

INTRODUCTION

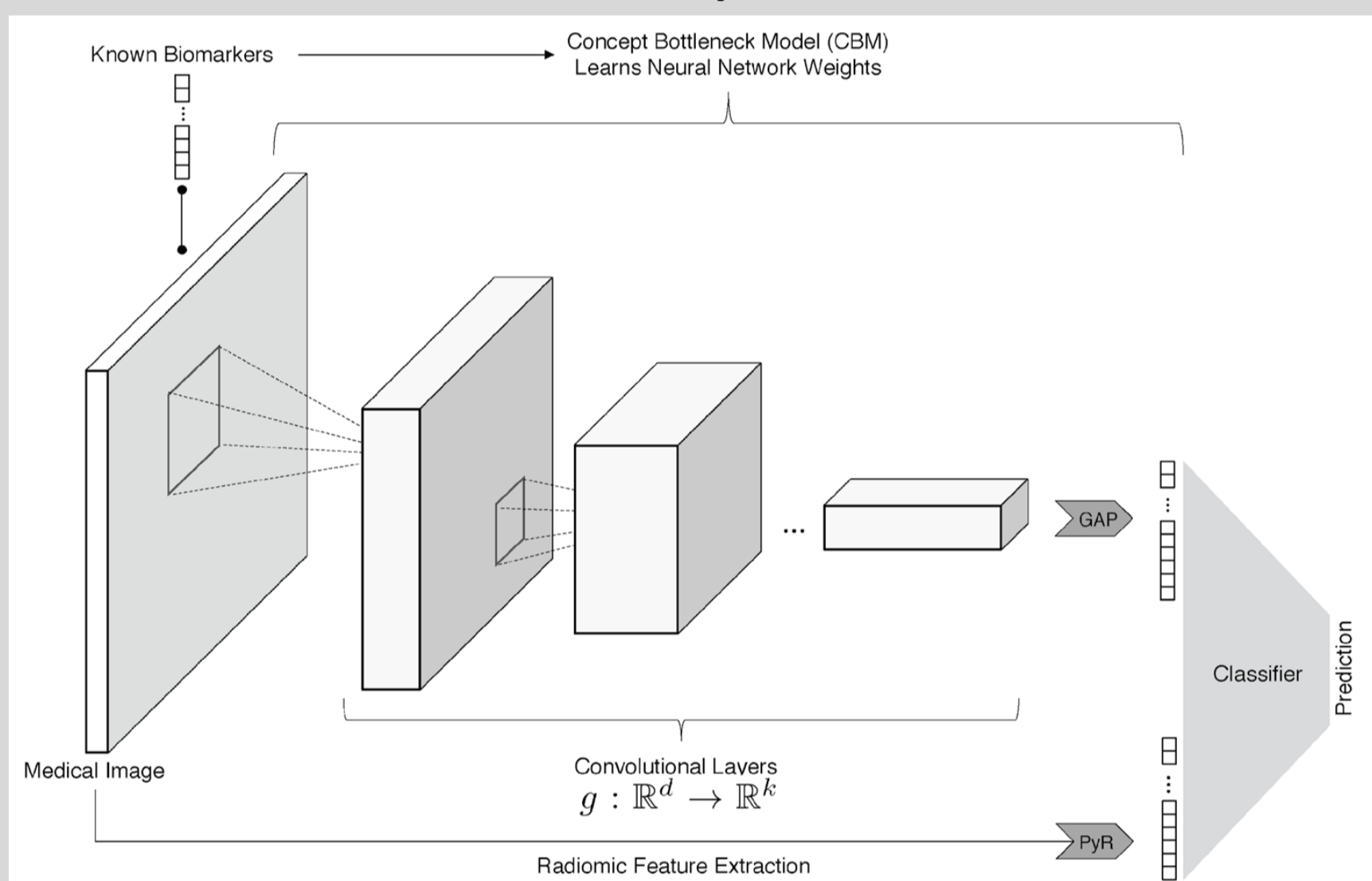
The **lack of interpretability** of DNN-based models prevents their utilization in healthcare, despite the exhibited huge success of Deep Neural Networks (DNNs) in Computer Vision and Bioinformatics.

- ❖ We built a **web application to visualize the developed explainable DNN model**, to contribute to the acceptance and implementation of DNN-based AI models in the field of medical imaging and oncology in clinical practice.
- ❖ **Clinicians can interact** with the developed model altering its meaningful features to understand and evaluate the underlying prediction mechanism, and eventually trust it.

METHODOLOGY

The proposed app integrates the interpretable Machine Learning model trained on segmented lung CT scans from LIDC-IDRI dataset [1].

- **Training dataset:** 1018 thoracic CT scans along with segmentations, likelihood of malignancy and annotated biomarkers for nodules with diameter > 3 mm obtained by up to 4 radiologists.
- **Model:** a radial SVM classifier to predict the tumor status (benign vs. malignant) using selected radiomic features and 8 DNN-predicted biomarkers [2].



Biomarkers:
subtlety, calcification, lobulation, diameter, spiculation, margin, sphericity, texture

Predicted biomarkers are obtained using a CBM, as a ResNet-50 model pre-trained on ImageNet and further fine-tuned. Class activation map (CAM) provides visualization of input features used to predict biomarkers [3].

Once this DNN model has been trained, the only required input is tumor image

Radiomics are extracted using the PyRadiomics package and are validated to be robust and reliable.

- **Web app:** Streamlit web app framework was used. It allows to rapidly deploy ML models by providing high-level functions to create the GUI and webserver.

