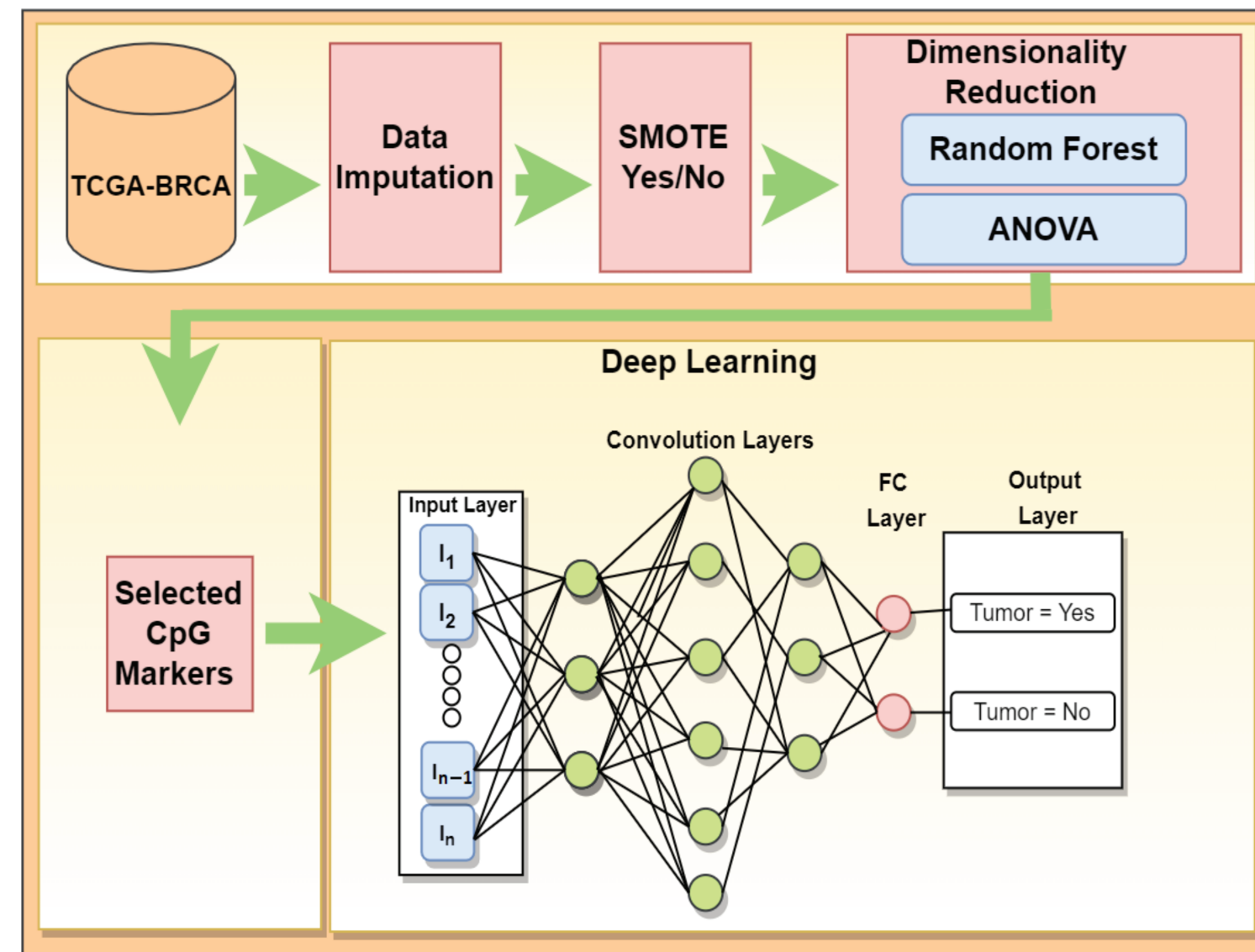




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*Application of Feature Selection and Deep Learning  
for Cancer Prediction Using DNA Methylation Markers*  
*Genes 13, no. 9*

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DNA methylation can affect gene accessibility and therefore gene expression. In this study, a machine learning pipeline is proposed for the prediction of breast cancer and the identification of significant genes that contribute to the prediction. The current study utilized breast cancer methylation data from The Cancer Genome Atlas (TCGA), specifically the TCGA-BRCA dataset. Feature engineering techniques have been utilized to reduce data volume and make deep learning scalable. Comparative analysis of the proposed approach on Illumina 27K and 450K methylation data reveals that deep learning methodologies for cancer prediction can be coupled with feature selection to enhance prediction accuracy.