

# Conformal Association Rule Mining (CARM)

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September 14, 2023

# Introduction

- ▶ CARM is an integration of two frameworks: *conformal prediction* and *association rule mining*.
- ▶ It enables detection of errors within a set of binary labels, with the usual CP guarantees on validity.
- ▶ XAI angle
- ▶ As an extension, we analyse the errors using *probabilistic prediction* to suggest corrections.



# Association Rule Mining

- ▶ A rule-based ML method for discovering relationships between items in a dataset.
- ▶ E.g for supermarkets:  $\{\text{bread}\} \rightarrow \{\text{butter}\}$
- ▶ In general terms:  $\{\textit{antecedent}\} \rightarrow \{\textit{consequent}\}$
- ▶ In a ML setting, an example rule might be:

IF feature  $F = a$  THEN feature  $G = b$

$G$  could alternatively refer to a label.

- ▶ **Implication:** Given a set of rules, errors can be identified as deviations from rules that hold true for most of the data

# ARM concepts

- ▶ **Support:** the proportion of examples where the rule holds.
- ▶ **Confidence:** the conditional probability of the rule's consequent given its antecedent.
- ▶ Most common way to generate rules: *apriori algorithm*
  - ▶ Requires user-defined thresholds for minimum support and confidence

# Apriori algorithm: lack of statistical rigor

- ▶ No notion of statistical significance
- ▶ Arbitrary choice of thresholds can lead to spurious and missed rules
- ▶ Solution: use a different approach to ARM...

# Our approach to ARM

- ▶ As per Hamalainen et al. (2009)
- ▶ Idea: subject any possible rule to a binomial test
- ▶ Each example is treated as an independent Bernoulli trial, whose outcome is either 1 or 0
  - ▶ 1 means the rule  $(F = a) \rightarrow (G = b)$  occurs
  - ▶ 0 means the rule doesn't occur
- ▶  $H_0$ : no association between antecedent and consequent
- ▶ Interpretation of  $p$ -values: the 'weight' of a given rule
  - ▶ a small value provides evidence against  $H_0$

# Non-conformity measure

- ▶ So we have...
  - ▶ A complete pool of rules with associated weights  $p_r$
  - ▶ A set of examples  $Z$  which either comply with those rules or not
- ▶ So for a given example  $z \in Z$ , we have an expectation for its label based on each rule  $r$  (assuming the antecedent of  $r$  is true for  $z$ )
- ▶ If the expected label doesn't match the observed label, then  $z$  is an exception to that rule, i.e. non-conforming.
- ▶ Non-conformity score  $\alpha$  for  $z$ :
  - ▶ Initialise  $\alpha$  at 0, then add  $-\log p_r$  for every broken rule
  - ▶ accumulates degree of non-conformity



# Converting NCM to conformal $p$ -values

- ▶ NB. Different kind of  $p$ -values!
- ▶ **Input:** The data sequence  $Z' = ((x_1, y_1), \dots, (x_N, y_N))$ , a non-conformity measure  $\mathcal{A}$ , and a threshold  $\varepsilon$ .
- ▶ **Non-conformity scores:** For each data point  $i = 1, \dots, N$ , compute:

$$\alpha_i = \mathcal{A}((x_i, y_i), Z' \setminus \{(x_i, y_i)\})$$

- ▶  **$p$ -value Calculation:** Determine  $p_N$  using:

$$p_N = \frac{|\{j : y_j = y_N, \alpha_j \geq \alpha_N\}|}{|\{j : y_j = y_N\}|}$$

- ▶ **Error Detection:** If  $p_N < \varepsilon$ , flag the example  $z_N$  as an error.

