Deep learning for computational biology

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Abstract

Technological advances in genomics and imaging have led to an explosion of molecular and cellular profiling data from large numbers of samples. This rapid increase in biological data dimension and acquisition rate is challenging conventional analysis strategies. Modern machine learning methods, such as deep learning, promise to leverage very large data sets for finding hidden structure within them, and for making accurate predictions. In this review, we discuss applications of this new breed of analysis approaches in regulatory genomics and cellular imaging. We provide background of what deep learning is, and the settings in which it can be successfully applied to derive biological insights. In addition to presenting specific applications and providing tips for practical use, we also highlight possible pitfalls and limitations to guide computational biologists when and how to make the most use of this new technology.

Keywords cellular imaging; computational biology; deep learning; machine learning; regulatory genomics

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Introduction

Machine learning methods are general-purpose approaches to learn functional relationships from data without the need to define them a priori (Hastie et al., 2005; Murphy, 2012; Michalski et al., 2013). In computational biology, their appeal is the ability to derive predictive models without a need for strong assumptions about underlying mechanisms, which are frequently unknown or insufficiently defined. As a case in point, the most accurate prediction of gene expression levels is currently made from a broad set of epigenetic features using sparse linear models (Karlic et al., 2010; Cheng et al., 2011) or random forests (Li et al., 2015); how the selected features determine the transcript levels remains an active research topic. Predictions in genomics (Libbrecht & Noble, 2015; Märtens et al., 2016), proteomics (Swan et al., 2013), metabolomics (Kell, 2005) or sensitivity to compounds (Eduati et al., 2015) all rely on machine learning approaches as a key ingredient.

Most of these applications can be described within the canonical machine learning workflow, which involves four steps: data cleaning and pre-processing, feature extraction, model fitting and evaluation (Fig 1A). It is customary to denote one data sample, including all covariates and features as input $x$ (usually a vector of numbers), and label it with its response variable or output value $y$ (usually a single number) when available.

A supervised machine learning model aims to learn a function $f(x) = y$ from a list of training pairs $(x_1,y_1), (x_2,y_2), \ldots$ for which data are recorded (Fig 1B). One typical application in biology is to predict the viability of a cancer cell line when exposed to a chosen drug (Menden et al., 2013; Eduati et al., 2015). The input features $(x)$ would capture somatic sequence variants of the cell line, chemical make-up of the drug and its concentration, which together with the measured viability (output label $y$) can be used to train a support vector machine, a random forest classifier or a related method (functional relationship $f$). Given a new cell line (unlabelled data sample $x^*$) in the future, the learnt function predicts its survival (output label $y^*$) by calculating $f(x^*)$, even if $f$ resembles more of a black box, and its inner workings of why particular mutation combinations influence cell growth are not easily interpreted. Both regression (where $y$ is a real number) and classification (where $y$ is a categorical class label) can be viewed in this way. As a counterpart, unsupervised machine learning approaches aim to discover patterns from the data samples $x$ themselves, without the need for output labels $y$. Methods such as clustering, principal component analysis and outlier detection are typical examples of unsupervised models applied to biological data.

The inputs $x$, calculated from the raw data, represent what the model “sees about the world”, and their choice is highly problem-specific (Fig 1C). Deriving most informative features is essential for performance, but the process can be labour-intensive and requires domain knowledge. This bottleneck is especially limiting for high-dimensional data; even computational feature selection methods do not scale to assess the utility of the vast number of possible input combinations. A major recent advance in machine learning is automating this critical step by learning a suitable representation of the data with deep artificial neural networks (Bengio et al., 2013; LeCun et al., 2015; Schmidhuber, 2015) (Fig 1D). Briefly, a deep neural network takes the raw data at the lowest (input) layer and transforms them into increasingly abstract feature representations by successively combining outputs from the preceding layer in a data-driven manner, encapsulating highly complicated functions in the
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Deep learning is now one of the most active fields in machine learning and has been shown to improve performance in image and speech recognition (Hinton et al., 2012; Krizhevsky et al., 2012; Graves et al., 2013; Zeller & Fergus, 2014; Deng & Togneri, 2015), natural language understanding (Bahdanau et al., 2014; Sutskever et al., 2014; Lipton, 2015; Xiong et al., 2016), and most recently, in computational biology (Eickholt & Cheng, 2013; Dahl et al., 2014; Leung et al., 2014; Senderby & Winther, 2014; Alipanahi et al., 2015; Wang et al., 2015; Zhou & Troyanskaya, 2015; Kelley et al., 2016).

