

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	3.421052631578946
CHC	1.5263157894736836
G-CMA-ES	1.8157894736842102
VXQR1	3.2368421052631575

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 32.00526315789453. P-value computed by Friedman Test: 5.220599126332104E-7.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 23.04864181933005. P-value computed by Iman and Davenport Test: 9.727388894376077E-10.

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

Algorithm	Ranking
DE	47.6578947368421
CHC	28.263157894736842
G-CMA-ES	26.921052631578945
VXQR1	51.1578947368421

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.282357742537313. P-value computed by Aligned Friedman Test: 0.0025449538687558615.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.3815789473684212
CHC	1.5736842105263156
G-CMA-ES	1.6789473684210527
VXQR1	3.3657894736842104

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 29.93041425758753. P-value computed by Quade Test: 1.5569767697343195E-11.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-1097	-1711	26.15
CHC	1097	0.000	-613.4	1124
G-CMA-ES	1711	613.4	0.000	1737
VXQR1	-26.15	-1124	-1737	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	4.52362220955031	6.0790192071150225E-6	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.026868574890093144
2	VXQR1	4.083825605844032	4.430028241597432E-5	0.025	0.025320565519103666	0.025	0.033361747021845407	0.026868574890093144
1	G-CMA-ES	0.6911089486812981	0.48949707708823026	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 $\leq 0.026868574890093144$.

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	3.38279983333023	7.175090755566114E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.00782058785947852
2	DE	2.894295622871033	0.0038001020330031988	0.025	0.025320565519103866	0.025	0.03361747021845407	0.00782058785947852
1	CHC	0.1873211634091662	0.8514088306699081	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 ≤ 0.00782058785947852 .

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	DE	3.0909591294743732	0.0019951109339498923	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.007516984670415505
2	VXQR1	3.063963853234422	0.0021842529979374313	0.025	0.025320565519103666	0.025	0.03361747021845407	0.007516984670415505
1	G-CMA-ES	0.17996850826633956	0.8571772912621054	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 $\leq 0.007516984670415505$.

Table 8: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	DE	6.0790192071150225E-6	1.8237057621345068E-5	1.8237057621345068E-5	1.8237057621345068E-5	1.8237057621345068E-5
2	VXQR1	4.430028241597432E-5	1.3290084724792295E-4	8.860056483194864E-5	8.860056483194864E-5	8.860056483194864E-5
3	G-CMA-ES	0.48949707708823026	1.4684912312646907	0.48949707708823026	0.48949707708823026	0.48949707708823026

Table 9: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Hol}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	6.0790192071150225E-6	1.8236946758176664E-5	1.8237057621345068E-5	1.8236946758176664E-5	1.1907761046566098E-5
2	VXQR1	4.430028241597432E-5	8.859860231691385E-5	8.860056483194864E-5	6.644968767544057E-5	8.67701955929056E-5
3	G-CMA-ES	0.48949707708823026	0.4894970770882303	0.48949707708823026	0.4894970770882303	0.48949707708823026

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hom}
1	VXQR1	7.175090755566114E-4	0.0021525272266698344	0.0021525272266698344	0.0021525272266698344	0.0021525272266698344
2	DE	0.0038001020330031988	0.011400306099009596	0.0076002040660063976	0.0076002040660063976	0.0076002040660063976
3	CHC	0.8514088306699081	2.5542264920097244	0.8514088306699081	0.8514088306699081	0.8514088306699081

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	VXQR1	7.175090755566114E-4	0.002150983138236695	0.0021525272266698344	0.002150983138236695	0.004805541668564304
2	DE	0.0038001020330031988	0.007585763290545167	0.0076002040660063976	0.005694734324033668	0.0249364809349801
3	CHC	0.8514088306699081	0.8514088306699081	0.8514088306699081	0.8514088306699081	0.8514088306699081

Table 12: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hom}
1	DE	0.0019951109339498923	0.005985332801849676	0.005985332801849676	0.004368505995874863	0.0039902218678997846
2	VXQR1	0.0021842529979374313	0.006552758993812293	0.005985332801849676	0.004368505995874863	0.004368505995874863
3	G-CMA-ES	0.8571772912621054	2.5715318737863164	0.8571772912621054	0.8571772912621054	0.8571772912621054

Table 13: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Hom}	p_{Finn}	p_{Li}
1	DE	0.0019951109339498923	0.005973399340407859	0.004368505995874863	0.005973399340407859	0.013776695012193868
2	VXQR1	0.0021842529979374313	0.005973399340407859	0.004368505995874863	0.005973399340407859	0.01506309057020736
3	G-CMA-ES	0.8571772912621054	0.8571772912621054	0.8571772912621054	0.8571772912621054	0.8571772912621054