**Table 1.**Performance comparison of two models on the DeepFE-PPI’s *S. cerevisiae* dataset. We report the mean values and standard deviations for the test sets

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Methods | Accuracy (%) | Precision (%) | Sensitivity (%) | Specificity (%) | F1-score (%) | MCC (%) |
| MOP | 92.29 ± 0.77 | 95.30 ± 0.54 | 88.96 ± 1.12 | 95.61 ± 0.52 | 92.02 ± 0.80 | 84.76 ± 1.50 |
| DeepTrio | 92.57 ± 0.63 | 96.33 ± 0.88 | 88.53 ± 1.19 | 96.62 ± 0.83 | 92.26 ± 0.65 | 85.43 ± 1.22 |

MOP: the model applies max-pooling on the outer-product of two sequences after the convolution module.

**Table 2.**Performance of MOP on each fold of 5-fold cross-validation of the DeepFE-PPI’s *S. cerevisiae* dataset

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Fold (No.) | Accuracy (%) | Precision (%) | Sensitivity (%) | Specificity (%) | F1-score (%) | MCC (%) |
| 1 | 93.50 | 0.95.98 | 90.49 | 96.38 | 93.15 | 87.12 |
| 2 | 92.13 | 0.94.82 | 89.3 | 95.01 | 91.97 | 84.4 |
| 3 | 91.41 | 0.95.07 | 87.44 | 95.42 | 91.10 | 83.1 |
| 4 | 91.60 | 0.94.74 | 87.93 | 95.2 | 91.21 | 83.4 |
| 5 | 92.79 | 0.95.91 | 89.66 | 96.03 | 92.68 | 85.77 |