RESEARCH ARTICLE

Editorial Process: Submission:03/11/2025 Acceptance:07/13/2025

Survival Prediction in Stomach Cancer with Deep Learning: Unveiling Model Decisions with LIME and SHAP

Diana Padhi*, Saroj Kumar Das Majumdar, Anupam Muralidharan

Abstract

Objective: Stomach cancer is anticipated to remain a significant global health concern, underscoring the urgent need for sophisticated prognostic models. The aim of the study is to build an intuitive deep learning model for predicting survival probabilities in stomach cancer patients, validating it with external data and merging SHAP and LIME to improve the therapeutic relevance and reliability. **Methods:** A deep learning survival model was developed with multilayer perceptron, on 1,350 documented stomach cancer cases from the AIIMS, Bhubaneswar Cancer Registry (2018–2022). The model was refined utilizing the Adam optimizer (learning rate = 0.002) with dropout regularization. External validation was performed on an independent cohort of 388 patients from Hi-Tech Medical College and Hospital. Performance was assessed using accuracy, precision, sensitivity, specificity, F1-score, balanced accuracy, Matthews correlation coefficient, concordance index, and AUROC score. LIME and SHAP were utilized to improve interpretability by evaluating both local and global feature contributions. **Result:** Complex interactions between important prognostic factors such as age, stage, treatment approaches, and socioeconomic level were well explained by LIME and SHAP, thus exposing important elements impacting survival results. Performance measures of the model measured through various metrics showed good generalizability over several datasets. **Conclusion:** This article focused on interpretable artificial intelligence models in the prognosis for stomach cancer with patient-specific survival projections. Artificial intelligence techniques such as LIME and SHAP improves clinician trust, hence promoting patient specific treatment recommendations.

Keywords: Stomach Cancer- LIME- SHAP

Asian Pac J Cancer Prev, **26 (7)**, 2669-2677

Introduction

In 2020, stomach cancer estimated over 1 million new cases and 769,000 related deaths worldwide, ranked as fourth in mortality and fifth as most common malignancy [1]. Although the AJCC staging system is usually used to direct treatment and predict prognosis, it has great shortcomings in precisely predicting the results of specific patients [2]. Improved customized treatment depends on advanced prediction model as stomach cancer is heterogeneous and the interaction of prognostic factors is complicated [3]. Healthcare might undergo a dramatic transformation if machine learning explores vast databases for patterns enhancing accuracy prediction [4-7]. Researcher interest has been sparked by deep learning's ability to independently extract significant traits from raw data and expose complicated, nonlinear relationships [8–11].

However, the "black box" quality renders them opaque and challenging to grasp, which may restrict clinician confidence to adopt them. These issues can be addressed by LIME (Local Interpretable Model-agnostic Explanations) and SHAP (Shapley Additive explanations). SHAP guarantees mathematically reasonable explanations by using game-theoretic ideas to divide feature contributions both locally and globally. LIME approximatively describes and explains complicated model activity using simpler surrogate model, for certain predictions. Since health care is a high-stakes sector, these approaches enable practitioners to better grasp how clinical, demographic and course of treatment affect survival rates [12, 13]. Though little is known about how effectively deep learning model predict survival in stomach cancer, they have been extensively applied in cancer research for things like digital histopathology, automated image interpretation, and biomarker identification [14–18]. Furthermore, limited research has been conducted to ensure these model' interpretability through SHAP and LIME. The aim of the study is to build an intuitive deep learning model for predicting survival probabilities in stomach cancer patients, validating it with external data and merging SHAP and LIME to improve the therapeutic relevance

*Department of Radiation Oncology, All India Institute of Medical Sciences, Bhubaneswar, India. *For Correspondence: dianapadhi@gmail.com*

and reliability.

Materials and Methods

The AIIMS, Bhubaneswar Cancer Registry produced a dataset of 1,350 stomach cancer diagnosed between 2018 and 2022 (21 to 95 years), we followed these patients all the way through 2024. Each participant was thoroughly briefed on the objectives of the study and the consent was taken (Figure 1). The raw data was selected from the database to ensure compatibility with deep learning techniques. The standardizing of continuous variables guaranteed homogeneity throughout the dataset, the one-hot encoding technique was utilized to numerically represent categorical variables. Data with unknown values were excluded from the study. The dataset was arranged using an output variable showing general survival status (coded as "Alive" or "Dead") and input parameters (such as age, sex, treatment approaches, and other clinicopathological factors). The dataset was split ten times during training in order to assure strong performance and minimize bias (k-fold cross-validation). A Multilayer Perceptron (MLP) help to achieve the survival prediction. We found the ideal number of neurons and layers through hyper-parameter tuning with Python-based optimization methods. The design consists of 3 hidden layers with 48, 64, and 16 neurons each and an input layer of 16 neurons. Every hidden layer captured nonlinear interactions using corrected linear unit (ReLU) activation functions. One output layer neuron assesses the survival probability of the "Alive" class using the Softmax activation function. This architecture was selected through iterative validating which finds a balance between model complexity, performance, and interpretability (Figure 2). Following every hidden layer, we used dropout regularization of 50%, to guard against overfitting by ensuring the model was not overly dependent on any one feature. Using the Adam optimizer and a learning rate of 0.002, stable and effective convergence during training was attained. Cross entropy loss was chosen as the loss function as it offers a reasonable gauge of the variation between the actual and predicted probability of survival.

