# Results

March 23, 2013

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



Table 1: Average Rankings of the algorithms (Friedman)

| Algorithm | Ranking |
|---|---|
| L-Co-R | 2.5250000000000004 |
| ETS | 3.475 |
| Croston | 4.399999999999999 |
| Theta | 2.6999999999999993 |
| RW | 3.45 |
| ARIMA | 4.449999999999999 |

Friedman statistic (distributed according to chi-square with 5 degrees of freedom: 18.892857142857014. P-value computed by Friedman Test: 0.002012483956556732.

Iman and Davenport statistic (distributed according to F-distribution with 5 and 95 degrees of freedom: 4.425803610744128. P-value computed by Iman and Daveport Test: 0.0011463746083697631.

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

| Algorithm | Ranking |
|---|---|
| L-Co-R | 44.075 |
| ETS | 55.975 |
| Croston | 85.05 |
| Theta | 47.800000000000004 |
| RW | 58.65000000000001 |
| ARIMA | 71.44999999999999 |

Aligned Friedman statistic (distributed according to chi-square with 5 degrees of freedom: 16.937011402048096. P-value computed by Aligned Friedman Test: 0.004620818831952422.

Table 3: Average Rankings of the algorithms (Quade)

| Algorithm | Ranking |
|---|---|
| L-Co-R | 2.369047619047619 |
| ETS | 3.3357142857142854 |
| Croston | 4.766666666666667 |
| Theta | 2.8285714285714283 |
| RW | 3.571428571428571 |
| ARIMA | 4.128571428571427 |

Quade statistic (distributed according to F-distribution with 5 and 95 degrees of freedom: 5.707188328311547. P-value computed by Quade Test: 1.2002699582555516E-4.

Table 4: Contrast Estimation

| | L-Co-R | ETS | Croston | Theta | RW | ARIMA |
|---|---|---|---|---|---|---|
| L-Co-R | 0.000 | -0.08267 | -1.183 | -0.05508 | -0.07708 | -0.4376 |
| ETS | 0.08267 | 0.000 | -1.100 | 0.02758 | 0.005583 | -0.3549 |
| Croston | 1.183 | 1.100 | 0.000 | 1.128 | 1.106 | 0.7455 |
| Theta | 0.05508 | -0.02758 | -1.128 | 0.000 | -0.02200 | -0.3825 |
| RW | 0.07708 | -0.005583 | -1.106 | 0.02200 | 0.000 | -0.3605 |
| ARIMA | 0.4376 | 0.3549 | -0.7455 | 0.3825 | 0.3605 | 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 |
|---|---|---|---|---|---|---|---|---|
| 5 | ARIMA | 3.253843880704787 | 0.0011385483161214366 | 0.01 | 0.010206218313011495 | 0.010515350115740741 | 0.010206218313011495 | 0.012243169665332404 |
| 4 | Croston | 3.169328455231934 | 0.001527916221622385 | 0.0125 | 0.012741455098566168 | 0.013109375000000001 | 0.0203082697337702 | 0.012243169665332404 |
| 3 | ETS | 1.6057930839841812 | 0.10831938073000413 | 0.016666666666666666 | 0.016952427508441503 | 0.016666666666666666 | 0.03030721741231923 | 0.012243169665332404 |
| 2 | RW | 1.5635353712477553 | 0.11792672274114391 | 0.025 | 0.025320565519103666 | 0.025 | 0.040204113647960726 | 0.012243169665332404 |
| 1 | Theta | 0.295803989154979 | 0.7673797763586844 | 0.05 | 0.050000000000000044 | 0.05 | 0.050000000000000044 | 0.05 |

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq 0.01$.
Holm's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.
Hochberg's procedure rejects those hypotheses that have a p-value $\leq 0.0125$.
Hommel's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.
Holland's procedure rejects those hypotheses that have a p-value $\leq 0.016952427508441503$.
Rom's procedure rejects those hypotheses that have a p-value $\leq 0.013109375000000001$.
Finner's procedure rejects those hypotheses that have a p-value $\leq 0.03030721741231923$.
Li's procedure rejects those hypotheses that have a p-value $\leq 0.012243169665332404$.

