

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 | 3.473684210526314 |
| CHC | 1.5263157894736836 |
| G-CMA-ES | 1.7631578947368416 |
| VXQR1 | 3.2368421052631575 |

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 33.99473684210508. P-value computed by Friedman Test: 1.9866505995835837E-7.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 26.598490048043562. P-value computed by Iman and Davenport Test: 1.0659428895110068E-10.

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

| Algorithm | Ranking |
|-----------|--------------------|
| DE | 47.97368421052631 |
| CHC | 27.421052631578945 |
| G-CMA-ES | 27.71052631578947 |
| VXQR1 | 50.89473684210526 |

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 14.276696910138039. P-value computed by Aligned Friedman Test: 0.002551720732487106.

Table 3: Average Rankings of the algorithms (Quade)

| Algorithm | Ranking |
|-----------|--------------------|
| DE | 3.455263157894737 |
| CHC | 1.5631578947368419 |
| G-CMA-ES | 1.6105263157894738 |
| VXQR1 | 3.371052631578947 |

Quade statistic (distributed according to F-distribution with 3 and 54 degrees of freedom: 36.16909807945108. P-value computed by Quade Test: 5.908606937055083E-13.

Table 4: Contrast Estimation

| | DE | CHC | G-CMA-ES | VXQR1 |
|----------|--------|-------|----------|-------|
| DE | 0.000 | -1178 | -1820 | 14.97 |
| CHC | 1178 | 0.000 | -641.3 | 1193 |
| G-CMA-ES | 1820 | 641.3 | 0.000 | 1835 |
| VXQR1 | -14.97 | -1193 | -1835 | 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 | 4.649278382037818 | 3.330983777894627E-6 | 0.016666666666666666 | 0.016952427508441503 | 0.016666666666666666 | 0.016952427508441503 | 0.02253864020376436 |
| 2 | VXQR1 | 4.083825605844032 | 4.430028241597432E-5 | 0.025 | 0.025320565519103666 | 0.025 | 0.03361747021845407 | 0.02253864020376436 |
| 1 | G-CMA-ES | 0.5654527761937891 | 0.5717658361284772 | 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 ≤ 0.02253864020376436 .

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 | 3.2762838776661947 | 0.0010518278004421138 | 0.016666666666666666 | 0.016952427508441503 | 0.016666666666666666 | 0.016952427508441503 | 0.0016962024023245807 |
| 2 | DE | 2.868584874952127 | 0.00412312557628376 | 0.025 | 0.025320565519103666 | 0.025 | 0.03361747021845407 | 0.0016962024023245807 |
| 1 | G-CMA-ES | 0.04040260387256484 | 0.967772154355833 | 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 $\leq 0.0016962024023245807$.

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 | 3.2349339360874443 | 0.0012167087932184295 | 0.016666666666666666 | 0.016952427508441503 | 0.016666666666666666 | 0.016952427508441503 | 0.003397198814408756 |
| 2 | VXQR1 | 3.0909591294743723 | 0.001995110933949898 | 0.025 | 0.025320565519103666 | 0.025 | 0.03361747021845407 | 0.003397198814408756 |
| 1 | G-CMA-ES | 0.08098582871985319 | 0.9354532225262336 | 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 $\leq 0.003397198814408756$.

Table 8: Adjusted p -values (FRIEDMAN)

| i | algorithm | unadjusted p | p_{Bonf} | p_{Holm} | p_{Hoch} | p_{Hommel} |
|-----|-----------|----------------------|-----------------------|----------------------|----------------------|----------------------|
| 1 | DE | 3.330983777894627E-6 | 9.992951333683881E-6 | 9.992951333683881E-6 | 9.992951333683881E-6 | 9.992951333683881E-6 |
| 2 | VXQR1 | 4.430028241597432E-5 | 1.3290084724792295E-4 | 8.860056483194864E-5 | 8.860056483194864E-5 | 8.860056483194864E-5 |
| 3 | G-CMA-ES | 0.5717658361284772 | 1.7152975083854316 | 0.5717658361284772 | 0.5717658361284772 | 0.5717658361284772 |

