

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	3.2894736842105248
CHC	1.6842105263157894
G-CMA-ES	1.9473684210526307
VXQR1	3.078947368421052

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 21.99473684210506. P-value computed by Friedman Test: 6.539583871434385E-5.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 11.309878213802264. P-value computed by Iman and Davenport Test: 7.2804975148610396E-6.

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

Algorithm	Ranking
DE	43.815789473684205
CHC	32.21052631578947
G-CMA-ES	26.684210526315788
VXQR1	51.28947368421053

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.753920110011828. P-value computed by Aligned Friedman Test: 0.0020394864923112266.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
DE	3.2578947368421054
CHC	1.7315789473684207
G-CMA-ES	1.8868421052631583
VXQR1	3.123684210526316

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 14.771456392788838. P-value computed by Quade Test: 3.838814646162092E-7.

Table 4: Contrast Estimation

	DE	CHC	G-CMA-ES	VXQR1
DE	0.000	-30.77	-26.55	2.925
CHC	30.77	0.000	4.223	33.70
G-CMA-ES	26.55	-4.223	0.000	29.48
VXQR1	-2.925	-33.70	-29.48	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	3.8325132608690105	1.2684075974808373E-4	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.024746317569958595
2	VXQR1	3.3298885709189787	8.688074530720151E-4	0.025	0.025320565519103866	0.025	0.033361747021845407	0.024746317569958595
1	G-CMA-ES	0.6282808624375416	0.5298199661707867	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 $\leq 0.024746317569958595$.

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	3.434221329168041	5.942587553982733E-4	0.016952427508441503	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.02944653494302304
2	DE	2.391099556458175	0.01679799719916822	0.025	0.025320565519103666	0.025	0.03361747021845407	0.02944653494302304
1	CHC	0.7713224375671536	0.44051583608256234	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 ≤ 0.02944653494302304 .

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	2.6095433698619166	0.00906631528454164	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.011017890075959304
2	VXQR1	2.380083521822334	0.017308714421212835	0.025	0.025320565519103866	0.025	0.033361747021845407	0.011017890075959304
1	G-CMA-ES	0.26545354969285145	0.7906600885567733	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 $\leq 0.011017890075959304$.

Table 8: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	$p_{Hos,f}$	$p_{Hol,m}$	$p_{Hoc,h}$	$p_{Hom,m}$
1	DE	1.2684075974808373E-4	3.805222792442512E-4	3.805222792442512E-4	3.805222792442512E-4	3.805222792442512E-4
2	VXQR1	8.688074530720151E-4	0.0026064223592160455	0.0017376149061440302	0.0017376149061440302	0.0017376149061440302
3	G-CMA-ES	0.5298199661707867	1.5894598985123602	0.5298199661707867	0.5298199661707867	0.5298199661707867

Table 9: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	$p_{Hos,l}$	$p_{Hol,m}$	$p_{Fin,n}$	p_{Li}
1	DE	1.2684075974808373E-4	3.8047401555008076E-4	3.805222792442512E-4	3.8047401555008076E-4	2.696978645250295E-4
2	VXQR1	8.688074530720151E-4	0.0017368600797535994	0.0017376149061440302	0.0013029280787107966	0.001844410551370755
3	G-CMA-ES	0.5298199661707867	0.5298199661707867	0.5298199661707867	0.5298199661707867	0.5298199661707867

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	VXQR1	5.942587553982733E-4	0.00178277626619482	0.00178277626619482	0.00178277626619482	0.00178277626619482
2	DE	0.01679799719916822	0.050393991597504656	0.03359599439833644	0.03359599439833644	0.03359599439833644
3	CHC	0.44051583608256234	1.321547508247687	0.44051583608256234	0.44051583608256234	0.44051583608256234

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	VXQR1	5.942587553982733E-4	0.0017817170456484455	0.00178277626619482	0.0017817170456484455	0.0010610277620807461
2	DE	0.01679799719916822	0.03331382168843311	0.03359599439833644	0.025090882904557854	0.029148910607644647
3	CHC	0.44051583608256234	0.44051583608256234	0.44051583608256234	0.44051583608256234	0.44051583608256234

Table 12: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	DE	0.00906631528454164	0.027198945853624923	0.027198945853624923	0.027198945853624923	0.025963071631819254
2	VXQR1	0.017308714421212835	0.05192614326363851	0.03461742884242567	0.03461742884242567	0.03461742884242567
3	G-CMA-ES	0.7906600885567733	2.3719802656703197	0.7906600885567733	0.7906600885567733	0.7906600885567733

Table 13: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	DE	0.00906631528454164	0.0269530968687528	0.027198945853624923	0.0269530968687528	0.04151124910848955
2	VXQR1	0.017308714421212835	0.034317837247510585	0.03461742884242567	0.0269530968687528	0.07636805365661176
3	G-CMA-ES	0.7906600885567733	0.7906600885567733	0.7906600885567733	0.7906600885567733	0.7906600885567733