The potential of deep learning in high-throughput biology is clear: in principle, it allows to better exploit the availability of increasingly large and high-dimensional data sets (e.g. from DNA sequencing, RNA measurements, flow cytometry or automated microscopy) by training complex networks with multiple layers that capture their internal structure (Fig 1C and D). The learned networks discover high-level features, improve performance over traditional models, increase interpretability and provide additional understanding about the structure of the biological data.

In this review, we discuss recent and forthcoming applications of deep learning, with a focus on applications in regulatory genomics and biological image analysis. The goal of this review was not to provide comprehensive background on all technical details, which can be found in the more specialized literature (Bengio, 2012; Bengio et al., 2013; Deng, 2014; Schmidhuber, 2015; Goodfellow et al., 2016). Instead, we aimed to provide practical pointers and the necessary background to get started with deep architectures, review current software solutions and give recommendations for applying them to data. The applications we cover are deliberately broad to illustrate differences and commonalities between approaches;

reviews focusing on specific domains can be found elsewhere (Park & Kellis, 2015; Gawehn et al., 2016; Leung et al., 2016; Mamoshina et al., 2016). Finally, we discuss both the potential and possible pitfalls of deep learning and contrast these methods to traditional machine learning and classical statistical analysis approaches.

Deep learning for regulatory genomics

Conventional approaches for regulatory genomics relate sequence variation to changes in molecular traits. One approach is to leverage variation between genetically diverse individuals to map quantitative trait loci (QTL). This principle has been applied to identify regulatory variants that affect gene expression levels (Montgomery et al., 2010), histone marks (Grubert et al., 2011), DNA methylation (Gibbs et al., 2010; Bell et al., 2011), histone marks (Grubert et al., 2015; Waszak et al., 2015) and proteome variation (Vincent et al., 2010; Albert et al., 2014; Parts et al., 2014; Battle et al., 2015) (Fig 2A). Better statistical methods have helped to increase the power to detect regulatory QTL (Kang et al., 2008; Stegle et al., 2010; Parts et al., 2011; Rakitsch & Stegle, 2016); however, any mapping approach is intrinsically limited to variation that is present in the training population. Thus, studying the effects of rare mutations in particular requires data sets with very large sample size.

An alternative is to train models that use variation between regions within a genome (Fig 2A). Splitting the sequence into windows centred on the trait of interest gives rise to tens of thousands of training examples for most molecular traits even when using a single individual. Even with large data sets, predicting molecular traits from DNA sequence is challenging due to multiple layers
of abstraction between the effect of individual DNA variants and the trait of interest, as well as the dependence of the molecular traits on a broad sequence context and interactions with distal regulatory elements.

The value of deep neural networks in this context is twofold. First, classical machine learning methods cannot operate on the sequence directly, and thus require pre-defining features that can be extracted from the sequence based on prior knowledge (e.g. the presence or absence of single-nucleotide variants (SNVs), k-mer frequencies, motif occurrences, conservation, known regulatory variants or structural elements). Deep neural networks can help circumventing the manual extraction of features by learning them from data. Second, because of their representational richness, they can capture nonlinear dependencies in the sequence and interaction effects and span wider sequence context at multiple genomic scales. Attesting to their utility, deep neural networks have been success-fully applied to predict splicing activity (Leung et al., 2014; Xiong et al., 2015), specificities of DNA- and RNA-binding proteins...
Early applications of neural networks in regulatory genomics

The first successful applications of neural networks in regulatory genomics replaced a classical machine learning approach with a deep model, without changing the input features. For example, Xiong et al. (2015) considered a fully connected feedforward neural network to predict the splicing activity of individual exons. The model was trained using more than 1,000 pre-defined features extracted from the candidate exon and adjacent introns. Despite the relatively low number of 10,700 training samples in combination with the model complexity, this method achieved substantially higher prediction accuracy of splicing activity compared to simpler approaches, and in particular was able to identify rare mutations implicated in splicing misregulation.

