IAES International Journal of Artificial Intelligence (IJ-AI)
Vol. 14, No. 6, December 2025, pp. 4494~4501
ISSN: 2252-8938, DOI: 10.11591/ijai.v14.i6.pp4494-4501

Explainable artificial intelligence with anchors method for breast cancer treatment recommendation

Reena Lokare[1], Mansing Rathod[1], Jyoti Sunil More[2]
[1]Department of Information Technology, Faculty of Information Technology, K. J. Somaiya Institute of Technology, Mumbai, India
[2]Department of Computer Engineering, Faculty of Computer Engineering, Fr. C. Rodrigues Institute of Technology, Mumbai, India

Article Info

Article history:

Received Jun 16, 2024
Revised Sep 8, 2025
Accepted Oct 16, 2025

Keywords:

Anchors explanation method
Explainable artificial intelligence
Interpretability
Precision medicine
Transparency

ABSTRACT

In the search of precision medicine for breast cancer, the integration of artificial intelligence (AI) offers unprecedented opportunities to improve diagnosis, prognosis, and treatment strategies. This paper discovers the prospective of explainable artificial intelligence (XAI) to demystify the black-box landscape of AI, fostering both transparency and trust. We introduce an XAI-based approach, anchored by the anchors explanation method, to provide interpretable predictions for breast cancer treatment. Our results demonstrate that while anchors improve the interpretability of model predictions, the precision and coverage of these explanations vary, highlighting the challenges of achieving high-fidelity explanations in complex clinical scenarios. Our findings underscore the importance of balancing the trade-off between model complexity and explainability. They advocate for the iterative development of AI systems with iterative feedback loops from clinicians to align the model's logic with clinical reasoning. We propose a framework for the clinical deployment of XAI in breast cancer. Ultimately, XAI, equipped with techniques like Anchors, holds the promise of enhancing precision medicine by making AI-assisted decisions more transparent and trustworthy, empowering clinicians and enabling patients to engage in informed discussions about their treatment options. However, anchors lag in the accuracy of rules and remains a challenge to the AI developers.

Corresponding Author:

Reena Lokare
Department of Information Technology, Faculty of Information Technology
K. J. Somaiya Institute of Information Technology
Mumbai, Maharashtra, India
Email: reena.l@somaiya.edu

1. INTRODUCTION

Precision medicine for breast cancer studies various approaches to find and recommend suitable treatment to the individual patient based on clinical and genomic observations of breast cancer tumor samples [1]. This includes using advanced technologies such as genomic profiling, pharmacogenomics, biomarker discovery, and artificial intelligence (AI) to understand the underlying biology of the disease to an individual patient and recommend suitable medicine termed as precision medicine accordingly. While these innovations are showing great promise and flexibility, there is an increasing need for ensuring transparency and trust in the decision-making process in order to increase acceptance and adoption of precision medicine approaches. This study mainly focuses on the use of explainable artificial intelligence (XAI) techniques, such as the anchors method. Explainable AI, or XAI, aims to make the model internals and prediction done by AI models more interpretable and understandable to humans. The anchors method identifies the most important

features or "anchors" that contribute to an AI model's prediction, providing clinicians and patients with clear and useful explanations for the model's decisions. This allows for greater transparency and trust in the application of AI-powered precision medicine tools for breast cancer [2], [3]. By leveraging XAI techniques like anchors, healthcare providers and patients can better comprehend the rationale behind AI-driven predictions and treatment recommendations, facilitating more informed and collaborative decision-making approach [4]–[6].

The use of XAI methods in precision medicine for breast cancer can have several key benefits:

- Improved transparency: XAI techniques like anchors provide clear and interpretable explanations for AI-based predictions and recommendations, allowing clinicians and patients to understand the reason behind the model's outputs.
- Enhanced trust and acceptance: transparent explanations build greater trust in AI-powered precision medicine tools, increasing the likelihood of their adoption and integration into clinical practice [7].
- Precision and personalization: by identifying the key factors driving AI predictions, anchors can help tailor treatment strategies to the characteristics of an individual and needs of each breast cancer patient.
- Validation and verification: XAI methods enable the validation and verification of AI models, ensuring their reliability and alignment with medical expertise and best practices.

