Metabolize Neural Network

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Abstract

The metabolism of cells is the most basic and important part of human function. Neural networks in deep learning stem from neuronal activity. It is self-evident that the significance of metabolize neuronal network (MetaNet) in model construction. In this study, we explore neuronal metabolism for shallow network from proliferation and autophagy two aspects. First, we propose different neuron proliferate methods that constructive the self-growing network in metabolism cycle. Proliferate neurons alleviate resources wasting and insufficient model learning problem when network initializes more or less parameters. Then combined with autophagy mechanism in the process of model self construction to ablate under-expressed neurons. The MetaNet can automatically determine the number of neurons during training, further, save more resource consumption. We verify the performance of the proposed methods on datasets: MNIST, Fashion-MNIST and CIFAR-10.

Introduction

Human cells and tissues by proliferation and autophagy to build fresh ones and replacing outdated, living organisms are needed to support metabolism. Cell proliferation and autophagy are the mechanisms to grow and degrade structures, it can be a self-proliferation, protection or procedural death mechanism (Heiden, Cantley, and Thompson 2009; Rabinowitz and White 2010). The theory development of neural networks originates from biology, the activity of neuronal in deep network should analogy with the metabolism in cells. The neurons activity foundations in the model guarantee the vitality of generalization.

Deep neural networks with some hidden layers have led to the substantial tremendous progress in many applications. The deep networks are trained with initialize various parameters, like weights, bias, the neurons number in each layer, etc. Those networks suffer from the waste of computing resources when initialize a large number of model parameters and construct complex structure in training process. However, the network function limited when the data mapping simply by initialize few parameters can not be learned with efficiently results. Networks which can depict different data structures is extremely important, it are easily overfit the data when networks are large, lack of learning ability when simply construct the network structures.

Ideally, what is desired is a network large enough to learn the function mapping, and as small as possible to generalize well (Huyser and Horowitz 1988). There are destructive and constructive two general approaches to finding such networks. The destructive is using a larger and deeper than needed network, training it until meet the required tasks. After this, elements of the network are pruned off if they have little influence on result, The constructive approach starts with a small network and grows until a solution is found (Ash 1989; Alvarez and Salzmann 2016).

In this work we study techniques for how to metabolize the network with proliferate new and phagocytose decayed neurons by exploiting the fact that the network how to self-regulation. The method we present is a dynamic self-growth network with general applicability. Our MetaNet take advantage of the growth network to scientifically and comprehensively deduce the development behavior of shallow neural network as we learn from it. Given a small and initial model, we first proliferate some new hidden neurons that using static or dynamic technique, similar to the meta learning methods (Sung et al. 2017; Sohn and Lee 2012), then utilize autoregression technique to set weights for those introduced neurons. Further, consider the combining pre-growth network to phagocytose decayed neurons based on various metrics.

The contributions of this paper are threefold. First, We design the ideology of MetaNet based on the cell metabolic mechanism, and explore neurons metabolism for shallow network from proliferation and autophagy two aspects. Second, we propose various methods of proliferate and phagocyte decayed neurons in the metabolism process, which are not affect the training process of the overall network as far as possible. Finally, we make some experiments to verify our ideas on MNIST, Fashion MNIST and CIFAR-10 datasets, which compare and analyse the results of diverse proliferation and autophagy methods.

Related Work

Model growing for neural network, such as deep growing learning, network pruning, network distillation and weights learning have been explored in many literature, but the neu-
rous number in each layer, and how to proliferate additional and phagocytose failed neurons starts with a small network has not been widely studied. Currently, most works about this part is achieved by manually tuning hyper-parameters, or by relying on a trained network that cost resources. Furthermore, if the amount of initial hyper-parameter are small, the network lack of adequate learning ability, conversely, most of the parameters are redundant and resource consuming (Cheng et al. 2015).

