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Introduction to Machine Learning
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What Is Bioinformatics? How Deep Neural Networks Work

~~A basic introduction to drugs, drug targets, and molecular interactions.~~

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Deep learning has advanced rapidly since the early 2000s and now demonstrates state-of-the-art performance in various fields. Accordingly, application of deep learning in bioinformatics to gain insight from data has been emphasized in both academia and industry .

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A novel deep learning method for predictive modeling of microbiome data. With the development and decreasing cost of next-generation sequencing technologies, the study of the human microbiome has become a rapid expanding research field, which provides an unprecedented opportunity in various clinical applications such as drug response predictions and disease diagnosis.

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Deep learning is the emerging generation of the artificial intelligence techniques, specifically in machine learning. The earliest artificial intelligence was firstly implemented on hardware system in the 1950s. The newer concept with the more systematic theorems, named machine learning, appeared in the 1960s.

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Learning in ...

The aim of this summer school was to “ give [the participants] the theoretical and practical basis for understanding [deep learning] ” . A few members of the platform and myself participated to these five days of training. I must be honest, I was a little afraid of deep learning the first time it was presented to me.

A Week of Deep Learning – IRIC's Bioinformatics Platform

Jangu is a python package that facilitates deep learning in the context of genomics. The package is freely available under a GPL-3.0 license. In particular, the package allows for easy access to typical Genomics data formats and out-of-the-box evaluation (for keras models specifically) so that you can

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concentrate on designing the neural network architecture for the purpose of quickly testing biological hypothesis.

GitHub - BIMSBbioinfo/jangu: Deep learning infrastructure ...

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Zhao ' s Bioinformatics and Systems Medicine Laboratory (BSML, www.uth.edu/bioinfo/), Center for Precision Health, School of Biomedical Informatics, University of Texas Health Science at Houston (UTHealth).

Postdoctoral Fellow in Bioinformatics, Deep Learning

This example shows a secondary structure prediction method that uses a feed-forward neural network and the functionality available with the Deep Learning Toolbox™. It is a simplified example intended to illustrate the steps for setting up a neural network with the purpose of predicting secondary structure of proteins.

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