

May 25, 2011

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

Table 1: Average Rankings of the algorithms (Friedman)

| Algorithm | Ranking |
|--|--------------------|
| CADD _G M _t st | 5.1428571428571415 |
| CAIM _G M _t st | 3.0476190476190474 |
| Chi2Merge _G M _t st | 3.1904761904761907 |
| ChiMerge _G M _t st | 2.7142857142857144 |
| Fayyad _G M _t st | 2.6666666666666656 |
| ID3 _G M _t st | 6.047619047619048 |
| USD _G M _t st | 5.19047619047619 |

Friedman statistic (distributed according to chi-square with 6 degrees of freedom: 107.18367346938768. P-value computed by Friedman

Test: 8.797129691373584E-11.

Iman and Davenport statistic (distributed according to F-distribution with 6 and 246 degrees of freedom: 30.34554678692217. P-value computed by Iman and Davenport Test: 3.668679551129473E-27.

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

| Algorithm | Ranking |
|-----------------------|--------------------|
| $CADD_G M_{tst}$ | 199.7619047619048 |
| $CAIM_G M_{tst}$ | 97.42857142857142 |
| $Chi2Merge_G M_{tst}$ | 110.07142857142857 |
| $ChiMerge_G M_{tst}$ | 89.16666666666667 |
| $Fayyad_G M_{tst}$ | 96.9047619047619 |
| $ID3_G M_{tst}$ | 235.23809523809518 |
| $USD_G M_{tst}$ | 203.92857142857147 |

Aligned Friedman statistic (distributed according to chi-square with 6 degrees of freedom: 36.80029097156058. P-value computed by Aligned Friedman Test: 1.9260144252797318E-6.

Table 3: Average Rankings of the algorithms (Quade)

| Algorithm | Ranking |
|-----------------------|--------------------|
| $CADD_G M_{tst}$ | 5.260243632336656 |
| $CAIM_G M_{tst}$ | 3.0088593576965663 |
| $Chi2Merge_G M_{tst}$ | 3.1893687707641183 |
| $ChiMerge_G M_{tst}$ | 2.5559246954595785 |
| $Fayyad_G M_{tst}$ | 2.4651162790697687 |
| $ID3_G M_{tst}$ | 6.294573643410852 |
| $USD_G M_{tst}$ | 5.2259136212624595 |

Quade statistic (distributed according to F-distribution with 6 and 246 degrees of freedom: 26.35121632852374. P-value computed by Quade Test: 3.724204682611438E-24.

Table 4: Contrast Estimation

| | CADD G_{Mfst} | CAIM G_{Mfst} | Chi2Merge G_{Mfst} | ChiMerge G_{Mfst} | Fayyad G_{Mfst} | ID3 G_{Mfst} | USD G_{Mfst} |
|----------------------|-----------------|-----------------|----------------------|---------------------|-------------------|----------------|----------------|
| CADD G_{Mfst} | 0.00000000 | -0.10531786 | -0.10358786 | -0.11226286 | -0.10754714 | 0.01821214 | -0.02541143 |
| CAIM G_{Mfst} | 0.10531786 | 0.00000000 | 0.00173000 | -0.00694500 | -0.00222929 | 0.12353000 | 0.07990643 |
| Chi2Merge G_{Mfst} | 0.10358786 | -0.00173000 | 0.00000000 | -0.00867500 | -0.00395929 | 0.12180000 | 0.07817643 |
| ChiMerge G_{Mfst} | 0.11226286 | 0.00694500 | 0.00867500 | 0.00000000 | 0.00471571 | 0.13047500 | 0.08685143 |
| Fayyad G_{Mfst} | 0.10754714 | 0.00222929 | 0.00395929 | -0.00471571 | 0.00000000 | 0.12575929 | 0.08213571 |
| ID3 G_{Mfst} | -0.01821214 | -0.12353000 | -0.12180000 | -0.13047500 | -0.12575929 | 0.00000000 | -0.04362357 |
| USD G_{Mfst} | 0.02541143 | -0.07990643 | -0.07817643 | -0.08685143 | -0.08213571 | 0.04362357 | 0.00000000 |