Convolutional designs

More recent work using convolutional neural networks (CNNs) allowed direct training on the DNA sequence, without the need to define features (Alipanahi et al., 2015; Zhou & Troyanskaya, 2015; Angermueller et al., 2016; Kelley et al., 2016). The CNN architecture allows to greatly reduce the number of model parameters compared to a fully connected network by applying convolutional operations to only small regions of the input space and by sharing parameters between regions. The key advantage resulting from this approach is the ability to directly train the model on larger sequence windows (Box 2; Fig 2B).

Alipanahi et al. (2015) considered convolutional network architectures to predict specificities of DNA- and RNA-binding proteins.
Their DeepBind model outperformed existing methods, was able to recover known and novel sequence motifs, and could quantify the effect of sequence alterations and identify functional SNVs. A key innovation that enabled training the model directly on the raw DNA sequence was the application of a one-dimensional convolutional layer. Intuitively, the neurons in the convolutional layer scan for motif sequences and combinations thereof, similar to conventional position weight matrices (Stormo et al., 1982). The learning signal from deeper layers informs the convolutional layer which motifs are the most relevant. The motifs recovered by the model can then be visualized as heatmaps or sequence logos (Fig 2D).
In silico prediction of mutation effects

An important application of deep neural networks trained on the raw DNA sequence is to predict the effect of mutations in silico. Such model-based assessments of the effect of sequence changes complement methods based on QTL mapping, and can in particular help to uncover regulatory effects of rare SNVs or to fine-map likely causal genes. An intuitive approach for visualizing such predicted regulatory effects is mutation maps (Alipanahi et al., 2015), whereby the effect of all possible mutations for a given input sequence is represented in a matrix view (Fig 2E). The authors could further reliably identify deleterious SNVs by training an additional neural network with predicted binding scores for a wild-type and mutant sequence (Fig 2C).

Joint prediction of multiple traits and further extensions

Following their initial successes, convolutional architectures have been extended and applied to a range of tasks in regulatory genomics. For example, Zhou and Troyanskaya (2015) considered these architectures to predict chromatin marks from DNA sequence. The authors observed that the size of the input sequence window is a major determinant of model performance, where larger windows (now up to 1 kb) coupled with multiple convolutional layers enabled capturing sequence features at different genomic length scales. A second innovation was to use neural network architectures with multiple output variables (so-called multitask neural networks) to predict multiple chromatin states in parallel. Multitask architectures allow learning shared features between outputs, thereby improving generalization performance, and markedly reducing the computational cost of model training compared to learning independent models for each trait (Dahl et al., 2014).

In a similar vein, Kelley et al (2016) developed the open-source deep learning framework Basset, to predict DNase I hypersensitivity across multiple cell types and to quantify the effect of SNVs on chromatin accessibility. Again, the model improved prediction performance compared to conventional methods and was able to retrieve both known and novel sequence motifs that are associated with DNase I hypersensitivity. A related architecture has also been considered by Angermueller et al to predict DNA methylation states in single-cell bisulphite sequencing studies (Angermueller et al., 2016). This approach combined convolutional architectures to detect informative DNA sequence motifs with additional features derived from neighbouring CpG sites, thereby accounting for methylation context. Most recently, Koh, Pierson and Kundaje applied CNNs to de-noise genomewide chromatin immunoprecipitation followed by sequencing data in order to obtain a more accurate prevalence estimate for different chromatin marks (Koh et al., 2016).