Overall, the integration of XAI techniques, such as the anchors method, into precision medicine frameworks for breast cancer can play a vital role in attractive transparency, trust, and the personalization of care, ultimately improving patient outcomes and the overall acceptance of these transformative technologies in clinical practice [8]. Breast cancer disease is a complex and varied disease, with various factors contributing to its progression, evolution, and response to treatment. Healthcare providers must have a deeper understanding of the underlying biological and clinical characteristics of each patient's tumor in order to provide personalized and precise care. AI-powered predictive models have shown great potential in this domain, leveraging large datasets and advanced algorithms to uncover hidden patterns and make accurate predictions about prognosis, disease risk and treatment response. However, for these models to be widely adopted in clinical practice, it is essential to ensure their transparency and interpretability. This is where XAI techniques, such as the anchors method, come into picture [9].

The anchors method identifies the most important features or "anchors" that contribute to an AI model's predictions. Thus, providing clear and actionable explanations for its decision-making process [10]. Clinicians and patients can gain insights into the key factors driving the model's outputs by applying anchors to breast cancer prediction models, such as specific molecular or genomic biomarkers those are most predictive of disease risk, treatment response, or prognosis. Also, clinical and demographic characteristics (e.g., age, tumor stage, and comorbidities) that meaningfully influence the model's predictions. Interactions between various factors that collectively contribute to the decision-making of AI model. This level of interpretability and transparency is crucial for building trust in AI-powered precision medicine tools, as it allows healthcare providers and patients to better understand the justification behind the model's commendations and make more informed decisions about treatment options [11].

A complex approach is required that addresses both technical and organizational challenges for the successful integration of XAI techniques, like the anchors method, into precision medicine for breast cancer [12]. First, from a technical perspective, AI model developers must work closely with domain experts, like pathologists and oncologists, to ensure that the explanations provided by the anchors method are clinically meaningful and aligned with medical best practices. This may involve iterative model refinement and feature engineering, and the incorporation of domain-specific knowledge to enhance the interpretability and clinical relevance of the AI-based predictions. Second, healthcare organizations have to decide evaluation criteria and clear instructions for the assessment of XAI systems in a clinical context. These strategies should address the timeliness of the clinical task and the ability of the explanations to truthfully reflect the model's decision-making process the computational resources required to generate explanations [13], [14]. Finally, patients and healthcare providers must be cultured on how to interpret the explanations provided by tools like anchors and the principles of XAI. This will foster greater trust and acceptance of these technologies, ultimately leading to their more extensive adoption in precision medicine for breast cancer [15].

2. RELATED WORK

The ground of precision medicine has seen a significant change with the beginning of machine learning (ML) and AI techniques [16]. In case of breast cancer, these progresses have enabled more adapted and targeted approaches to prognosis, diagnosis, and treatment. However, the complexity of these AI models can often lead to a lack of transparency, making it thought-provoking for clinicians and patients to appreciate and trust the conclusion-making process [17]. Specifically, the application of XAI and anchor-based methods in the context of breast cancer diagnosis and treatment has garnered substantial attention from the research

community. This literature review aims to synthesize the current state of the art in this domain, highlighting the key advancements, challenges, and opportunities for further exploration [18].

XAI has appeared as a fruitful approach in facilitating the transparency and interpretability and of complex ML models, particularly in impact-creating fields such as healthcare. By providing interpretable explanations for AI-based decisions, XAI can bridge the gap between the black-box nature of these models and the need for healthcare professionals and patients to understand the reasoning behind treatment recommendations [19]. The anchors explanation method, in particular, has been leveraged to offer a succinct and intuitive rationale for AI predictions in breast cancer management. Anchors identify the most salient features—such as genetic markers and clinical indicators—that "anchor" a model's predictions, thus offering a clear and concise justification for its outcomes [20].

This approach has been active in enhancing the trustworthiness and transparency of precision medicine policies in breast cancer, as it allows healthcare providers and patients to better understand the decision-making process and make informed choices [21]. Moreover, the integration of XAI and anchors has the potential to rationalize the clinical adoption of AI-powered tools, as healthcare professionals and patients can more readily understand and trust the underlying logic behind the AI's recommendations [22]. As the field of precision medicine continues to grow, the exploration of XAI and anchor-based methods will likely play a crucial role in advancing the development of trustworthy and transparent AI-driven solutions for breast cancer prognosis, diagnosis and treatment [23], [24]. Previous research on XAI in breast cancer quantification underlines the need for interpretable models to improve clinical decision-making and trust. Studies indicate that XAI improves diagnostic accuracy by making AI predictions transparent and understandable for healthcare professionals. In Saudi Arabia, XAI's application is particularly valuable for addressing region-specific demographic and genetic factors. Overall, XAI facilitates personalized treatment plans and supports the adoption of precision medicine in breast cancer management [25].

