siRNA efficacy prediction with Deep Learning

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Introduction

RNAi is widely used in functional genomics. SiRNA based gene silencing is one of the preferred techniques among gene silencing methods. Designing small interfering RNAs (siRNAs) that can greatly reduce the expression of the target transcripts, but not of other unintended targets is a critical step in RNAi experiments. The importance of siRNA-based gene silencing has motivated work to develop methods of designing and predicting functional siRNAs. Although various statistical and computational methods have been proposed, predicting siRNA efficacy remains challenging. Recently, deep learning has shown to be a useful method to perform classification tasks that were previously difficult. This study introduces a deep learning based method to predict siRNA efficacy.

Results and discussion

Classification of siRNAs was performed on a dataset of 280 non-redundant, experimentally evaluated set of siRNAs collected from several published studies. Two types of deep learning based classifiers were trained for prediction. Classification results suggest that both of the deep learning methods can perform equally or better at classification.(Table.1)

Table.1 Comparison with other classification methods

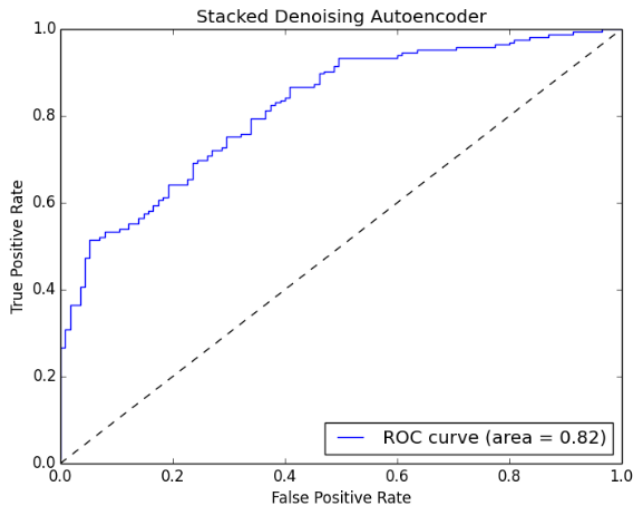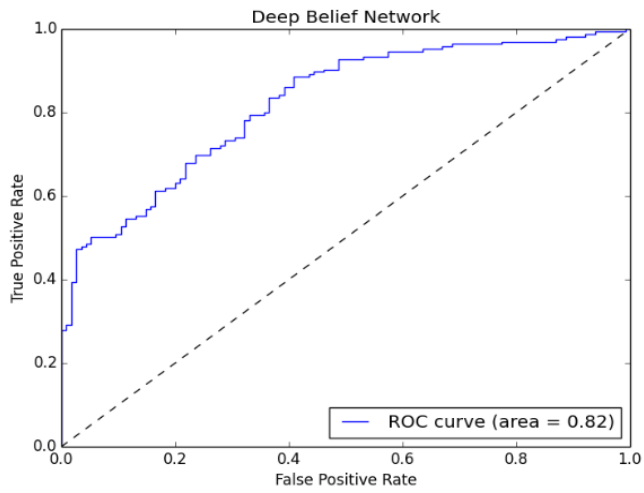| Classifier	ROC curve AUC
Gaussian naïve Bayes	0.69
Random Forest	0.75
DBN	0.82
SdA	0.82
SVM	0.82

Figure1.Reciever operating curve of SdA

Figure2. Receiver operating curve of DBN