At present, CNNs are among the most widely used architectures to extract features from fixed-size DNA sequence windows. However, alternative architectures could also be considered. For example, recurrent neural networks (RNNs) are suited to model sequential data (Lipton, 2015) and have been applied for modelling natural language and speech (Hinton et al., 2012; Graves et al., 2013; Sutskever et al., 2014; Che et al., 2015; Deng & Togneri, 2015; Xiong et al., 2016), protein sequences (Agathocles et al., 2010; Sendereby & Winther, 2014), clinical medical data (Che et al., 2015; Lipton et al., 2015) and to a limited extent DNA sequences (Xu et al., 2007; Lee et al., 2015). RNNs are appealing for applications in regulatory genomics, because they allow modelling sequences of variable length, and to capture long-range interactions within the sequence and across multiple outputs. However, at present, RNNs are more difficult to train than CNNs, and additional work is needed to better understand the settings where one should be preferred over the other.

Complementary to supervised methods, unsupervised deep learning architectures learn low-dimensional feature representations from high-dimensional unlabelled data, similarly to classical principal component analysis or factor analysis, but using a nonlinear model. Examples of such approaches are stacked autoencoders (Vincent et al., 2010), restricted Boltzmann machines and deep belief networks (Hinton et al., 2006). The learnt features can be used to visualize data or as input for classical supervised learning tasks. For example, sparse autoencoders have been applied to classify cancer cases using gene expression profiles (Fakoor et al., 2015) or to predict protein backbones (Lyons et al., 2014). Restricted Boltzmann machines can also be used for unsupervised pre-training of deep networks to subsequently train supervised models of protein secondary structures (Spencer et al., 2015), disordered protein regions (Eickholt & Cheng, 2013) or amino acid contacts (Eickholt & Cheng, 2012). Skip-gram neural networks have been applied to learn low-dimensional representations of protein sequences and improve protein classification (Aggarri & Mofrad, 2015). In general, unsupervised models are a powerful approach if large quantities of unlabelled data are available to pre-train complex models. Once trained, these models can help to improve performance on classification tasks, for which smaller numbers of labelled examples are typically available.

Deep learning for biological image analysis

Historically, perhaps the most important successes of deep neural networks have been in image analysis. Deep architectures trained on millions of photographs can famously detect objects in pictures better than humans do (He et al., 2015). All current state-of-the-art models in image classification, object detection, image retrieval and semantic segmentation make use of neural networks.

The convolutional neural network (Box 2) is the most common network architecture for image analysis. Briefly, a CNN performs pattern matching (convolution) and aggregation (pooling) operations (Box 2). At a pixel level, the convolution operation scans the image with a given pattern and calculates the strength of the match for every position. Pooling determines the presence of the pattern in a region, for example by calculating the maximum pattern match in smaller patches (max-pooling), thereby aggregating region information into a single number. The successive application of convolution and pooling operations is at the core of most network architectures used in image analysis (Box 2).

First applications in computational biology—pixel-level classification

The early applications of deep networks for biological images focused on pixel-level tasks, with additional models building on the network outputs. For example, Ning et al (2005) applied...
convolutional neural networks in a study that predicted abnormal development in C. elegans embryo images. They trained a CNN on 40 × 40 pixel patches to classify the centre pixel to cell wall, cytoplasm, nucleus membrane, nucleus or outside medium, using three convolutional and pooling layers, followed by a fully connected output layer. The model predictions were then fed into an energy-based model for further analysis. CNNs have outperformed standard methods, for example Markov random fields and conditional random fields (Li, 2009) in such raw data analysis tasks, for example restoring noisy neural circuitry images (Jain et al., 2007).

Adding layers allows moving from clearing up pixel noise to modelling more abstract image features. Ciresan et al. (2013) used five convolutional and pooling layers, followed by two fully connected layers, to find mitosis in breast histology images. This model won the mitosis detection challenge at the International Conference of Pattern Recognition 2012, outperforming competitors by a substantial margin. The same approach was also used to segment neuronal structures in electron microscopy images, classifying each pixel as membrane or non-membrane (Ciresan et al., 2012). In these applications, while the CNNs were trained in an end-to-end manner, additional post-processing was required to obtain class probabilities from the outputs for new images.