The evolution of network structure have destructive and constructive two general approaches, destructive methods to structure evolution be required for a pretrained large and deep network, then prune or mimic it to network self-repairing or forming a new shallower or thinner student network. Network pruning by (Hanson and Pratt 1989; LeCun, Denker, and Solla 1990; Whitley, Starkweather, and Bogart 1990; Reed 1993; Setiono and Liu 1997) delete redundant parameters to improve network generalization ability. Recent explored (Han, Mao, and Dally 2016) have introduced deep compression by pruning, trained quantization and Huffman coding. Anwar S et al. (Anwar, Hwang, and Sung 2017) proposed structured pruning in deep convolutional neural networks (DCNN) which made channel wise, kernel wise and intra kernel strided structured sparsity. (Anwar S 2017) showed layer-wise pruning, feature map pruning, $k \times k$ kernel pruning and intra-kernel pruning four possible pruning granularities, used pruning to reduce the computational complexity of a DCNN. Optimizing the number of neurons in a network (Liu, Starzyk, and Zhu 2007; Murray and Chiang 2015; Zhou, Alvarez, and Porikli 2016; Alvarez and Salzmann 2016). The core concept of these studies are remove some network elements that have less effect on the model performance.

The main idea of model compression (Bucilua, Caruana, and Niculescu-Mizil 2006) is used a fast and compact model to approximate the function learned by a slower, larger, but better performing model. This concept has been extended in (Hinton, Vinyals, and Dean 2015) to formed network distillation, which transferred the knowledge from the cumbersome model to a small model that is more suitable for deployment. The more recent works often to training shallower or thinner model when distilled the acquired knowledge from a large model. (Ba and Caruana 2014) designd a shallow feedforward nets that could learned the complex functions from trained deep nets. (Chen, Goodfellow, and Shlens 2016) and (Li and Hoiem 2017) learned a continually growing model by pretrained network knowledge.

Another constructive method is dynamic growingth neurons or layers for initial small network structure that satisfies certain conditions. For add new neurons or layers, (Ash 1989) showed dynamic node creation that automatically grows backpropagation networks. (Rusu et al. 2016) by combining transfer analysis and reinforcement learning, progressive network achieved old and new features to multiple tasks. (Terekhov, Montone, and Oregan 2015) added an additional block when learned to solve new tasks. These network expansion by learning between different tasks. Not only are these processes increasing nodes, but need to consider the setting of the parameters. As Glorot and Bengio (Glorot and Bengio 2010) and (He et al. 2015) proposed a new initialization scheme for different activation function, respectively. (Denil et al. 2013) predicted parameters in deep network. (Wang et al. 2017) proposed deep growing learning framework by selected the confident prediction examples as the next iteration.

The destructive methods have higher requirements for prior knowledge or pretrained model, take major resources in trained a network that is larger than necessary, it may get stuck in one of the intermittently sized optimal solutions (Ash 1989). To construction, on the existing conditions to growth when add additional neurons or layers. In this paper, we introduce metabolism ideology into neural network, use proliferation and autophagy to gradually self-regulation in different model training stages.

The Proposed Method

Our model only need relatively small retraining effort when some new neurons is introduced, the overall framework is show in Figure 1 and detailed diagram in Figure 2. This section we first introduce metabolism cycle, then proliferate neurons number in each layer, descibe weight learning for adding neurons and discuss the autophagy process in MetaNet.

Given a simple initialize network, the main parameters in the model are expressed as $n = \{n_1, n_2, \ldots, n_l\}$, $W = \{W_1, W_2, \ldots, W_l\}$, $h = \{h_1, h_2, \ldots, h_l\}$, neurons number $n_l$, weights $W_l$ and each hidden output $h_l$ in layer $L_l$.

**Metabolism Cycle**

In MetaNet, some new hidden neurons are introduced when the curve slope of loss function value $\Delta c = c_g - c_b$ begins to lower than $\omega$, it means that the initialization weights couldn’t satisfied network learning ability, where $c_g$ and $c_b$ are the epoch in training process, the
initial neurons \( n \)

Online parturition

Proliferate new neurons

Metabolize neurons of each layers

Recovery pool

Online autophagy

\[ \{ \text{dis,low,den} \} \]

\[ \{ \text{rand,rep,ker} \} \]

\[ \Delta \]

\[ \text{E} \]

where

with epochs time, the metabolism cycle \( \Delta c \) also can changes depending on the situation.

