

Results

June 18, 2010

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

1

Table 1: Average Rankings of the algorithms (Friedman)

Algorithm	Ranking
DE	3.394736842105262
CHC	1.5263157894736836
G-CMA-ES	1.8684210526315788
VXQR1	3.2105263157894735

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 30.236842105263033. P-value computed by Friedman Test: 1.2304948693309115E-6.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 20.33628318584053. P-value computed by Iman and Davenport Test: 5.998261887185663E-9.

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

Algorithm	Ranking
DE	47.68421052631579
CHC	28.157894736842103
G-CMA-ES	26.868421052631575
VXQR1	51.28947368421052

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.282233728171565. P-value computed by Aligned Friedman Test: 0.002545101922689086.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.376315789473684
CHC	1.5736842105263156
G-CMA-ES	1.689473684210526
VXQR1	3.3605263157894734

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 29.24311688021163. P-value computed by Quade Test: 2.290079237354803E-11.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-1106	-1730	44.44
CHC	1106	0.000	-623.6	1151
G-CMA-ES	1730	623.6	0.000	1774
VXQR1	-44.44	-1151	-1774	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	4.460794123306556	8.165650609903694E-6	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.030838806940565136
2	VXQR1	4.020997519600278	5.7952215291898184E-5	0.025	0.025320565519103866	0.025	0.033361747021845407	0.030838806940565136
1	G-CMA-ES	0.8167651211688072	0.41406266812926257	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 $\leq 0.030838806940565136$.

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	3.408510581249135	6.531855193257145E-4	0.01666666666666666	0.016952427508441503	0.01666666666666666	0.016952427508441503	0.007517262632290713
2	DE	2.9053145148362782	0.0036688423151319946	0.025	0.025320565519103666	0.025	0.03361747021845407	0.007517262632290713
1	CHC	0.17997523543233596	0.8571720099864765	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 $\leq 0.007517262632290713$.

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	3.0819607040610557	0.002056419826045023	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.008259359644450091
2	VXQR1	3.0549654278211045	0.0022508646685696484	0.025	0.025320565519103666	0.025	0.03361747021845407	0.008259359644450091
1	G-CMA-ES	0.19796535909297278	0.8430721667554483	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 $\leq 0.008259359644450091$.

Table 8: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	DE	8.165650609903694E-6	2.449695182971108E-5	2.449695182971108E-5	2.449695182971108E-5	2.449695182971108E-5
2	VXQR1	5.7952215291898184E-5	1.7385664587569454E-4	1.1590443058379637E-4	1.1590443058379637E-4	1.1590443058379637E-4
3	G-CMA-ES	0.41406266812926257	1.2421880043877878	0.41406266812926257	0.41406266812926257	0.41406266812926257

Table 9: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Holm}	p_{Finn}	p_{Li}
1	DE	8.165650609903694E-6	2.449675179672095E-5	2.449675179672095E-5	1.3935853495667829E-5
2	VXQR1	5.7952215291898184E-5	1.159010721245579E-4	1.1590443058379637E-4	8.6927063503355017E-5
3	G-CMA-ES	0.41406266812926257	0.41406266812926257	0.41406266812926257	0.41406266812926257

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homn}
1	VXQR1	6.531855193257145E-4	0.0019595565579771435	0.0019595565579771435	0.0019595565579771435	0.0019595565579771435
2	DE	0.0036688423151319946	0.011006526945395983	0.007337684630263989	0.007337684630263989	0.007337684630263989
3	CHC	0.8571720099864765	2.5715160299594295	0.8571720099864765	0.8571720099864765	0.8571720099864765

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Romn}	p_{Finn}	p_{Li}
1	VXQR1	6.531855193257145E-4	0.0019582768826915675	0.0019595565579771435	0.0019582768826915675	0.004552412655527562
2	DE	0.0036688423151319946	0.007324224226330611	0.007337684630263989	0.005498212730462471	0.02504383375949862
3	CHC	0.8571720099864765	0.8571720099864765	0.8571720099864765	0.8571720099864765	0.8571720099864765

Table 12: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	DE	0.002056419826045023	0.00616925947813507	0.00616925947813507	0.004501729337139297	0.004112839652090046
2	VXQR1	0.0022508646685696484	0.006752594005708945	0.00616925947813507	0.004501729337139297	0.004501729337139297
3	G-CMA-ES	0.8430721667554483	2.5292165002663447	0.8430721667554483	0.8430721667554483	0.8430721667554483

Table 13: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	0.002056419826045023	0.006156581586948762	0.004501729337139297	0.006156581586948762	0.012934739046966315
2	VXQR1	0.0022508646685696484	0.006156581586948762	0.004501729337139297	0.006156581586948762	0.014140489261937257
3	G-CMA-ES	0.8430721667554483	0.8430721667554483	0.8430721667554483	0.8430721667554483	0.8430721667554483