Successive pooling operations lose information on localization, as only summaries are retained from larger and larger regions. To avoid this, skip links can be added to carry information from early, fine-grained layers forward to deeper ones. The currently best-performing pixel-level classification method for neuronal structures (U-Net; Ronneberger et al., 2015) employs an architecture in which neurons take inputs from lower layers to localize high-resolution features, as well as to overcome the arbitrary choice of context size.

Analysis of whole cells, cell populations and tissues

In many cases, pixel-level predictions are not required. For example, Xu et al. directly classified colon histopathology images into cancerous and non-cancerous, finding that supervised feature learning with deep networks was superior to using handcrafted features (Xu et al., 2014). Parnamaa and Parts used CNNs to classify pre-segmented image patches of individual yeast cells carrying a fluorescent protein to different subcellular localization patterns (Parnamaa & Parts, 2016). Again, deep networks outperformed methods based on traditional features. Further, Kraus et al. combined the segmentation and classification tasks into a single architecture that can be learned end-to-end and applied the model to full resolution yeast microscopy images (Kraus et al., 2015). This approach allowed classifying entire images without performing segmentation as a preprocessing step. CNNs have even been applied to count bacterial colonies in agar plates (Ferrari et al., 2015). Since the early denoising applications on the pixel level, the field has been moving towards end-to-end image analysis pipelines that make use of large bioimage data sets, and the representational power of CNNs.

Interpreting and visualizing convolutional networks

Convolutional neural networks have been successful across many domains. In interpreting their performance, it is useful to understand the features they capture.

Visualizing input weights

One way to understand what a particular neuron represents is to look for inputs that maximally activate it. Under some mathematical constraints, these patterns are proportional to the incoming weights (see also Box 1). Krizhevsky et al. visualized weights in the first convolutional layer (Krizhevsky et al., 2012) and found that these maximally activating patterns correspond to colour blobs, edges at different orientations and Gabor-like filters (Fig 4). Gabor filters are widely used pre-defined features in image analysis; neural networks rediscover them in a data-driven way as a useful component of the image model. Higher layer weights can be visualized as well, but as the inputs are not pixels, their weights are more difficult to interpret.

Finding images that maximize neuron activity

To understand the deeper layers in terms of input pixels, Girshick et al. (2014) retrieved and Simonyan et al. (2013) generated images that maximize the output of individual neurons (Fig 4). While this approach yields no explicit representation, it can provide an overview of the type of features that differentiate images with large neuron activity from all others. Such visualizations tend to show that second-layer features combine edges from the first layer,
Learning Center and is written in C++.

Rampasek & Goldenberg, 2016) (Table 1), which differ in modular-
TensorFlow provides the most efficient implementation for RNNs. The software is recent and under active development; hence, only few pre-trained models are currently available.

### Data preparation

Training data are key for every machine learning application. Since more data with informative features usually result in better performance, effort should be spent on collecting, labelling, cleaning and normalizing data.

#### Required data set sizes

Most of the successful applications of deep learning have been in supervised learning settings, where sufficient labelled training samples are available to fit complex models. As a rule of thumb, the number of training samples should be at least as high as the number of model parameters, although special architectures and model regularization can help to avoid overfitting if training data are scarce (Bengio, 2012).

Central problems in regulatory genomics, for example predicting molecular traits from genotype, are limited in the number of training instances; hundreds to at most tens of thousands of training examples are typical. The strategy of considering sequence windows centred on the trait of interest (e.g. splice site, transcription factor binding site or epigenetic marks; see Fig 2A) is now a widely used approach and helps increasing the number of input–output pairs from a single individual.

In image analysis, data can be abundant, but manually curated and labelled training examples are typically difficult to obtain. In such instances, the training set can be augmented by scaling, rotating or cropping the existing images, an approach that also enhances robustness (Krizhevsky et al., 2012). Another strategy is to reuse a network that was pre-trained on a large data set for image recognition [e.g. AlexNet (Krizhevsky et al., 2012), VGG (Simonyan & Zisserman, 2014), GoogleNet (Szegedy et al., 2015b) or ResNet (He et al., 2015)], and to fine-tune its parameters on the data set of interest (e.g. microscopy images for a particular segmentation task). Such an approach exploits the fact that different data sets share important characteristics and features, such as edges or curves, which can be transferred between them. Caffe, Lasagne, Torch and to a limited extend TensorFlow provide repositories with pre-trained models.

