

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	3.1578947368421044
CHC	2.0526315789473686
G-CMA-ES	1.81578947368421
VXQR1	2.973684210526315

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 15.110526315789338. P-value computed by Friedman Test: 0.0017245915712698068.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 6.49302676215597. P-value computed by Iman and Davenport Test: 7.83655419746232E-4.

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

Algorithm	Ranking
DE	45.210526315789465
CHC	36.21052631578947
G-CMA-ES	22.868421052631582
VXQR1	49.71052631578947

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.480989993963734. P-value computed by Aligned Friedman Test: 0.00231844952866489.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.144736842105263
CHC	2.2842105263157895
G-CMA-ES	1.673684210526316
VXQR1	2.8973684210526316

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 9.876723856290035. P-value computed by Quade Test: 2.7109683984782862E-5.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-8.337e-09	-2.100	0.000
CHC	8.337e-09	0.000	-2.100	8.337e-09
G-CMA-ES	2.100	2.100	0.000	2.100
VXQR1	0.000	-8.337e-09	-2.100	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	3.2042323984314702	0.001354231159512026	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.022538640203764414
2	VXQR1	2.76443579472519	0.005702132761524356	0.025	0.025320565519103666	0.025	0.03361747021845407	0.022538640203764414
1	CHC	0.5654527761937908	0.5717658361284762	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 $\leq 0.022538640203764414$.

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	3.746423268183316	1.793738365927101E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.04933810909963207
2	DE	3.1183464261643477	0.001818688954693522	0.025	0.025320565519103666	0.025	0.03361747021845407	0.04933810909963207
1	CHC	1.8621927421264128	0.06257592710699075	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 ≤ 0.04933810909963207 .

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	2.515059903022087	0.011901216054177119	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.0370226366642980625
2	VXQR1	2.0921339085961903	0.03642653862777755	0.025	0.025320565519103666	0.025	0.03361747021845407	0.0370226366642980625
1	CHC	1.0438173479447657	0.2965699037833682	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 ≤ 0.025 .

Hochberg's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

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

Holland's procedure rejects those hypotheses that have a p-value $\leq 0.025320565519103666$.

Rom's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

Finner's procedure rejects those hypotheses that have a p-value ≤ 0.03361747021845407 .

Li's procedure rejects those hypotheses that have a p-value $\leq 0.0370226366642980625$.

Table 8: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homn}
1	DE	0.001354231159512026	0.004062693478536078	0.004062693478536078	0.004062693478536078	0.004062693478536078
2	VXQR1	0.005702132761524356	0.01710639828457307	0.011404265523048712	0.011404265523048712	0.011404265523048712
3	CHC	0.5717658361284762	1.7152975083854285	0.5717658361284762	0.5717658361284762	0.5717658361284762

Table 9: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	0.001354231159512026	0.004057194136017461	0.004062693478536078	0.004057194136017461	0.0031522392325249356
2	VXQR1	0.005702132761524356	0.011371751205018543	0.011404265523048712	0.008540994660616752	0.0131404833535873196
3	CHC	0.5717658361284762	0.5717658361284762	0.5717658361284762	0.5717658361284762	0.5717658361284762

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	VXQR1	1.793738365927101E-4	5.381215097781303E-4	5.381215097781303E-4	5.381215097781303E-4	5.381215097781303E-4
2	DE	0.001818688954693522	0.0054560668640805665	0.003637377909387044	0.003637377909387044	0.003637377909387044
3	CHC	0.06257592710699075	0.18772778132097226	0.06257592710699075	0.06257592710699075	0.06257592710699075

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	VXQR1	1.793738365927101E-4	5.38024906297152E-4	5.381215097781303E-4	5.38024906297152E-4	1.9131098250371536E-4
2	DE	0.001818688954693522	0.0036340702798730584	0.003637377909387044	0.0027267926947440735	0.0019363353422237183
3	CHC	0.06257592710699075	0.06257592710699078	0.06257592710699075	0.06257592710699078	0.06257592710699075

Table 12: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hom}
1	DE	0.011901216054177119	0.035703648162531354	0.035703648162531354	0.035703648162531354	0.035703648162531354
2	VXQR1	0.03642653862777755	0.10927961588333264	0.0728530772555551	0.0728530772555551	0.0728530772555551
3	CHC	0.2965699037833682	0.8897097113501047	0.2965699037833682	0.2965699037833682	0.2965699037833682

Table 13: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	0.011901216054177119	0.03528041700749596	0.035703648162531354	0.03528041700749596	0.016637348107126585
2	VXQR1	0.03642653862777755	0.07152618453915416	0.0728530772555551	0.05413916025819032	0.049234590746676195
3	CHC	0.2965699037833682	0.2965699037833682	0.2965699037833682	0.2965699037833682	0.2965699037833682