CPU5006-20: Artificial Intelligence: Assessment 1: Rule-based AI Scientific Research Paper

22nd November 2024

1. Introduction

The classifications of objects and entities using rule-based artificial intelligence have been a foundational concept since the birth of AI back in 1956 when John McCarthy first coined the term. From its origin to its renewed optimism and advancements in expert systems in the early 1980s (AI spring), rule-based AI has evolved into a robust methodology for solving problems in domains where logic and predefined knowledge play a critical role (Russell & Norvig, 2021). This research investigates the application of two distinct rule-based forward-chaining algorithms to the UCI mushroom dataset, aiming to classify mushrooms as either edible or poisonous. The ultimate goal is to evaluate and determine which of the two AI approaches is better suited for this particular task.

Forward chaining operates by iteratively applying rules to known facts until reaching a goal (Davis & King, 1977). It differs from backward chaining, which starts with a hypothesis and works backwards to find supporting facts. Forward chaining is well-suited for problems involving large datasets with numerous potential starting points (Mitchell, 1977). In this research, two distinct forward-chaining rule-based algorithms were developed and evaluated on a publicly available mushroom dataset. These algorithms classify mushrooms based on their physical and chemical characteristics, such as odour, cap shape, and habitat. This research aims to evaluate the performance of these two forward-chaining approaches using key metrics, including overall accuracy and precision, computational efficiency, interpretability and confusion matrix.

The motivation behind using such a dataset was because of its balance and comprehensive feature set, offering detailed information about mushroom characteristics. Its simplicity and structure make it an ideal dataset for exploring rule-based artificial intelligence. This research seeks to provide insight into the strengths and limitations of the two different rule-based reasoning in solving real-world classification problems by critically evaluating the two distinct approaches.

2. Literature Review

Rule-based reasoning has long been regarded as a fundamental approach to problem-solving in systems and as a foundation for artificial intelligence. Early studies on this, such as by Randall Davis and Jonathan J. King (1977), demonstrated the importance and usefulness of this rule-based system in applying established knowledge and rules to deduce conclusions from a structured data set. Later on, these systems started getting more acknowledged with the development of expert systems like MYCIN, when Edward H. Shortliffe showcased the potential of forward chaining in diagnosing infectious diseases where decisions were derived by iteratively applying rules to known patient data (Shortliffe, 1976). The success of such systems highlighted the strengths and ability of artificial intelligence to incorporate domain-specific knowledge into decision-making processes, leading to various advancements of AI in areas such as medical diagnosis, fraud detection and environmental modelling (Dutta et al., 2019).

Forward chaining, in particular, started getting more recognised for making classification tasks easier. It begins with known facts and systematically applies rules to reach conclusions, making it great for problems involving large datasets and complex decision trees (Mitchell, 1997). In contrast, backward chaining operates by starting with a hypothesis and working backwards to validate it, often requiring more profound rule sets to achieve the necessary conditions for a hypothesis (Giarratano & Riley, 2005). Despite all its advantages, forward chaining faces notable challenges when applied to complex datasets with diverse and interdependent features. Tom M. Mitchell (1997) observed that although forward chaining ensures a comprehensive exploration of possibilities, it can become computationally inefficient when the rule set expands and becomes more complex. Additionally, Peter Jackson (1998) further emphasised the difficulty of designing set rules that are both comprehensive and free from redundancies or conflicts, especially in dynamic domains where the data is constantly changing.

Recent efforts have sought to overcome these limitations by combining forward chaining with other methods, such as heuristic or data-driven approaches, to improve scalability and accuracy (Dutta, Ghosh, & Jana, 2019). However, its application still remains relatively underexplored, especially in biological classification, particularly in domains where features and relationships are subject to constant variability. Overcoming this gap requires using domain-specific knowledge or machine learning as an approach to design rules that adapt to evolving biological contexts.

The UCI mushroom dataset provides an ideal structure for evaluating such rule-based reasoning. It contains comprehensive features, such as odour, cap shape, habitat and colour, to classify whether a mushroom is either edible or poisonous. These features offer clear opportunities to design rules, based on domain-specific knowledge, such as associating foul odours or green spore prints with poisonous mushrooms. However, the dataset also presents challenges, as certain features, such as habitat and population, are less definitive, introducing variability into the rule base. This research develops and evaluates two distinct forward-chaining rule-based algorithms to determine their effectiveness on this dataset. By comparing their performance in terms of accuracy and precision, interpretability, computation efficiency and confusion matrix, this research aims to identify which of the two algorithms is better suited for this classification task.

