

Results

March 23, 2013

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
L-Co-R	1.5000000000000004
ETS	4.25
Croston	4.8
Theta	3.1500000000000004
RW	4.125
ARIMA	3.1750000000000007

Friedman statistic (distributed according to chi-square with 5 degrees of freedom: 39.264285714285734. P-value computed by Friedman Test: 2.1012737416725713E-7.

Iman and Davenport statistic (distributed according to F-distribution with 5 and 95 degrees of freedom: 12.283076561213699. P-value computed by Iman and Davenport Test: 3.415900232737556E-9.

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

Algorithm	Ranking
L-Co-R	29.35
ETS	69.4
Croston	84.7
Theta	60.35000000000001
RW	68.825
ARIMA	50.37499999999999

Aligned Friedman statistic (distributed according to chi-square with 5 degrees of freedom: 16.923381262328157. P-value computed by
Aligned Friedman Test: 0.004647422237445631.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
L-Co-R	1.5095238095238093
ETS	4.238095238095238
Croston	5.023809523809524
Theta	3.2952380952380946
RW	3.9571428571428564
ARIMA	2.9761904761904763

Quade statistic (distributed according to F-distribution with 5 and 95 degrees of freedom: 12.082053820948609. P-value computed by Quade Test: 4.5738614445137335E-9.

Table 4: Contrast Estimation

	L-Co-R	ETS	Croston	Theta	RW	ARIMA
L-Co-R	0.000	-6.933	-14.03	-6.173	-7.376	-5.528
ETS	6.933	0.000	-7.094	0.7601	-0.4429	1.406
Croston	14.03	7.094	0.000	7.854	6.651	8.499
Theta	6.173	-0.7601	-7.854	0.000	-1.203	0.6454
RW	7.376	0.4429	-6.651	1.203	0.000	1.848
ARIMA	5.528	-1.406	-8.499	-0.6454	-1.848	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	Croston	5.578018081208208	2.4327437355602848E-8	0.01	0.010206218313011495	0.010515350115740741	0.010206218313011495	0.052353317951792704
4	ETS	4.6483484010068405	3.346034047178284E-6	0.0125	0.012741455098566168	0.01310937500000000001	0.0203082697337702	0.052353317951792704
3	RW	4.437059837324711	9.11959490915456E-6	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.03030721741231923	0.052353317951792704
2	ARIMA	2.831266753340531	0.004636403572904565	0.025	0.025320565519103666	0.025	0.040204113647960726	0.052353317951792704
1	Theta	2.7890090406041046	0.005286958915938802	0.05	0.050000000000000044	0.05	0.050000000000000044	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value ≤ 0.01 .

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	Holland/Hommel	Holland	Rom	Finner	Li
5	Croston	5.0318181818182	4.858499308565756E-7	0.01	0.01	0.010206218313011495	0.010515350115740741	0.010206218313011495	0.04968642808555686
4	ETS	3.6409090909091	2.7167705973685837E-4	0.0125	0.0125	0.012741455098566168	0.01310937500000000001	0.0203082697337702	0.04968642808555686
3	RW	3.5886363636364	3.324121112500655E-4	0.016666666666666666	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.03030721741231923	0.04968642808555686
2	Theta	2.8181818181819	0.004829645255939948	0.025	0.025	0.025320565519103666	0.025	0.040204113647960726	0.04968642808555686
1	ARIMA	1.91136363636355	0.05595786637441985	0.05	0.05	0.050000000000000044	0.05	0.050000000000000044	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value ≤ 0.01 .

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 ≤ 0.04968642808555686 .

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	Holland	Rom	Finner	Li
5	Croston	3.293035322108322	9.91120223131925E-4	0.01	0.010206218313011495	0.010515350115740741	0.010206218313011495	0.04371897185908375
4	ETS	2.5567875874906076	0.010564370499639505	0.0125	0.012741455098566168	0.0131093750000000001	0.0203082697337702	0.04371897185908375
3	RW	2.2935232460212425	0.021817898605735526	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.03030721741231923	0.04371897185908375
2	Theta	1.6732903059493502	0.09427015990831819	0.025	0.02532056519103666	0.025	0.040204113647960726	0.04371897185908375
1	ARIMA	1.3743291046197337	0.16933953467740884	0.05	0.050000000000000044	0.05	0.050000000000000044	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value ≤ 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 ≤ 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 $\leq 0.040204113647960726$.
 Li's procedure rejects those hypotheses that have a p-value ≤ 0.04371897185908375 .