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 |
|-----|-----------------------------|------------------------|-----------------------|----------------------|-----------------------|----------------------|-----------------------|------------------|
| 6 | ID _{3G} $M_{t,st}$ | 7.1720830663207 | 7.386509761453864E-13 | 0.008333333333333333 | 0.008512444610847103 | 0.008764162596519848 | 0.008512444610847103 | 0.00423482364137 |
| 5 | USD $M_{t,st}$ | 5.3538084861267174 | 8.61220122214416E-8 | 0.01 | 0.010206218313011495 | 0.010515350115740741 | 0.016952427508441503 | 0.00423482364137 |
| 4 | CADD $M_{t,st}$ | 5.252793231671495 | 1.4980968650032732E-7 | 0.0125 | 0.012741455098566168 | 0.013109375000000001 | 0.025320565519103666 | 0.00423482364137 |
| 3 | Chi2Merge $M_{t,st}$ | 1.1111677990074345 | 0.26649612895753083 | 0.016666666666666666 | 0.016952427508441503 | 0.016666666666666666 | 0.03361747021845407 | 0.00423482364137 |
| 2 | CAIM $M_{t,st}$ | 0.8081220356417704 | 0.41902033333431484 | 0.025 | 0.025320565519103666 | 0.025 | 0.04184374797610979 | 0.00423482364137 |
| 1 | ChiMerge $M_{t,st}$ | 0.1010152544522354 | 0.9195383508138865 | 0.05 | 0.0500000000000000044 | 0.05 | 0.0500000000000000044 | 0.05 |

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq 0.008333333333333333$.

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 ≤ 0.03361747021845407 .

Li's procedure rejects those hypotheses that have a p-value $\leq 0.004234823641374397$.

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 |
|-----|-----------------------------------|----------------------|-----------------------|----------------------|-----------------------|----------------------|-----------------------|-------------------|
| 6 | ID _{3G} $M_{t,st}$ | 7.873736447902937 | 3.442036332881378E-15 | 0.008333333333333333 | 0.008512444610847103 | 0.008764162596519848 | 0.008512444610847103 | 0.017021125944553 |
| 5 | USD _G $M_{t,st}$ | 6.18604884741519 | 6.169089873678664E-10 | 0.01 | 0.010206218313011495 | 0.010515350115740741 | 0.016952427508441503 | 0.017021125944553 |
| 4 | CADD _G $M_{t,st}$ | 5.961451638224804 | 2.5000691326170854E-9 | 0.0125 | 0.012741455098566168 | 0.013109375000000001 | 0.025320565519103666 | 0.017021125944553 |
| 3 | Chi2Merge _G $M_{t,st}$ | 1.126836283823762 | 0.25981170658187064 | 0.016666666666666666 | 0.016952427508441503 | 0.016666666666666666 | 0.03361747021845407 | 0.017021125944553 |
| 2 | CAIM _G $M_{t,st}$ | 0.4453441805089348 | 0.656071044561814 | 0.025 | 0.025320565519103666 | 0.025 | 0.04184374797610979 | 0.017021125944553 |
| 1 | Fayyad _G $M_{t,st}$ | 0.4171091027821438 | 0.6765986070534792 | 0.05 | 0.0500000000000000044 | 0.05 | 0.0500000000000000044 | 0.05 |

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq 0.008333333333333333$.

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 ≤ 0.03361747021845407 .

Li's procedure rejects those hypotheses that have a p-value ≤ 0.01702112594455373 .

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 |
|-----|---------------------------------|------------------------|-----------------------|----------------------|-----------------------|----------------------|-----------------------|------------------|
| 6 | ID _{3G} $M_t.st$ | 4.085575707849393 | 4.396766080051999E-5 | 0.008333333333333333 | 0.008512444610847103 | 0.008764162596519848 | 0.008512444610847103 | 0.00406209077648 |
| 5 | CADD _G $M_t.st$ | 2.9820685617732416 | 0.0028630787290009987 | 0.01 | 0.010206218313011495 | 0.010515350115740741 | 0.016952427508441503 | 0.00406209077648 |
| 4 | USD _G $M_t.st$ | 2.9454425215929843 | 0.003224930604223344 | 0.0125 | 0.012741455098566168 | 0.013109375000000001 | 0.025320565519103666 | 0.00406209077648 |
| 3 | Chi2Merge _G $M_t.st$ | 0.7726912992867249 | 0.4397050971248901 | 0.016666666666666666 | 0.016952427508441503 | 0.016666666666666666 | 0.03361747021845407 | 0.00406209077648 |
| 2 | CAIM _G $M_t.st$ | 0.5801092170485962 | 0.5618409685333685 | 0.025 | 0.025320565519103666 | 0.025 | 0.04184374797610979 | 0.00406209077648 |
| 1 | ChiMerge _G $M_t.st$ | 0.09688178370261509 | 0.9228202752468165 | 0.05 | 0.0500000000000000044 | 0.05 | 0.0500000000000000044 | 0.05 |

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq 0.008333333333333333$.