**Proliferate Neurons**

The proliferate neurons number \( \mathcal{P} = \{ P_1, P_2, \ldots, P_l \} \), introduced \( P_l \) new nodes in each layer \( L_l \). There should be two basic approaches to decide adding neurons numbers, one is static methods that using a constant value to network grow and training it until end the iteration process, an alternative approach is dynamically increasing that as some variables grow automatically, in this section, we select the variance of test error \( \text{Var}(E) \) in \( \Delta c \) cycle period as the independent variable of the number of neurons in all layers, where \( E = \{ E_0, \ldots, E_\text{g} \} \), \( E_n \) is the test error at epoch \( n \). The proliferation neurons operation as \( \text{ProN} \), the number of neurons is given by:

\[ P_l = c_l(1 + e^{f(\text{Var}(E), \vartheta_l)}) \]

Here \( c_l \) is the constant value in each layer \( L_l \) and \( \vartheta_l \) is the dynamic proliferation rate. This function \( f \) can static or dynamic to obtain the neurons number \( P_l \) rely on the linear or nonlinear relation between \( \text{Var}(E) \) and parameter \( \vartheta_l \). In our model, we make \( f(\text{Var}(E), \vartheta_l) = -\vartheta_l \text{Var}(E) \), where \( \vartheta_l = 1 \).

**Weights Learning**

Training network with a large number of neurons and parameters from beginning to end, each neurons may not try to play their due role and function. While initialize a large number of neurons at the first, would bring a little free parameters number, exploiting the weights structure of each layers in deep network is necessary. To such problems is to define a autoregression model for the prior weights, the autoregression weights function \( \mathcal{G}_l : \mathbb{R}^{n_l} \mapsto \mathbb{R} \), generative neuron weights as \( W'_l = \mathcal{G}_l(W_l, P_l) \), \( W'_l = \{ W'_1, W'_2, \ldots, W'_l \} \). In this section, we will introduce three methods of weight learning.

**Random Parameterization** For the weights obtained from the initial rounds of training, function \( \mathcal{F}_{\text{rand}} \) is a randomly select the number of \( P_l \) neuron weights from original weights \( W \) as newly generated neuron weights \( W'_l = \{ W'_1, W'_2, \ldots, W'_l \} \), this process is expressed as:

\[ W' = \mathcal{F}_{\text{rand}}(W, \mathcal{P}) \]

**Higher Representational Power of Neurons**

For training samples, the ability of each neuron to express may reflect its value to some extent. Each single neurons \( N_s \) has an activations values \( \varphi(N_s) = \{ \varphi_1, \varphi_2, \ldots, \varphi_n \} \) and representation power \( \mathcal{R}(N_s, X) = \text{Var}(\varphi(N_s)) \) for different input \( X = \{ X_1, X_2, \ldots, X_n \} \). Select the top \( P_l \) with the highest variance values from \( \mathcal{R}_l(N_s, X) \) in layer \( l \) to form new weights.

\[ W' = \mathcal{F}_{\text{rep}}(\mathcal{R}(N_s, X), \mathcal{P}) \]

**Autoregression Strategy** In the process of proliferate neurons, our model start with a small amount of original neuron weights to get new weights. These weights as initial samples, we can use meta-learning methods to obtain some new samples. [Denil et al. 2013] analysed the low rank weight meatics and proposed three ways to constructed an apporriate dictionary: trained a single layer unsupervised model, exploit prior knowledge about the structure of features space and used kernel to encode prior knowledge. On the basis of this study, we use kernel ridge regressive [Murphy 2012] to make online weights prediction, as it is a autoregressive new parameter in all weight regions. This method is expressed as:

\[ W' = \mathcal{F}_{\text{ker}}(K^T(K + \lambda I)^{-1}W, \mathcal{P}) \]

\[ K(w_i, w_j) = \exp(-\frac{||w_i - w_j||^2}{2\delta^2}) \]

Here kernel matrix \( K_n \), \( \delta \) is known as the bandwidth that controls the degree of smoothness.
Neurons Selection for Autophagy

Survival of the fittest in the neurons dynamic growth is the effective mode of network development. The question is just how many neurons are needed for a particular problem in design the dynamic growth network, what conditions does these neurons meet and whether they have any help in training process. In this section, we propose three methods of neurons autophagy.

