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	1.850000000000005
ETS	4.075
Croston	5.149999999999995
Theta	2.949999999999997
RW	4.05
ARIMA	2.925000000000003

Friedman statistic (distributed according to chi-square with 5 degrees of freedom: 38.35000000000004. P-value computed by Friedman Test: 3.2094248447744489E-7.

Iman and Davenport statistic (distributed according to F-distribution with 5 and 95 degrees of freedom: 11.819140308191422. P-value computed by Iman and Daveport Test: 6.717110126731175E-9.

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

Algorithm	Ranking
L-Co-R	32.55000000000004
ETS	64.47500000000001
Croston	88.45
Theta	60.9
RW	69.45000000000002
ARIMA	47.175

Aligned Friedman statistic (distributed according to chi-square with 5 degrees of freedom: 17.175936685816534. P-value computed by Aligned Friedman Test: 0.004177936278873529.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
L-Co-R	1.847619047619473
ETS	3.935714285714855
Croston	5.109523809523809
Theta	3.333333333333326
RW	3.888095238095238
ARIMA	2.885714285714857

Quade statistic (distributed according to F-distribution with 5 and 95 degrees of freedom: 9.45114871205464. P-value computed by Quade Test: 2.44254136115375E-7.

Table 4: Contrast Estimation

	L-Co-R	ETS	Croston	Theta	RW	ARIMA
L-Co-R	0.000	-4.956	-12.55	-4.545	-5.833	-3.346
ETS	4.956	0.000	-7.595	0.4109	-0.8772	1.610
Croston	12.55	7.595	0.000	8.006	6.718	9.205
Theta	4.545	-0.4109	-8.006	0.000	-1.288	1.199
RW	5.833	0.8772	-6.718	1.288	0.000	2.487
ARIMA	3.346	-1.610	-9.205	-1.199	-2.487	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	5.578018081208207	2.4327437355602974E-8	0.01	0.010206218313011495	0.010515350115740741	0.010206218313011495	0.04898923092559697
4	ETS	3.7609364335418984	1.6927844756719902E-4	0.0125	0.012741455098566168	0.013109375000000001	0.020308269733702	0.04898923092559697
3	RW	3.718678720805472	2.0026757491716922E-4	0.016666666666666666	0.016952442750844 1503	0.016666666666666666	0.030307217412231923	0.04898923092559697
2	Theta	1.8593393360402735	0.06297905121445545	0.025	0.025320565519103666	0.025	0.040204113647960726	0.04898923092559697
1	ARIMA	1.81708164766663103	0.06920461241365775	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 ≤ 0.025.

Hochberg's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

Hommel's procedure rejects those hypotheses that have a p-value ≤ 0.025.

Holland's procedure rejects those hypotheses that have a p-value $\leq 0.025320565519103666$.

Rom's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

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 ≤ 0.04898923092559697.

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	5.0818181818182	3.73839159916893943E-7	0.01	0.01020621831301495	0.0105153501157441	0.01020621831301495	0.04296483789728828
4	RW	3.354545454545456	7.949549150799624E-4	0.0125	0.01274145509856168	0.0131093750000000001	0.02030826973377702	0.04296483789728828
3	ETS	2.902272727272728	0.0037046586278312935	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.030307217412231923	0.04296483789728828
2	Theta	2.5772727272727267	0.009958334446764907	0.025	0.025320565519103666	0.025	0.040204113647960726	0.04296483789728828
1	ARIMA	1.329545454545454	0.18366807995115228	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 ≤ 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 ≤ 0.050000000000000044.

Li's procedure rejects those hypotheses that have a p-value ≤ 0.04296483789728828.

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	3.056543625534147	0.0022390489534412313	0.01	0.010206218313011495	0.0105153501157740741	0.010206218313011495	0.035227219872080266
4	ETS	1.9566343110901074	0.050390499203719324	0.0125	0.012741455098566168	0.01310937500000001	0.0203082697337702	0.035227219872080266
3	RW	1.9120130562647917	0.055874519423078695	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.030307217412231923	0.035227219872080266
2	Theta	1.3921775345498593	0.16386864394254461	0.025	0.025320565519103666	0.025	0.040204113647960726	0.035227219872080266
1	ARIMA	0.9727394311918894	0.3306828224304751	0.05	0.05000000000000044	0.05	0.05000000000000044	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 ≤ 0.0125.

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

Hommel's procedure rejects those hypotheses that have a p-value ≤ 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 $\leq 0.0105153501157740741$.