Table 8: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hom}
1	Croston	2.4327437355602848E-8	1.2163718677801425E-7	1.2163718677801425E-7	1.2163718677801425E-7	1.2163718677801425E-7
2	ETS	3.346034047178284E-6	1.673017023589142E-5	1.3384136188713136E-5	1.3384136188713136E-5	1.3384136188713136E-5
3	RW	9.11959490915456E-6	4.5597974545772806E-5	2.7358784727463682E-5	2.7358784727463682E-5	2.7358784727463682E-5
4	ARIMA	0.004636403572904565	0.023182017864522824	0.00927280714580913	0.005286958915938802	0.005286958915938802
5	Theta	0.005286958915938802	0.02643479457969401	0.00927280714580913	0.005286958915938802	0.005286958915938802

Table 9: Adjusted p -values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	Croston	2.4327437355602848E-8	1.2163718110524968E-7	1.1567583146464321E-7	1.2163718110524968E-7	2.445673853247211E-8
2	ETS	3.346034047178284E-6	1.3384069013189226E-5	1.276198921450597E-5	8.365064125492871E-6	3.363807101713094E-6
3	RW	9.11959490915456E-6	2.735853522706222E-5	2.7358784727463682E-5	1.5199278644573155E-5	9.167982045287672E-6
4	ARIMA	0.004636403572904565	0.009251310907718135	0.005286958915938802	0.005792141777838489	0.004639421773527923
5	Theta	0.005286958915938802	0.009251310907718135	0.005286958915938802	0.005792141777838489	0.005286958915938802

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homn}
1	Croston	4.858499308565756E-7	2.429249654282878E-6	2.429249654282878E-6	2.429249654282878E-6	2.429249654282878E-6
2	ETS	2.7167705973685837E-4	0.0013583852986842919	0.0010867082389474335	9.972363337501966E-4	8.150311792105751E-4
3	RW	3.324121112500655E-4	0.0016620605562503274	0.0010867082389474335	9.972363337501966E-4	9.972363337501966E-4
4	Theta	0.004829645255939948	0.0241148226279699737	0.009659290511879895	0.009659290511879895	0.009659290511879895
5	ARIMA	0.05595786637441985	0.27978933187209926	0.05595786637441985	0.05595786637441985	0.05595786637441985

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	Croston	4.858499308565756E-7	2.429247293767034E-6	2.3101937905486013E-6	2.429247293767034E-6	5.146483017117415E-7
2	ETS	2.7167705973685837E-4	0.0010862654686014661	9.972363337501966E-4	6.790542648121844E-4	2.876978570711511E-4
3	RW	3.324121112500655E-4	0.0010862654686014661	9.972363337501966E-4	6.790542648121844E-4	3.519918159067992E-4
4	Theta	0.004829645255939948	0.009635965038581773	0.009659290511879895	0.006033407554861592	0.005089881861206662
5	ARIMA	0.05595786637441985	0.055957866374419796	0.05595786637441985	0.055957866374419796	0.05595786637441985

Table 12: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Hommel}
1	Croston	9.91120223131925E-4	0.004955601115659625	0.004955601115659625	0.004955601115659625	0.004955601115659625
2	ETS	0.010564370499639505	0.05282185249819753	0.04225748199855802	0.04225748199855802	0.04225748199855802
3	RW	0.021817898605735526	0.10908949302867763	0.06545369581720659	0.06545369581720659	0.06545369581720659
4	Theta	0.09427015990831819	0.471350799541591	0.18854031981663638	0.16933953467740884	0.16933953467740884
5	ARIMA	0.16933953467740884	0.8466976733870442	0.18854031981663638	0.16933953467740884	0.16933953467740884

Table 13: Adjusted p -values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	Croston	9.91120223131925E-4	0.004945787653834244	0.0047127304950516456	0.004945787653834244	0.0011917493339251674
2	ETS	0.010564370499639505	0.04159255018368058	0.040293189033190006	0.026202034081583725	0.012558319785356396
3	RW	0.021817898605735526	0.06403601948985371	0.06545369581720659	0.03609806259117154	0.025593492490760615
4	Theta	0.09427015990831819	0.17965345676749656	0.16933953467740884	0.1164149782205467	0.10192133046171284
5	ARIMA	0.16933953467740884	0.17965345676749656	0.16933953467740884	0.1693395346774088	0.16933953467740884