

## Highlights of Proposed Model

To develop a framework that

- Detction and Staging of Hepatocellular Carcinoma
- Stain Colour Agnostic.
- Segmentation of nuclei masks
- Extraction of relevant features from segmented nuclei masks..

### Challenges in effectively staging HCC:

- No Explainability in the current methods for staging
- Stain colour variability .

## Proposed Framework

- System employs ADASYN for class imbalance, generating synthetic samples.
- Stain Colour Normalization ensures consistent stain representation.
- U-Nets generate precise image masks for disease severity assessment.
- Cell Profiler extracts metrics like area, perimeter etc. for each nuclei.
- Aggregate features are computed from the above metrics for each image.
- These features are fed into various machine learning models to perform staging.

## Performance metrics of Deep Learning Models

Model	Test Accuracy (%)
ResNet	52.29
AlexNet	20.59

Table 1. Test accuracies of ResNet and AlexNet models

## Functional Modules and Dataset Description

- Data Preprocessing
    - Data Augmentation via ADASYN
    - Stain Color Normalization
  - Nuclei Segmentation using U-Nets
  - Generation of metrics using Cell Profiler
  - Identification of aggregate features
  - Staging
- The dataset comprises a total of 673 histopathologic images obtained from a private hospital.
  - Among these images, 261 are labeled as "Non Cancerous," indicating the absence of HCC cells.
  - There are 57 images labeled as stage 1, 88 as stage 2, 80 as stage 3, and 187 as stage 4.
  - For the purpose of analysis, stage 1 and Non Cancerous samples were combined into a single category to enhance the robustness of the model.
  - Data augmentation was performed using ADASYN to address the class imbalance issue.

## Functional pipeline of Proposed Framework

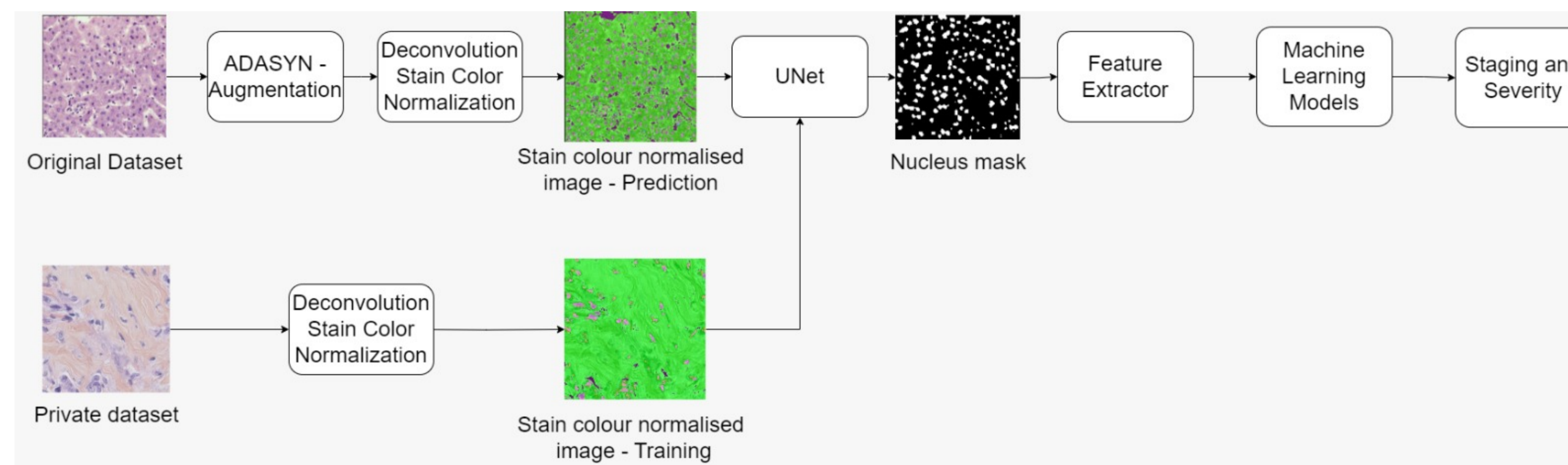


Figure 1. Proposed Framework

## Performance Analysis

The following bar chart shows a comparative study between feeding images directly to Neural Networks and our proposed model involving relevant extracted features