The effectiveness of combining convolutional neural networks (CNNs) with XAI techniques for the breast cancer diagnosis is discussed in [24]. The research focuses on CNNs and making them more interpretable with the integration of XAI, thus increasing their effectiveness in clinical use. By providing clear and understandable explanations for model predictions, this integration aims to improve clinician trust and accuracy, and also support for more informed decision-making in fields such as mammography. The study highlights various XAI methods to identify the most effective approaches for elucidating CNN decisions, thus highlighting the potential for these advanced AI tools to transform breast cancer detection and treatment.

Kothari *et al.* [25] explores the implementation and development of a web-based application that leverages XAI to predict the value of cancer drugs. The application integrates advanced ML algorithms with XAI techniques to provide transparent and interpretable predictions regarding drug efficacy and value. This transparency is critical for healthcare providers, researchers and patients to understand the rationale behind AI-driven recommendations, ensuring trust and facilitating informed decision-making. Kothari *et al.* [25] work highlights the importance of user-friendly interfaces and the practical application of XAI in real-world healthcare scenarios. Thus, demonstrates how such technologies can improve drug selection processes and personalized treatment strategies in oncology.

Ali *et al.* [26] examines the growing importance of XAI across various medical and healthcare applications. The review associates' findings from numerous studies, highlighting how XAI enhances the interpretability and transparency of AI models, which is essential for gaining the trust of healthcare professionals and patients. The work debates the benefits of XAI in improving treatment planning, diagnostic accuracy and patient outcomes by making AI predictions more understandable. Also, the review identifies key XAI techniques and their applications in different healthcare settings, emphasizing the potential of XAI to bridge the hole between compound AI models and reliable, practical medical practices. Ali *et al.* [26] inclusive analysis underscores the transformative impact of XAI in promoting more effective and responsible AI-driven healthcare solutions.

3. METHOD

To provide a comprehensive overview, this research paper will examine the role of XAI, particularly the anchors method, in improving the transparency, trust, and acceptance of AI-driven precision medicine for breast cancer. Anchors, a technique introduced by Sawangarreerak *et al*. [27], is a model-agnostic method that identifies the most important features contributing to a model's predictions. By highlighting the "anchor" features that are sufficient to explain a prediction, anchors allows users to understand the underlying logic and rationale behind AI-generated recommendations.

In the context of breast cancer, anchors can be leveraged to provide physicians and patients with interpretable insights into AI-powered diagnostic and prognostic models. For example, an anchors analysis might reveal that a model's prediction of a patient's risk of developing breast cancer is primarily driven by factors such as family history, age, and mammographic breast density. This level of transparency can help build trust in the AI system, as clinicians can verify that the model's decision-making aligns with their medical expertise. Patients can be empowered to make more informed decisions about their care, as they can understand the rationale behind the AI's recommendations.

3.1. Dataset used

The dataset used in the study is taken from cBioPortal. The cBioPortal for cancer genomics is an open-access reserve for the communicating exploration of multidimensional cancer genomics datasets. It provides visualization, analysis, and download of large-scale cancer genomics data sets. The description and specifics of a particular dataset used in an existing study would depend on the scope of that study, but generally, cBioPortal datasets can include: i) genomic information like mutations, copy-number alterations, and structural variants from sequencing data; ii) gene expression profiles which measure the movement of thousands of genes at once to create a global image of cellular function; iii) proteomics data which may include levels of proteins and their modifications, if available; iv) clinical data such as patient demographics, treatment histories, survival details, and clinical outcomes; and v) biomarker data indicating the presence or absence of certain biological markers linked to cancer pathology or treatment response.

These datasets are often derived from large cohorts of patients and are used to perform comprehensive analyses that identify genetic alterations that drive cancer progression. They also correlate genomic changes with clinical outcomes, and support the development of targeted cancer therapies. Researchers accessing cBioPortal datasets for studies are expected to carefully consider the source, context, and relevance of the data they extract, as well as any potential limitations, such as sample size or completeness of the clinical annotations [28], [29].

