0.0022175855545903955	0.0020766858930127167	0.0022175855545903955	0.0013780650245587306
3	G-CMA-ES	0.2475594228651804	0.2475594228651804	0.2475594228651804	0.2475594228651804	0.2475594228651804