All of the many measures used to evaluate the model's performance including precision, accuracy, sensitivity, specificity, F1 score, balanced accuracy, and Matthews Correlation Coefficient (MCC). Computing the Concordance Index (C-index) and the Area Under the Receiver Operating Characteristic (AUROC) allowed one to assess the model's discriminative performance in survival analysis. Particularly in cases of survival studies, if datasets are imbalanced, these indicators provide a whole view of performance for the model. External validity of the model was evaluated using an independent dataset of a Geographically Distinct Hospital (Hi-Tech Medical College & Hospital). For this group, all pre-processing systems and assessment tools were reproduced. The performance evaluation of metrics was validated with external datasets so as to evaluate how well the model suited to various patient groups and healthcare situations, and not confined to the AIIMS dataset.

LIME and SHAP two model agnostic interpretability techniques were merged to address the "black-box" feature of deep learning model. LIME was applied to modify input characteristics and explain about their influence on predictions and therefore enabling explanations at the instance level. This was done to highlight how the survival probability prediction is affected by elements like age, cancer stage, chemotherapy, socioeconomic status, tumor differentiation, and patient habits. Simultaneously, by quantifying the contributions of local and global variables, SHAP values provide a comprehensive picture of the elements significantly influencing the projections of the model. The linking of complex computational findings with clinical insights, these approaches of interpretability increase confidence and enable more customized treatment strategie.

All data analysis was done using Python (version 3.10) included into the Visual Studio Code environment. The deep learning model was developed with Tensor Flow and Keras frameworks. Grid search were used for hyper parameters optimization. Statistical evaluations including cross-valuation and performance metric computations were frequently conducted to the trained and external validation datasets in order to ensure a complete assessment of the performance of the model.

Results

Model performance of the trained data with validation cohorts help to determine the generalizability and robustness of clinical research prediction model. Using demographic, clinical, and outcome-related criteria, this article compares the trained dataset (n=1,350) with the validation dataset (n=388). It underscores the need of careful recalibration for broader applicability and the necessity of these variants for model transferability. The distribution of age shows a clear demographic trend in Table 1. Higher proportion of "Old Adult (60–79)" (44.6%) are included in the trained dataset than in the validation dataset, which mostly consists of "Middle Age (40–59)" patients (52.5%). Men make 62% of the trained group and 64.9% of the validation group, so the sex ratio stays unchanged. Important clinical factors displaying clear consistency throughout the datasets which includes stage of cancer, the co-morbidity, and the treatment approaches. The capacity of the model to generalize throughout the multiple patient health states which is supported by the homogeneity of the fraction of comorbid disorders (17.3% in trained vs. 18.5% in validation). Comparatively, the proportion of Stage IV diagnosis (49.3% in trained vs. 46.3% in validation) suggests that the degree of the disease remained the same. The patterns of treatment vary as Chemotherapy application is equal (76.6% in trained vs 75.2% in validation) but the surgical intervention is less common (10.6% in trained vs 6.1% in validation). The cohorts mostly comprise of data from rural areas. The validation group comprises more Non-BPL patients (54.6%) than the trained cohort, which has 49.3%. The generalizing capacity of the model is supported by the fact that lifestyle elements, including alcohol and tobacco usage, show no considerable difference (36% in validation vs. 34.6% in trained). Survival model particularly in

Table 1. Comparison of Clinical and Demographic Characteristics Between AIIMS Bhubaneswar and Hi-Tech Medical College & Hospital Cohorts (2018–2022)

Variable		Aiims,Bhubaneswar	Hi-Tech Medical College & Hospital
Age	Young Adult(19-39)	144 (10.6%)	28 (7.2%)
	Middle Age (40-59)	585 (43.3%)	204 (52.5%)
	Old Adult (60-79)	603 (44.6%)	144 (37.1%)
	Elderly (80>)	18 (1.3%)	12 (3%)
Sex	Female	513 (38%)	136 (35%)
	Male	837 (62%)	252 (64.9%)
Coomorbidity	Condition	234 (17.3)	72(18.5%)
	NA	1116 (82.6)	312 (80.4%)
Settlement	Urban	297 (22%)	104 (26.8%)
	Rural	1053 (78%)	284 (73.1%)
Socioeconomic Status	Bpl	684 (50.6%)	176 (45.3%)
	Non-BPL	666 (49.3%)	212 (54.6%)
Habbit	Usage	468 (34.6%)	140 (36%)
	NA	882 (65.3%)	248 (63.9%)
Stage	I	27 (2%)	4 (1%)
	II	189 (14%)	72 (18.5%)
	III	468 (34.6%)	132 (34%)
	IV	666 (49.3%)	180 (46.3%)
Differentiation	Well	63 (4.6%)	12 (3%)
	Moderate	459 (34%)	160 (41.2%)
	Poor	828 (61.3)	216 (55.6%)
LVI	Positive	144 (10.6%)	32 (8.2%)
	Negative	1206 (89.3%)	356 (91.7%)
PNI	Positive	153 (11.3%)	40 (10.3%)
	Negative	1197 (88.6%)	348 (89.6%)
Surgery	Yes	144 (10.6%)	24 (6.1%)
	No	1206 (89.3%)	364 (93.8%)
Chemotherapy	Yes	1035 (76.6%)	292 (75.2%)
	No	315 (23.3%)	96 (24.7%)
Radiation	Yes	18 (1.3%)	4 (1%)
	No	1332 (98.6%)	384 (98.9%)
HER 2	Positve	144 (10.6%)	24 (6.1%)
	Negative	1206 (89.3%)	364 (93.8%)
MSI	Positve	63 (4.6%)	20 (5.1%)
	Negative	1287 (95.3%)	368 (94.8%)
Survival Time	365 Days	216 (16%)	68 (17.5%)
	365-730 Days	360 (26.6%)	48 (12.3%)
	730-1095 Days	144 (10.6%)	60 (15.4%)
	1095-1460 Days	558 (41.3%)	192 (49.4%)
	> 1460 Days	72 (5.3%)	20 (5.1%)
Event	Dead	549 (40.6%)	72 (18.5%)
	Alive	801(59.3%)	316 (81.4%)