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 ≤ 0.03361747021845407 .

Li's procedure rejects those hypotheses that have a p-value $\leq 0.004062090776483334$.

Table 8: Adjusted p -values (FRIEDMAN)

| i | algorithm | unadjusted p | p_{Bonf} | p_{Holm} | p_{Hoch} | p_{Hommel} |
|-----|-----------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|
| 1 | ID3 $_G M_t st$ | 7.386509761453864E-13 | 4.4319058568723186E-12 | 4.4319058568723186E-12 | 4.4319058568723186E-12 | 4.4319058568723186E-12 |
| 2 | USD $_G M_t st$ | 8.61220122214416E-8 | 5.167320733286496E-7 | 4.30610061107208E-7 | 4.30610061107208E-7 | 3.745242162508183E-7 |
| 3 | CADD $_G M_t st$ | 1.4980968650032732E-7 | 8.988581190019638E-7 | 5.992387460013093E-7 | 5.992387460013093E-7 | 5.992387460013093E-7 |
| 4 | Chi2Merge $_G M_t st$ | 0.26649612895753083 | 1.598976773745185 | 0.7994883868725925 | 0.7994883868725925 | 0.6285305003014723 |
| 5 | CAIM $_G M_t st$ | 0.41902033353431484 | 2.514122001205589 | 0.8380406670686297 | 0.8380406670686297 | 0.8380406670686297 |
| 6 | ChiMerge $_G M_t st$ | 0.9195383508138865 | 5.5172301048833186 | 0.9195383508138865 | 0.9195383508138865 | 0.9195383508138865 |

Table 9: Adjusted p -values (FRIEDMAN)

| i | algorithm | unadjusted p | p_{Hall} | p_{Rom} | p_{Finn} | p_{Li} |
|-----|-----------------------|-----------------------|-----------------------|-----------------------|----------------------|-----------------------|
| 1 | ID3 $_G M_t st$ | 7.386509761453864E-13 | 4.4317882696987E-12 | 4.214041946453027E-12 | 4.4317882696987E-12 | 9.180162022655691E-12 |
| 2 | USD $_G M_t st$ | 8.61220122214416E-8 | 4.3060998677901807E-7 | 4.0950615658780105E-7 | 2.583660143606892E-7 | 1.070347437718563E-6 |
| 3 | CADD $_G M_t st$ | 1.4980968650032732E-7 | 5.9923386115094561E-7 | 5.713837864136441E-7 | 2.996193506632494E-7 | 1.8618734401917517E-6 |
| 4 | Chi2Merge $_G M_t st$ | 0.26649612895753083 | 0.6053544314710881 | 0.7994883868725925 | 0.37179177932081164 | 0.7680938308499267 |
| 5 | CAIM $_G M_t st$ | 0.41902033353431484 | 0.6624626271534211 | 0.8380406670686297 | 0.47881354608950444 | 0.8380908066202926 |
| 6 | ChiMerge $_G M_t st$ | 0.9195383508138865 | 0.9195383508138865 | 0.9195383508138865 | 0.9195383508138865 | 0.9195383508138865 |

Table 10: Adjusted p -values (ALIGNED FRIEDMAN)

| i | algorithm | unadjusted p | p_{Bonf} | p_{Holm} | p_{Hoch} | p_{Hommel} |
|-----|-----------------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|
| 1 | ID _{3G} $M_{t,st}$ | 3.442036332881378E-15 | 2.065221799728827E-14 | 2.065221799728827E-14 | 2.065221799728827E-14 | 2.065221799728827E-14 |
| 2 | USD $G M_{t,st}$ | 6.169089873678664E-10 | 3.701453924207198E-9 | 3.084544936839332E-9 | 3.084544936839332E-9 | 3.084544936839332E-9 |
| 3 | CADD $G M_{t,st}$ | 2.5000691326170854E-9 | 1.5000414795702514E-8 | 1.0000276530468342E-8 | 1.0000276530468342E-8 | 1.0000276530468342E-8 |
| 4 | Chi2Merge $G M_{t,st}$ | 0.25981170658187064 | 1.558870239491224 | 0.779435119745612 | 0.6765986070534792 | 0.6765986070534792 |
| 5 | CAIM $G M_{t,st}$ | 0.656071044561814 | 3.9364262673708836 | 1.312142089123628 | 0.6765986070534792 | 0.6765986070534792 |
| 6 | Fayyad $G M_{t,st}$ | 0.6765986070534792 | 4.059591642320875 | 1.312142089123628 | 0.6765986070534792 | 0.6765986070534792 |

