Publications Template

#	Research Title	Field	Abstract	Year of Publication Publishing	Publishing Link "URL"
1	"Noisy Epistasis Using Deep Learning." 2018 International Japan- Africa Conference on Electronics, Communications and Computations (JAC-ECC). IEEE, 2018.	Deep Learning - Bioinformatics	Nowadays, the analysis of the complex diseases through the epistatic interactions between single nucleotide polymorphisms (SNPs), for the detection of their statistical association with the disease is challenging due to curse of dimensionality, time complexity, absence of marginal effect and effect of the environmental factors. Studies of deep Learning (DL) techniques are shown to have more accurate results compared to other techniques such as Logistic Regression (LR), Multifactor dimensionality reduction (MDR) and associative classification-based multifactor dimensionality reduction (MDRAC). However, DL is not tested against different sources of noise. In this paper, we are concerned about studying the effect of different types of noise on a DL technique. Experiments are designed to compare the performance of the technique for different data models. The empirical results show that the DL approach gives robust and accurate results when compared to LR, MDR and MDRAC approaches.	2018	https://ieeexplore.ieee.org/abstract/document/8679568

2	"High Performance Computing for Detecting Complex Disease Using Deep Learning" 2019 International Conference on Advances in the Emerging Computing Technologies (AECT 2019).	High Performance Computing – Complex Diseases- Deep Learning	The study of the Genome-wide association study (GWAS) and the complex diseases is of high importance nowadays. The epistasis describes the analysis of the single nucleotide polymorphisms (SNPs) interactions and their effects on the complex diseases. However, enormous number of SNPs interactions should be tested against the disease that is highly computational expensive. In this paper, High Performance Computing (HPC) is being applied on a supercomputer to reduce the processing time. Parallel Deep Learning (PDL) is applied and tested using different datasets. Simulated datasets of 12 different models and the real WTCCC Rheumatoid arthritis (RA) dataset are being tested. Results show the high accuracy, specificity and true positive rate values. Moreover, they show low values of the false discovery rate and the robustness of power through the different simulated models. When tested on the real RA dataset, our model shows the ability to detect the 2-way interaction SNPs with their promising related genes with high accuracy due to the parallel deep learning architecture.	2020	https://ieeexplore.ieee.org/abstract/document/9194158