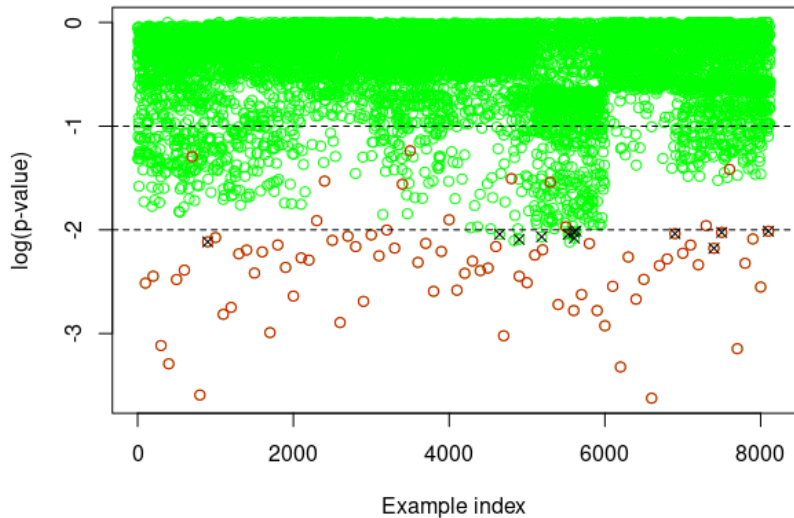
# Validity

- ▶ All conformal predictors automatically come with the property of *validity*, i.e. the probability of incorrectly rejecting  $H_0$  is at most  $\varepsilon$ .
- ▶ In our setting of error detection,  $\varepsilon$  becomes an upper bound on the probability of a false positive (false alarm).

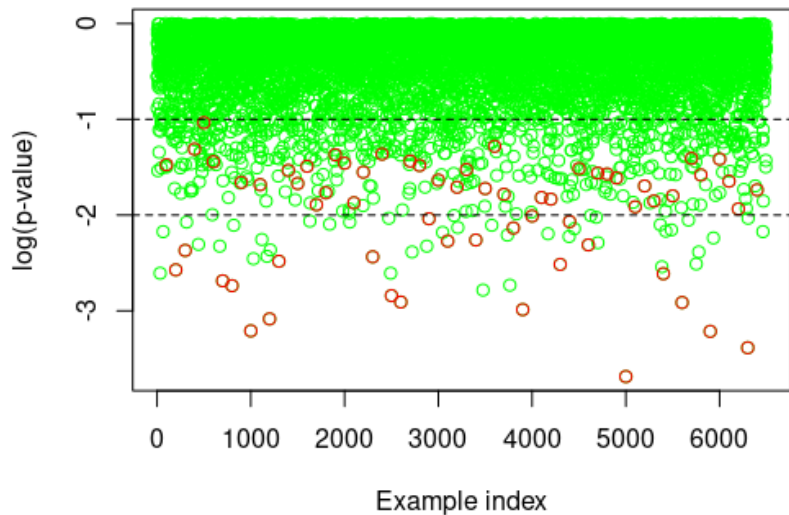
# Datasets & pre-processing

1. **Mushrooms.** Label: edible or posionous
  2. **Wine Quality.** Label: red or white
  3. **Adult Income.** Label: salary greater/less than \$50K
- ▶ Introduced known errors into the labels for 1% of examples
  - ▶ Remaining features converted to binary form by one-hot encoding

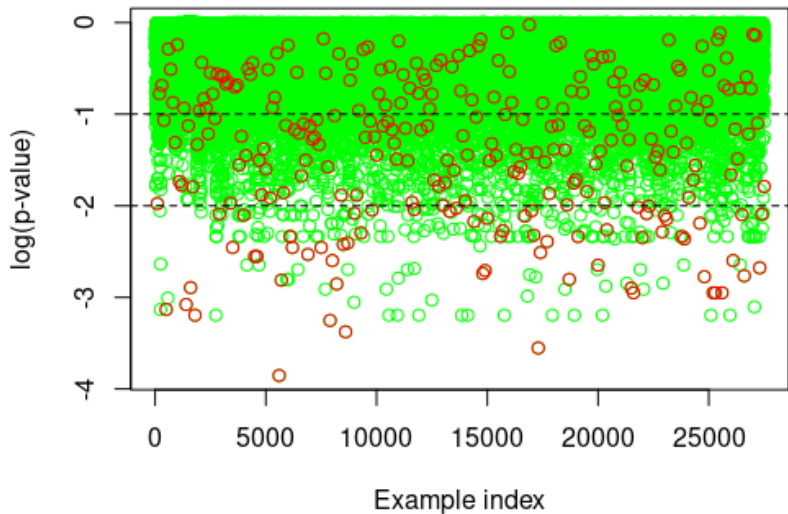
# CARM $p$ -values (log scale) - Mushrooms