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 |
|---|---|---|---|---|---|---|---|---|
| 5 | Croston | 3.7249999999999996 | 1.953152219838016 4E-4 | 0.01 | 0.010206218313011495 | 0.010515350115740741 | 0.010206218313011495 | 0.013953490250670551 |
| 4 | ARIMA | 2.4886363636363624 | 0.012823404999015473 | 0.0125 | 0.012741455098566168 | 0.013109375000000001 | 0.0203082697337702 | 0.013953490250670551 |
| 3 | RW | 1.3250000000000008 | 0.18517115131358966 | 0.016666666666666666 | 0.016952427508441503 | 0.016666666666666666 | 0.03030721741231923 | 0.013953490250670551 |
| 2 | ETS | 1.0818181818181818 | 0.2793333259447317 | 0.025 | 0.025320565519103666 | 0.025 | 0.040204113647960726 | 0.013953490250670551 |
| 1 | Theta | 0.3386363636363638 | 0.7348836852372596 | 0.05 | 0.050000000000000044 | 0.05 | 0.050000000000000044 | 0.05 |

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq 0.01$.
Holm's procedure rejects those hypotheses that have a p-value $\leq 0.0125$.
Hochberg's procedure rejects those hypotheses that have a p-value $\leq 0.01$.
Hommel's procedure rejects those hypotheses that have a p-value $\leq 0.0125$.
Holland's procedure rejects those hypotheses that have a p-value $\leq 0.012741455098566168$.
Rom's procedure rejects those hypotheses that have a p-value $\leq 0.013109375000000001$.
Finner's procedure rejects those hypotheses that have a p-value $\leq 0.03030721741231923$.
Li's procedure rejects those hypotheses that have a p-value $\leq 0.013953490250670551$.

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 |
|---|---|---|---|---|---|---|---|---|
| 5 | Croston | 2.246671117454661 | 0.02466105341680431 | 0.01 | 0.010206218313011495 | 0.010515350115740741 | 0.010206218313011495 | 0.017538733615913085 |
| 4 | ARIMA | 1.6487487147954256 | 0.09919912555062183 | 0.0125 | 0.012741455098566168 | 0.013109375000000001 | 0.0203082697337702 | 0.017538733615913085 |
| 3 | RW | 1.1266821393392292 | 0.25987689656740265 | 0.016666666666666666 | 0.016952427508441503 | 0.016666666666666666 | 0.03030721741231923 | 0.017538733615913085 |
| 2 | ETS | 0.9058078189539148 | 0.3650375817619201 | 0.025 | 0.025320565519103666 | 0.025 | 0.040204113647960726 | 0.017538733615913085 |
| 1 | Theta | 0.43059337206429926 | 0.6667640612976514 | 0.05 | 0.050000000000000044 | 0.05 | 0.050000000000000044 | 0.05 |

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq 0.01$.
Holm's procedure rejects those hypotheses that have a p-value $\leq 0.01$.
Hommel's procedure rejects those hypotheses that have a p-value $\leq 0.01$.
Holland's procedure rejects those hypotheses that have a p-value $\leq 0.010206218313011495$.
Finner's procedure rejects those hypotheses that have a p-value $\leq 0.010206218313011495$.
Li's procedure rejects those hypotheses that have a p-value $\leq 0.017538733615913085$.

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Table 8: Adjusted $p$-values (FRIEDMAN)

| i | algorithm | unadjusted $p$ | $p_{Bonf}$ | $p_{Holm}$ | $p_{Hoch}$ | $p_{Homm}$ |
|---|---|---|---|---|---|---|
| 1 | ARIMA | 0.0011385483161214366 | 0.005692741580607183 | 0.005692741580607183 | 0.005692741580607183 | 0.0045541932644857465 |
| 2 | Croston | 0.001527916221622385 | 0.007639581108111925 | 0.00611166488648954 | 0.00611166488648954 | 0.00611166488648954 |
| 3 | ETS | 0.10831938073000413 | 0.5415969036500207 | 0.3249581421900124 | 0.23585344548228782 | 0.21663876146000827 |
| 4 | RW | 0.11792672274114391 | 0.5896336137057195 | 0.3249581421900124 | 0.23585344548228782 | 0.23585344548228782 |
| 5 | Theta | 0.7673797763586844 | 3.836898881793422 | 0.7673797763586844 | 0.7673797763586844 | 0.7673797763586844 |

Table 9: Adjusted $p$-values (FRIEDMAN)

| i | algorithm | unadjusted $p$ | $p_{Holl}$ | $p_{Rom}$ | $p_{Finn}$ | $p_{Li}$ |
|---|---|---|---|---|---|---|
| 1 | ARIMA | 0.0011385483161214366 | 0.005679793408439826 | 0.0054137442100815536 | 0.005679793408439826 | 0.004870612155375046 |
| 2 | Croston | 0.001527916221622385 | 0.006097671981010522 | 0.005827570809525186 | 0.005679793408439826 | 0.006525425410241451 |
| 3 | ETS | 0.10831938073000413 | 0.29102979831721254 | 0.23585344548228782 | 0.1739324819093101 | 0.3177084132825845 |
| 4 | RW | 0.11792672274114391 | 0.29102979831721254 | 0.23585344548228782 | 0.1739324819093101 | 0.33640778776740937 |
| 5 | Theta | 0.7673797763586844 | 0.7673797763586844 | 0.7673797763586844 | 0.7673797763586844 | 0.7673797763586844 |