3. Methodology

The methodology employed in this study is designed to systematically evaluate and compare the effectiveness of the two forward-chaining rule-based algorithms for classifying mushrooms as either poisonous or edible. The process breakdown is analysed below, and a detailed exploration of the UCI Mushroom dataset serves as the foundation for constructing and testing the algorithms. This section explains the steps taken and highlights the challenges of applying rule-based reasoning to biological classification tasks.

3.1.   Dataset Description

The UCI Mushroom dataset, sourced from the UCI Machine Learning Repository (Dua & Graff, 2019), consists of 8,124 samples, each described by 22 categorical features. Each mushroom sample is classified as edible (e) or poisonous (p). Key features such as odour, spore print colour, and habitat are beneficial for distinguishing between edible and poisonous mushrooms. The dataset was analysed to identify patterns and correlations between mushroom classifications and their attributes to create rule-based algorithms. Additionally, general mushroom classification methods were reviewed to contextualise the dataset and better understand domain-specific classification criteria. Insights from this review, combined with the visualisation of feature patterns using bar charts, were used to guide the construction of decision rules for the two forward-chaining algorithms.

```
Dataset Information:
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RangeIndex: 8124 entries, 0 to 8123
Data columns (total 23 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   class                     8124 non-null   object
 1   cap-shape                 8124 non-null   object
 2   cap-surface               8124 non-null   object
 3   cap-color                 8124 non-null   object
 4   bruises                   8124 non-null   object
 5   odor                      8124 non-null   object
 6   gill-attachment           8124 non-null   object
 7   gill-spacing              8124 non-null   object
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 19  ring-type                 8124 non-null   object
 20  spore-print-color         8124 non-null   object
 21  population                8124 non-null   object
 22  habitat                   8124 non-null   object
dtypes: object(23)
memory usage: 1.4+ MB
```

Figure 1. Overview of the UCI Mushroom Dataset

3.2. Rule Constructions

The set rules for the algorithms were developed based on patterns identified during the dataset analysis and exploration. Visualising these patterns with bar charts provided insights into how specific features may correlate with mushroom classification, helping to distinguish poisonous mushrooms from edible mushrooms. For instance, a consistent pattern observed was that mushrooms with no odour were predominantly edible, while those with foul or fishy odours were almost exclusively poisonous. Similarly, other features such as spore print colour and gill size played a significant role in classification, as mushrooms with broad gills were often edible. In contrast, those with narrow gills tended to be poisonous.
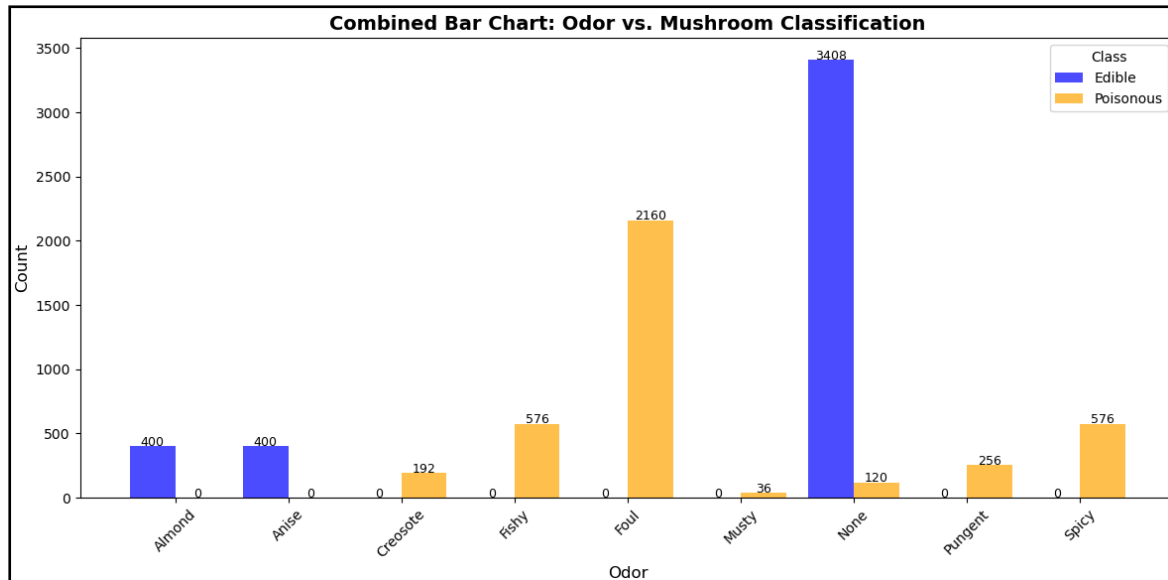

Figure 2. Combined bar chart illustrating the relationship between mushroom odour and classification

3.3. System Desing and Implementation

With such patterns identified, the next step was to implement the rules, ensuring that sufficient and distinct patterns were established to construct two forward-chaining algorithms. Each algorithm was codified carefully to reflect the observed relationships in the dataset. The goal was to evaluate the algorithm's effectiveness by analysing various metrics to aid my research claims.

