

# Results

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## 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	3.394736842105262
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	47.23684210526315
CHC	20.736842105263158
G-CMA-ES	34.89473684210526
VXQR1	51.131578947368425

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.45143111495407. P-value computed by Aligned Friedman Test: 0.002350844759526627.

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	-153.2	-151.3	80.38
CHC	153.2	0.000	1.897	233.6
G-CMA-ES	151.3	-1.897	0.000	231.7
VXQR1	-80.38	-233.6	-231.7	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  $\leq 0.05$ .

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  $\leq 0.04724434075935377$ .

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	4.242273406619344	2.2126690116448753E-5	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.05009744259553303
2	DE	3.6986747363339205	2.1672812324984025E-4	0.025	0.025320565519103866	0.025	0.033361747021845407	0.05009744259553303
1	G-CMA-ES	1.9760546257672786	0.04814859068487259	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  $\leq 0.05$ .

Hommel's procedure rejects all hypotheses.

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

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

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	3.374409529993856	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  $\leq 0.05$ .

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  $\leq 0.03960213563867472$ .

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	4.370062249153539E-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	2.2126690116448753E-5	6.638007034934626E-5	6.638007034934626E-5	6.638007034934626E-5	6.638007034934626E-5
2	DE	2.1672812324984025E-4	6.501843697495208E-4	4.334562464996805E-4	4.334562464996805E-4	4.334562464996805E-4
3	G-CMA-ES	0.04814859068487259	0.14444577205461775	0.04814859068487259	0.04814859068487259	0.04814859068487259

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

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Rom}$	$p_{Finn}$	$p_{Li}$
1	VXQR1	2.2126690116448753E-5	6.63786015889789E-5	6.638007034934626E-5	6.63786015889789E-5	2.32454094777225E-5
2	DE	2.1672812324984025E-4	4.334092754202379E-4	4.334562464996805E-4	3.250745700833572E-4	2.2763929883523487E-4
3	G-CMA-ES	0.04814859068487259	0.04814859068487254	0.04814859068487259	0.04814859068487254	0.04814859068487259

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