

# Results

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## 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	1.5263157894736838
G-CMA-ES	1.973684210526316
VXQR1	3.1052631578947367

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 27.268421052631457. P-value computed by Friedman Test: 5.171789589919484E-6.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 16.50876261285169. P-value computed by Iman and Davenport Test: 9.783145860087217E-8.

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

Algorithm	Ranking
DE	47.76315789473683
CHC	22.157894736842106
G-CMA-ES	34.71052631578947
VXQR1	49.36842105263158

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.241131633509253. P-value computed by Aligned Friedman Test: 0.0025946447609277445.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.2736842105263158
CHC	1.5578947368421052
G-CMA-ES	1.9868421052631575
VXQR1	3.1815789473684215

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 17.605929685096125. P-value computed by Quade Test: 4.26721932234031E-8.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-13.38	-9.100	-0.1310
CHC	13.38	0.000	4.280	13.25
G-CMA-ES	9.100	-4.280	0.000	8.969
VXQR1	0.1310	-13.25	-8.969	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	4.460794123306555	8.165650609903726E-6	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.03760602265468399
2	VXQR1	3.7696851746252604	1.634535987808786E-4	0.025	0.025320565519103666	0.025	0.03361747021845407	0.03760602265468399
1	G-CMA-ES	1.0680774661438248	0.28548556956100424	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  $\leq 0.03760602265468399$ .

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	3.7978447640211273	1.459596832056775E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.0484329920715017
2	DE	3.573793960727809	3.518458291317768E-4	0.025	0.025320565519103866	0.025	0.033361747021845407	0.0484329920715017
1	G-CMA-ES	1.7520038224739627	0.07977315064146778	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  $\leq 0.0484329920715017$ .

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	2.933486684741326	0.0033517803083335847	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.028245696184991814
2	VXQR1	2.7760142400082803	0.005502979818493291	0.025	0.025320565519103666	0.025	0.033361747021845407	0.028245696184991814
1	G-CMA-ES	0.7333716711853309	0.4633317724851555	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  $\leq 0.028245696184991814$ .

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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hom}$
1	DE	8.165650609903726E-6	2.4496951829711176E-5	2.4496951829711176E-5	2.4496951829711176E-5	2.4496951829711176E-5
2	VXQR1	1.634535987808786E-4	4.903607963426357E-4	3.269071975617572E-4	3.269071975617572E-4	3.269071975617572E-4
3	G-CMA-ES	0.28548556956100424	0.8564567086830127	0.28548556956100424	0.28548556956100424	0.28548556956100424

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

$i$	algorithm	unadjusted $p$	$p_{Hol}$	$p_{Rom}$	$p_{Finn}$	$p_{Li}$
1	DE	8.165650609903726E-6	2.449675179672095E-5	2.4496951829711176E-5	2.449675179672095E-5	1.1428120894415635E-5
2	VXQR1	1.634535987808786E-4	3.2688048048279406E-4	3.269071975617572E-4	2.4517037899374206E-4	2.287094681836254E-4
3	G-CMA-ES	0.28548556956100424	0.28548556956100424	0.28548556956100424	0.28548556956100424	0.2854855695610043



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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hommel}$
1	VXQR1	1.4595968320556775E-4	4.378790496167033E-4	4.378790496167033E-4	4.378790496167033E-4	4.378790496167033E-4
2	DE	3.518458291317768E-4	0.0010555374873953303	7.036916582635536E-4	7.036916582635536E-4	7.036916582635536E-4
3	G-CMA-ES	0.07977315064146778	0.23931945192440335	0.07977315064146778	0.07977315064146778	0.07977315064146778

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

$i$	algorithm	unadjusted $p$	$p_{Hol}$	$p_{Rom}$	$p_{Finn}$	$p_{Li}$
1	VXQR1	1.4595968320556775E-4	4.378151400387109E-4	4.378790496167033E-4	4.378151400387109E-4	1.585875655730597E-4
2	DE	3.518458291317768E-4	7.035678627759223E-4	7.036916582635536E-4	5.277223176670676E-4	3.82200708066627E-4
3	G-CMA-ES	0.07977315064146778	0.07977315064146784	0.07977315064146778	0.07977315064146784	0.07977315064146778

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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Homn}$
1	DE	0.0033517803083335847	0.010055340925000754	0.010055340925000754	0.010055340925000754	0.008254469727739936
2	VXQR1	0.005502979818493291	0.016508939455479873	0.011005959636986582	0.011005959636986582	0.011005959636986582
3	G-CMA-ES	0.4633317724851555	1.3899953174554665	0.4633317724851555	0.4633317724851555	0.4633317724851555

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

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Hom}$	$p_{Finn}$	$p_{Li}$
1	DE	0.0033517803083335847	0.01002167528664022	0.010055340925000754	0.01002167528664022	0.00620677060067574
2	VXQR1	0.005502979818493291	0.0109756768501037	0.011005959636986582	0.01002167528664022	0.010149893140876344
3	G-CMA-ES	0.4633317724851555	0.46333177248515556	0.4633317724851555	0.46333177248515556	0.4633317724851555