3.3.1. Forward Chaining System 1

The first rule-based algorithm focused more on chemical and physical characteristics, such as odour and spore print colour, to classify the mushrooms. For example, foul odour and green spore prints were associated with poisonous mushrooms, while mushrooms with a none or anise odour were classified as edible. Broad gill size also indicated that mushrooms were edible, whereas narrow gills were more commonly associated with poisonous mushrooms. The first algorithm systematically applied these rules iteratively to the dataset until a classification was reached.

3.3.2. Forward Chaining System 2

The second rule-based algorithm incorporated additional contextual and environmental features alongside physical and chemical properties. Although similar physical characteristics such as veil colour and ring type were still considered, the second rule-based algorithm also introduced rules based on contextual features such as habitat and population to account for variability in the dataset. For instance, mushrooms found in grassy or meadow habitats were more likely to be classified as edible, while mushrooms in wooded or dense populations were features of more poisonous mushrooms. Unlike the first algorithm, the second algorithm introduced more complexity to the rule set by introducing these contextual features.

3.4. Experimental Setup and Procedure

The algorithms were implemented using Python 3.9 on a machine with an Intel Core i7 processor and 16GB of RAM. This is important because different machines using more powerful processors or RAM may show differences in the computation efficiency of the algorithms. Libraries such as Pandas and NumPy facilitated data processing and numerical computation, while libraries such as Matplotlib helped visualise the findings. The dataset was split into training (70%) and test (30%) subsets to ensure fair evaluation of the algorithms. The whole procedure can be summarised into:

Procedure

- The dataset was pre-processed by encoding categorical variables.

- Two forward-chaining rule-based algorithms were implemented using distinct rule sets.

- Each algorithm was applied to the test dataset to classify mushrooms as edible or poisonous.

- Performance metrics were calculated and compared across the two algorithms.

4. Results and Discussion

After designing and implementing the two forward chaining algorithms, the next step was to evaluate their performance on the UCI Mushroom Dataset. Performance metrics, including accuracy, computational efficiency, interpretability, and confusion matrix analysis, were used to evaluate both algorithms. These metrics provided insights into the constructed rule's effectiveness and highlighted each algorithm's strengths and limitations.

4.1. Results

The two forward chaining systems were evaluated based on the following metrics to support research claims:

4.1.1. Accuracy

The first rule-based forward-chaining algorithm demonstrated a higher accuracy of approximately 91.96% compared to the second algorithm, achieving an accuracy of approximately 77.69%. This discrepancy may be attributed to the simplicity and feasibility of the rules used in the first algorithm, which focused on a smaller subset of correlated features, such as odour and spore colour. These straightforward rules allowed the first algorithm to classify mushrooms more reliably. In contrast, the second algorithm incorporated additional contextual features, such as habitat and population, which introduced variability and increased the potential for misclassifications. While these features provided

flexibility for handling variable cases, they may have reduced the precision of the rules for more straightforward classifications.

4.1.2. Precision

Precision, the proportion of true positive classifications among all positive predictions, further highlights this contrast. The first algorithm achieved a precision score of approximately 0.93, indicating that when the algorithm predicted a mushroom as poisonous, it was correct 93% of the time. This high precision reflects the strong alignment between the selected features and the classification task. On the other hand, the second algorithm achieved a lower precision score of 0.78, largely due to the inclusion of less definitive features, as mentioned before.

4.1.3. Computational Efficiency

The first chaining algorithm also outperformed the second in terms of computational efficiency. It averaged an execution time of approximately 1.5 Ms per classification, compared to almost 2.2 Ms for the second algorithm. There were even instances where the first algorithm almost had an execution time of as low as 1.0 Ms, showcasing this algorithm's efficiency. This performance difference can again be rooted back to using more straightforward rules set for the first algorithm, which almost required fewer iterations and evaluations to conclude. While the second algorithm, a more complex rule set, increased the computational power. Although this difference remains relatively small, it highlights the trade-off between simplicity and flexibility in rule-based systems, as Peter Jackson (1998) observed.