**Weight Distribution** Weight plays a key role in model training. As Glorot and Bengio (Glorot and Bengio 2010) found that the weights are initialized independently and the inputs features variances are the same with $Var(X)$. For the function Relu and forward propagation, with L layers put together, the weight variance of each layer should satisfy the following conditions (He et al. 2015):

$$Var(h_l) = Var(h_l) \prod_{i=1}^{L} \frac{1}{2} n_i Var(W_i) = 1$$ (7)

$$\frac{1}{2} n_i Var(W_i) = 1$$ (8)

It is constantly in a condition of growingth and updating. If the weight is small, the effect may not be obvious, use distribution $\overrightarrow{T}(\beta)$ as absolute value less than threshold $\beta$. Before neurons proliferate, We make a distribution adjustment for weights. Some neurons that do not satisfy this distribution are self autophagy. If the initialization parameter is uniform distribution, the weight are retained if the following conditions satisfy with:

$$\overrightarrow{w_l} = F_{dis}(w_l)$$ (9)

$$w_l \in \{x \sim a\mathcal{U}(-\sqrt{\frac{6}{n_l}}, \sqrt{\frac{6}{n_l}}) \} - \{x \sim T(\beta)\}$$ (10)

Where threshold $\alpha$ determine the range of values. When the weight is initialized as gaussian distribution, the condition as:

$$w_l \in \{x \sim a\mathcal{N}(0, \frac{6}{n_l}) \} - \{x \sim T(\beta)\}$$ (11)

After phagocytose neurons, those parameters is updated to $W_l \xrightarrow{update} \tilde{W}_l$, $n_l \xrightarrow{update} \tilde{n}_l$ and $h_l \xrightarrow{update} \tilde{h}_l$. Those parameters will be used for next proliferate neurons, the autophagy condition would update as:

$$Var(\tilde{h}_l \otimes \tilde{h}_l') = Var(\tilde{h}_l \otimes \tilde{h}_l') \times \prod_{i=1}^{L} \frac{1}{2} (\tilde{n}_l + P_l) \times Var(\tilde{W}_l \otimes \tilde{W}_l')$$ (12)

$$\frac{1}{2} (\tilde{n}_l + P_l) Var(\tilde{W}_l \otimes \tilde{W}_l') = 1$$ (13)

$h_l', w_l'$ are new hidden layer activation and weights value, respectively. $\otimes$ is the concatenate, can operate in weights and activation values. $n_l = \tilde{n}_l + P_l$, $h_l \xrightarrow{growth} \tilde{h}_l \otimes \tilde{h}_l'$, $W_l \xrightarrow{growth} \tilde{W}_l \otimes \tilde{W}_l'$. From these definitions, With the metabolism of proliferation and autophagy, the weights, number of neurons and hidden layer activitions in the neuronal network would updated.

**Lower Representational Power of Neurons** This part of the representational power of neurons is calculated in the same way as weights learning. In the weights learning, we select the top $P_l$ variance values from neurons in layer $l$. In this section, our model phagocytose neurons which its representational power below a certain level $\nu$, the method is expressed as:

$$\overrightarrow{w_l} = F_{low}(w_l, \nu)$$ (14)

**Weight Density** Density indicates the distribution of the data. According to the principle of fine density division, we subdivide the weights by ultra-fine density, referred to as $\mathcal{D} = \{D_1, D_2, \cdots, D_m\}$. The smaller the distance between weight samples, the more the density division area is. If the density of a certain area is much larger than other areas, the neurons in the area are randomly deleted the number $r$ of neurons. This method is a hypothesis and we will be verified in the experiment, it is expressed as:

$$\overrightarrow{w_l} = F_{den}(Max(D), r)$$ (15)

**Experiments**

In this sectoin, we present two basic architectures which are two fully-connected layers on MNIST, Fashion MNIST data sets and two-layers convolution neural network on CIFAR-10 to demonstrate the metabolism ability of our method, abbreviated as MetaNetNLP and MetaNetCNN. We discuss the experiment results, analyze the various parturition and autophagy behavior of our model on three different datasets. As for parameter calculation, we get average value of all epoch parameters with add new neurons.