cancer prediction.

In Conclusion, our study has constructed and validated a deep learning model for predicting survival in stomach cancer patients. Strong prediction performance of the model makes it therapeutically relevant. Combining SHAP with LIME improves model interpretability thereby providing the evidence to trust AI- driven model Settlement, treatment modalities, and socioeconomic level are among the key survival elements. Even though the model performs well, differences in how well it generalizes across datasets highlight the need for ongoing study, better data balancing strategies, and external

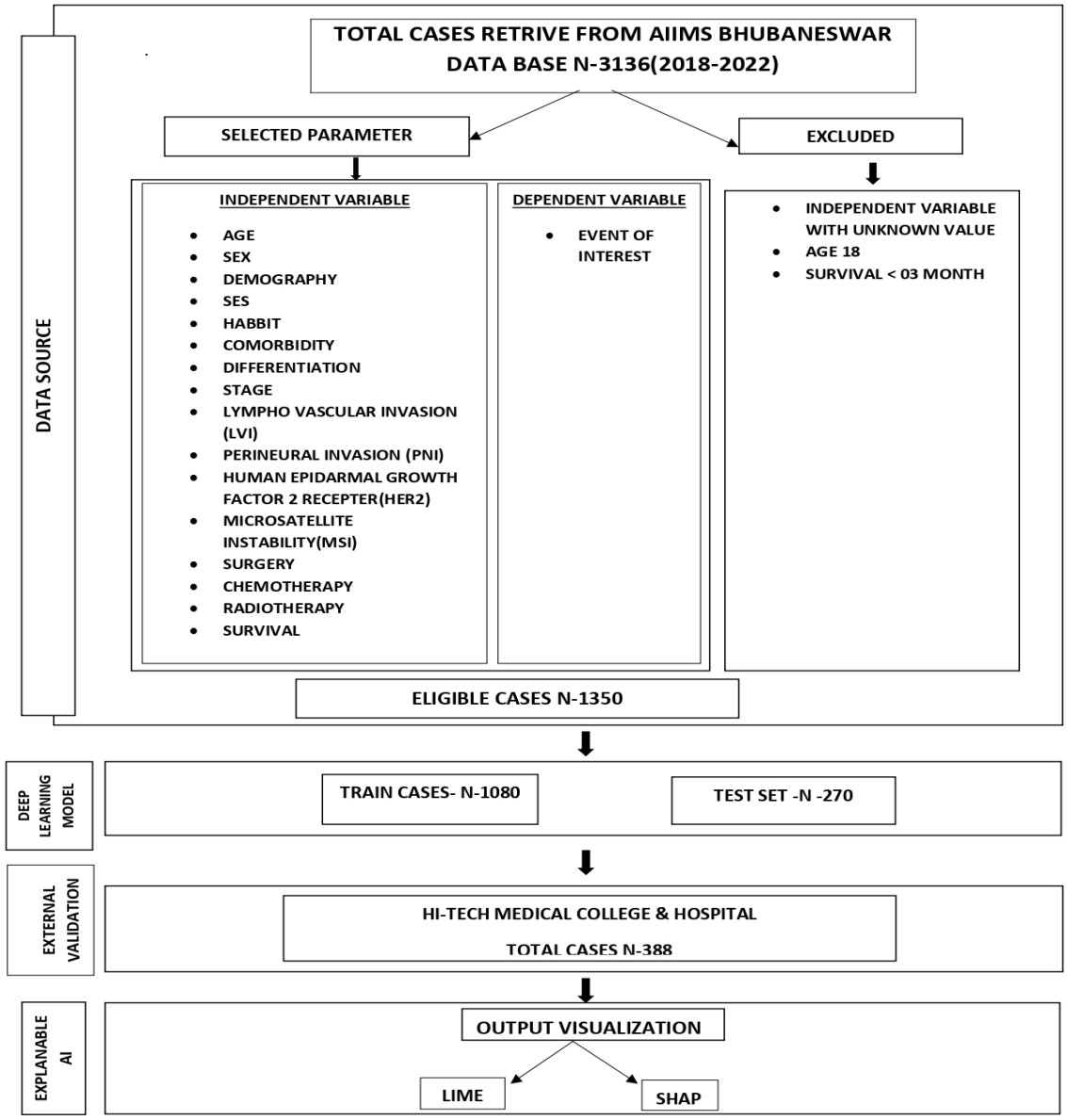

Figure 1. Workflow for Deep Learning-Based Predictive Modeling and Explainable AI Using Clinical Data from AIIMS Bhubaneswar (2018–2022)