4.1.4. Interpretability

Regarding interpretability, the first algorithm again excelled due to its reliance on straightforward and highly correlated features. Each classification rule in the first algorithm corresponds to an observable characteristic, as mentioned above, making its decision-making process easy. In contrast, while the second algorithm is still interpretable, more complex rules result in a problematic classification process.

4.1.5. Confusion Matrix Analysis

The confusion matrices further highlight the performance differences between the two algorithms. For the first algorithm, the number of false positives (edible mushrooms misclassified as poisonous) was significantly lower than that of the second algorithm, as seen in Figure 3 and Figure 4.
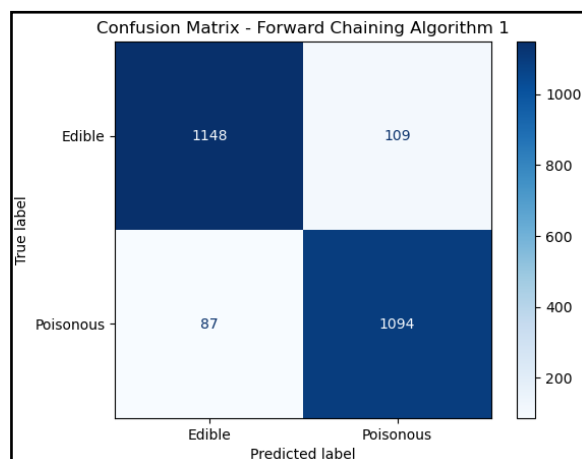

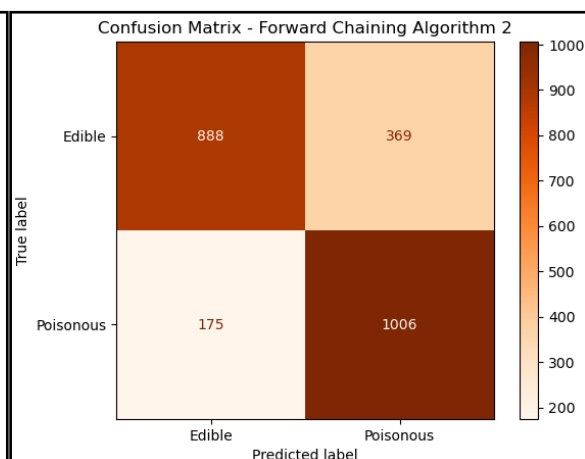Figure 3. Confusion matrix for forward chaining algorithm 1   Figure 4. Confusion Matrix for forward chaining algorithm 2

4.2. Discussion

The evaluation highlights the apparent differences between both of the rule-based systems. The first forward chaining algorithm prioritised simplicity, focusing on more direct and domain-specific rules. This design ensured that the rules produced more accurate, computationally efficient and precise interpretability results. However, it still has drawbacks regarding being less adaptable and involving more common feature combinations.

Similarly, although the second algorithm lacked that accuracy, it showcased the potential of incorporating more dynamic and contextual features to enhance flexibility. Using uncommon or ambiguous feature combinations showcased a more adaptable approach to rule-based AI problem-solving. However, this came at the cost of a less accurate and reduced computationally efficient algorithm.

The results show that the algorithm choice should depend on the specific application context. Scenarios requiring quick and transparent decision-making may favour the first algorithm, while those involving more complex or variable datasets could benefit from rules in such a second algorithm.

4.3. Implications for Future Work

This research shows several future work and development opportunities in rule-based artificial intelligence. One of the critical limitations of this research lies in the use of the UCI Mushroom Dataset, which, while serving as a significant benchmark for machine learning models and AI models for over 30 years, was last updated over 8 years ago, meaning that the data is not well up to date. While the dataset is comprehensive and well-structured for easy classification tasks, its age and lack of recent updates may not reflect current insights or variations in mushroom species. Again, one of the drawbacks of using rule-based algorithms is that they need to be updated constantly as new features are discovered over time.

Another important thing for future work involves integrating rule-based systems with data-driven approaches, such as combining forward chaining with machine learning algorithms. Such an approach could resolve the scalability challenges and tackle dataset variability, notably when datasets feature highly interdependent attributes.

Future studies could also explore methods for automating rule discovery through heuristic or evolutionary techniques, reducing manual looking for patterns in the dataset and rule construction. This would allow rule-based systems to scale efficiently and remain adaptable across diverse domains. It would also improve the second chain-based rule algorithm by looking for more domain-specific patterns to improve the algorithm overall.

By addressing these limitations and opportunities, future research can refine the balance between accuracy, precision, computational efficiency and interpretability in rule-based AI systems, ensuring their relevance in structured and dynamic problem-solving tasks.

