Deep neural network architectures such as convolutional and long short-term memory networks have become increasingly popular as machine learning tools during the recent years. The availability of greater computational resources, more data, new algorithms for training deep models, and easy to use libraries for implementation and training of neural networks are the drivers of this development. The use of deep learning has been especially successful in image recognition; and the development of tools, applications, and code examples are in most cases centered within this field rather than within biology. Here, we aim to further the development of deep learning methods within biology by providing application examples and ready to apply and adapt code templates. Given such examples, we illustrate how architectures consisting of convolutional and long short-term memory neural networks can relatively easily be designed and trained to state-of-the-art performance on three biological sequence problems: prediction of subcellular localization, protein secondary structure and the binding of peptides to MHC Class II molecules. All implementations and datasets are available online at https://github.com/vanessajurtz/lasagne4bio. Supplementary data are available at Bioinformatics online.
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