contexts with limited resources should provide priority to socioeconomic inequalities. The percentage of patients whose survival span "365–730 days" is greater in the trained dataset (26.6% vs. 12.3% in the validation cohort). The proportion of patients surviving "1095-1460 days" is higher in the validation dataset (49.4% vs. 41.3% in trained). Furthermore, the death's in the trained set (40.6%) and the validation cohort (18.5%) clearly indicates probable variations reflecting possible changes in patient characteristics, cancer development, or medication efficacy. Moving from the trained set to the validation set brings the accuracy from 0.911 to 0.855 (Table 2). However, the model's continual of stable precision 0.941 against 0.945 represent its accuracy in identifying affirmative cases. On the other hand, sensitivity spans 0.905 to 0.873, suggesting that some real positive occurrences could have been missed in the validation sample. The fact that the balanced accuracy is roughly the same (0.838 to 0.965) and the F1 score is really good (0.923 vs. 0.907) imply that the model can handle slightly imbalanced survival outcome. The great discriminative power of the model is confirmed by several experiments. Model high discriminative power is further supported by the concordance index (ranging from 0.923 to 0.936) and the auroc curve score (ranging from 0.93 to 0.94), so implying that the model can strongly be reliable for predicting patient's survival. Though accuracy declines, it stays within an anticipated range (usually 5–10%), therefore confirming the generalizability. Even in an independent validation cohort, the model's robustness and capacity in survival prediction are shown by the continuous strength of important metrics including AUROC and F1-score.

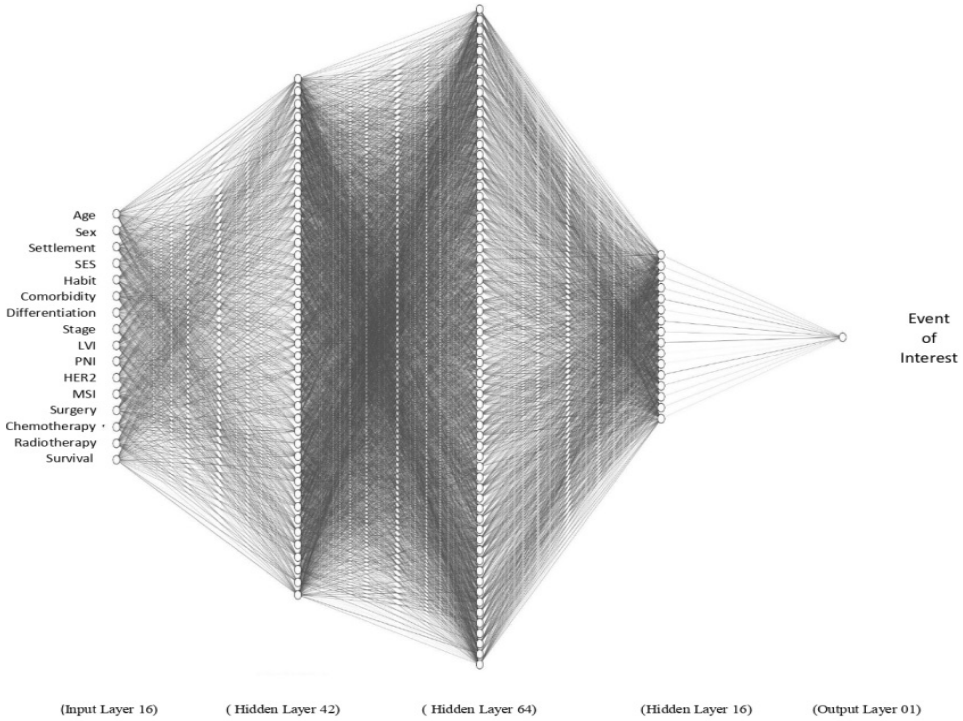

Figure 2. Layered Architecture of Deep Neural Network Model for Clinical Outcome Prediction

Discussion

Deep learning models have regularly surpassed traditional and alternative AI-based survival prediction approaches; yet, their opaque "black-box" character has hindered their extensive clinical use [19-20]. Personalized treatment planning is still difficult without artificial intelligence interpretability as every patient shows different patterns of disease development and therapeutic responses. The open views of model predictions, methods like SHAP and LIME help to overcome this restriction. Studies show that by raising openness and physician confidence in model predictions, these approaches improve the therapeutic value of artificial intelligence [13, 21-23]. Most artificial intelligence studies on stomach cancer prediction have concentrated on contrasting many machine learning models, therefore overlooking interpretability, which is crucial for clinical decision-making. Furthermore, existing publications validated on internal datasets and lack external validation, therefore restricting generalizability and raising questions regarding robustness over different populations [24-25]. AI models remain challenging to apply in normal clinical practice without interpretability and external evaluation. Our deep learning model can augment the TNM staging system by combining SHAP and LIME, therefore giving doctors a strong tool for survival prediction and tailored treatment planning.