Finner's procedure rejects those hypotheses that have a p-value ≤ 0.0203082697337702.

Li's procedure rejects those hypotheses that have a p-value $\leq 0.035227219872080266$.

Table 8: Adjusted p-values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	Croston	2.4327437355602974E-8	1.2163718677801488E-7	1.2163718677801488E-7	1.2163718677801488E-7	1.2163718677801488E-7
2	ETS	1.6927844756719902E-4	8.463922378359511E-4	6.771137902687961E-4	6.0080272475150768E-4	5.0783534270159776E-4
3	RW	2.0026757491716922E-4	0.0010013378745858462	6.771137902687961E-4	6.0080272475150768E-4	6.0080272475150768E-4
4	Theta	0.06297905121445545	0.3148952560722725	0.1259581024289109	0.06920461241365775	0.06920461241365775
5	ARIMA	0.06920461241365775	0.3460230620682887	0.1259581024289109	0.06920461241365775	0.06920461241365775

Table 9: Adjusted p-values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	Croston	2.4327437355602974E-8	1.2163718110524968E-7	1.1567583146464388E-7	1.2163718110524968E-7	2.6136180995464683E-8
2	ETS	1.6927844756719902E-4	6.769418785139703E-4	6.0080272475150768E-4	4.2314239194740644E-4	1.8183122705221256E-4
3	RW	2.0026757491716922E-4	6.769418785139703E-4	6.0080272475150768E-4	4.2314239194740644E-4	2.151118103175307E-4
4	Theta	0.06297905121445545	0.12199174153703796	0.06920461241365775	0.07809403385463187	0.06337358736098425
5	ARIMA	0.06920461241365775	0.12199174153703796	0.06920461241365775	0.07809403385463187	0.06920461241365775

Table 10: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	Croston	3.73839159168943E-7	1.86919579958844715E-6	1.86919579958844715E-6	1.86919579958844715E-6	1.86919579958844715E-6
2	RW	7.94954915079964E-4	0.0039747457533998115	0.00317981966603198495	0.00317981966603198495	0.00317981966603198495
3	ETS	0.0037046586278312935	0.018523293139156467	0.0111139758349388	0.0111139758349388	0.0111139758349388
4	Theta	0.00995833446764907	0.049791672233382454	0.0199166688935329815	0.0199166688935329815	0.0199166688935329815
5	ARIMA	0.1836680799515228	0.918340399757614	0.1836680799515228	0.1836680799515228	0.1836680799515228

Table 11: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	Croston	3.73839159168943E-7	1.869194402259744E-6	1.7775877921424761E-6	1.869194402259744E-6	4.5794973776738877E-7
2	RW	7.94954915079964E-4	0.003176029949516046	0.0030320092112704165	0.0019862025322238135	9.7286591955645115E-4
3	ETS	0.0037046586278312935	0.011072853241418 49	0.0111139758349388	0.0061166803184199316	0.004517674850323508
4	Theta	0.00995833446764907	0.0198175004685761 1	0.0199166688935329815	0.012432384246799488	0.012051859976066375
5	ARIMA	0.1836680799515228	0.1836680799515228	0.1836680799515228	0.1836680799515228	0.1836680799515228

Table 12: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	Croston	0.0022390489534412313	0.011195244767206156	0.011195244767206156	0.011195244767206156	0.011195244767206156
2	ETS	0.050390499203719324	0.2519524960185966	0.2015619968148773	0.16762355826923608	0.15171497611157797
3	RW	0.055874519423078695	0.2793725971153935	0.2015619968148773	0.16762355826923608	0.16762355826923608
4	Theta	0.1638686439425461	0.8193432197127305	0.3277372878850922	0.3277372878850922	0.3277372878850922
5	ARIMA	0.3306828224304751	1.6534141121523755	0.3306828224304751	0.3306828224304751	0.3306828224304751

Table 13: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	Croston	0.0022390489534412313	0.011145223490576894	0.010646573479705313	0.011145223490576894	0.0033341198622103157
2	ETS	0.050390499203719324	0.1868321415140748	0.16762355826923608	0.1212554841363731	0.0700152309471553 4
3	RW	0.055874519423078695	0.1868321415140748	0.16762355826923608	0.1212554841363731	0.07704793043658988
4	Theta	0.1638686439425461	0.3008843554177523 23	0.3277372878850922	0.20045458351538104	0.19667718738318932
5	ARIMA	0.3306828224304751	0.3306828224304751	0.3306828224304751	0.3306828224304751	0.3306828224304751