## CARM $p$ -values (log scale) - Wine



# CARM $p$ -values (log scale) - Adult



# Evaluation of CARM

Precision at three  $p$ -value thresholds

Dataset	$p < 0.1\%$	$p < 1\%$	$p < 10\%$
Mushrooms	100%	87%	10%
Wine	100%	37%	10%
Adult Income	29%	23%	6%

Recall at three  $p$ -value thresholds

Dataset	$p < 0.1\%$	$p < 1\%$	$p < 10\%$
Mushrooms	9%	87%	100%
Wine	8%	37%	100%
Adult Income	2%	23%	62%

# Example report

<b>Index in data</b>	6600
<b>Observed label</b>	1 (= edible)
<i>p</i> -value	0.000237
<b>Broken rules</b>	(listed if significant at the threshold $10^{-9}$ ) <b>Confidence</b>
<i>One-feature rules</i>	IF cap-shape = k THEN Y = 0 0.72 IF cap-surface = y THEN Y = 0 0.54 IF bruises = f THEN Y = 0 0.69 IF odor = y THEN Y = 0 0.99 IF gill-spacing = c THEN Y = 0 0.56 IF gill-size = n THEN Y = 0 0.88 IF gill-color = b THEN Y = 0 0.99 IF stalk-root = ? THEN Y = 0 0.71 IF stalk-surface-above-ring = k THEN Y = 0 0.93 IF stalk-surface-below-ring = k THEN Y = 0 0.93 IF stalk-color-above-ring = p THEN Y = 0 0.69 IF ring-type = e THEN Y = 0 0.63 IF spore-print-color = w THEN Y = 0 0.75 IF population = v THEN Y = 0 0.70 IF habitat = p THEN Y = 0 0.88
<i>Two-feature rules</i>	IF gill-attachment = f AND ring-number = o THEN Y = 0 0.47 IF veil-color = w AND ring-number = o THEN Y = 0 0.47



# Probabilistic Prediction

- ▶ When a data example is identified as an error, it is important to conduct a thorough investigation that includes also a suggested correction for it.
- ▶ For this purpose, we can employ the *Venn-ABERS (VA) framework*.
- ▶ VA works in same assumptions as CP.
- ▶ Like CP, VA framework can be linked to an underlying method as well.
- ▶ The difference is in output: where CP produces *p-values*, VA outputs *lower and upper probabilities*.

# CARM & VA results for 10 most suspicious examples

Index	Label.	$p$ -value	VA probs	VA prediction	True label	Comment
6600	1	0.00024	0.0074–0.0078	0	0	1 corrected to 0
800	0	0.00026	0.990–0.991	1	1	0 corrected to 1
6200	1	0.00048	0.0074 – 0.0078	0	0	1 corrected to 0
400	0	0.00051	0.990 – 0.991	1	1	0 corrected to 1
7700	1	0.00071	0.0074 – 0.0078	0	0	1 corrected to 0
300	0	0.00077	0.990 – 0.991	1	1	0 corrected to 1
4700	1	0.00095	0.00780 – 0.98	0	0	1 corrected to 0
1700	0	0.001	0.990 – 0.991	1	1	0 corrected to 1
6000	1	0.0012	0.00737 – 0.00780	0	0	1 corrected to 0
2600	0	0.0013	0.990 – 0.991	1	1	0 corrected to 1

- ▶  $p$ -values for alternative labels are all close to 1, i.e. no longer suspicious.
- ▶ VA predictions indicate high confidence in alternative labels.

# Conclusions and further work

- ▶ Demonstrated integration of modified ARM with the CP framework for *explainable* error detection in data labels.
- ▶ Validity property limits false alarms during error detection.
- ▶ Association rules enhances interpretability and serve as basis for probabilistic analysis using Venn-ABERS

## Further work:

- ▶ Exploration of more complex rules.
- ▶ Extension of the methodology for multi-class labels
- ▶ Extension of methodology to correcting features, not just labels