**Meiqi Wu** used A deep learning method(**Deep Learning classifier, Multi-Layer perceptron(MLP)**) to construct a novel predictor model named **DeepAcet** to more accurately predict lysine acetylation site. They have been used Human lysine acetylation site from CPLM database(human sequence) and proteins from UniProt database(corresponding protein) .

Initially 16107 positive dataset (After Under-Sampling it’s remain same) and initially 57443 negative dataset (After Under-sampling it’s have 16,107) . Developed a independent set by selecting 1/5 dataset from both dataset.

They have been used six encoding schemes (**One-hot encoding, BLOSUM62 matrix, Composition of *K*-space amino acid pairs (CKSAAP), Information gain (IG), Physicochemical and biochemical properties, Position-specific scoring matrix (PSSM)**) to represent modification residue.

The method’s best prediction achieved 84.95% accuracy, 83.45% specificity, 86.44% sensitivity, 0.8540 AUC, and 0.6993 MCC in a 10-fold cross-validation with 2199 optimal feature and another prediction achieved 84.87% accuracy, 83.46% specificity, 86.28% sensitivity, 0.8407 AUC, and 0.6977 MCC for an independent test set.

They has been compared with existing methods approach by **Machine Learning , Bayesian Discrimination, Logistic Regression** such as PAIL , PSKAcePred, LAceP, N-Ace, BRABSB-PHKA.

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