**Week 6-1: Paper Summaries**

***CE-510 Seminar: Social Media Mining***

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* **A Survey of Deep Neural Network Architectures and Their Applications**
* **ImageNet Classification with Deep Convolutional Neural Networks**

In this paper, the author proposes a groundbreaking structure, ImageNet, which contains five convolutional layers and three fully connected layers. Its characteristics can be summarized as follows:

1. **Convergence/training was accelerated** with the use of linear correction unit, **ReLU**. ReLU is a kind of nonlinear neuron (when input x is greater than 0, output x; The input x is less than 0, then the output 0) with faster calculation speed and faster convergence than the previous activation function.
2. **Data augmentation:** This ensures the diversity of data and makes the model fit better, the data augmentation methods used by the author include flipping the image horizontally and changing the pixel intensity value of RGB on the image
3. **Dropout:** The dropout model training will soon overfit, adding a double to the iteration times.
4. **Muti GPU training:** The author divided the network into two parts, divided it into two Gpus, and solved the problem by parallel computing

In addition, this paper also proves the importance of data and model size, that is, to solve the task of thousands classification level, a sufficiently large model is required, and a sufficiently large model requires enough data with a certain diversity for fitting. According to the experiment, even removing a single convolutional layer will have a huge impact on the final classification result.

* **Mastering the game of Go with deep neural networks and tree search**

Go has long been considered the most challenging classic game in the field of artificial intelligence because of its vast search space and the difficulty of evaluating moves and moves. Here, the author of this paper introduces a new approach to go calculation, which uses a "value network" to evaluate the game and a "strategy network" to select positions. The chess games played by go masters are supervised to learn, and the chess games played by themselves are strengthened to learn, and the two are combined to train the deep neural network.

In AlphaGo, the author represented the checkerboard position as 19x19 image and used convolutional neural network to construct position representation. At the same time, the authors use neural networks to reduce the effective depth and breadth of the search tree. The training process can be summarized as follows:

1. First, supervised learning (SL) is used to train a strategy network , and the training data is human expert knowledge. The supervised learning method makes the gradient of high quality and fast update.
2. Secondly, they train a fast strategy network with shallow network depth, which can quickly select behaviors in Monte Carlo Rollouts.
3. A reinforcement learning (RL) strategy network is trained to improve the SL strategy network by optimizing the results of **selfplay**, which adjusts the strategy to win the game rather than maximize the prediction accuracy.
4. Finally, a value network is trained to predict the winner of the game between RL strategy network and itself.

* **Highly accurate protein structure prediction with AlphaFold**

1. Motivation

Protein is the material basis of all living systems. Each protein has a specific structure due to the composition, torsion, bending and so on of the basic acid chain, which determines the function of the protein. Normally, proteins need to be properly folded into a specific 3D configuration to perform their biological functions. The folding of protein quaternary structure is affected by many non-covalent interactions. To understand the mechanism of action at the molecular level, it is necessary to accurately measure the 3D structure of a protein. Existing methods of measuring protein structure are expensive because only a few proteins can be crystallized.

1. Alphafold

**Transformer** is a model based on encoder-decoder structure. Transformer emerged in the NLP field using the attention mechanism to process a series of text sequences. The addition of **self-attention** can help the current node not only pay attention to the current word, to obtain the semantic meaning of the context and improve the decoding effect. Amino acid sequence is a data structure like text. Alphafold uses multiple sequence alignment to integrate protein structure and biological information into the deep learning algorithm.

Alphafold 2 uses the target amino acid sequence, MSA and template as input to directly predict the three-dimensional structure of the target from end to end and uses Transformer for pre-training.

Using such a network system, Alphafold determined the structure of proteins that cover almost the entire human proteome (98.5% of all human proteins, i.e., all proteins under 2700AA in Uniprot)