3.2. Machine learning model

In order to find out important features or biomarkers, a random forest classifier is trained with the dataset mentioned in sub-section 3.1. The classifier with 50 estimators is giving an accuracy of 93.26% as shown in Figure 1. This random forest classifier is giving an accuracy of 93.26%.

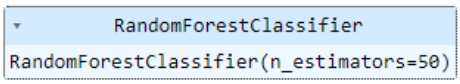
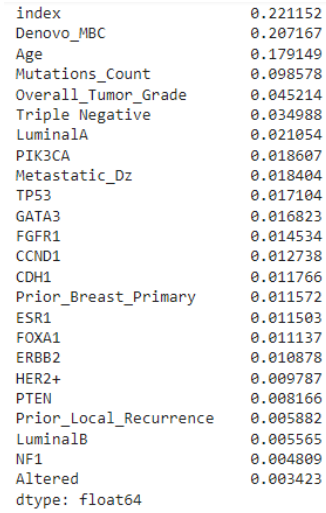


Figure 1. Structure of random forest classifier

3.3. Biomarkers derived from feature importance of machine learning models

ML models trained on cancer genomics datasets can identify important features or biomarkers that contribute to their predictive performance. The cBioPortal for cancer genomics is an open-access resource for the interactive exploration of multidimensional cancer genomics datasets [30], [31]. It provides visualization, analysis, and download of large-scale cancer genomics data sets. The description and specifics of a particular dataset used in an existing study would depend on the scope of that study, but generally, cBioPortal datasets can include: i) genomic information like mutations, copy-number alterations, and structural variants from sequencing data; ii) gene expression profiles which measure the activity of thousands of genes at once to create a global picture of cellular function; iii) proteomics data which may include levels of proteins and their modifications, if available; iv) clinical data such as patient demographics, treatment histories, survival details, and clinical outcomes; and v) biomarker data indicating the presence or absence of certain biological markers linked to cancer pathology or treatment response.

These datasets are often derived from large cohorts of patients and are used to perform comprehensive analyses that identify genetic alterations that drive cancer progression, correlate genomic changes with clinical outcomes, and support the development of targeted cancer therapies. Researchers accessing cBioPortal datasets for studies are expected to carefully consider the source, context, and relevance of the data they extract, as well as any potential limitations, such as sample size or completeness of the data. The dataset used in the study contains 1,198 breast cancer tumor samples. This dataset contains clinical, treatment and genomic details of the patient. Figure 2 shows biomarkers discovered from the feature importance of random forest classifier. The features listed are both clinical and genomic.



index	0.221152
Denovo_MBC	0.207167
Age	0.179149
Mutations_Count	0.098578
Overall_Tumor_Grade	0.045214
Triple Negative	0.034988
LuminalA	0.021054
PIK3CA	0.018607
Metastatic_Dz	0.018404
TP53	0.017104
GATA3	0.016823
FGFR1	0.014534
CCND1	0.012738
CDH1	0.011766
Prior_Breast_Primary	0.011572
ESR1	0.011503
FOXA1	0.011137
ERBB2	0.010878
HER2+	0.009787
PTEN	0.008166
Prior_Local_Recurrence	0.005882
LuminalB	0.005565
NF1	0.004809
Altered	0.003423

dtype: float64

Figure 2. Feature importance of random forest classifier

4. RESULTS AND DISCUSSION

The aim of this research work is to predict and explain suitable therapy for breast cancer patients based on clinical and genomic details. The therapies used in this study are chemotherapy, hormone single therapy, Anti_HER2 therapy and HormoneCDK46i therapy. The results of anchor method for recommendation of suitable therapy based on discovered clinical and genomic biomarkers are discussed.

4.1. Prediction: chemotherapy

Chemotherapy is one of the treatments on breast cancer. In order to predict suitable treatment as chemotherapy, attributes and their values used for the prediction by the anchor method of explainability are explained in the anchor text.

