

Results

June 18, 2010

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	3.4999999999999982
CHC	1.4210526315789471
G-CMA-ES	2.1052631578947367
VXQR1	2.973684210526316

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 29.00526315789461. P-value computed by Friedman Test: 2.2337529722582516E-6.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 18.649746192893236. P-value computed by Iman and Davenport Test: 1.9821753793891617E-8.

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

Algorithm	Ranking
DE	47.97368421052631
CHC	19.263157894736842
G-CMA-ES	35.8421052631579
VXQR1	50.921052631578945

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.377178159781728. P-value computed by Aligned Friedman Test: 0.0024342158576324824.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.4842105263157896
CHC	1.4157894736842105
G-CMA-ES	2.1052631578947367
VXQR1	2.9947368421052625

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 21.590754002474597. P-value computed by Quade Test: 2.547346777959092E-9.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-206.5	-183.6	68.68
CHC	206.5	0.000	22.90	275.1
G-CMA-ES	183.6	-22.90	0.000	252.2
VXQR1	-68.68	-275.1	-252.2	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	4.963418813256589	6.926300149983597E-7	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.04724434075935377
2	VXQR1	3.7068570883815064	2.0984727918566809E-4	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 ≤ 0.05 .

Hochberg's procedure rejects those hypotheses that have a p-value ≤ 0.025 .

Hommel's procedure rejects those hypotheses that have a p-value ≤ 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 ≤ 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 ≤ 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	4.418575678063265	9.935349136097724E-6	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.051543709725242
2	DE	4.007203711360782	6.144186609211445E-5	0.025	0.025320565519103666	0.025	0.03361747021845407	0.051543709725242
1	G-CMA-ES	2.3139673127014606	0.02066951522040226	0.05	0.0500000000000000044	0.05	0.0500000000000000044	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 ≤ 0.05 .

Hommel's procedure rejects all hypotheses.

Rom's procedure rejects those hypotheses that have a p-value ≤ 0.05 .

Li's procedure rejects those hypotheses that have a p-value ≤ 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	3.5363811874335616	4.0564891998053385E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.040079983053929125
2	VXQR1	2.6995276239950843	0.0069437990858534655	0.025	0.0253205655191038666	0.025	0.033361747021845407	0.040079983053929125
1	G-CMA-ES	1.1787937291445205	0.23848032197534663	0.05	0.0500000000000000044	0.05	0.0500000000000000044	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 ≤ 0.05 .

Hochberg's procedure rejects those hypotheses that have a p-value ≤ 0.025 .

Hommel's procedure rejects those hypotheses that have a p-value ≤ 0.05 .

Holland's procedure rejects those hypotheses that have a p-value $\leq 0.0500000000000000044$.

Rom's procedure rejects those hypotheses that have a p-value ≤ 0.025 .

Finner's procedure rejects those hypotheses that have a p-value $\leq 0.0500000000000000044$.

Li's procedure rejects those hypotheses that have a p-value $\leq 0.040079983053929125$.

Table 8: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homn}
1	DE	6.926300149983597E-7	2.077890044995079E-6	2.077890044995079E-6	2.077890044995079E-6	2.077890044995079E-6
2	VXQR1	2.0984727918566809E-4	6.295418375570043E-4	4.1969455837133617E-4	4.1969455837133617E-4	4.1969455837133617E-4
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_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	6.926300149983597E-7	2.077888605844791E-6	2.077890044995079E-6	2.077888605844791E-6	7.716095219313464E-7
2	VXQR1	2.0984727918566809E-4	4.19650522490822E-4	4.1969455837133617E-4	3.147544047457096E-4	2.337213750104554E-4
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	9.935349136097724E-6	2.980604740829317E-5	2.980604740829317E-5	2.980604740829317E-5	2.980604740829317E-5
2	DE	6.144186609211445E-5	1.8432559827634334E-4	1.228837321842289E-4	1.228837321842289E-4	1.228837321842289E-4
3	G-CMA-ES	0.02066951522040226	0.062008545661206775	0.02066951522040226	0.02066951522040226	0.02066951522040226

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Hol}	p_{Rom}	p_{Finn}	p_{Li}
1	VXQR1	9.935349136097724E-6	2.9805751275757686E-5	2.980604740829317E-5	2.9805751275757686E-5	1.0144939320274076E-5
2	DE	6.144186609211445E-5	1.2287995708137878E-4	1.228837321842289E-4	9.216138346013203E-5	6.273470754710642E-5
3	G-CMA-ES	0.02066951522040226	0.02066951522040228	0.02066951522040226	0.02066951522040228	0.02066951522040226

Table 12: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{occh}	p_{Hom}
1	DE	4.0564891998053385E-4	0.0012169467599416016	0.0012169467599416016	0.0012169467599416016	0.0012169467599416016
2	VXQR1	0.0069437990858534655	0.020831397257560398	0.013887598171706931	0.013887598171706931	0.013887598171706931
3	G-CMA-ES	0.23848032197534663	0.7154409659260399	0.23848032197534663	0.23848032197534663	0.23848032197534663

Table 13: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Hom}	p_{Finn}	p_{Li}
1	DE	4.0564891998053385E-4	0.0012164531735526785	0.0012169467599416016	0.0012164531735526785	5.323998371431098E-4
2	VXQR1	0.0069437990858534655	0.013839381825962338	0.013887598171706931	0.010397596519159613	0.009035951990799599
3	G-CMA-ES	0.23848032197534663	0.23848032197534663	0.23848032197534663	0.23848032197534663	0.23848032197534663