**Results on MNIST**

The two hidden fully-connected network in this MNIST experiment have two basic architectures with BasicNLP(64) and BasicNLP(1024), that the number of neurons in all layers is 64 and 1024, respectively. Our model from the number of neurons in all layers is 32, 64 and 256 to constructive MetaNet, the final neuron number goal is no more than 1024 in each layers, those methods as MetaNetNLP(32-1024), MetaNetNLP(64-1024) and MetaNetNLP(256-1024).

| Model                  | Test Error(%) | Time(s) | #Params(k) |
|------------------------|---------------|---------|------------|
| BasicNLP(64)           | 2.42          | 135.87  | 54.26      |
| BasicNLP(1024)         | 1.71          | 185.27  | 1828.04    |
| MetaNetNLP(32-1024)    | 1.48          | 179.42  | 697.37     |
| MetaNetNLP(64-1024)    | **1.39**      | 180.46  | 735.76     |
| MetaNetNLP(256-1024)   | 1.51          | 184.63  | 895.91     |

Table 1: Test error, training time and parameter on Mmit Datasets.

$\alpha$ shows performance using BasicNLP(64), BasicNLP(1024) as the several different baseline for the neurons region, and MetaNetNLP(64-1024). The dashed line as train error(TnE), solid line as test error(TsE). During the training process, our method is slightly fluctuating due to the addition
of neurons, but this has no effect on the final classification result. Generally, the performance of MetaNetNLP(64-1024) is not outstanding before 50 epochs, but at same point, such epoch 32, 37 and 47, it is even better than BasicNLP(1024). After this critical point, the model becomes excellent, and the best results is 1.39%, more than the 1.71% of Basic1024. The final number of neurons in each layer of MetaNetNLP(32-1024), MetaNetNLP(64-1024) and MetaNetNLP(256-1024) is 942, 964 and 992, respectively. Combined with Table 1 for the number of initialized neurons in the model, if we want to make the training time and resources cost less, that can set a smaller value, if want better results that can set a larger value. The fewer running time and neurons, parameter is less than half of BasicNLP(1024). Our method is better than baseline in terms of parameter, time and performance.

For MetaNet, the middle of Figure 3 we can see the role of different weight learning methods, the random parameterization as MetaNetNLP(64-1024)Rand, representational power of each neurons to all samples as MetaNetNLP(64-1024)Rep, the kernel ridge predictor we take it as a basic weights learning method, as MetaNetNLP(64-1024). From Figure 3(b) kernel ridge predictor method is better. Figure 3(c) is the different weights autophagy comparison method, weights selection based on distribution as MetaNetNLP(64-1024)Dis, the power of neurons representational as MetaNetNLP(64-1024)Low, the density as MetaNetNLP(64-1024)Den. These autophagy methods do not have a big impact on the experimental results. MetaNetNLP(64-1024) is self-growth but not ablate any neurons, relatively speaking, weights selection based on the power of neuronal representational is better than other methods for the MNIST dataset.

During the metabolism of neurons, we use kernel ridge technology to learning the weights for proliferate neurons. Figure 4 shows the correlation between the original and predicted parameters in in different epochs and layers. We choose epoch 13, 33, 43 and 53 as a few samples in the training process to draw the dispersive points of corresponding weights. The upper half of Figure 4 are the first layer, at epoch 13 moment, the original and predicted parameters are more dispersed, then for epoch 33, 43 and 53, the original training parameters gathered together, but the predicted parameters are still dispersed, the weight diversity can learn as many features as possible on the initial layer, and provide more information for the next layer. For the bottom half of Figure 4 this part are the parameters of second layer. Because our model has only two layers, the second layer learns the important feature representations for the task. Almost all predicted values are within the original parameter range, and gathered together. Compared with the predicted parameters in first layer, the prediction parameters of this layer are more conservative, maybe we can add some noise disturbance information in the parameter prediction process to improve the generalization of the model. But in any case, these prediction parameters can help MetaNet to training.