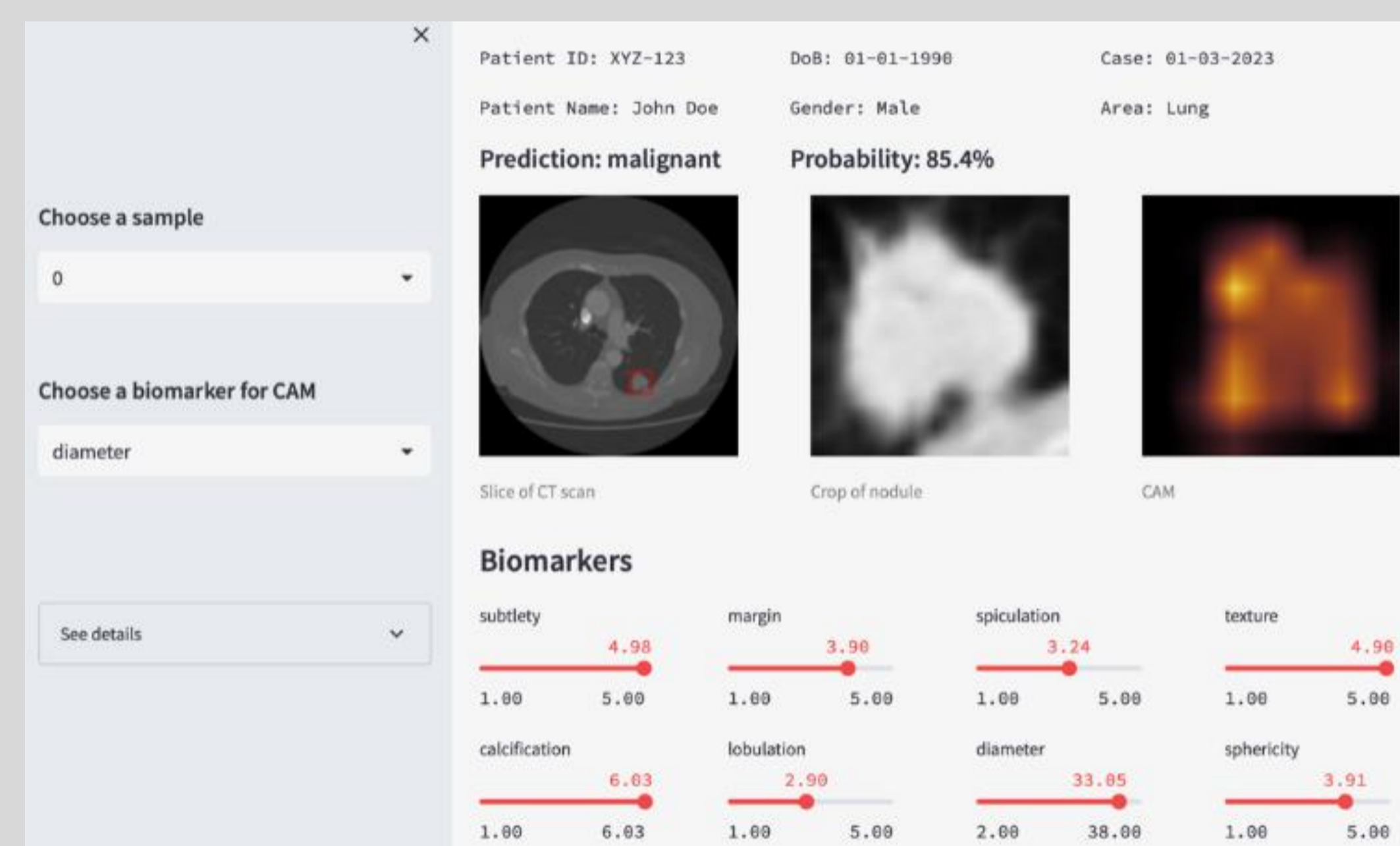
RESULTS

• AI model

The developed classifier exhibits high performance, with accuracy of 0.895 and area under the curve (AUC) of 0.961. (evaluated with 5-fold cross-validation).

• Web app

The user chooses a sample nodule, which is fed to the CBM for biomarker and subsequent malignancy prediction.



User can interact with the predicted biomarkers, (altering their values) and observe the updated prediction in real-time.

For example, if the user upon inspection finds that the diameter has been predicted incorrectly, the diameter can be set to the corrected value, which is then fed to the classifier model to update the malignancy prediction.

Additionally, the user chooses a biomarker for visualization via CAM [3], which highlights the region of the image that was most important for the biomarker prediction.

CONCLUSIONS

- ✓ The proposed interactive XAI methodology can be generalized and implemented for other oncological applications, applied on relevant imaging dataset and characteristics, and is expected to exhibit similarly high model performance and interpretability.
- ✓ With the proposed human-in-the-loop approach, the user does not have to blindly trust the model's predictions but rather the user is an active participant in the decision-making process, aided by the underlying ML model and trust it.
- ✓ In this framework our study is anticipated to facilitate the acceptability of DNN decision-aid models in medical imaging and oncology, on optimizing patient management and clinical treatment strategies.

Next Steps

- In future version the user will be able to upload their own data for classification and inspection.
- Users' feedback on model evaluation can be used to further improve both the algorithm and the GUI.
- The proposed methodology will be additionally applied on head and neck PET/CT data from HECKTOR dataset, to be generalized in more cancer cases.

Acknowledgements

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References

- [1] S.G. Armato 3rd *et al.* Med. Phys. 2011
- [2] L. Brocki, N.C. Chung, Cancers 15, 2023
- [3] B. Zhou *et al.* Proceedings of the IEEE Conf. on Computer Vision and Pattern Recognition. 2016