#### Partitioning data into training, validation and test sets

Machine learning models need to be trained, selected and tested on independent data sets to avoid overfitting and assure that the model will generalize to unseen data. Holdout validation, partitioning the data into a training, validation and test sets, is the standard for deep neural networks (Fig 5C). The training set is used to learn models with different hyper-parameters, which are then assessed on the validation set. The model with best performance, for example prediction accuracy or mean-squared error, is selected and further evaluated on the test set to quantify the performance on unseen data and for comparison to other methods. Typical data set proportions are 60% for training, 10% for validation and 30% for model testing. If the data set is small, k-fold cross-validation or bootstrapping can be used instead (Hastie et al., 2005).

#### Normalization of raw data

Appropriate choices for data normalization can help to accelerate training and the identification of a good local minimum.

Categorical features such as DNA nucleotides first need to be encoded numerically. They are typically represented as binary vectors with all but one entry set to zero, which indicates the category (one-hot coding). For example, DNA nucleotides (categories)
are commonly encoded as $A = (1 \ 0 \ 0 \ 0), G = (0 \ 1 \ 0 \ 0), C = (0 \ 0 \ 1 \ 0)$ and $T = (0 \ 0 \ 0 \ 1)$ (Fig 5A). A DNA sequence can then be represented as a binary string by concatenating the encoding nucleotides, and treating each nucleotide as an independent input feature of a feedforward neural network. In a CNN, the four bits of each encoded base are commonly considered analogously to colour channels of an image to preserve the entity of a nucleotide.

Numerical features are typically zero-centred by subtracting their mean value. Image pixels are usually not zero-centred individually, but jointly by subtracting the mean pixel intensity per colour channel. An additional common normalization step is to standardize features to unit variance. Whiting can be used to decorrelate features (Fig 5B), but can be computationally involved, since it requires computing the feature covariance matrix (Hastie et al., 2005). If the distribution of features is skewed due to a few extreme values, log transformations or similar processing steps may be appropriate. Validation and test data need to be normalized consistently with the training data. For example, features of the validation data need to be zero-centred by subtracting the mean computed on the training data, not on the validation data.

Model building

Choice of model architecture
After preparing the data, design choices about the model architectures need to be made. The default architecture is a feedforward neural network with fully connected hidden layers, which is an appropriate starting point for many problems. Convolutional architectures are well suited for multi- and high-dimensional data, such as two-dimensional images or abundant genomic data. Recurrent neural networks can capture long-range dependencies in sequential data of varying lengths, such as text, protein or DNA sequences. More sophisticated models can be built by combining different architectures. To describe the content of an image, for example, a CNN can be combined with an RNN, where the CNN encodes the image and the RNN generates the corresponding image description (Vinyals et al., 2015; Xu et al., 2015). Most deep learning frameworks provide modules for different architectures and their combinations.

Determining the number of neurons in a network
The optimal number of hidden layers and hidden units is problem-dependent and should be optimized on a validation set. One common heuristic is to maximize the number of layers and units without overfitting the data. More layers and units increase the number of representable functions and local optima, and empirical evidence shows that it makes finding a good local optimum less sensitive to weight initialization (Dauphin et al., 2014).

Model training
The goal of model training is to find parameters $w$ that minimize an objective function $L(w)$, which measures the fit between the predictions the model parameterized by $w$ and the actual observations.
The most common objective functions are the cross-entropy for classification and mean-squared error for regression. Minimizing $L(w)$ is challenging since it is high-dimensional and non-convex (Fig 5C); see also Box 1 and Fig 2.

