

# 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	3.421052631578946
CHC	1.368421052631579
G-CMA-ES	1.973684210526316
VXQR1	3.2368421052631575

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 33.615789473684096. P-value computed by Friedman Test: 2.388199845659855E-7.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 25.875759621876895. P-value computed by Iman and Davenport Test: 1.648247094365729E-10.

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

Algorithm	Ranking
DE	48.52631578947368
CHC	20.57894736842105
G-CMA-ES	34.868421052631575
VXQR1	50.0263157894737

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.239903343942235. P-value computed by Aligned Friedman Test: 0.002596139910455597.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.276315789473684
CHC	1.3684210526315788
G-CMA-ES	2.0105263157894733
VXQR1	3.344736842105263

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 25.923897274840247. P-value computed by Quade Test: 1.6007384306959693E-10.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-55.23	-33.70	-4.475
CHC	55.23	0.000	21.53	50.75
G-CMA-ES	33.70	-21.53	0.000	29.22
VXQR1	4.475	-50.75	-29.22	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	4.900590727012835	9.554891997363964E-7	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.044818685795656565
2	VXQR1	4.460794123306556	8.165650609903694E-6	0.025	0.025320565519103666	0.025	0.03361747021845407	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	VXQRI	4.110046703036406	3.955791025157527E-5	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.05020493499133545
2	DE	3.900687755696747	9.591980133083663E-5	0.025	0.025320565519103666	0.025	0.03361747021845407	0.05020493499133545
1	G-CMA-ES	1.9944194457093536	0.046106235164626544	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	3.378908742700515	7.277416083453931E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.03830061153095814
2	DE	3.2619292123273946	0.0011065677232189308	0.025	0.025320565519103666	0.025	0.033361747021845407	0.03830061153095814
1	G-CMA-ES	1.0978079004246677	0.27228838091179547	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  $\leq 0.03830061153095814$ .

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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Homn}$
1	DE	9.554891997363964E-7	2.866467599209189E-6	2.866467599209189E-6	2.866467599209189E-6	2.866467599209189E-6
2	VXQR1	8.165650609903694E-6	2.449695182971108E-5	1.6331301219807388E-5	1.6331301219807388E-5	1.6331301219807388E-5
3	G-CMA-ES	0.148444496988252537	0.4453349096475761	0.148444496988252537	0.148444496988252537	0.148444496988252537

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

$i$	algorithm	unadjusted $p$	$p_{Hol}$	$p_{Rom}$	$p_{Finn}$	$p_{Li}$
1	DE	9.554891997363964E-7	2.866464860362683E-6	2.866467599209189E-6	2.866464860362683E-6	1.122050946604147E-6
2	VXQR1	8.165650609903694E-6	1.633123454192198E-5	1.6331301219807388E-5	1.2248450910634645E-5	9.589013065012187E-6
3	G-CMA-ES	0.148444496988252537	0.148444496988252542	0.148444496988252537	0.148444496988252542	0.148444496988252537



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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Homn}$
1	VXQR1	3.955791025157527E-5	1.186737307547258E-4	1.186737307547258E-4	1.186737307547258E-4	1.186737307547258E-4
2	DE	9.591980133083663E-5	2.877594039925099E-4	1.9183960266167327E-4	1.9183960266167327E-4	1.9183960266167327E-4
3	G-CMA-ES	0.046106235164626544	0.13831870549387965	0.046106235164626544	0.046106235164626544	0.046106235164626544

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

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Rom}$	$p_{Finn}$	$p_{Li}$
1	VXQR1	3.955791025157527E-5	1.1866903633184211E-4	1.1866903633184211E-4	1.1866903633184211E-4	4.146821303790825E-5
2	DE	9.591980133083663E-5	1.9183040205339452E-4	1.9183960266167327E-4	1.4387625171297103E-4	1.0054595230488739E-4
3	G-CMA-ES	0.046106235164626544	0.04610623516462653	0.046106235164626544	0.04610623516462653	0.046106235164626544

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

$i$	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holm}$	$p_{Hoch}$	$p_{Hommel}$
1	VXQR1	7.277416083453931E-4	0.0021832248250361792	0.0021832248250361792	0.0021832248250361792	0.0016598515848283962
2	DE	0.0011065677232189308	0.0033197031696567923	0.0022131354464378617	0.0022131354464378617	0.0022131354464378617
3	G-CMA-ES	0.272228838091179547	0.8168651427353864	0.272228838091179547	0.272228838091179547	0.272228838091179547

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

$i$	algorithm	unadjusted $p$	$p_{Holl}$	$p_{Holm}$	$p_{Sinn}$	$p_{Li}$
1	VXQR1	7.277416083453931E-4	0.002181636386908381	0.0021832248250361792	0.002181636386908381	9.9904212706121566E-4
2	DE	0.0011065677232189308	0.0022119109543118354	0.0022131354464378617	0.002181636386908381	0.0015183042125501288
3	G-CMA-ES	0.272228838091179547	0.27222883809117955	0.272228838091179547	0.27222883809117955	0.272228838091179547