

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	3.342105263157893
CHC	1.736842105263157
G-CMA-ES	1.7631578947368418
VXQR1	3.1578947368421053

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 25.847368421052465. P-value computed by Friedman Test: 1.0265613766380355E-5.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 14.934617334008948. P-value computed by Iman and Davenport Test: 3.3664419685219826E-7.

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

Algorithm	Ranking
DE	45.8421052631579
CHC	35.8421052631579
G-CMA-ES	20.289473684210527
VXQR1	52.026315789473685

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.381468962558792. P-value computed by Aligned Friedman Test: 0.0024293193383729816.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.386842105263158
CHC	1.8210526315789473
G-CMA-ES	1.4921052631578948
VXQR1	3.3

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 27.057365813069058. P-value computed by Quade Test: 8.111644689279274E-11.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-378.6	-1589	22.58
CHC	378.6	0.000	-1210	401.2
G-CMA-ES	1589	1210	0.000	1611
VXQR1	-22.58	-401.2	-1611	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	3.832513260869012	1.268407597480831E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.00263666631338654288
2	VXQR1	3.392716657162736	6.920318080538578E-4	0.025	0.025320565519103866	0.025	0.03361747021845407	0.00263666631338654288
1	G-CMA-ES	0.06282808624375558	0.9499034004565569	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 $\leq 0.00263666631338654288$.

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	4.4295945700285095	9.44104063420638E-6	0.016952427508441503	0.016952427508441503	0.016952427508441503	0.016952427508441503	0.05105514660304771
2	DE	3.5664480327509813	3.6185252557375164E-4	0.025	0.025320565519103866	0.025	0.033361747021845407	0.05105514660304771
1	CHC	2.170721717153275	0.029952214542093666	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 ≤ 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	3.239433148794102	0.0011976753860850902	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.02242934541379925
2	VXQR1	3.090959129474372	0.0019951109339499023	0.025	0.025320565519103866	0.025	0.03361747021845407	0.02242934541379925
1	CHC	0.5624015883323091	0.5738424371378142	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 ≤ 0.02242934541379925 .

Table 8: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	DE	1.268407597480831E-4	3.805222792442493E-4	3.805222792442493E-4	3.805222792442493E-4	3.805222792442493E-4
2	VXQR1	6.920318080538578E-4	0.0020760954241615735	0.0013840636161077157	0.0013840636161077157	0.0013840636161077157
3	G-CMA-ES	0.9499034004565569	2.8497102013696707	0.9499034004565569	0.9499034004565569	0.9499034004565569

Table 9: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Hol}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	1.268407597480831E-4	3.8047401555008076E-4	3.805222792442493E-4	3.8047401555008076E-4	0.0025255290952265466
2	VXQR1	6.920318080538578E-4	0.0013835847080844177	0.0013840636161077157	0.0010378681008529345	0.01362572271862293
3	G-CMA-ES	0.9499034004565569	0.9499034004565569	0.9499034004565569	0.9499034004565569	0.9499034004565569

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	VXQR1	9.44104063420638E-6	2.8323121902619136E-5	2.8323121902619136E-5	2.8323121902619136E-5	2.8323121902619136E-5
2	DE	3.6185252557375164E-4	0.001085557576721255	7.237050511475033E-4	7.237050511475033E-4	7.237050511475033E-4
3	CHC	0.029952214542093666	0.089856643626281	0.029952214542093666	0.029952214542093666	0.029952214542093666

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	VXQR1	9.44104063420638E-6	2.8322854503604056E-5	2.8323121902619136E-5	2.8322854503604056E-5	9.732457401801113E-6
2	DE	3.6185252557375164E-4	7.235741138972296E-4	7.237050511475033E-4	5.427296839300988E-4	3.728863681998093E-4
3	CHC	0.029952214542093666	0.029952214542093625	0.029952214542093666	0.029952214542093625	0.029952214542093666

Table 12: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homn}
1	DE	0.0011976753860850902	0.0035930261582552705	0.0035930261582552705	0.0035930261582552705	0.0029926664009248534
2	VXQR1	0.0019951109339499023	0.005985332801849707	0.0039902218678998045	0.0039902218678998045	0.0039902218678998045
3	CHC	0.5738424371378142	1.7215273114134426	0.5738424371378142	0.5738424371378142	0.5738424371378142

Table 13: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	0.0011976753860850902	0.003588724597241022	0.0035930261582552705	0.003588724597241022	0.0028025288539678637
2	VXQR1	0.0019951109339499023	0.003986241400261048	0.0039902218678998045	0.003588724597241022	0.004659811922370176
3	CHC	0.5738424371378142	0.5738424371378142	0.5738424371378142	0.5738424371378142	0.5738424371378142