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	2.6578947368421058
CHC	0.9999999999999996
VXQR1	2.342105263157894

Friedman statistic (distributed according to chi-square with 2 degrees of freedom: 29.44736842105258. P-value computed by Friedman Test: 4.03277710669947E-7.

Iman and Davenport statistic (distributed according to F-distribution with 2 and 36 degrees of freedom: 61.975384615384144. P-value computed by Iman and Daveport Test: 2.1962967524993484E-12.

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

Algorithm	Ranking
DE	35.763157894736835
CHC	11.31578947368421
VXQR1	39.92105263157895

Aligned Friedman statistic (distributed according to chi-square with 2 degrees of freedom: 12.953645011035965. P-value computed by Aligned Friedman Test: 0.0015386921215805316.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	2.5500000000000003
CHC	1.0
VXQR1	2.4499999999999997

Quade statistic (distributed according to F-distribution with 2 and 36 degrees of freedom: 24.73972602739726. P-value computed by Quade Test: 1.7375362808383028E-7.

Table 4: Contrast Estimation

	DE	CHC	VXQR1
DE	0.000	-1899	178.8
CHC	1899	0.000	2078
VXQR1	-178.8	-2078	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	5.109974765619023	3.222018441378448E-7	0.025	0.025320565519103666	0.025	0.025320565519103666	0.05262972411163838
1	VXQR1	4.136646238834443	3.524187887096871E-5	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 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	5.311864015748826	1.0850956297527696E-7	0.025	0.025320565519103666	0.025	0.025320565519103666	0.05263128253858566
1	DE	4.539762346486346	5.631766872610135E-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	4.190075270115177	2.788619345680359E-5	0.025	0.025320565519103666	0.025	0.025320565519103666	0.052626913596485914
1	VXQR1	3.919747833333551	8.864166676775197E-5	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_{Homm}
1	DE	3.222018441378448E-7	6.444036882756896E-7	6.444036882756896E-7	6.444036882756896E-7	6.444036882756896E-7
2	VXQR1	3.524187887096871E-5	7.048375774193742E-5	3.524187887096871E-5	3.524187887096871E-5	3.524187887096871E-5

Table 9: Adjusted p-values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	3.222018441378448E-7	6.444035843822249E-7	6.444036882756896E-7	6.444035843822249E-7	3.2221309571508097E-7
2	VXQR1	3.524187887096871E-5	3.524187887093966E-5	3.524187887096871E-5	3.524187887093966E-5	3.524187887096871E-5

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Table 10: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	VXQR1	1.0850956297527696E-7	2.1701912595055392E-7	2.1701912595055392E-7	2.1701912595055392E-7	2.1701912595055392E-7
2	DE	5.631766872610135E-6	1.126353374522027E-5	5.631766872610135E-6	5.631766872610135E-6	5.631766872610135E-6

Table 11: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	VXQR1	1.0850956297527696E-7	2.1701911423477327E-7	2.1701912595055392E-7	2.1701911423477327E-7	1.0851016230482409E-7
2	DE	5.631766872610135E-6	5.631766872626898E-6	5.631766872610135E-6	5.631766872626898E-6	5.631766872610135E-6

Table 12: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	DE	2.788619345680359E-5	5.577238691360718E-5	5.577238691360718E-5	5.577238691360718E-5	5.577238691360718E-5
2	VXQR1	8.864166676775197E-5	1.7728333353550393E-4	8.864166676775197E-5	8.864166676775197E-5	8.864166676775197E-5

Table 13: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	2.788619345680359E-5	5.5771609273946865E-5	5.577238691360718E-5	5.5771609273946865E-5	2.788788779862643 6E-5
2	VXQR1	8.864166676775197E-5	8.864166676769702E-5	8.864166676775197E-5	8.864166676769702E-5	8.864166676775197E-5