Local Interpretable Model-Agnostic Explanations, or LIME, examine input data to evaluate how it influences certain predictions. For example, in one occasion a patient with Stage III cancer, male gender, and a history of treatment had a 95% estimated survival probability (Figure 3). LIME found three most important factors affecting this prediction to be tumor stage, age, and treatment. Through feature significance on both local and global levels, SHAP (Shapley Additive Explanations) improves interpretability. Patients in rural locations who

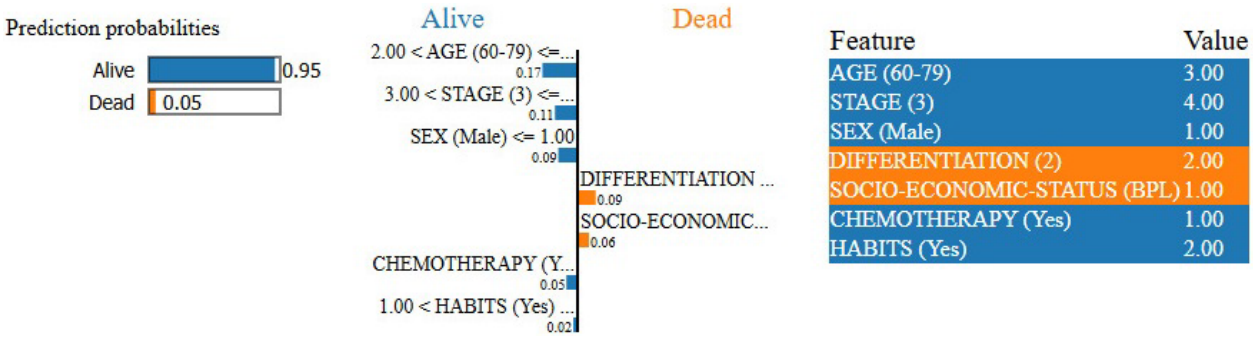

Figure 3. Individual Patient Prediction Interpretation Using LIME: Probability of Survival with Key Contributing Features

Table.2 Performance Metrics of the Deep Learning Model on Internal Training and External Validation Datasets

Performance Matrix	Trained Model	External Validation
Accuracy	0.911	0.855
Sensititivity	0.905	0.873
Specificity	0.918	0.777
Precision	0.941	0.945
Negative Predictive Value	0.871	0.583
False Positive Rate	0.081	0.222
False Discovery Rate	0.058	0.054
False Negative Rate	0.094	0.126
F1 Score	0.923	0.907
Matthews Correlation Co-Efficent	0.818	0.586
Concordance Index	0.923	0.936
Balanced Accuracy	0.838	0.825
Auroc Score	0.93	0.94

completed chemotherapy and had better socioeconomic level showed lower risk scores (0.47, Figure 4), according to SHAP force plots. Whereas, urban individuals without treatment who had poor tumor differentiation had a noticeably greater death risk (0.99, Figure 4). These interpretability methods improve confidence in AI-driven survival predictions and promote tailored treatment regimens by tying computational results with clinical insights. Our model found three most important determinants of survival: socioeconomic level, treatment history, and tumor differentiation. SHAP summary graphs (Figure 5 and 6) also showed that settlement type, urban vs. rural had the maximum influence, therefore underlining the importance of healthcare accessibility in survival results. These results match other studies demonstrating that early cancer detection and thorough treatment plans increase survival rates [26-27]. Early-stage cancers greatly increase survival with surgical intervention; but, in advanced instances, especially with metastases, its advantages become less common. Early screening and new treatments are more easily available to patients from higher socioeconomic backgrounds or well-resourced

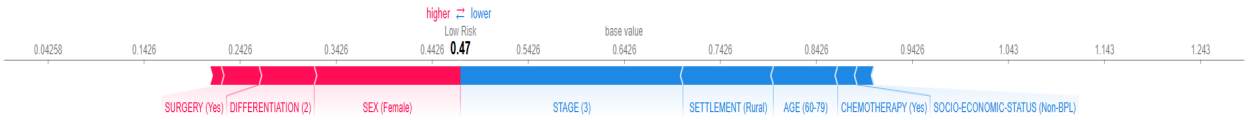

Figure 4 (a). SHAP Force Plot Showing Feature Contributions to Low Predicted Risk in a Single Patient

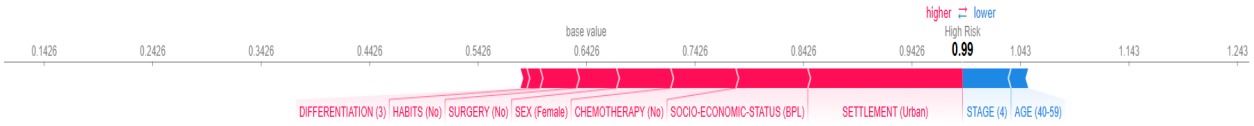

Figure 4 (b). SHAP Force Plot Showing Feature Contributions to High Predicted Risk in a Single Patient