Anchor text: ['GATA3 <=0.00', '42.00 <Age <=50.00', '2.00 <Overall_Tumor_Grade <=3.00', 'HER2+ <=0.00', 'Denovo_MBC <=0.00', 'ESR1 <=0.00', 'FGFR1 <=0.00', 'Altered <=1.00', 'NF1 <=0.00', 'Metastatic_Dz <=1.00', 'FOXA1 <=0.00', 'TP53 <=1.00', 'LuminalA <=1.00', 'LuminalB <=0.00', 'PTEN <=0.00', 'Prior_Breast_Primary <=0.00', 'CCND1 <=0.00', 'Mutations_Count <=4.00', 'PIK3CA <=0.00', 'ERBB2 <=0.00', 'CDH1 <=0.00', 'Prior_Local_Recurrence <=0.00']

Precision: 0.15847665847665848

Coverage: 0.0084

Prediction explanation: anchor method is used to explain the prediction. The important features for predicting chemotherapy:

GATA3 expression level: age between 42 and 50, tumor grade between 2 and 3, HER2 status (positive or negative), and prior occurrence of metastatic disease. The model achieved a precision of 0.1585 with a coverage of 0.0084.

4.2. Prediction: hormone single therapy

Hormone single therapy is one of the treatments on breast cancer. In order to predict suitable treatment as hormone single therapy, attributes and their values used for the prediction by the anchor method of explainability are explained in the anchor text.

Anchor text: ['LuminalA <=0.00', 'Age <=50.00', 'CCND1 <=0.00', 'FOXA1 <=0.00', 'HER2+ <=0.00', 'Denovo_MBC <=0.00', 'Prior_Breast_Primary <=0.00', 'ESR1 <=0.00', 'ERBB2 <=0.00', 'Overall_Tumor_Grade >2.00', 'Mutations_Count <=4.00', 'CDH1 <=0.00', 'LuminalB <=0.00', 'PTEN <=0.00', 'NF1 <=0.00', 'PIK3CA <=1.00', 'Metastatic_Dz <=1.00', 'GATA3 <=0.00', 'TP53 <=1.00']

Precision: 0.11004784688995216

Coverage: 0.0193

Prediction explanation: the model predicts the effectiveness of hormone single therapy for a specific case based on several features such as: LuminalA status, age, CCND1 expression level, FOXA1 status, HER2+ status, De novo MBC occurrence, prior breast primary condition, ESR1 and ERBB2 levels, overall tumor grade, mutations count in the genes CDH1, PTEN NF1, and PIK3CA, and metastatic disease involvement is also taken into account alongside GATA3 and TP53 gene statuses. The model achieved a precision of 0.110 and coverage of 0.019.

4.3. Prediction: Anti_HER2 therapy

Anti_HER2 therapy is one of the treatments on breast cancer. In order to predict suitable treatment as anti_HER2 therapy, attributes and their values used for the prediction by the anchor method of explainability are explained in the anchor text.

Anchor text: ['GATA3 <=0.00', '42.00 <Age <=50.00', '2.00 <Overall_Tumor_Grade <=3.00', 'HER2+ <=0.00', 'Denovo_MBC <=0.00', 'ESR1 <=0.00', 'FGFR1 <=0.00', 'Altered <=1.00', 'NF1 <=0.00', 'Metastatic_Dz <=1.00', 'FOXA1 <=0.00', 'TP53 <=1.00', 'LuminalA <=1.00', 'LuminalB <=0.00', 'PTEN <=0.00', 'Prior_Breast_Primary <=0.00', 'CCND1 <=0.00', 'Mutations_Count <=4.00', 'PIK3CA <=0.00', 'ERBB2 <=0.00', 'CDH1 <=0.00', 'Prior_Local_Recurrence <=0.00']

Precision: 0.15847665847665848

Coverage: 0.0084

Prediction explanation: the prediction for Anti-HER2 therapy is based on the following criteria: GATA3 score, age range between 42 and 50, overall tumor grade between 2 and 3, absence of HER2 amplification, non-de novo metastatic breast cancer status, low ESR1 expression level, lack of FGFR1 alteration, presence of genetic alterations in at least one gene among altered genes list (NF1 exclusion), limited metastatic disease burden (Metastatic_Dz <=1.00), absence of FOXA1 overexpression, TP53 mutation presence but with luminal a subtype predominance. It is with as low PTEN score as well as never experiencing local recurrence before. The model's precision for this prediction is approximately 0.1585 with a coverage rate of about 0.0084.

4.4. Prediction: HormoneCDK46i therapy

HormoneCDK46i therapy is one of the treatments on breast cancer. In order to predict suitable treatment as HormoneCDK46i therapy, attributes and their values used for the prediction by the anchor method of explainability are explained in the anchor text.