Table 10: Adjusted $p$-values (ALIGNED FRIEDMAN)

| i | algorithm | unadjusted $p$ | $p_{Bonf}$ | $p_{Holm}$ | $p_{Hoch}$ | $p_{Homm}$ |
|---|---|---|---|---|---|---|
| 1 | Croston | 1.9531522198380164E-4 | 9.765761099190082E-4 | 9.765761099190082E-4 | 9.765761099190082E-4 | 9.765761099190082E-4 |
| 2 | ARIMA | 0.012823404999015473 | 0.06411702499507736 | 0.05129361999606189 | 0.05129361999606189 | 0.05129361999606189 |
| 3 | RW | 0.18517115131358966 | 0.9258557565679483 | 0.555513453940769 | 0.555513453940769 | 0.41899998891709755 |
| 4 | ETS | 0.2793333259447317 | 1.3966666297236585 | 0.5586666518894634 | 0.5586666518894634 | 0.5586666518894634 |
| 5 | Theta | 0.7348836852372596 | 3.674418426186298 | 0.7348836852372596 | 0.7348836852372596 | 0.7348836852372596 |

Table 11: Adjusted $p$-values (ALIGNED FRIEDMAN)

| i | algorithm | unadjusted $p$ | $p_{Holl}$ | $p_{Rom}$ | $p_{Finn}$ | $p_{Li}$ |
|---|---|---|---|---|---|---|
| 1 | Croston | 1.9531522198380164E-4 | 9.76194704061184E-4 | 9.287147828365147E-4 | 9.76194704061184E-4 | 7.361728620605408E-4 |
| 2 | ARIMA | 0.012823404999015473 | 0.050315389369322006 | 0.04890929201054769 | 0.03175084805240935 | 0.04613736032405669 |
| 3 | RW | 0.18517115131358966 | 0.4589976023279928 | 0.555513453940769 | 0.2891510476336189 | 0.41122874888594063 |
| 4 | ETS | 0.2793333259447317 | 0.4806395449061177 | 0.5586666518894634 | 0.3360000461430823 | 0.5130563142290968 |
| 5 | Theta | 0.7348836852372596 | 0.7348836852372596 | 0.7348836852372596 | 0.7348836852372596 | 0.7348836852372596 |

Table 12: Adjusted $p$-values (QUADE)

| i | algorithm | unadjusted $p$ | $p_{Bonf}$ | $p_{Holm}$ | $p_{Hoch}$ | $p_{Homm}$ |
|---|---|---|---|---|---|---|
| 1 | Croston | 0.02466105341680431 | 0.12330526708402154 | 0.12330526708402154 | 0.12330526708402154 | 0.12330526708402154 |
| 2 | ARIMA | 0.09919912555062183 | 0.4959956277531091 | 0.3967965022024873 | 0.3967965022024873 | 0.3967965022024873 |
| 3 | RW | 0.25987689656740265 | 1.2993844828370134 | 0.779630689702208 | 0.6667640612976514 | 0.5475563726428802 |
| 4 | ETS | 0.3650375817619201 | 1.8251879088096004 | 0.779630689702208 | 0.6667640612976514 | 0.6667640612976514 |
| 5 | Theta | 0.6667640612976514 | 3.3338203064882572 | 0.779630689702208 | 0.6667640612976514 | 0.6667640612976514 |

Table 13: Adjusted $p$-values (QUADE)

| i | algorithm | unadjusted $p$ | $p_{Holl}$ | $p_{Rom}$ | $p_{Finn}$ | $p_{Li}$ |
|---|---|---|---|---|---|---|
| 1 | Croston | 0.02466105341680431 | 0.11737173183596417 | 0.11726216029596791 | 0.11737173183596417 | 0.06890545033861034 |
| 2 | ARIMA | 0.09919912555062183 | 0.3415615310525164 | 0.37835184953753254 | 0.22985589101843873 | 0.2293965817087193 |
| 3 | RW | 0.25987689656740265 | 0.5945737320361731 | 0.6667640612976514 | 0.3944175667015578 | 0.4381576002299951 |
| 4 | ETS | 0.3650375817619201 | 0.5968227274252496 | 0.6667640612976514 | 0.4331932329240813 | 0.5227716232447331 |
| 5 | Theta | 0.6667640612976514 | 0.6667640612976514 | 0.6667640612976514 | 0.6667640612976514 | 0.6667640612976514 |