**Title:** *A deep Learning method to more accurately recall known lysine acetylation sites.*

**Year:** 2019

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**Country:** China

**Objective:**

* A deep learning method to more accurately predict lysine acetylation site
* Develop a tool to predict acetylation site

**Previous Approach:** Machine Learning Approach, Bayesian Discrimination, Logistic Regression

**Encoding Schemes:** one-hot, BLOSUM62 matrix, CKSAAP, Information Gain (IG), physiochemical properties, Position Specific Scoring Matrix (PSSM), F- Score

**Contains:** sequence location information,evolutionary information,amino acid composition information, physiochemical properties.

**Contribution:** The 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. For an independent test set, the prediction  
achieved 84.87% accuracy, 83.46% specificity, 86.28% sensitivity, 0.8407 AUC, and 0.6977 MCC

**Performance Measure:** 10-Fold Cross validation, Independent Test set.

**Data:** Human lysine acetylation site from CPLM database, and their proteins from UniProt

**Methodology:** Deep Learning classifier, Multi-Layer perceptron was utilized to construct a model to predict lysine acetylation site

**Keyword:** acetylation, multilayer perceptron, protein localization, protein stabilization, peptide chain backbone, histone acetyltransferase, antibodies, SVM, evolutionary information, shallow machine learning algorithm, Independent test set, multilayer perceptron, acetylated substrate, rectified linear unit, softmax loss function, pseudo amino acid

**Acetylation:**

**Multilayer Perceptron:**

**protein localization:**

**protein stabilization:**

**peptide chain backbone:**

**histone acetyltransferase:**

**antibodies:**

**SVM:**

**evolutionary information:**

**shallow machine learning algorithm:**

**Independent test set:**

**multilayer perceptron:**

**acetylated substrate:**

**rectified linear unit:**

**softmax loss function:**

**pseudo amino acid:**