Results on Fashion MNIST

The basic model and parameter settings of Fashion MNIST are the same as MNIST. Figure 5(a) shows the experimental results of BasicNLP(64), BasicNLP(1024) and MetaNetNLP(64-1024). For the different proliferate and ablate neurons methods, the experiments results Figure 5(b) shows that random select some weights are better than the weights from higher representation power neurons. The higher representation power of the neurons may have insufficient ability to capture important features and have strong learning ability for less important features, which may result in poor performance. For the autophagy process, most methods are the same except that the method of ablating neurons based on distribution will converge faster and get the best results.

Table 2 shows the test error, cost time and parameters with different model. From the above results, the final test error result BasicNLP(1024) is 9.06%, MetaNetNLP(64-1024) is 9.34%, MetaNetNLP(256-1024) is 9.02%. For MetaNetNLP(64-1024) and MetaNetNLP(256-1024) only need fewer neurons and resources, can be almost achieve the same or even better results. It can be seen from the experimental results that our method save time and memory when achieve similar or even better results.

Results on CIFAR-10

MetaNet on CIFAR-10 is different from the previous two datasets. We use two-layers convolution neural network to construct metabolism CNN. Due to the large amount of parameters in the CNN, the setting of smaller number of channels is adopted in the experimental model. The basic compari-
Figure 5: Comparison of experimental results for baseline, neurons proliferation and autophagy in Fashion MNIST datasets. Left: (a) the dashed and solid line are the train and test error for different methods. Middle: (b) test error of various neurons proliferation methods. Right: (c) test error of diverse neurons autophagy methods.

Table 2: Test error, training time and parameter on Fashion Mniast Datasets.

| Model               | Test Error(%) | Time(s)  | #Params(k) |
|---------------------|---------------|----------|------------|
| BasicNLP(64)        | 10.93         | 171.77   | 54.26      |
| BasicNLP(1024)      | 9.06          | 185.34   | 1828.04    |
| MetaNetNLP(32-1024) | 9.44          | 174.18   | 697.37     |
| MetaNetNLP(64-1024) | 9.34          | 177.58   | 735.76     |
| MetaNetNLP(256-1024)| **9.02**      | 181.26   | 895.91     |

Table 3: Test error, training time and parameter on CIFAR-10 Datasets.

| Model               | Test Error(%) | Time(s)  | #Params(k) |
|---------------------|---------------|----------|------------|
| BasicCNN(60)        | 26.90         | 3757.28  | 493.23     |
| BasicCNN(80)        | **25.76**     | 4850.81  | 671.69     |
| MetaNetCNN(40-80)   | 26.70         | 3344.31  | 430.64     |
| MetaNetCNN(60-80)   | 25.86         | 3615.79  | 499.80     |

Figure 6: Comparison of experimental results for baseline, neurons proliferation and autophagy in CIFAR-10 datasets. Left: (a) the dashed and solid line are the train and test error for different methods. Middle: (b) test error of various neurons proliferation methods. Right: (c) test error of diverse neurons autophagy methods.

We have introduced parturition and autophagy mechanism to metabolize neural network that automatically self growth and ablate neurons in each layers. The idea of MetaNet are verify on two fully-connected layers and two-layers convolutional neural network, the experiments have demonstrated the benefits of our model. For deliver dynamic neurons number, we intend to study better function expression where each layers fits of our model. For deliver dynamic neurons number, we intend to study better function expression where each layers fits of our model. For deliver dynamic neurons number, we intend to study better function expression where each layers fits of our model.

Conclusion

We have introduced parturition and autophagy mechanism to metabolize neural network that automatically self growth and ablate neurons in each layers. The idea of MetaNet are verify on two fully-connected layers and two-layers convolutional neural network, the experiments have demonstrated the benefits of our model. For deliver dynamic neurons number, we intend to study better function expression where each layers can get the more adaptable neurons number. The autophagy in our model didn’t play a better role, we plan to design a appropriate autophagy mechanism that reflect the effectiveness of its behavior. The framework can applicable to different architectures and generalizability is well in theory, furthermore, we could extend it multiple layers network and test its generalization by more data sets.
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