Output tables for 1xN statistical comparisons.

April 4, 2023

1 Average rankings of Friedman test

Average ranks obtained by each method in the Friedman test.

| Algorithm | Ranking |
|---------------------------------|---------|
| B2 | 2.375 |
| F11 | 3 |
| I1 | 1.8125 |
| HAPPENN-MAIN | 6.125 |
| HemoPI(SVM+Motif-HemoPI-1based) | 4.0625 |
| HemoPred | 6.2812 |
| HLPpred-Fuse | 4.3438 |

Table 1: Average Rankings of the algorithms (Friedman)

Friedman statistic (distributed according to chi-square with 6 degrees of freedom): 62.631696. P-value computed by Friedman Test: 0.

2 Post hoc comparison (Friedman)

P-values obtained in by applying post hoc methods over the results of Friedman procedure.

| i | algorithm | $z = (R_0 - R_i)/SE$ | p | Holm Hochberg Hommel | Holland | Li |
|---|---------------------------------|----------------------|----------|----------------------|----------|----------|
| 6 | HemoPred | 5.850967 | 0 | 0.008333 | 0.008512 | 0.028346 |
| 5 | HAPPENN-MAIN | 5.646388 | 0 | 0.01 | 0.010206 | 0.028346 |
| 4 | HLPpred-Fuse | 3.314184 | 0.000919 | 0.0125 | 0.012741 | 0.028346 |
| 3 | HemoPI(SVM+Motif-HemoPI-1based) | 2.945942 | 0.00322 | 0.016667 | 0.016952 | 0.028346 |
| 2 | F11 | 1.554802 | 0.119993 | 0.025 | 0.025321 | 0.028346 |
| 1 | B2 | 0.736485 | 0.461435 | 0.05 | 0.05 | 0.05 |

Table 2: Post Hoc comparison Table for $\alpha = 0.05$ (FRIEDMAN)

Bonferroni-Dunn's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.008333 .

Holm's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.025 .

Hochberg's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.016667 .

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

Holland's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.025321 .

Li's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.028346 .

3 Adjusted P-Values (Friedman)

Adjusted P-values obtained through the application of the post hoc methods (Friedman).

| i | algorithm | unadjusted p | p_{Bonf} | p_{Holm} | $p_{Hochberg}$ | p_{Hommel} |
|---|---------------------------------|----------------|------------|------------|----------------|--------------|
| 1 | HemoPred | 0 | 0 | 0 | 0 | 0 |
| 2 | HAPPENN-MAIN | 0 | 0 | 0 | 0 | 0 |
| 3 | HLPpred-Fuse | 0.000919 | 0.005515 | 0.003676 | 0.003676 | 0.003676 |
| 4 | HemoPI(SVM+Motif-HemoPI-1based) | 0.00322 | 0.019318 | 0.009659 | 0.009659 | 0.009659 |
| 5 | F11 | 0.119993 | 0.719959 | 0.239986 | 0.239986 | 0.239986 |
| 6 | B2 | 0.461435 | 2.768612 | 0.461435 | 0.461435 | 0.461435 |

Table 3: Adjusted *p*-values (FRIEDMAN) (I)

| i | algorithm | unadjusted p | $p_{Holland}$ | p_{Li} |
|---|---------------------------------|----------------|---------------|----------|
| 1 | HemoPred | 0 | 0 | 0 |
| 2 | HAPPENN-MAIN | 0 | 0 | 0 |
| 3 | HLPpred-Fuse | 0.000919 | 0.003671 | 0.001704 |
| 4 | HemoPI(SVM+Motif-HemoPI-1based) | 0.00322 | 0.009628 | 0.005943 |
| 5 | F11 | 0.119993 | 0.225588 | 0.182206 |
| 6 | B2 | 0.461435 | 0.461435 | 0.461435 |

Table 4: Adjusted p-values (FRIEDMAN) (II)