5. Conclusion

This research used the UCI Mushroom Dataset to compare the application of two distinct forward-chaining rule-based AI systems for classifying mushrooms as either edible or poisonous. The evaluation focused on key metrics: accuracy, precision, computational efficiency, interpretability and confusion matrices. The first algorithm, designed with straightforward and highly correlated features,

demonstrated better performance in terms of accuracy (91.96%), precision (0.93), and computational efficiency (~1.5 Ms). The high interpretability of its decision-making allowed it to classify mushrooms reliably and transparently, making it more well-suited for this particular research.

In contrast, the second algorithm incorporated additional contextual features, introducing flexibility and adaptability. However, this approach resulted in a reduced accuracy (77.69%), lower precision (0.78) and increased computational complexity (~2.0 Ms). While the second algorithm highlighted the potential of interpreting contextual features, its performance trade-offs suggest that such approaches must be carefully designed based on the specific requirements of the classification task.

The results underscore the importance of tailoring rule-based systems to the application context. For tasks where precision and accuracy are essential, simpler algorithms like the first forward chaining algorithm are better. Conversely, tasks requiring more adaptability with limited data compressing of complex or ambiguous features could benefit from algorithms such as the second system despite their trade-offs.

Overall, this study demonstrates how rule-based algorithms remain valuable for structured classification tasks and, when combined with machine learning or other models, could offer vast improvements in the world of AI.
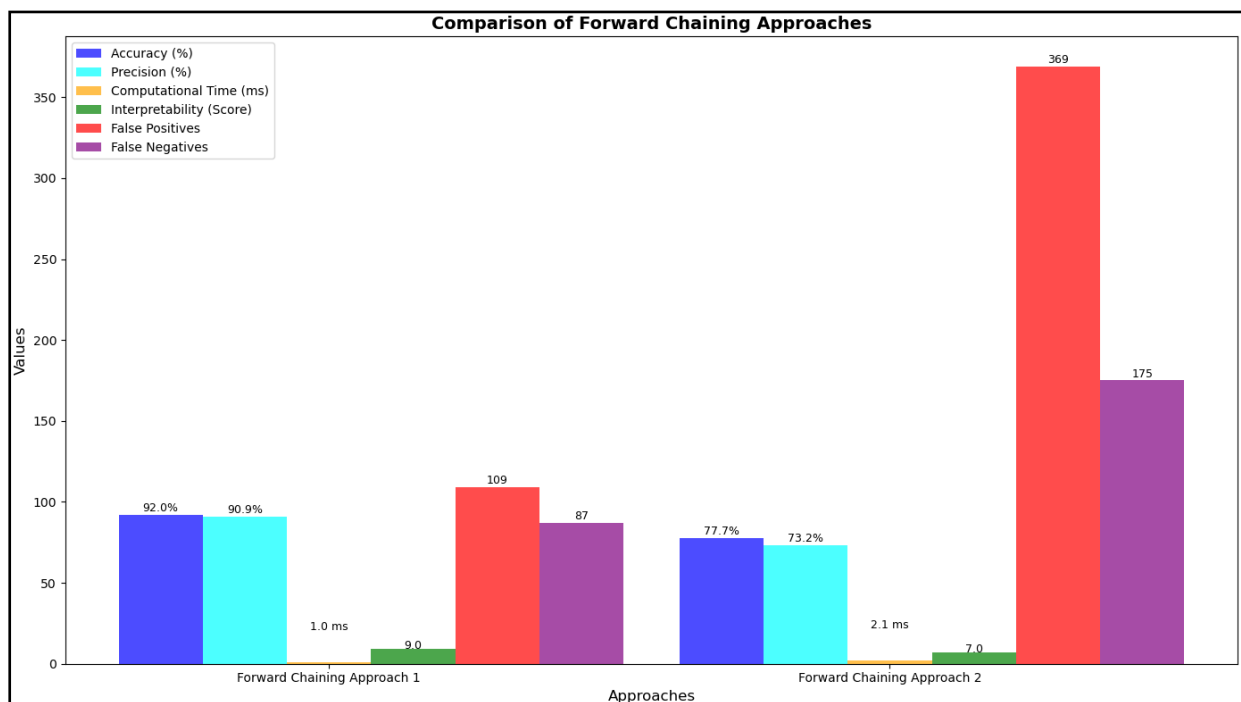

Figure 5. Combined bar chart comparing forward algorithms 1 and 2

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Links

Github Repository Link - https://github.com/RJay02/Artificial-Intelligence

UCI Mushroom Dataset Link - Mushroom Classification