

13<sup>th</sup> International Conference on

# Metabolomics and Systems Biology

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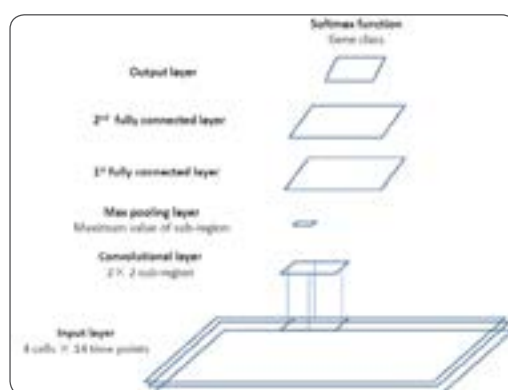


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### The applications of deep learning in biomedicine

Artificial intelligence has shown great power in processing big data and achieving better performance than human in many complex tasks. The underlying algorithms are machine learning, especially deep learning, a revolutionary development in computer sciences. The deep learning algorithm is based neural network which mimics how the human brain works. There are input layer, hidden layers and output layer. Each layer performs linear combinations using the output from the previous layers as input, and operate non-linear functions on the weighted sums. At last, softmax function is applied to the output units of the hidden layers for classification purpose. Deep learning has been applied to analyze images, sound, text and various data. It is very useful method in biomedicine. To illustrate the applications of deep learning, an example of identifying cell-cycle genes based on time course gene expression profiles will be demonstrated. The cells and the gene expression levels on each time points formed the input layer and the output layer was the gene class. We found that the Convolutional Neural Network (CNN) had better prediction performance than traditional methods. The results provided novel insight to the cell cycle mechanisms.



### Recent Publications

1. Cai Y D, Zhang Q, Zhang Y H, Chen L and Huang T (2017) Identification of genes associated with breast cancer metastasis to bone on a protein-protein interaction network with a shortest path algorithm. *Journal of Proteome Research*. 16(2):1027-1038.
2. Zhang N, Wang M, Zhang P and Huang T (2016) Classification of cancers based on copy number variation landscapes. *Biochimica et Biophysica Acta*. 860(11, Part B):2750-2755.
3. Huang T et al. (2016) SNHG8 is identified as a key regulator of epstein-barr virus (EBV)-associated gastric cancer by an integrative analysis of lncRNA and mRNA expression. *Oncotarget*. 7(49):80990-81002.

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4. Huang T et al. (2016) A new method for identifying causal genes of schizophrenia and anti-tuberculosis drug-induced hepatotoxicity. *Scientific Reports*. 6:32571.
5. Chen L et al. (2016) Identification of novel candidate drivers connecting different dysfunctional levels for lung adenocarcinoma using protein-protein interactions and a shortest path approach. *Scientific Reports*. 6:29849

## Biography

Tao Huang has been the Director of Bioinformatics Core Facility at Institute of Health Sciences, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences since 2014. From 2012 to 2014, he was a Postdoctoral Fellow at Department of Genetics and Genomics Sciences, Icahn School of Medicine at Mount Sinai, New York City, USA. His research interests include bioinformatics, computational biology, systems genetics and big data research. He has published over 100 articles in peer-reviewed journals. His works have been cited for 3138 times with an h-index of 26 and an i10-index of 64. He has been independent reviewer for about 30 journals. He is Editor for Book Computational Systems Biology - Methods and Protocols of Springer, Guest Editor for BBA Molecular Basis of Disease, BBA General Subjects, Artificial Intelligence in Medicine, BioMed Research International, Combinatorial Chemistry & High Throughput Screening and Computational and Mathematical Methods in Medicine.

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