

# 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	3.473684210526314
CHC	1.368421052631579
G-CMA-ES	1.973684210526316
VXQR1	3.1842105263157894

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 33.8999999999987. P-value computed by Friedman Test: 2.0802191524893487E-7.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 26.415584415584167. P-value computed by Iman and Davenport Test: 1.1894707441229002E-10.

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

Algorithm	Ranking
DE	48.99999999999999
CHC	19.47368421052632
G-CMA-ES	35.763157894736835
VXQR1	49.76315789473685

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.161308650356803. P-value computed by Aligned Friedman Test: 0.0026936070406256007.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.3815789473684212
CHC	1.3578947368421053
G-CMA-ES	2.0078947368421045
VXQR1	3.2526315789473683

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 26.831154770813097. P-value computed by Quade Test: 9.277656420891844E-11.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-77.81	-63.44	21.55
CHC	77.81	0.000	14.37	99.36
G-CMA-ES	63.44	-14.37	0.000	84.99
VXQR1	-21.55	-99.36	-84.99	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	5.026246899500343	5.001718578552741E-7	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.044818685795656565
2	VXQR1	4.335137950819048	1.4566874163845129E-5	0.025	0.025320565519103866	0.025	0.033361747021845407	0.044818685795656565
1	G-CMA-ES	1.4450459836063498	0.14844496988252537	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  $\leq 0.044818685795656565$ .

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	4.22758155065684	2.362165717909932E-5	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.05142146466488338
2	DE	4.121065595001647	3.771240221706378E-5	0.025	0.025320565519103666	0.025	0.03361747021845407	0.05142146466488338
1	G-CMA-ES	2.2735647088288937	0.022992171367215864	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	DE	3.4598945714203673	5.403869207281134E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.03860858651538743
2	VXQR1	3.239433148794102	0.0011976753860850902	0.025	0.025320565519103666	0.025	0.033361747021845407	0.03860858651538743
1	G-CMA-ES	1.1113055385446422	0.266436856207639	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  $\leq 0.03860858651538743$ .

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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hommel}$
1	DE	5.001718578552741E-7	1.5005155735658224E-6	1.5005155735658224E-6	1.5005155735658224E-6	1.5005155735658224E-6
2	VXQR1	1.4566874163845129E-5	4.3700622491535539E-5	2.9133748327690257E-5	2.9133748327690257E-5	2.9133748327690257E-5
3	G-CMA-ES	0.14844496988252537	0.4453349096475761	0.14844496988252537	0.14844496988252537	0.14844496988252537

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

$i$	algorithm	unadjusted $p$	$p_{Rom}$	$p_{Finn}$	$p_{Li}$
1	DE	5.001718578552741E-7	1.5005148229496612E-6	1.5005148229496612E-6	5.873625853681333E-7
2	VXQR1	1.4566874163845129E-5	2.9133536133763016E-5	2.9133748327690257E-5	1.7105911501897083E-5
3	G-CMA-ES	0.14844496988252537	0.14844496988252542	0.14844496988252542	0.14844496988252537

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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hommel}$
1	VXQR1	2.362165717909932E-5	7.086497153729796E-5	7.086497153729796E-5	7.086497153729796E-5	5.656860332559567E-5
2	DE	3.771240221706378E-5	1.1313720665119134E-4	7.542480443412756E-5	7.542480443412756E-5	7.542480443412756E-5
3	G-CMA-ES	0.022992171367215864	0.0689765141016476	0.022992171367215864	0.022992171367215864	0.022992171367215864

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

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Rom}$	$p_{Sinn}$	$p_{Li}$
1	VXQR1	2.362165717909932E-5	7.086329760230825E-5	7.086497153729796E-5	7.086329760230825E-5	2.4176967048592842E-5
2	DE	3.771240221706378E-5	7.542338220889455E-5	7.542480443412756E-5	7.086329760230825E-5	3.859840778467131E-5
3	G-CMA-ES	0.022992171367215864	0.022992171367215875	0.022992171367215864	0.022992171367215875	0.022992171367215864

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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hommel}$
1	DE	5.403869207281134E-4	0.0016211607621843403	0.0016211607621843403	0.0016211607621843403	0.0016211607621843403
2	VXQR1	0.0011976753860850902	0.0035930261582552705	0.0023953507721701803	0.0023953507721701803	0.0023953507721701803
3	G-CMA-ES	0.266436856207639	0.799310568622917	0.266436856207639	0.266436856207639	0.266436856207639

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

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Rom}$	$p_{Finn}$	$p_{Li}$
1	DE	5.403869207281134E-4	0.0016202848659148117	0.0016211607621843403	0.0016202848659148117	7.361181333690026E-4
2	VXQR1	0.0011976753860850902	0.0023939163458397417	0.0023953507721701803	0.0017959750618318227	0.0016300207561751048
3	G-CMA-ES	0.266436856207639	0.266436856207639	0.266436856207639	0.266436856207639	0.266436856207639