Stochastic gradient descent
Stochastic gradient descent is widely used to train deep models. Starting from an initial set of parameters $w_0$, the gradient $dw$ of $L$ with respect to $w$ is computed for a random batch of only few, for example 128, training samples. $dw$ points to the direction of steepest descent, towards which $w$ is updated with step size $\eta$, the learning rate (Fig 1C). At each step, the parameters are updated into the direction of steepest descent until a minimum is reached, analogously to a ball running down a hill to a valley (Bengio, 2012). The training performance strongly depends on parameter initialization, learning rate and batch size.

Parameter initialization
In general, model parameters should be initialized randomly to avoid local optima determined by a fixed initialization. Starting points for model parameters can be sampled independently from a normal distribution with small variance, or more commonly from a normal distribution with its variance scaled inversely by the number of hidden units in the input layer (Glorot & Bengio, 2010; He et al, 2015).

Learning rate and batch size
The learning rate and batch size of stochastic gradient descent need to be chosen with care, since they can strongly impact training speed and model performance. Different learning rates are usually explored on a logarithmic scale such as 0.1, 0.01 or 0.001, with 0.01 as the recommended default value (Bengio, 2012). A batch size of 128 training samples is suitable for most applications. The batch size can be increased to speed up training or decreased to reduce memory usage, which can be important for training complex models on memory-limited GPUs. The optimum learning rate and batch size are connected, with larger batch sizes typically requiring smaller learning rates.

Learning rate decay
The learning rate can be gradually reduced during training, which is based on the idea that larger steps may be helpful in early training stages in order to overcome possible local optima, whereas smaller step sizes allow exploring narrow parameter regions of the loss function in advanced stages of training. Common approaches include to linearly reduce the learning rate by a constant factor such as 0.5 after the validation loss stops improving, or exponentially after every training iteration or epoch (Bengio, 2012; Gawehn et al, 2016).

Momentum
Vanilla stochastic gradient descent can be extended by “momentum”, which usually improves training (Sutskever et al, 2013). Instead of updating the current parameter vector $w_t$ at time $t$ by the gradient vector $dw_{t+1}$ directly, a fraction of the previous update is added to the current one. With momentum rate $\nu$, weights are updated by a momentum vector $m_{t+1} = \nu \cdot m_{t} - \eta dW_{t+1}$. This approach can help to take larger steps in directions where gradients point consistently, and therefore speed up the convergence. The momentum rate $\nu$ can be set between [0, 1], and a typical value is 0.9. Nesterov momentum (Nesterov, 1983, 2013) is a special form of the same concept, which sometimes provides additional advantages.

Per-parameter adaptive learning rate methods
To reduce the sensitivity to the specific choice of the learning rate, adaptive learning rate methods, such as RMSprop, Adagrad (Srivastava et al, 2014) and Adam (Kingma & Ba, 2014), have been developed in order to appropriately adapt the learning rate per parameter during training. The most recent method, Adam, combines the strengths of previous methods RMSprop and Adagrad and is generally recommended for many applications.

Batch normalization
Batch normalization (Ioffe & Szegedy, 2015) is a recently described approach to reduce the dependency of training to the parameter initialization, speed up training and reduce overfitting. It is easy to implement, has marginal additional compute costs and has hence become common practice. Batch normalization zero centres and normalizes data not only at the input layer, but also at hidden layers before the activation function. This approach allows using higher learning rates and hence also accelerates training.

Analysing the learning curve
To validate the learning process, the loss should be monitored as a function of the number of training epochs, that is the number of times the full training set has been traversed (Fig 5D). If the learning curve decreases slowly, the learning rate may be too small and should be increased. If the loss decreases steeply at the beginning but saturates quickly, the learning rate may be too high. Extreme learning rates can result in an increasing or fluctuating learning curve (Bengio, 2012).

Monitoring training and validation performance
In parallel with the training loss, it is recommended to monitor the target performance such as the accuracy for both the training and validation set during training (Fig 5E). A low or decreasing validation performance relative to the training performance indicates overfitting (Bengio, 2012).

