

Results

June 18, 2010

1 Tables of Friedman, Aligned Friedman, Bonferroni-Dunn, Holm, Hochberg and Hommel Tests

Table 1: Average Rankings of the algorithms (Friedman)

Algorithm	Ranking
DE	2.710526315789474
CHC	0.9999999999999996
VXQR1	2.289473684210525

Friedman statistic (distributed according to chi-square with 2 degrees of freedom: 30.184210526315706. P-value computed by Friedman Test: 2.7902518784372887E-7.

Iman and Davenport statistic (distributed according to F-distribution with 2 and 36 degrees of freedom: 69.51515151515058. P-value computed by Iman and Davenport Test: 4.3391694430168896E-13.

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

Algorithm	Ranking
DE	36.289473684210535
CHC	11.26315789473684
VXQR1	39.44736842105263

Aligned Friedman statistic (distributed according to chi-square with 2 degrees of freedom): 12.939317989268568. P-value computed by Aligned Friedman Test: 0.0015497541329241304.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	2.660526315789474
CHC	1.0
VXQR1	2.3394736842105264

Quade statistic (distributed according to F-distribution with 2 and 36 degrees of freedom: 26.636785162287477. P-value computed by Quade Test: 7.951201211016793E-8.

Table 4: Contrast Estimation

	DE	CHC	VXQR1
DE	0.000	-2168	148.3
CHC	2168	0.000	2317
VXQR1	-148.3	-2317	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
2	DE	5.272196186749785	1.3480086707903467E-7	0.025	0.025320565519103666	0.025	0.025320565519103666	0.05262786581355037
1	VXQR1	3.97442481770368	7.054954254317046E-5	0.05	0.050000000000000044	0.05	0.050000000000000044	0.05

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

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 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
2	VXQR1	5.233676504937435	1.6617117494706561E-7	0.025	0.025320565519103666	0.025	0.025320565519103666	0.05263140191762721
1	DE	4.64727017385201	3.3635650830086325E-6	0.05	0.050000000000000044	0.05	0.050000000000000044	0.05

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

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
2	DE	4.488858226558025	7.160593091336521E-6	0.025	0.025320565519103666	0.025	0.025320565519103666	0.052616131244078435
1	VXQR1	3.6209648768907043	2.935063625097434E-4	0.05	0.050000000000000044	0.05	0.050000000000000044	0.05

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

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 8: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	DE	1.3480086707903467E-7	2.6960173415806934E-7	2.6960173415806934E-7	2.6960173415806934E-7	2.6960173415806934E-7
2	VXQR1	7.054954254317046E-5	1.410990850863409E-4	7.054954254317046E-5	7.054954254317046E-5	7.054954254317046E-5

Table 9: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Hol}	p_{Rom}	p_{Firm}	p_{Li}
1	DE	1.3480086707903467E-7	2.696017158410058E-7	2.6960173415806934E-7	2.696017158410058E-7	1.348103597156893E-7
2	VXQR1	7.054954254317046E-5	7.054954254315238E-5	7.054954254317046E-5	7.054954254315238E-5	7.054954254317046E-5

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	VXQR1	1.6617117494706561E-7	3.3234234989413123E-7	3.3234234989413123E-7	3.3234234989413123E-7	3.3234234989413123E-7
2	DE	3.3635650830086325E-6	6.727130166017265E-6	3.3635650830086325E-6	3.3635650830086325E-6	3.3635650830086325E-6

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Firm}	p_{Li}
1	VXQR1	1.6617117494706561E-7	3.323423222179045E-7	3.3234234989413123E-7	3.323423222179045E-7	1.661717062634669E-7
2	DE	3.3635650830086325E-6	3.363565083014386E-6	3.3635650830086325E-6	3.363565083014386E-6	3.363565083008633E-6

Table 12: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	DE	7.160593091336521E-6	1.4321186182673042E-5	1.4321186182673042E-5	1.4321186182673042E-5	1.4321186182673042E-5
2	VXQR1	2.935063625097434E-4	5.870127250194868E-4	2.935063625097434E-4	2.935063625097434E-4	2.935063625097434E-4

Table 13: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	7.160593091336521E-6	1.4321134908623634E-5	1.4321186182673042E-5	1.4321134908623634E-5	7.162644084167873E-6
2	VXQR1	2.935063625097434E-4	2.935063625097989E-4	2.935063625097989E-4	2.935063625097989E-4	2.935063625097434E-4