

# 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	3.1842105263157885
CHC	1.8421052631578942
G-CMA-ES	1.81578947368421
VXQR1	3.1578947368421053

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 20.5421052631578. P-value computed by Friedman Test: 1.3103245664169982E-4.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 10.142052836725782. P-value computed by Iman and Davenport Test: 2.1154654878619006E-5.

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

Algorithm	Ranking
DE	45.34210526315789
CHC	32.473684210526315
G-CMA-ES	24.23684210526316
VXQR1	51.94736842105263

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.563257778095243. P-value computed by Aligned Friedman Test: 0.002230599473714845.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.131578947368421
CHC	1.9684210526315786
G-CMA-ES	1.7526315789473688
VXQR1	3.1473684210526316

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 12.461718209093007. P-value computed by Quade Test: 2.641201541142557E-6.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-7.343	-11.32	5.180
CHC	7.343	0.000	-3.975	12.52
G-CMA-ES	11.32	3.975	0.000	16.50
VXQR1	-5.180	-12.52	-16.50	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	3.2670604846752243	0.0010867046009095658	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.002636663133865382
2	VXQR1	3.204232398431472	0.0013542311595120182	0.025	0.025320565519103666	0.025	0.03361747021845407	0.002636663133865382
1	CHC	0.06282808624375452	0.9499034004565577	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  $\leq 0.002636663133865382$ .

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	3.867631079801012	1.0989775761343075E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.03945825725839225
2	DE	2.945717118708842	0.0032220692545615235	0.025	0.025320565519103866	0.025	0.03361747021845407	0.03945825725839225
1	CHC	1.1496377283738997	0.25029311209054744	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  $\leq 0.03945825725839225$ .

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	2.3845827345289914	0.01709850280270441	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.016952427508441503	0.015148639730926367
2	DE	2.35758745828904	0.01839412185377731	0.025	0.025320565519103666	0.025	0.03361747021845407	0.015148639730926367
1	CHC	0.36893544194599387	0.7121758451123991	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  $\leq 0.016666666666666666$ .

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  $\leq 0.016952427508441503$ .

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  $\leq 0.016952427508441503$ .

Li's procedure rejects those hypotheses that have a p-value  $\leq 0.015148639730926367$ .

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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hommel}$
1	DE	0.0010867046009095658	0.003260113802728697	0.003260113802728697	0.0027084623190240364	0.0021734092018191316
2	VXQR1	0.0013542311595120182	0.0040626934785360546	0.003260113802728697	0.0027084623190240364	0.0027084623190240364
3	CHC	0.9499034004565577	2.8497102013696733	0.9499034004565577	0.9499034004565577	0.9499034004565577

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

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Rom}$	$p_{Finn}$	$p_{Li}$
1	DE	0.0010867046009095658	0.003256572305378347	0.0027084623190240364	0.003256572305378347	0.021231622676112175
2	VXQR1	0.0013542311595120182	0.003256572305378347	0.0027084623190240364	0.003256572305378347	0.02632088036305035
3	CHC	0.9499034004565577	0.9499034004565577	0.9499034004565577	0.9499034004565577	0.9499034004565579



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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hommel}$
1	VXQR1	1.0989775761343075E-4	3.296932728402923E-4	3.296932728402923E-4	3.296932728402923E-4	3.296932728402923E-4
2	DE	0.0032220692545615235	0.00966620776368457	0.006444138509123047	0.006444138509123047	0.006444138509123047
3	CHC	0.25029311209054744	0.7508793362716424	0.25029311209054744	0.25029311209054744	0.25029311209054744

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

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Rom}$	$p_{Finn}$	$p_{Li}$
1	VXQR1	1.0989775761343075E-4	3.2965704161602716E-4	3.296932728402923E-4	3.2965704161602716E-4	1.465661475098366E-4
2	DE	0.0032220692545615235	0.006433756778841726	0.006444138509123047	0.00482920863979075	0.004279380177776381
3	CHC	0.25029311209054744	0.2502931120905474	0.25029311209054744	0.2502931120905474	0.25029311209054744

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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hommel}$
1	VXQR1	0.01709850280270441	0.051295508408113234	0.051295508408113234	0.03678824370755462	0.03419700560540882
2	DE	0.01839412185377731	0.05518236556133192	0.051295508408113234	0.03678824370755462	0.03678824370755462
3	CHC	0.7121758451123991	2.1365275353371973	0.7121758451123991	0.7121758451123991	0.7121758451123991

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

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Rom}$	$p_{Finn}$	$p_{Li}$
1	VXQR1	0.01709850280270441	0.05042343091155954	0.03678824370755462	0.05042343091155954	0.05607488447142719
2	DE	0.01839412185377731	0.05042343091155954	0.03678824370755462	0.05042343091155954	0.060068660987575115
3	CHC	0.7121758451123991	0.7121758451123991	0.7121758451123991	0.7121758451123991	0.7121758451123992