

# 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	3.473684210526314
CHC	1.4736842105263157
G-CMA-ES	1.973684210526316
VXQR1	3.0789473684210527

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 29.794736842105117. P-value computed by Friedman Test: 1.52434283906544E-6.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 19.713290771909257. P-value computed by Iman and Davenport Test: 9.271603484961588E-9.

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

Algorithm	Ranking
DE	48.39473684210526
CHC	21.263157894736842
G-CMA-ES	34.34210526315789
VXQR1	50.0

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.15556661471473. P-value computed by Aligned Friedman Test: 0.0027008684022683527.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.402631578947368
CHC	1.4736842105263155
G-CMA-ES	2.007894736842105
VXQR1	3.1157894736842104

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 20.863099975616826. P-value computed by Quade Test: 4.172619139097833E-9.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-24.30	-16.80	-0.8999
CHC	24.30	0.000	7.507	23.40
G-CMA-ES	16.80	-7.507	0.000	15.90
VXQR1	0.8999	-23.40	-15.90	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	4.774934554525325	1.7976570566878026E-6	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.04039041170620342
2	VXQR1	3.832513260869014	1.2684075974808194E-4	0.025	0.025320565519103866	0.025	0.033361747021845407	0.04039041170620342
1	G-CMA-ES	1.1937336386313329	0.232582177582135	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  $\leq 0.05$ .

Hochberg's procedure rejects those hypotheses that have a p-value  $\leq 0.025$ .

Hommel's procedure rejects those hypotheses that have a p-value  $\leq 0.05$ .

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  $\leq 0.025$ .

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  $\leq 0.04039041170620342$ .

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	4.0108766753491985	6.0493704442605904E-5	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.0490562539812078
2	DE	3.7868258720558816	1.5258394734477356E-4	0.025	0.025320565519103866	0.025	0.033361747021845407	0.0490562539812078
1	G-CMA-ES	1.8254631022422625	0.06793117435705194	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  $\leq 0.05$ .

Hochberg's procedure rejects those hypotheses that have a p-value  $\leq 0.025$ .

Hommel's procedure rejects those hypotheses that have a p-value  $\leq 0.05$ .

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  $\leq 0.025$ .

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  $\leq 0.0490562539812078$ .

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	3.297922913980662	9.740287079100409E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.03362822859349808
2	VXQR1	2.807508728954889	0.004992632675188102	0.025	0.025320565519103666	0.025	0.03361747021845407	0.03362822859349808
1	G-CMA-ES	0.91333401794516705	0.36106365672353663	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  $\leq 0.05$ .

Hochberg's procedure rejects those hypotheses that have a p-value  $\leq 0.025$ .

Hommel's procedure rejects those hypotheses that have a p-value  $\leq 0.05$ .

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  $\leq 0.025$ .

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  $\leq 0.03362822859349808$ .

Table 8: Adjusted  $p$ -values (FRIEDMAN)

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hom}$
1	DE	1.7976570566878026E-6	5.392971170063408E-6	5.392971170063408E-6	5.392971170063408E-6	5.392971170063408E-6
2	VXQR1	1.2684075974808194E-4	3.805222792442458E-4	2.5368151949616387E-4	2.5368151949616387E-4	2.5368151949616387E-4
3	G-CMA-ES	0.232582177582135	0.697746532746405	0.232582177582135	0.232582177582135	0.232582177582135

Table 9: Adjusted  $p$ -values (FRIEDMAN)

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Hom}$	$p_{Finn}$	$p_{Li}$
1	DE	1.7976570566878026E-6	5.392961475281233E-6	5.392971170063408E-6	5.392961475281233E-6	2.3424695038580076E-6
2	VXQR1	1.2684075974808194E-4	2.5366543091787097E-4	2.5368151949616387E-4	1.902551062777924E-4	1.6525521684036576E-4
3	G-CMA-ES	0.232582177582135	0.23258217758213506	0.232582177582135	0.23258217758213506	0.232582177582135



Table 10: Adjusted  $p$ -values (ALIGNED FRIEDMAN)

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hommel}$
1	VXQR1	6.0493704442605904E-5	1.8148111332781772E-4	1.8148111332781772E-4	1.8148111332781772E-4	1.8148111332781772E-4
2	DE	1.5258394734477356E-4	4.577518420343207E-4	3.051678946895471E-4	3.051678946895471E-4	3.051678946895471E-4
3	G-CMA-ES	0.06793117435705194	0.20379352307115384	0.06793117435705194	0.06793117435705194	0.06793117435705194

Table 11: Adjusted  $p$ -values (ALIGNED FRIEDMAN)

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Holm}$	$p_{Finn}$	$p_{Li}$
1	VXQR1	6.0493704442605904E-5	1.8147013508440502E-4	1.8148111332781772E-4	1.8147013508440502E-4	6.489840324404688E-5
2	DE	1.5258394734477356E-4	3.051446128284896E-4	3.051678946895471E-4	2.288671900971817E-4	1.636777977581887E-4
3	G-CMA-ES	0.06793117435705194	0.06793117435705198	0.06793117435705194	0.06793117435705198	0.06793117435705195

Table 12: Adjusted  $p$ -values (QUADE)

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hommel}$
1	DE	9.740287079100409E-4	0.0029220861237301225	0.0029220861237301225	0.0029220861237301225	0.0029220861237301225
2	VXQR1	0.004992632675188102	0.014977898025564306	0.009985265350376204	0.009985265350376204	0.009985265350376204
3	G-CMA-ES	0.36106365672353663	1.08319097017061	0.36106365672353663	0.36106365672353663	0.36106365672353663

Table 13: Adjusted  $p$ -values (QUADE)

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Rom}$	$p_{Finn}$	$p_{Li}$
1	DE	9.740287079100409E-4	0.002919240852050864	0.0029220861237301225	0.002919240852050864	0.0015221330213629144
2	VXQR1	0.004992632675188102	0.009960338969346894	0.009985265350376204	0.007479593827280917	0.0077533390298688727
3	G-CMA-ES	0.36106365672353663	0.3610636567235366	0.36106365672353663	0.3610636567235366	0.36106365672353663