Anchor text: ['GATA3 <=0.00', '42.00 <Age <=50.00', '2.00 <Overall_Tumor_Grade <=3.00', 'HER2+ <=0.00', 'Denovo_MBC <=0.00', 'ESR1 <=0.00', 'FGFR1 <=0.00', 'Altered <=1.00', 'NF1 <=0.00', 'Metastatic_Dz <=1.00', 'FOXA1 <=0.00', 'TP53 <=1.00', 'LuminalA <=1.00', 'LuminalB <=0.00', 'PTEN <=0.00', 'Prior_Breast_Primary <=0.00', 'CCND1 <=0.00', 'Mutations_Count <=4.00', 'PIK3CA <=0.00', 'ERBB2 <=0.00', 'CDH1 <=0.00', 'Prior_Local_Recurrence <= 0.00']

Precision: 0.15847665847665848

Coverage: 0.0084

Prediction explanation: HormoneCDK46i therapy will be effective for patients who have the following characteristics: GATA3 <=0.00 age between 42 and 50↵- overall tumor grade between 2 and 3 HER2+ status <=0.00. Denovo MBC status <=0.00. ESR1 expression level <=0.00↵and more factors as per anchor text. Precision of this prediction is approximately at 15.85% with a coverage of only 0.84%.

5. CONCLUSION

The development of XAI and anchor-based approaches holds immense promise for enhancing the transparency and trustworthiness of precision medicine in breast cancer. By providing interpretable and understandable insights into the decision-making process of AI models, these techniques can empower clinicians and patients to make more informed decisions, leading to improved treatment outcomes and increased patient trust in the healthcare system. The role of explainability in creating trustworthy AI for healthcare cannot be overstated, as the lack of transparency has been identified as a key barrier to the wider adoption of these technologies. The ability to explain the reasoning behind AI predictions, as demonstrated by the anchors method, can foster a deeper understanding of the underlying factors that drive treatment decisions, thereby enabling more informed and collaborative decision-making between healthcare providers and patients. So, the integration of clinically relevant features, such as genetic markers and clinical indicators, into the explanation process can enhance the relevance and utility of the XAI-based approach, aligning it with the clinical reasoning patterns of healthcare professionals. As the field of precision medicine in breast cancer continues to evolve, the synergistic integration of XAI and anchor-based techniques can pave the way for more transparent, trustworthy, and personalized treatment strategies. Ongoing research and collaboration between AI researchers, clinicians, and regulatory bodies will be crucial in ensuring the responsible and ethical development of these technologies, ultimately leading to improved patient outcomes and a stronger bond of trust between patients and the healthcare system.

FUNDING INFORMATION

Authors state no funding involved.

AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

Name of Author	C	M	So	Va	Fo	I	R	D	O	E	Vi	Su	P	Fu
Reena Lokare	✓	✓	✓		✓	✓	✓	✓	✓		✓	✓	✓	
Mansing Rathod	✓			✓		✓	✓	✓	✓	✓	✓	✓		
Jyoti Sunil More	✓	✓	✓	✓	✓		✓	✓		✓	✓		✓	✓

C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

The data that support the findings of this study are openly available in CBioportal at https://www.cbioportal.org/study/summary?id=breast_msk_2018.

REFERENCES

[1] T. Sethi, A. Kalia, A. Sharma, and A. Nagori, "Interpretable artificial intelligence: closing the adoption gap in healthcare," in *Artificial Intelligence in Precision Health*, 2020, pp. 3–29, doi: 10.1016/B978-0-12-817133-2.00001-X.

[2] A. Bennetot *et al.*, "A practical guide on explainable AI techniques applied on biomedical use case applications," *ACM Computing Surveys*, vol. 57, no. 2, pp. 1-44, 2024, doi: 10.1145/3670685.

[3] F. Giuste *et al.*, "Explainable artificial intelligence methods in combating pandemics: a systematic review," *IEEE Reviews in Biomedical Engineering*, vol. 16, pp. 5–21, 2023, doi: 10.1109/RBME.2022.3185953.

[4] A. Chaddad, J. Peng, J. Xu, and A. Bouridane, "Survey of explainable AI techniques in healthcare," *Sensors*, vol. 23, no. 2, Jan. 2023, doi: 10.3390/s23020634.