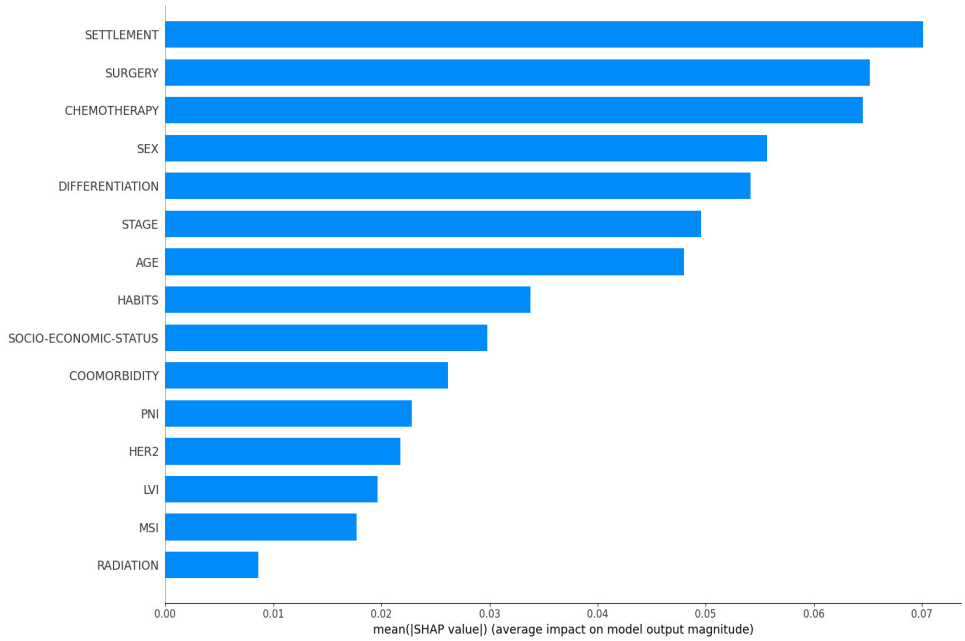

Figure 5. Feature Importance Ranked by Mean SHAP Values in Predictive Clinical Model

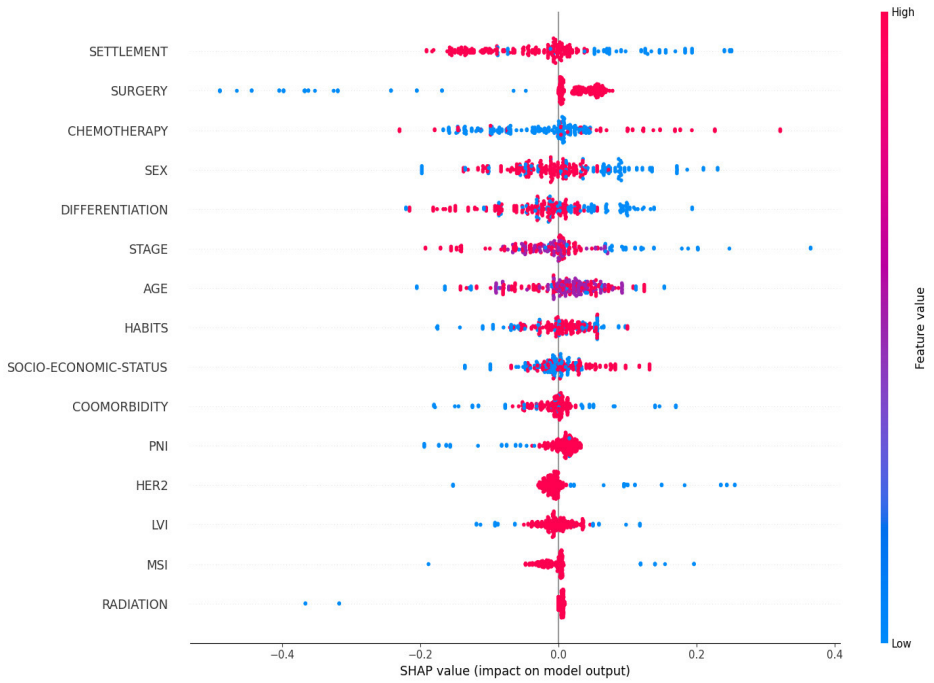

Figure 6. SHAP Summary Plot: Feature Contributions to Predicting Patient Outcome in Clinical Model

healthcare environments, therefore improving their prognosis (2024). Consistent improvement in survival across all cancer stages by chemotherapy helps to lower tumor load and enhance surgical treatment [28-30]. These realizations support the need of customized treatment planning grounded on patient-specific criteria. Using AI-driven interpretability tools can help doctors alter chemotherapy regimens, change course of treatment, and scheduling surgical intervention to improve patient outcomes. Hospitals can approach precision oncology by combining artificial intelligence survival prediction with AJCC staging, therefore assuring that treatment strategies are customized not just to cancer stage but also to individual patient features, socioeconomic level, and treatment response. This hybrid strategy maximizes healthcare resource allocation, improves survival outcomes, and sharpens clinical decision-making. Explainable artificial intelligence techniques should be included into multidisciplinary team meetings (MDTs) involving surgeons, radiologists, and oncologists for actual adoption. By means of integrated dashboards, AI-powered visualizations including SHAP force charts can help in real-time patient monitoring, therefore enabling doctors to dynamically change treatment strategies. Improve risk assessment so that doctors may give high-risk patients top priority for extensive follow-ups. Such artificial intelligence-driven decision-support systems might lower mortality connected to cancer and enhance quality of life. The results show that we need public health strategies that are specific to the differences in cancer outcomes depending on where people live and how much money they have. It is important to have personalized healthcare treatments, better cancer screening infrastructure in rural areas, and fair access to chemotherapy and surgery. To close the gap in health between urban and rural areas, policymakers should use these findings in their national cancer control plans. Making sure that everyone has access to early diagnosis and high-quality treatment may greatly increase survival rates for people of all ages and backgrounds.

