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# A Fuzzy Logic-Based Diagnostic Model for Lung Cancer Detection: An Improved Clinical Decision Support Framework

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**ABSTRACT**
Lung disease, and lung cancer above all, remains one of the toughest problems in global health, taking a heavy toll each year because diagnosis so often arrives late or turns out to be wrong. The real clinical difficulty is not detection in general but catching disease at an early stage, when treatment has the best chance of working. Standard diagnostic methods tend to falter when symptom data is vague or overlapping in nature, which is exactly the situation fuzzy logic is built to handle: it reasons under uncertainty while still giving clinicians an interpretable output. This paper reports a full study built around five linked goals. First, the relevant diagnostic parameters for selected lung diseases were gathered and consolidated from the clinical literature. Second, a new Mamdani-type fuzzy inference system was designed, with membership functions chosen specifically for the parameters identified. Third, established fuzzy diagnostic models from the literature were re-implemented and run against real patient data so their reported performance could be checked rather than simply cited. Fourth, the newly proposed model was tested under the same conditions. Fifth, all of the models were placed side by side in a structured comparison that looks beyond raw accuracy to include interpretability, execution time, confidence output, and treatment guidance. Testing on the benchmark UCI lung cancer dataset shows the proposed model reaching a mean accuracy of 97.10 percent under 10-fold cross-validation, without discarding any of the original features through dimensionality reduction, and producing confidence values that carry genuine clinical meaning. Taken together, the work delivers both a working diagnostic model and a comparison framework intended to steer future research in intelligent, fuzzy-logic-based healthcare decision support....
**Keywords:** Fuzzy logic, lung cancer, Mamdani inference system, clinical decision support, membership functions, fuzzy rule base, early detection, medical diagnosis, computer-aided diagnosis.

## INTRODUCTION:

Lung disease makes up a large share of the global disease burden, and lung cancer in particular is the leading cause of cancer death for both men and women in many countries [1]. Current estimates put lung cancer behind close to one in five cancer deaths worldwide, which makes early and accurate diagnosis less a clinical nicety and more a public-health necessity [2]. Even with the progress made in imaging and molecular diagnostics, a large share of lung cancer is still caught at an advanced stage, when treatment options narrow and outcomes worsen considerably [3].

Part of what makes early diagnosis hard is that the symptoms overlap so heavily with other conditions. A persistent cough, breathlessness, a hoarse voice, unexplained weight loss, and chest pain can all point toward several respiratory and non-respiratory illnesses at once. A physician has to weigh imprecise, multi-dimensional information and still reach a timely, dependable judgement [4]. That kind of ambiguity is precisely what fuzzy reasoning is designed for [5].

Fuzzy logic, introduced by Zadeh [5], gives computers a way of handling vague information that mirrors how people actually reason. Rather than forcing a decision into strict true/false categories as classical logic does, it allows degrees of truth, which fits naturally with how clinical symptoms present and progress [7]. A fuzzy inference system (FIS) turns linguistic rules -- for instance, "if cough duration is very high and weight loss is high, then cancer stage is advanced" -- into numerical outputs through clearly defined mathematical steps, keeping the system transparent to the clinicians who use it [6].

Fuzzy logic has already been applied to a range of diagnostic problems over the last two decades, including diabetes [15], breast cancer [14], Parkinson's disease [16], thyroid disorders [17], and lung cancer specifically [8]-[12]. What is missing from this body of work is a single study that consolidates diagnostic parameters, builds a new model from them, tests it against real data, and compares it rigorously with the models already in the literature.

This paper sets out to close that gap through five objectives: consolidating the diagnostic parameters used across the literature for selected lung diseases; proposing a new fuzzy logic model for lung disease diagnosis; evaluating existing models on real patient data; testing the proposed model under the same conditions; and comparing the proposed model against established fuzzy logic baselines.
The rest of the paper is organised as follows. Related work is surveyed next, followed by the identified diagnostic parameters, the proposed fuzzy model, the experimental results and comparison, a discussion of findings, and a concluding section with directions for future work.

## Related Work

The overlap between fuzzy logic and medical diagnosis has a long history. The survey below concentrates on systems built for lung disease detection while drawing on closely related medical applications for context.

### *Early Fuzzy Diagnostic Systems for Lung Cancer*

Durai et al. [18] produced one of the earliest formal fuzzy rule-based diagnostic models for lung cancer, using priority values and six categorical output stages running from "no cancer" to "critical stage." Their design laid useful groundwork for symptom-driven inference, though it drew on symptoms not exclusively tied to lung cancer, which introduced some diagnostic noise. Phuong et al. [19] proposed LDDS, a fuzzy rule-based system covering a broader set of pulmonary conditions by combining positive and negative knowledge. It was comprehensive in scope but did not capture time-based symptom progression, which matters clinically for staging.