[5] A. F. Markus, J. A. Kors, and P. R. Rijnbeek, "The role of explainability in creating trustworthy artificial intelligence for health care: a comprehensive survey of the terminology, design choices, and evaluation strategies," *Journal of Biomedical Informatics*, vol. 113, Jan. 2021, doi: 10.1016/j.jbi.2020.103655.

[6] C. C. Yang, "Explainable artificial intelligence for predictive modeling in healthcare," *Journal of Healthcare Informatics Research*, vol. 6, no. 2, pp. 228–239, June 2022, doi: 10.1007/s41666-022-00114-1.

[7] M. L. Ferla, "An XAI approach to deep learning models in the detection of DCIS," *Artificial Intelligence Applications and Innovations. AIAI 2023 IFIP WG 12.5 International Workshops*, pp. 409-420, 2023, doi: 10.1007/978-3-031-34171-7_33.

[8] S. K. Mandala, "XAI renaissance: redefining interpretability in medical diagnostic models," *arXiv:2306.01668,* 2023.

[9] M. Bohacek and H. Farid, "The making of an AI news anchor—and its implications," *Proceedings of the National Academy of Sciences*, vol. 121, no. 1, Jan. 2024, doi: 10.1073/pnas.2315678121.

[10] M. A. Chaudhry, M. Cukurova, and R. Luckin, "A transparency index framework for AI in education," in *Artificial Intelligence in Education. Posters and Late Breaking Results, Workshops and Tutorials, Industry and Innovation Tracks, Practitioners' and Doctoral Consortium, 23rd International Conference*, 2022, pp. 195–198, doi: 10.1007/978-3-031-11647-6_33.

[11] A. Rosen and S. L. Zeger, "Precision medicine: discovering clinically relevant and mechanistically anchored disease subgroups at scale," *Journal of Clinical Investigation*, vol. 129, no. 3, pp. 944–945, Jan. 2019, doi: 10.1172/JCI126120.

[12] W. Samek and K.-R. Müller, "Towards explainable artificial intelligence," *Explainable AI: Interpreting, Explaining and Visualizing Deep Learning*, pp. 5-22, 2019, doi: 10.1007/978-3-030-28954-6_1.

[13] K. Sokol and P. Flach, "Explainability is in the mind of the beholder: establishing the foundations of explainable artificial intelligence," *arXiv:2112.14466,* 2021.

[14] R. Massafra *et al.*, "Analyzing breast cancer invasive disease event classification through explainable artificial intelligence," *Frontiers in Medicine*, vol. 10, Feb. 2023, doi: 10.3389/fmed.2023.1116354.

[15] F. Li, N. Ruijs, and Y. Lu, "Ethics & AI: a systematic review on ethical concerns and related strategies for designing with AI in healthcare," *AI*, vol. 4, no. 1, pp. 28–53, Dec. 2022, doi: 10.3390/ai4010003.

[16] D. Dave, H. Naik, S. Singhal, and P. Patel, "Explainable AI meets healthcare: a study on heart disease dataset," *arXiv:2011.03195*, 2020.

[17] A. A. Kuwaiti *et al.*, "A review of the role of artificial intelligence in healthcare," *Journal of Personalized Medicine*, vol. 13, no. 6, June 2023, doi: 10.3390/jpm13060951.

[18] W. Oleszkiewicz *et al.*, "Understanding the robustness of deep neural network classifiers for breast cancer screening," *arXiv:2003.10041*, 2020.

[19] E. Frullanti and M. J. Serrano, "Editorial: current trends and future perspectives about liquid biopsy," *Frontiers in Genetics*, vol. 14, Dec. 2023, doi: 10.3389/fgene.2023.1345876.

[20] I. D.-Mullan, J. Bull, and F. Sy, "Precision medicine and health disparities: advancing the science of individualizing patient care," *American Journal of Public Health*, vol. 105, no. S3, pp. S368–S368, Jul. 2015, doi: 10.2105/AJPH.2015.302755.