Although this research showed some encouraging results, it does have certain drawbacks. The dataset only includes variables from two hospitals, which might lead to selection bias and make the model less applicable to other types of patients. The model performance gets impacted by the difference of treatment regimens in between the two institutions, so there is a need of uniform clinical data integration. Further validation is needed in real-world clinical contexts to generalize the model in other patients and even the interpretability approaches can be further examined for decision-making. The expansion of the dataset to include multi-institutional and geographically varied populations can be the focus of future research to increase the robustness of the model. Although the model is quite good in predicting the survival outcome, the predictions and tailored treatment suggestions can be made more precise if there is an inclusion of genetic and molecular data into the model. Further research is needed in Learning methods which are necessary in to overcome data privacy and allow distributed artificial intelligence. Using digital twin technology, which creates virtual models that mimic how each patient reacts, is a potential area for future research. This might improve treatment planning by allowing for dynamic, individualized simulations, which would make the model more useful in treating stomach cancer. The longitudinal studies can be used to evaluate the effect of AI-driven predictions on decision making and patient survival outcome. Resolving these limitations in the future will help to clarify the effect of deep learning on precision oncology and stomach

validation across a range of demographics. model robustness, future developments should revolve around federated learning. The results show promise and will pave the path for more open and customized clinical decision-making for the treatment of stomach cancer by means of AI-driven precision oncology tools. Our work paves the road for the use of interpretable artificial intelligence in tailored cancer treatment with an aim of enhancing patient outcomes and more informed clinical decision-making for stomach cancer treatment.

Author Contribution Statement

All authors contributed equally in this study.

Acknowledgements

General

We acknowledge the contributions of the cancer Registry team at AIIMS, Bhubaneswar and Hi-Tech Medical Collage and Hospital for the valuable data.