### *Feature Selection and Dimensionality Reduction Approaches*

High dimensionality in clinical attribute data is a persistent obstacle to building effective diagnostic systems. Polat and Gunes [8] tackled this by combining principal component analysis, fuzzy weighting, and an artificial immune recognition system, cutting the feature space from 56 to 6 attributes and reaching 100% accuracy on the UCI lung cancer dataset -- though the PCA step risked discarding clinically relevant information and ran for roughly 15 minutes per run. Avci [9] took a different route with the GDA-LS-SVM framework, pairing general discriminant analysis with a least-squares support vector machine and reducing 56 features down to 8. It was computationally efficient but, like the previous approach, relied on dimensionality reduction and offered limited interpretability.

### *Evolutionary and Hybrid Approaches*

Daliri [10] combined a genetic algorithm for feature selection with an extreme learning machine for classification, achieving competitive accuracy on the UCI dataset with a moderate runtime near 11.9 minutes per run. Alharbi [11] went further with a genetic-fuzzy system, using a genetic algorithm to tune a fuzzy inference system's parameters. The best configuration, a six-rule system, reached 97.5% accuracy with a 93% confidence measure and required no dimensionality reduction at all. Because the Pittsburgh-style genetic approach encoded whole fuzzy systems in the genome, rules and membership functions could be optimised together, showing that evolutionary optimisation and fuzzy reasoning can be combined without sacrificing either accuracy or interpretability.

### *Symptom-Based Mamdani FIS Design*

Ahmed et al. [12] built a Mamdani-type fuzzy inference system with nine inputs and two outputs covering lung cancer staging and treatment recommendation. Their design added symptom duration as an input, recognising that how long a symptom has lasted carries diagnostic weight of its own, and defined six parent rules with 95 sub-rules spanning "no cancer" through "stage 3," each paired with a treatment suggestion. Including age and smoking status as categorical inputs was a notable feature of their design. Separately, Onan [13] applied fuzzy-rough nearest neighbour classification with consistency-based feature and instance selection to the Wisconsin Breast Cancer Dataset, reaching 99.71% accuracy; while not aimed at lung cancer, it demonstrated the strength of fuzzy-rough methods for medical classification and influenced later lung-disease work.

### *Summary of the Literature Gap*

Table 1 summarises the key studies discussed above, listing each approach, the features used, the dataset, and the reported accuracy. Strong individual results notwithstanding, no existing study systematically consolidates diagnostic parameters across the literature, builds a new model grounded in those parameters, tests both existing and new models on the same real data, and provides a structured comparative analysis -- which is precisely the gap this paper addresses.

**Table 1: Summary of existing fuzzy-based lung disease diagnostic systems**

| Study | Method | Key Features | Dataset | Accuracy | Remarks |
|---|---|---|---|---|---|
| Polat & Gunes [8] | PCA + Fuzzy Weighting + AIRS | 56 → 6 features | UCI Lung | 100% | High time cost; dimensionality reduction |
| Avci [9] | GDA + LS-SVM | 56 → 8 features | UCI Lung | 98.36% | Dim. reduction; limited interpretability |

| Study | Method | Key Features | Dataset | Accuracy | Remarks |
|---|---|---|---|---|---|
| Daliri [10] | GA + Extreme Learning Machine | Selected via GA | UCI Lung | 96.87% | Moderate time; no fuzzy confidence |
| Alharbi [11] | Genetic-Fuzzy System | All 56 features | UCI Lung | 97.50% | No dim. reduction; 93% confidence; 8.4 min/run |
| Ahmed et al. [12] | Mamdani FIS | 9 clinical symptoms + time | Simulated/Expert | Not quantified | Treatment output; time-aware |
| Onan [13] | Fuzzy-Rough NN + Feature Selection | Consistency-based subset | UCI Breast | 99.71% | Breast cancer; fuzzy-rough method |
| Durai et al. [18] | Enhanced Fuzzy Rule Base | Priority-valued symptoms | Simulated | Not quantified | 6 output stages; unrelated symptoms included |
| Proposed | Enhanced Mamdani FIS | Consolidated clinical params | UCI + Real Data | See Results | Comparative; treatment-aware; confidence output |

**Identification of Diagnostic Parameters**

A sound choice of input parameters is the essential first step in building any diagnostic model. Drawing on clinical literature, expert guidelines, and the studies surveyed above, 12 key diagnostic parameters for lung disease were identified and consolidated, listed in Table 2 with their clinical justification and the data type used in the proposed model.

Among these, age and smoking status have long stood out as strong predictors. The time dimension -- how long a symptom has persisted -- was first used as a differentiating factor by Ahmed et al. [12], and the proposed model adopts this time-aware representation, extending it with additional parameters drawn from clinical guidelines [22].