[21] T. Hulsen, "Explainable artificial intelligence (XAI): concepts and challenges in healthcare," *AI*, vol. 4, no. 3, pp. 652–666, Aug. 2023, doi: 10.3390/ai4030034.
[22] A. Sharma, A. Lysenko, S. Jia, K. A. Boroevich, and T. Tsunoda, "Advances in AI and machine learning for predictive medicine," *Journal of Human Genetics*, vol. 69, no. 10, pp. 487–497, Oct. 2024, doi: 10.1038/s10038-024-01231-y.
[23] T. Alelyani, M. M. Alshammari, A. Almuhanna, and O. Asan, "Explainable artificial intelligence in quantifying breast cancer factors: Saudi Arabia context," *Healthcare*, vol. 12, no. 10, May 2024, doi: 10.3390/healthcare12101025.
[24] M. Ahmed, T. Bibi, R. A. Khan, and S. Nasir, "Enhancing breast cancer diagnosis in mammography: evaluation and integration of convolutional neural networks and explainable AI," *2024 26th International Multi-Topic Conference (INMIC),* 2024, pp. 1-6, doi: 10.1109/INMIC64792.2024.11004362.
[25] S. Kothari, S. Sharma, S. Shejwal, A. Kazi, M. D'Silva, and M. Karthikeyan, "An explainable AI-assisted web application in cancer drug value prediction," *MethodsX*, vol. 12, Jun. 2024, doi: 10.1016/j.mex.2024.102696.
[26] S. Ali, F. Akhlaq, A. S. Imran, Z. Kastrati, S. M. Daudpota, and M. Moosa, "The enlightening role of explainable artificial intelligence in medical & healthcare domains: a systematic literature review," *Computers in Biology and Medicine*, vol. 166, Nov. 2023, doi: 10.1016/j.compbiomed.2023.107555.
[27] S. Sawangarreerak, P. Thanathamathee, P. Lakkanawanit, and N. S. A. Wahab, "Anchor-based explainable and causal artificial intelligence for enhancing financial predictions of future earnings," *IEEE Access*, vol. 13, pp. 61026–61047, 2025, doi: 10.1109/ACCESS.2025.3557264.
[28] E. Cerami *et al.*, "The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data," *Cancer Discovery*, vol. 2, no. 5, pp. 401–404, May 2012, doi: 10.1158/2159-8290.CD-12-0095.
[29] J. Gao *et al.*, "Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal," *Science Signaling*, vol. 6, no. 269, Apr. 2013, doi: 10.1126/scisignal.2004088.
[30] I. D. Bruijn *et al.*, "Analysis and visualization of longitudinal genomic and clinical data from the AACR project GENIE biopharma collaborative in cBioPortal," *Cancer Research*, vol. 83, no. 23, pp. 3861–3867, Dec. 2023, doi: 10.1158/0008-5472.CAN-23-0816.
[31] P. Razavi *et al.*, "The genomic landscape of endocrine-resistant advanced breast cancers," *Cancer Cell*, vol. 34, no. 3, pp. 427-438.e6, Sept. 2018, doi: 10.1016/j.ccell.2018.08.008.

BIOGRAPHIES OF AUTHORS

Reena Lokare holds a Doctor of Philosophy in Computer Engineering degree from Mumbai University, India in 2023. She is working as an Assistant Professor at K. J. Somaiya Institute of Technology, Mumbai, India. She has nearly 21 years of teaching experience. Her areas of expertise include data structures, algorithms, automata theory, soft computing, machine learning, deep learning, and bioinformatics. She has nearly 20 research publications and 2 collaborative research projects in the healthcare domain. She can be contacted at email: reena.l@somaiya.edu.

Mansing Rathod is Associate Professor in the Department of Information Technology, K. J. Somaiya Institute of Technology, Mumbai University and having 24 years' experience in teaching. Completed his Ph.D. in image processing domain with research area i.e., resolution enhancement of satellite image. He has authored over 34 peer reviewed conference and journal papers. He conducted several national level faculty development programs under AICTE. He can be contacted at email: rathodm@somaiya.edu.

Dr. Jyoti Sunil More B.E. Computer Science Engineering (2003) from Shivaji University, M.Tech. in Computer Engineering (2006) from Dr. B.A.T.U., Lonere and Ph.D. in Computer Engineering from University of Mumbai in 2019. She has more than 20 years of teaching experience and is currently affiliated to Fr. C. Rodrigues Institute of Technology, affiliated to Mumbai University. She has published several research papers in international conferences and journals. Her area of expertise are computer networks, databases, data mining, machine learning, data science, and artificial intelligence. She can be contacted at email: jyoti.more@fcrit.ac.in.