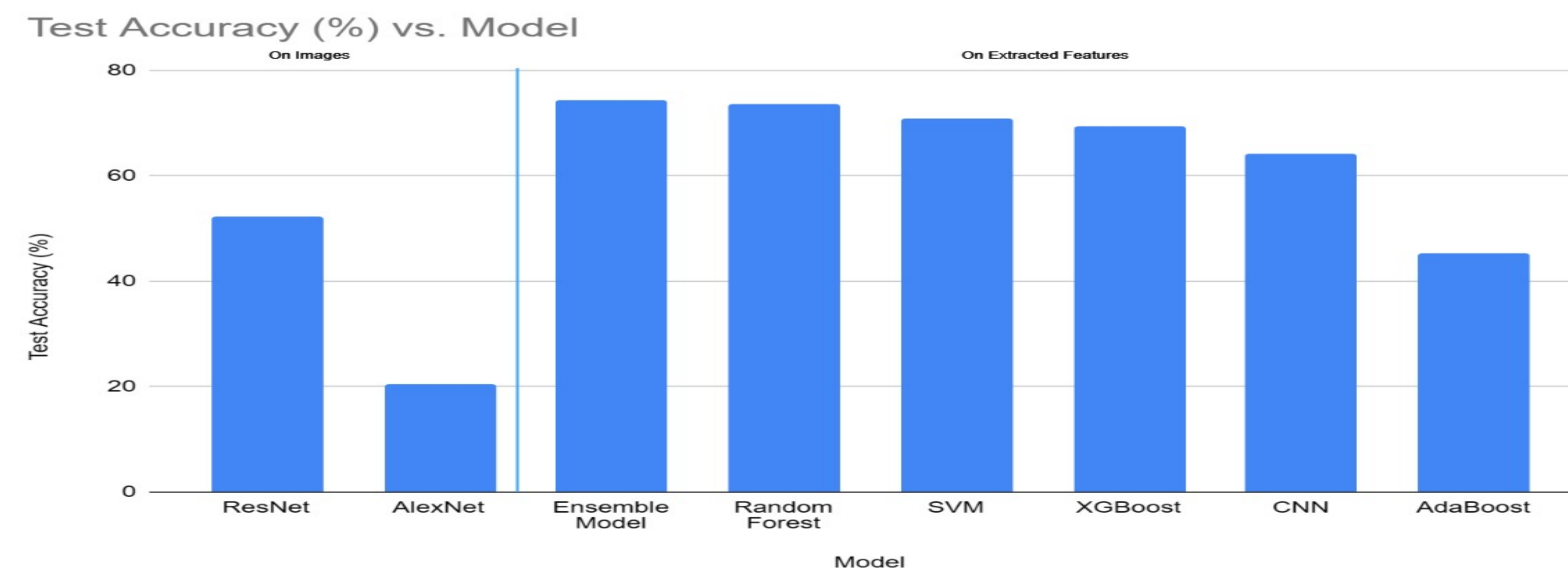


Figure 2. Comparative results between Deep learning and Machine learning models

## Performance of Machine Learning Models

Model	Test Accuracy (%)	Precision	Recall	F1-score
Ensemble model	74.45	0.696	0.745	0.709
Random Forest	73.72	0.691	0.737	0.704
Support Vector Machine (SVM)	70.80	0.689	0.708	0.671
XGBoost	69.34	0.699	0.693	0.683
Convolutional Neural Network (CNN)	66.42	0.621	0.664	0.634
AdaBoost	45.26	0.439	0.409	0.402

Figure 3. Test metrics of individual machine learning models

## Impact of Moments on the Performance

Model	Test Accuracy (%)
Convolutional Neural Network (CNN)	71.53
Support Vector Machine (SVM)	68.61
Ensemble Model	68.61
XGBoost	67.88
Random Forest	65.69
AdaBoost	45.26

Figure 4. Test accuracies after including average of new features

## Inferences

- Deep learning models failed to match the accuracy of the machine learning models which used the features computed from the the given pipeline.
- A comparative Study was conducted to gather the importance of certain features extracted such as moments of a given image
- Inclusion of the moments decreased the performance of the models significantly

## References

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- Konstantina Kourou et al. "Applied machine learning in cancer research: A systematic review for patient diagnosis, classification and prognosis". In: *Computational and Structural Biotechnology Journal* 19 (2021), pp. 5546–5555. ISSN: 2001-0370
- Miriam Seoane Santos et al. "A new cluster-based oversampling method for improving survival prediction of hepatocellular carcinoma patients". In: *Journal of biomedical informatics* 58 (2015), pp. 49–59