

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	3.368421052631578
CHC	1.5263157894736838
G-CMA-ES	2.1052631578947367
VXQR1	2.9999999999999996

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 24.03157894736834. P-value computed by Friedman Test: 2.460364766720957E-5.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 13.12068965517234. P-value computed by Iman and Davenport Test: 1.5026524985417566E-6.

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

Algorithm	Ranking
DE	47.57894736842104
CHC	21.947368421052634
G-CMA-ES	34.73684210526316
VXQR1	49.73684210526317

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.211453109251861. P-value computed by Aligned Friedman Test: 0.002631011259695226.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.2605263157894733
CHC	1.5578947368421052
G-CMA-ES	2.1052631578947363
VXQR1	3.076315789473684

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 14.994176395458291. P-value computed by Quade Test: 3.2093862389892536E-7.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-13.41	-9.027	-0.07372
CHC	13.41	0.000	4.382	13.34
G-CMA-ES	9.027	-4.382	0.000	8.953
VXQR1	0.07372	-13.34	-8.953	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	4.397966037062801	1.092700725019233E-5	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.0438471154539849
2	VXQR1	3.518372829650242	4.342018690566093E-4	0.025	0.025320565519103666	0.025	0.03361747021845407	0.0438471154539849
1	G-CMA-ES	1.3822178973625958	0.16690480637428703	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 ≤ 0.0438471154539849 .

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	3.8786499717662593	1.0503776342627205E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.04872360503330675
2	DE	3.5774669247162243	3.4694010368365623E-4	0.025	0.025320565519103866	0.025	0.033361747021845407	0.04872360503330675
1	G-CMA-ES	1.7850604983696976	0.07425150436671737	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 ≤ 0.04872360503330675 .

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	2.910990621208033	0.003602848319835953	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.03424434169082701
2	VXQR1	2.5960457317419396	0.009430351275790616	0.025	0.025320565519103666	0.025	0.03361747021845407	0.03424434169082701
1	G-CMA-ES	0.935836242984962	0.3493575078742867	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 ≤ 0.03424434169082701 .

Table 8: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	DE	1.0927007250192333E-5	3.278102175057699E-5	3.278102175057699E-5	3.278102175057699E-5	3.278102175057699E-5
2	VXQR1	4.342018690566093E-4	0.001302605607169828	8.684037381132186E-4	8.684037381132186E-4	8.684037381132186E-4
3	G-CMA-ES	0.16690480637428703	0.5007144191228611	0.16690480637428703	0.16690480637428703	0.16690480637428703

Table 9: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Sinn}	p_{Li}
1	DE	1.0927007250192333E-5	3.27806635327791E-5	3.278102175057699E-5	3.27806635327791E-5	1.3115984842231618E-5
2	VXQR1	4.342018690566093E-4	8.682152068502091E-4	8.684037381132186E-4	6.512320992441145E-4	5.209190837009858E-4
3	G-CMA-ES	0.16690480637428703	0.16690480637428706	0.16690480637428703	0.16690480637428706	0.16690480637428703

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	VXQR1	1.0503776342627205E-4	3.151132902788161E-4	3.151132902788161E-4	3.151132902788161E-4	3.151132902788161E-4
2	DE	3.4694010368365623E-4	0.0010408203110509686	6.938802073673125E-4	6.938802073673125E-4	6.938802073673125E-4
3	G-CMA-ES	0.07425150436671737	0.22275451310015212	0.07425150436671737	0.07425150436671737	0.07425150436671737

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	VXQR1	1.0503776342627205E-4	3.1508019264248066E-4	3.151132902788161E-4	3.1508019264248066E-4	1.1344965444039145E-4
2	DE	3.4694010368365623E-4	6.937598399316958E-4	6.938802073673125E-4	5.2036501512675558E-4	3.746267288398511E-4
3	G-CMA-ES	0.07425150436671737	0.07425150436671735	0.07425150436671737	0.07425150436671735	0.07425150436671737

Table 12: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	DE	0.003602848319835953	0.010808544959507858	0.010808544959507858	0.010808544959507858	0.010808544959507858
2	VXQR1	0.009430351275790616	0.028291053827371848	0.018860702551581232	0.018860702551581232	0.018860702551581232
3	G-CMA-ES	0.3493575078742867	1.04807252362286	0.3493575078742867	0.3493575078742867	0.3493575078742867

Table 13: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	0.003602848319835953	0.010769650178290902	0.010808544959507858	0.010769650178290902	0.005506876544787263
2	VXQR1	0.009430351275790616	0.018771771026396378	0.018860702551581232	0.01411212498952974	0.014286834203318974
3	G-CMA-ES	0.3493575078742867	0.3493575078742867	0.3493575078742867	0.3493575078742867	0.3493575078742867