Approval

It was approved by Institutional scientific body

Ethical Declaration

The Institutional ethics committee have provided consent for this study

References

1. Miller KD, Fidler-Benaoudia M, Keegan TH, Hipp HS, DVM AJ, Siegel RL. Cancer statistics for adolescents and young adults, 2020. CA Cancer J Clin. 2020;70:443–59. https://doi.org/10.3322/caac.21637
2. He X, Wu W, Lin Z, Ding Y, Si J, Sun LM. Validation of the American Joint Committee on Cancer (AJCC) stage system for gastric cancer patients: a population-based analysis. Gastric cancer. 2018;21:391-400. https://doi.org/10.1007/s10120-017-0740-7
3. Hao D, Li Q, Feng QX, Qi L, Liu XS, Arefan D, et al. Survivalcnn: A deep learning-based method for gastric cancer survival prediction using radiological imaging data and clinicopathological variables. Artif Intell Med. 2022;134:102424. https://doi.org/10.1016/j.artmed.2022.102424.
4. Sherazi SWA, Zheng H, Lee JY. A machine learning-based applied prediction model for identification of acute coronary syndrome outcomes and mortality in patients during the hospital stay. Sensors (Basel). 2023;23:1351. https://doi.org/10.3390/s23031351
5. Vollmer S, Mateen BA, Bohner G, Király FJ, Ghani R, Jonsson P, et al. Machine learning and artificial intelligence research for patient benefit: 20 critical questions on transparency, replicability, ethics, and effectiveness. Bmj. 2020;368:l6927. https://doi.org/10.1136/bmj.l6927.
6. Naqvi RA, Hussain D, Loh WK. Artificial intelligence-based semantic segmentation of ocular regions for biometrics and healthcare applications. Comput Mater Contin. 2020;66:715–32. https://doi.org/10.32604/cmc.2020.013249
7. Jiménez Fonseca P, Carmona-Bayonas A, Hernández R, Custodio A, Cano JM, Lacalle A, et al. Lauren subtypes of advanced gastric cancer influence survival and response to chemotherapy: real-world data from the AGAMENON National Cancer Registry. Br j cancer. 2017;117(6):775-82. https://doi.org/10.1038/bjc.2017.34
8. Sun D, Wang M, Li A. A multimodal deep neural network for human breast cancer prognosis prediction by integrating multi-dimensional data. IEEE Trans Comput Biol Bioinform. 2018;15:149–57. https://doi.org/10.1109/TCBB.2018.2806438
9. Lee C, Light A, Alaa A, Thurtle D, van der Schaar M, Gnanapragasam VJ. Application of a novel machine learning framework for predicting non-metastatic prostate cancer-specific mortality in men using the surveillance, epidemiology, and end results (seer) database. Lancet Digit Health. 2021;3(3):e158-e65. https://doi.org/10.1016/s2589-7500(20)30314-9.
10. Han JH, Lee S, Lee B, Baek OK, Washington III SL, Herlemann A, Lonergan PE, et al. Explainable ML models for a deeper insight on treatment decision for localized prostate cancer. Sci Rep. 2023;13(1):11532. https://doi.org/10.1038/s41598-023-38097-7
11. Brieu N, Gavriel CG, Nearchou IP, Harrison DJ, Schmidt G, Caie PD. Automated tumour budding quantification by machine learning augments TNM staging in muscle-invasive bladder cancer prognosis. Sci Rep. 2019;9:5174. https://doi.org/10.1038/s41598-019-41392-1
12. Ribeiro MT, Singh S, Guestrin C. Why should I trust you?: Explaining the predictions of any classifier. In: Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining. 2016;1135–44. https://doi.org/10.1145/2939672.2939778
13. Lundberg SM, Lee SI. A unified approach to interpreting model predictions. Adv Neural Inf Process Syst. 2017;30:4765–74. Available from: https://proceedings.neurips.cc/paper_files/paper/2017/hash/8a20a8621978632d76c43dfd28b67767-Abstract.html
14. Issa NT, Stathias V, Schürer S, Dakshanamurthy S. Machine and deep learning approaches for cancer drug repurposing. Semin Cancer Biol. 2021;68:132-42. https://doi.org/10.1016/j.semcancer.2019.12.011.
15. Chiu YC, Zheng S, Wang LJ, Iskra BS, Rao MK, Houghton PJ, et al. Predicting and characterizing a cancer dependency map of tumors with deep learning. Sci Adv. 2021;7(34). https://doi.org/10.1126/sciadv.abh1275
16. Daneshjou R, He B, Ouyang D, Zou JY. How to evaluate deep learning for cancer diagnostics - factors and recommendations. Biochim Biophys Acta Rev Cancer. 2021;1875(2):188515. https://doi.org/10.1016/j.bbcan.2021.188515
17. Kuntz S, Krieghoff-Henning E, Kather JN, Jutzi T, Höhn J, Kiehl L, et al. Gastrointestinal cancer classification and prognostication from histology using deep learning: Systematic review. Eur J Cancer. 2021;155:200-15. https://doi.org/10.1016/j.ejca.2021.07.012
18. Avanzo M, Wei L, Stancanello J, Vallières M, Rao A, Morin O, et al. Machine and deep learning methods for radiomics. Med Phys. 2020;47(5):e185-e202. https://doi.org/10.1002/mp.13678.
19. Nasejje JB, Mbuvha R, Mwambi H. Use of a deep learning and random forest approach to track changes in the predictive nature of socioeconomic drivers of under-5 mortality rates in sub-saharan africa. BMJ Open. 2022;12(2):e049786. https://doi.org/10.1136/bmjopen-2021-049786
20. Kar İ, Kocaman G, İbrahimov F, Enön S, Coşgun E, Elhan AH. Comparison of deep learning-based recurrence-free survival with random survival forest and cox proportional hazard models in stage-i nsclc patients. Cancer Med. 2023;12(18):19272-8. https://doi.org/10.1002/cam4.6479
21. Tjoa E, Guan C. A survey on explainable artificial intelligence

(xai): Toward medical xai. IEEE Trans Neural Netw Learn Syst. 2021;32(11):4793-813. https://doi.org/10.1109/tnnls.2020.3027314
22. Holzinger A, Langs G, Denk M, Zatloukal K, Müller H. Causability and explainability of artificial intelligence in medicine. WIREs Data Min Knowl Discov. 2019;9(4):e1312. https://doi.org/10.1002/widm.1312
23. Ahmad M, et al. Interpretable AI in healthcare: Enhancing trust and transparency. Artif Intell Med. 2022.
24. Zeng J, Li K, Cao F, Zheng Y. Development and validation of survival prediction model for gastric adenocarcinoma patients using deep learning: A seer-based study. Front Oncol. 2023;13:1131859. https://doi.org/10.3389/fonc.2023.1131859
25. Wang L, Ge J, Feng L, Wang Z, Wang W, Han H, et al. Establishment and validation of a prognostic nomogram for postoperative patients with gastric cardia adenocarcinoma: A study based on the surveillance, epidemiology, and end results database and a chinese cohort. Cancer Med. 2023;12(12):13111-22. https://doi.org/10.1002/cam4.5994
26. Fitzgerald RC, et al. Gastric cancer survival disparities: The role of socio-economic factors and treatment access. Lancet Oncol. 2021;22(3):198–210.
27. Torre LA, et al. Geographical disparities in gastric cancer survival rates: A global perspective. Gastroenterology. 2022;162(5):1305–21.
28. Ajani JA, et al. Gastric adenocarcinoma: ESMO Clinical Practice Guidelines for diagnosis, treatment, and follow-up. Ann Oncol. 2021;32(6):752–69.
29. Siegel RL, Miller KD, Fuchs HE, Jemal A. Cancer statistics, 2022. CA Cancer J Clin. 2022;72(1):7-33. https://doi.org/10.3322/caac.21708.
30. Katai H, et al. Surgical treatment of advanced gastric cancer: Current status and future directions. J Clin Oncol. 2019;37(8):626–36.