

An Uncertainty-Aware Sequential Approach for Predicting Response to Neoadjuvant Therapy in Breast Cancer

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- 1 Response to neoadjuvant therapies
The clinical problem
- 2 Uncertainty-Aware Sequential Approach
The solution
- 3 Experimental analysis
- 4 Conclusions and future work

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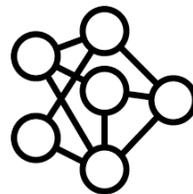
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- Not all patients respond in the same way.
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- Patients experiencing ineffective neoadjuvant therapy incur in toxicity and side effects without reaching the desired clinical benefit.
- **So we need tools to predict how a patient will respond to neoadjuvant therapies.**



Machine learning to the rescue!

Response to neoadjuvant therapy has been approached through different data modalities

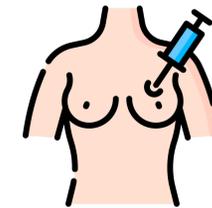
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- Dynamic contrast-enhanced MRI features.
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- Clinical and biomolecular predictors.
 - Gathered through invasive biopsy tests.
 - Allow a better understanding of biological processes.
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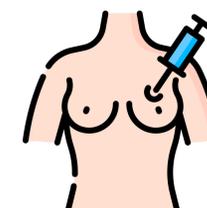


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- **What if we could efficiently use each feature set?**

Only in those cases in which the imaging features provide an uncertain prediction, should a biopsy be performed.

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Uncertainty-Aware Sequential Approach

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Let assume a set of patient triplets

$$(x_1^{\text{MRI}}, x_1^{\text{BIO}}, y_1), \dots, (x_n^{\text{MRI}}, x_n^{\text{BIO}}, y_n)$$

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Learn a predictive model using the whole set of features $f(x^{\text{MRI}}, x^{\text{BIO}})$.

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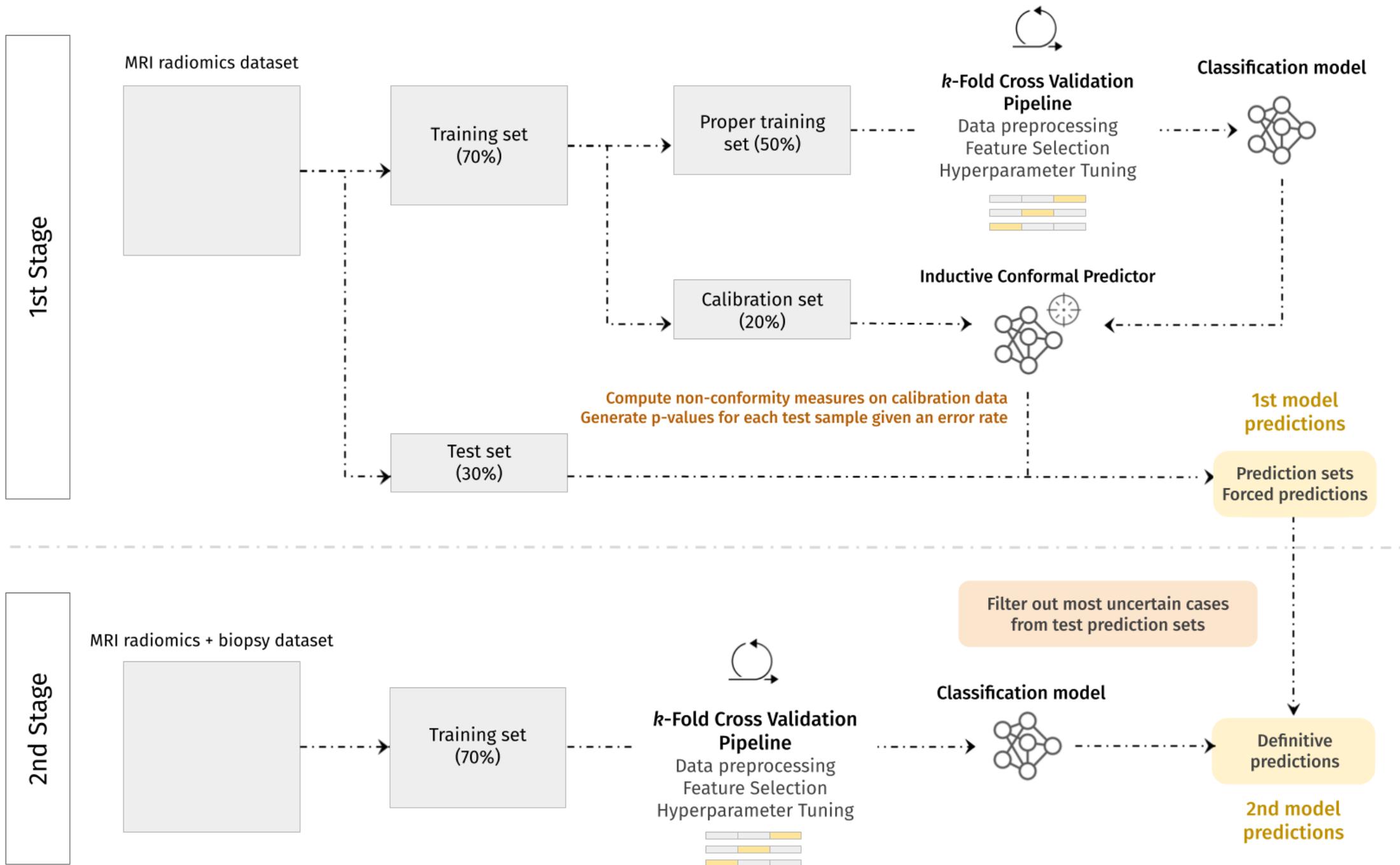
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- **Our proposal**

