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Tutorial title: **A tutorial on deep learning for computational genomics and drug response prediction**

Organizers

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Short description

The advances and decreasing costs of genome sequencing and other high throughput technologies have led to the creation of large volumes of diverse datasets for biomedical research and drug discovery. This explosion of extensive genomic data provides exciting opportunities for developing machine learning and especially deep learning solutions for the discovery of new knowledge that can be used for better understanding of human pathological conditions and for the development of a more personalized, less toxic and more potent treatment regimen.

Contents

This tutorial will provide a comprehensive survey of deep learning models for "omics" data analysis and drug response prediction. The goal is to educate audience about the deep learning basics and its applications to genomics data and the prediction of drug responses. In the first section, we will cover the deep learning basics and important deep learning models as well as an introduction to molecular biology, different high through sequencing data protocols, and public data resource. In the second section, we will survey existing work on deep learning models for genomics. In the third section, we will focus on discussing the deep learning models for drug response prediction.

CVs of the organizers

Dr. Yufei Huang is an expert in computational biology and machine learning. Currently, he focuses on epitranscriptome research and developing deep learning solutions for genomics data analysis and drug response prediction.

Dr. Chen is an expert in the area of bioinformatics methods for NGS data analysis, gene expression analysis, gene regulation networks, integrative genomic data analysis, genetic data visualization, and machine-learning techniques in translational cancer research. He authored and co-authored about 200 peer-reviewed publications in these areas.

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