Avoiding overfitting
Deep neural networks are notoriously difficult to train, and overfitting to data is a major challenge, since they are nonlinear and have many parameters. Overfitting results from a too complex model relative to the size of the training set, and can thus be reduced by decreasing the model complexity, for example the number of hidden layers and units, or by increasing the size of the training set, for example via data augmentation. The following training guidelines can help to avoid overfitting.

Dropout (Srivastava et al, 2014) is the most common regularization technique and often one of the key ingredients to train deep models. Here, the activation of some neurons is randomly set to zero (“dropped out”) during training in each forward pass, which intuitively results in an ensemble of different networks whose
predictions are averaged (Fig 5E). The dropout rate corresponds to the probability that a neuron is dropped out, where 0.5 is a sensible default value. In addition to dropping out hidden units, input units can be dropped, however usually at a lower rate. Dropout is often combined with regularizing the magnitude or parameter values by the L2 norm, and less commonly the L1 norm.

Another popular regularization method is “early stopping”. Here, training is stopped as soon as the validation performance starts to saturate or deteriorate, and the parameters with the best performance on the validation set chosen.

Layerwise pre-training (Bengio et al, 2007; Salakhutdinov & Hinton, 2012) should be considered if the model overfits despite the mentioned regularization techniques. Instead of training the entire network at once, layers are first pre-trained unsupervised using autoencoders or restricted Boltzmann machines. Afterwards, the entire network is fine-tuned using the actual supervised learning objective.

Hyper-parameter optimization

Table 2 summarizes recommendations and starting points for the most common hyper-parameters, excluding architecture-dependent hyper-parameters such as the size and number of filters of a CNN. Since the best hyper-parameter configuration is data- and application-dependent, models with different configurations should be trained and their performance be evaluated on a validation set. As the number of configurations grows exponentially with the number of hyper-parameters, trying all of them is impossible in practice (Bengio, 2012). It is therefore recommended to optimize the most important hyper-parameters such as the learning rate, batch size or length of convolutional filters independently via line search, which is exploring different values while keeping all other hyper-parameters constant. The refined hyper-parameter space can then be further explored by random sampling, and settings with the best performance on the validation set are chosen. Frameworks such as Spearmint (Snoek et al, 2012), Hyperopt (Bergstra & Cox, 2013) or SMAC (Hutter et al, 2011) allow to automatically explore the hyper-parameter space using Bayesian optimization. However, although conceptually more powerful, they are at present more difficult to apply and parallelize than random sampling.

Training on GPUs

Training neural networks is more time-consuming compared to shallow models and can take hours, days or even weeks, depending on the size of training set and model architecture. Training on GPUs can considerably reduce the training time (commonly by tenfold or more) and is therefore crucial for evaluating multiple models efficiently. The reason for this speedup is that learning deep networks requires large numbers of matrix multiplications, which can be parallelized efficiently on GPUs. All state-of-the-art deep learning frameworks provide support to train models on either CPUs or GPUs without requiring any knowledge about GPU programming. On desktop machines, the local GPU card can often be used if the framework supports the specific brand. Alternatively, commercial providers provide GPU cloud compute clusters.

Pitfalls

No single method is universally applicable, and the choice of whether and how to use deep learning approaches will be problem-specific. Conventional analysis approaches will remain valid and have advantages when data are scarce or if the aim is to assess statistical significance, which is currently difficult using deep learning methods. Another limitation of deep learning is the increased training complexity, which applies both to model design and the required compute environment.

Conclusion

Deep learning methods are a powerful complement to classical machine learning tools and other analysis strategies. Already, these approaches have found use in a number of applications in computational biology, including regulatory genomics and image analysis. The first publicly available software frameworks have help to reduce the overhead of model development and provided a rich, accessible toolbox to practitioners. We expect that continued improvement of software infrastructure will make deep learning applicable to a growing range of biological problems.

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Conflict of interest

The authors declare that they have no conflict of interest.
References


Deep learning for computational biology

Christof Angermueller et al


McCulloch WS, Pitts W (1943) A logical calculus of the ideas immanent in nervous activity. Bull Math Biophysics 5: 115–133


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