Learn an **inductive conformal predictor** on top of a non-invasive MRI predictive model.

If the model is certain enough for an specific patient, compute a prediction using the non-invasive model $f(x^{\text{MRI}})$

If not, compute a prediction with a biopsy-enriched invasive model $f(x^{\text{MRI}}, x^{\text{BIO}})$.



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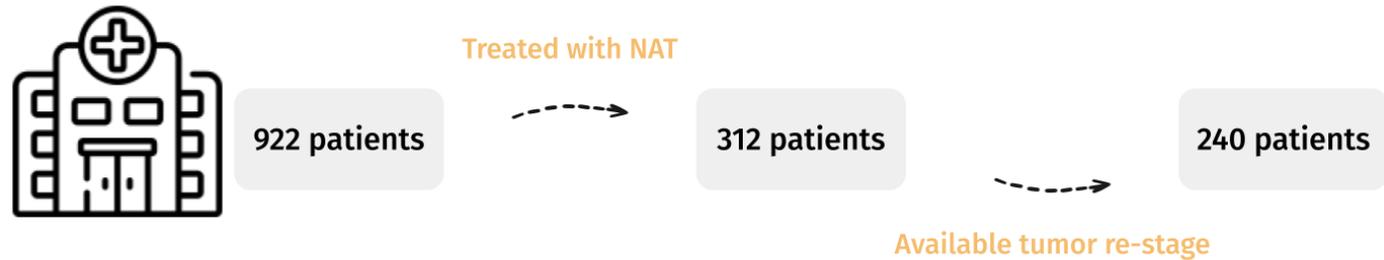
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Duke Breast Cancer MRI dataset

A fully annotated and anonymized collection of 922 breast cancer patients admitted at Duke University Hospital between January 1st, 2000 and March 23rd, 2014.



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Response to NAT	Cancer re-stage	Sample size
Pathological complete response	∅	71 (29.6 %)
Early stage	IA or IIA	104 (44.3 %)
Locally advanced or metastasis stage	From IIB to IV	65 (27.1 %)

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- **521 MRI numerical features** describing tumor and fibroglandular tissue characteristics.
- **12 clinical features** describing tumor biology from biopsy.

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We tested three different algorithms: **logistic regression**, **random forest** and **xgboost**.

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Non-conformity functions

- **Inverse Probability Error** : $\Delta(y, f(x)) = 1 - \hat{\mathbb{P}}(y_i | x)$
- **Margin Error** : $\Delta(y, f(x)) = 0.5 - \frac{\hat{\mathbb{P}}(y_i | x) - \max_{y' \neq y_i} \hat{\mathbb{P}}(y' | x)}{2}$

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Filtering strategy

Patients with $|\Gamma(x_i)| = 1$ will be retained within the 1st stage.

In order to produce prediction sets, we test two error rates: $\epsilon \in \{0.1, 0.2\}$

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Meaningful metrics

- **1st stage (conformal predictor)**

Single rate (patients assessed through 1st model) : $\frac{1}{N} \sum_i^N (|\Gamma(x_i)| = 1)$

- **Entire pipeline**

F1 macro (unweighted per-class F1) : $\frac{1}{3} (F1_{CR} + F1_{ES} + F1_{LA})$

True Positive Rate (TPR) for each class.

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Some key insights...

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RF_{MRI}	RF_{MRI+BIO}	Our approach	Single rate
0.408	0.525	0.513	12.6 %

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Even outperforming the model trained with the whole set of features!

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- TPR for early stage patients using a xgboost model ($\epsilon = 0.2$, inverse probability error)

XGB_{MRI}	XGB_{MRI+BIO}	Our approach	Single rate
0.461	0.672	0.659	13.7 %

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Conclusions

- Machine learning has the potential to assess how a breast cancer patient will respond to neoadjuvant therapies.
- Our conformal prediction-based approach helps identify patients whose prognosis is uncertain using non-invasive protocols.
- These patients are referred to a second assessment with invasive test, providing a more accurate prediction.
- Patients retained within the non-invasive model avoid unnecessary biopsies.

Future work

- Additional non-conformity measures (e.g., ordinal prediction sets).
- Other clinical applications in cost-variable problems.
- Limited data regime → cross-conformal prediction.

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