Table 9: Adjusted p -values (FRIEDMAN)

| i | algorithm | unadjusted p | p_{Holl} | p_{Rom} | p_{Sinn} | p_{Li} |
|-----|-----------|----------------------|----------------------|----------------------|----------------------|-----------------------|
| 1 | DE | 3.330983777894627E-6 | 9.992918047374566E-6 | 9.992918047374566E-6 | 9.992918047374566E-6 | 7.778356211008917E-6 |
| 2 | VXQR1 | 4.430028241597432E-5 | 8.859860231691385E-5 | 8.860056483194864E-5 | 6.644968767544057E-5 | 1.0343803418527997E-4 |
| 3 | G-CMA-ES | 0.5717658361284772 | 0.5717658361284772 | 0.5717658361284772 | 0.5717658361284772 | 0.5717658361284772 |

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

| i | algorithm | unadjusted p | p_{Bonf} | p_{Holm} | p_{Hoch} | p_{Hommel} |
|-----|-----------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|
| 1 | VXQR1 | 0.0010518278004421138 | 0.0031554834013263417 | 0.0031554834013263417 | 0.0031554834013263417 | 0.0031554834013263417 |
| 2 | DE | 0.00412312557628376 | 0.012369376728851281 | 0.00824625115256752 | 0.00824625115256752 | 0.00824625115256752 |
| 3 | G-CMA-ES | 0.967772154355833 | 2.903316463067499 | 0.967772154355833 | 0.967772154355833 | 0.967772154355833 |

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

| i | algorithm | unadjusted p | p_{Holl} | p_{Rom} | p_{Sinn} | p_{Li} |
|-----|-----------|-----------------------|----------------------|-----------------------|----------------------|---------------------|
| 1 | VXQR1 | 0.0010518278004421138 | 0.003152165539841989 | 0.0031554834013263417 | 0.003152165539841989 | 0.03160571278419488 |
| 2 | DE | 0.00412312557628376 | 0.00822925098804983 | 0.00824625115256752 | 0.006178308915080644 | 0.11342545846379279 |
| 3 | G-CMA-ES | 0.967772154355833 | 0.967772154355833 | 0.967772154355833 | 0.967772154355833 | 0.967772154355833 |

Table 12: Adjusted p -values (QUADE)

| i | algorithm | unadjusted p | p_{Bonf} | p_{Holm} | p_{Hoch} | p_{Homn} |
|-----|-----------|-----------------------|----------------------|----------------------|----------------------|----------------------|
| 1 | DE | 0.0012167087932184295 | 0.003650126379655288 | 0.003650126379655288 | 0.003650126379655288 | 0.002992666400924847 |
| 2 | VXQR1 | 0.001995110933949898 | 0.005985332801849694 | 0.003990221867899796 | 0.003990221867899796 | 0.003990221867899796 |
| 3 | G-CMA-ES | 0.9354532225262336 | 2.806359667578701 | 0.9354532225262336 | 0.9354532225262336 | 0.9354532225262336 |

Table 13: Adjusted p -values (QUADE)

| i | algorithm | unadjusted p | p_{Holl} | p_{Rom} | p_{Finn} | p_{Li} |
|-----|-----------|-----------------------|-----------------------|----------------------|-----------------------|---------------------|
| 1 | DE | 0.0012167087932184295 | 0.0036456870399845798 | 0.003650126379655288 | 0.0036456870399845798 | 0.01850128182497607 |
| 2 | VXQR1 | 0.001995110933949898 | 0.003986241400261048 | 0.003990221867899796 | 0.0036456870399845798 | 0.02998278199929385 |
| 3 | G-CMA-ES | 0.9354532225262336 | 0.9354532225262336 | 0.9354532225262336 | 0.9354532225262336 | 0.9354532225262336 |