



**NARASARAOPETA ENGINEERING COLLEGE (AUTONOMOUS)**  
**DEPARTMENT OF COMPUTER SCIENCE AND ENGINEERING**

<b>Batch Number</b>	DG4
<b>Team Members</b>	Ch.Chandrika Tirumala(22471A05L7) K.Jayamma(22471A05M7) P.Haseena(23475A0501)
<b>Guide</b>	Dr.K.Soma Sekhar
<b>Title</b>	<b>Survival Analysis Using Deep Gated Neural Network With Self-Attention Mechanism</b>
<b>Domain/Technology</b>	DEEP LEARNING
<b>Base Paper Link</b>	<a href="https://ieeexplore.ieee.org/document/10769011">https://ieeexplore.ieee.org/document/10769011</a>
<b>Dataset Link</b>	<a href="https://www.kaggle.com/datasets/raghadalharbi/breast-cancer-gene-expression-profiles-metabric">https://www.kaggle.com/datasets/raghadalharbi/breast-cancer-gene-expression-profiles-metabric</a>
<b>Software Requirements</b>	Browser: Any latest browser like Chrome Operating System: Windows 10/Linux(Ubuntu)/macOS /python 3.7 or higher(COLAB)
<b>Hardware Requirements</b>	SystemType: Intel Core i3 or above RAM: Minimum 8 GB Number of cores:5 Number of Threads: 4
<b>Abstract</b>	Survival analysis plays a crucial role in clinical risk prediction, particularly for diseases like cancer. However, traditional models are limited by assumptions such as proportional hazards and their inability to capture complex temporal and nonlinear feature relationships. This project introduces CNN-Attentive SA-DGNet, a novel hybrid deep learning framework that integrates Convolutional Neural Networks (CNNs) for gene expression encoding with a lightweight self-attention-enhanced Deep Gated Neural Network (SA-DGNet). The CNN module extracts localized gene-level patterns, while the SA-DGNet captures time-varying feature effects through gated mechanisms and efficient attention-based temporal modeling. The model is trained using a composite survival loss that robustly handles censored and uncensored data. Experimental results on the METABRIC breast cancer dataset demonstrate that CNN-Attentive SA-DGNet achieves superior performance compared to traditional and deep learning baselines in terms of concordance index and mean absolute error. Furthermore, it offers improved interpretability via time-varying feature importance matrices, making it a promising and practical tool for personalized survival prediction in clinical settings.

Signature of the student(s)

Signature of the Guide

Signature of the project coordinator