Parallelization Classificaiton of Cancer Gene Expression Dataset with Deep Neural Network Algorithm Using Stacked Sparse Autoencoder

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Abstract

Nowadays, research in bioinformatics can be one of the popular researches for the medical professional researcher. One of them is the classification using data gene expression. Deep learning has become an interesting research in bioinformatics fields. Many kinds of research about cancer classification are appointed using deep learning. Classification using gene expression dataset is useful in the medical profession. Because it can classify diseases using gene only. This research raised the classification gene expression cancer using deep neural network with stacked sparse autoencoder and autoencoder as an extraction method. In addition, sparse autoencoder is also used as a represented of neural network learning. Fine tuning is used as weight and bias optimization for neural network with gradient descent method. Classification of the learning result using the softmax classifier. This research, the data is sourced from the portal of National Center for Biotechnology Information. With this obtained, the highest accuracy of 97.3% for training and 92,6 % for testing. Parallelization for this algorithm work quite well, this shows to the efficiency of the computation time is faster with speed up 000% for sequential computation. Of course, this research becomes the best moment for other neural network algorithm development with parallelism technique.

Keyword : Deep Learning, SSAE, Parallel Computing, High Performance Computing, Cancer Classification, gene expression