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DeepOmics: Deep Learning for Understanding Genome Functioning and the Underlying Genetic Causes of Disease

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Abstract : Advancement in sequence data generation technologies is churning out voluminous omics data and posing a massive challenge to annotate the biological functional features. With so much data available, the use of machine learning methods and tools to make novel inferences has become obvious. Machine learning methods have been successfully applied to a lot of disciplines, including computational biology and bioinformatics. Researchers in computational biology are interested to develop novel machine learning frameworks to classify the huge amounts of biological data. In this proposal, it plan to employ novel machine learning approaches to aid the understanding of how apparently innocuous mutations (in intergenic DNA and at synonymous sites) cause diseases. We are also interested in discovering novel functional sites in the genome and mutations in which can affect a phenotype of interest.

Keywords : genome wide association studies (GWAS), next generation sequencing (NGS), deep learning, omics
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