Table 11: Adjusted p -values (ALIGNED FRIEDMAN)

| i | algorithm | unadjusted p | p_{Hol} | p_{Rom} | p_{Finn} | p_{Li} |
|-----|-----------------------------|-----------------------|------------------------|-----------------------|------------------------|-----------------------|
| 1 | ID _{3G} $M_{t,st}$ | 3.442036332881378E-15 | 2.0650148258027912E-14 | 1.96369949494571E-14 | 2.0650148258027912E-14 | 1.064323286155583E-14 |
| 2 | USD $G M_{t,st}$ | 6.169089873678664E-10 | 3.0845448417693433E-9 | 2.9333734995870318E-9 | 1.850726905061606E-9 | 1.9075644064807344E-9 |
| 3 | CADD $G M_{t,st}$ | 2.5000691326170854E-9 | 1.0000276606803027E-8 | 9.535424582091386E-9 | 5.00013883034015134E-9 | 7.730545284644496E-9 |
| 4 | Chi2Merge $G M_{t,st}$ | 0.25981170658187064 | 0.594466592857228 | 0.6765986070534792 | 0.36318449505996486 | 0.44548331783350614 |
| 5 | CAIM $G M_{t,st}$ | 0.656071044561814 | 0.8817128736111982 | 0.6765986070534792 | 0.7221806513147291 | 0.6698208335813749 |
| 6 | Fayyad $G M_{t,st}$ | 0.6765986070534792 | 0.8817128736111982 | 0.6765986070534792 | 0.7221806513147291 | 0.6765986070534792 |

Table 12: Adjusted p -values (QUADE)

| i | algorithm | unadjusted p | p_{Bonf} | p_{Holm} | p_{Hoch} | p_{Hommel} |
|-----|---------------------------------|-----------------------|----------------------|----------------------|----------------------|----------------------|
| 1 | ID _{3C} $M_t st$ | 4.396766080051999E-5 | 2.638059648031199E-4 | 2.638059648031199E-4 | 2.638059648031199E-4 | 2.638059648031199E-4 |
| 2 | CADD _G $M_t st$ | 0.0028630787290009987 | 0.017178472374005993 | 0.014315393645004993 | 0.012899722416893376 | 0.011452314916003995 |
| 3 | USD _G $M_t st$ | 0.003224930604223344 | 0.019349583625340065 | 0.014315393645004993 | 0.012899722416893376 | 0.012899722416893376 |
| 4 | Chi2Merge _G $M_t st$ | 0.4397050971248901 | 2.6382305827493404 | 1.3191152913746702 | 0.9228202752468165 | 0.8794101942497802 |
| 5 | CAIM _G $M_t st$ | 0.5618409685333685 | 3.371045811200211 | 1.3191152913746702 | 0.9228202752468165 | 0.9228202752468165 |
| 6 | ChiMerge _G $M_t st$ | 0.9228202752468165 | 5.536921651480899 | 1.3191152913746702 | 0.9228202752468165 | 0.9228202752468165 |

Table 13: Adjusted p -values (QUADE)

| i | algorithm | unadjusted p | p_{Holl} | p_{Rom} | p_{Finn} | p_{Li} |
|-----|---------------------------------|-----------------------|-----------------------|----------------------|-----------------------|----------------------|
| 1 | ID _{3C} $M_t st$ | 4.396766080051999E-5 | 2.6377696917490034E-4 | 2.508377438120023E-4 | 2.6377696917490034E-4 | 5.693545520306937E-4 |
| 2 | CADD _G $M_t st$ | 0.0028630787290009987 | 0.014233655803997713 | 0.012300092888575328 | 0.008564667996863395 | 0.03576934595548307 |
| 3 | USD _G $M_t st$ | 0.003224930604223344 | 0.014233655803997713 | 0.012300092888575328 | 0.008564667996863395 | 0.04010875477157637 |
| 4 | Chi2Merge _G $M_t st$ | 0.4397050971248901 | 0.8241064092437039 | 0.9228202752468165 | 0.5806033014480252 | 0.8506829345989401 |
| 5 | CAIM _G $M_t st$ | 0.5618409685333685 | 0.8241064092437039 | 0.9228202752468165 | 0.6285005958609009 | 0.8792218693948081 |
| 6 | ChiMerge _G $M_t st$ | 0.9228202752468165 | 0.9228202752468165 | 0.9228202752468165 | 0.9228202752468165 | 0.9228202752468165 |