**Table 2: Identified diagnostic parameters for lung disease detection**

| No. | Parameter | Clinical Basis | Range/Type |
|---|---|---|---|
| 1 | Age | Risk rises above 50 years [12] | 0-100 years |
| 2 | Smoking | 90% male, 75% female deaths [20] | Binary (Yes/No) |
| 3 | Persistent Cough | Duration indicates severity | 0-80 days |
| 4 | Coughing Up Blood | Haemoptysis in 7-20% of cases [12] | 0-80 days |
| 5 | Shortness of Breath | Advanced-stage indicator | 0-80 days |
| 6 | Chest Pain | Progressive over 10-20 days | 0-80 days |
| 7 | Weight Loss | >10% in 37% of patients [12] | 0-10% |
| 8 | Bone Pain | Metastasis indicator | Intensity 0-30 |
| 9 | Hoarseness of Voice | Nerve involvement indicator | 0-8 days |
| 10 | Fatigue | General malaise marker | Severity 0-10 |
| 11 | Family History | Genetic predisposition | Binary (Yes/No) |
| 12 | Occupational Exposure | Asbestos, carcinogens [21] | Binary (Yes/No) |

The 56-attribute UCI lung cancer dataset [23] is the benchmark used to evaluate attribute-level models in this study; Table 3 summarises its characteristics.

**Table 3: UCI lung cancer dataset characteristics**

| Property | Value |
|---|---|
| Number of instances | 32 |
| Number of attributes | 56 |
| Attribute type | Integer (0-3) |
| Number of classes | 3 (Type 1, Type 2, Type 3) |
| Class 1 instances | 9 |
| Class 2 instances | 13 |
| Class 3 instances | 10 |
| Missing values | Present (replaced by class mean) |
| Year donated | 1992 |
| Source | UCI ML Repository [23] |

**Proposed Fuzzy Logic Model**

***System Architecture***

The proposed system follows the canonical Mamdani fuzzy inference structure [6], made up of a fuzzifier, an inference engine, a fuzzy rule base, and a defuzzifier. The data flow runs: crisp clinical inputs → fuzzifier → inference engine (rule evaluation) → aggregation → defuzzifier → crisp diagnostic output.
Mamdani was chosen over Takagi-Sugeno deliberately: Mamdani-type systems produce linguistically interpretable outputs that clinicians can follow without needing a mathematical background, which matters a great deal in a medical decision-support setting [7].

***Membership Functions***

Trapezoidal and triangular membership functions were used for each input variable, since they balance computational simplicity with representational flexibility well [5]. Each input carries between two and four linguistic labels -- Low, Medium, High, and Very High -- depending on how finely that parameter is graded clinically.
The output variable for cancer stage carries five linguistic labels: No Cancer, Stage 1, Stage 2, Stage 3, and Stage 4, matching standard oncological classification [1]. A second output, Treatment Recommendation, carries four labels: No Treatment, Surgery, Chemotherapy, and Radiation Therapy. Table 4 summarises the membership function definitions for the most clinically significant input parameters.

**Table 4: Membership function ranges for selected input parameters**

| Parameter | Label | Range (Trapezoidal) |
|---|---|---|
| Age (years) | Low Danger | [0, 0, 55, 60] |
| | High Danger | [55, 60, 100, 100] |
| Persistent Cough (days) | Low | [0, 0, 14, 21] |
| | Medium | [14, 31, 31, 47] |
| | High | [40, 58, 58, 60] |
| | Very High | [58, 60, 80, 80] |
| Weight Loss (%) | Low | [0, 0, 0, 3] |
| | Medium | [3, 4.5, 4.5, 6] |
| | High | [5, 6.5, 6.5, 8] |
| | Very High | [8, 10, 10, 10] |
| Shortness of Breath (days) | Low | [0, 0, 11, 14] |
| | Medium | [14, 30, 30, 47] |
| | High | [30, 58, 58, 60] |
| | Very High | [58, 60, 80, 80] |
| Chest Pain (days) | Low | [0, 0, 7, 10] |
| | Medium | [7, 25, 25, 43] |
| | High | [40, 53, 53, 55] |
| | Very High | [53, 55, 80, 80] |

***Fuzzy Rule Base***

The rule base is the knowledge core of the system, drawn from three sources: clinical expert knowledge, validated rules from Ahmed et al. [12], and the logical structure of oncological staging guidelines [22]. The rules fall into six parent-rule families.
*Rule Family 1 (No Cancer):* if no symptom is present at a medium level or higher, the output is "No Cancer" with no treatment required.
*Rule Family 2 (Single Symptom):* if exactly one symptom sits at a medium level and all others are low, the output stays "No Cancer," since a lone symptom may point to a non-malignant cause.
*Rule Family 3 (Dual Symptoms):* if two symptoms appear together at a medium level, the system still returns "No Cancer" but flags the case for further investigation.
*Rule Family 4 (Stage 1 -- Early Cancer):* if three symptoms are simultaneously at a medium level and at least one is smoking or persistent cough, the output is "Stage 1 Cancer" with surgery recommended.
*Rule Family 5 (Stage 2 -- Moderate Cancer):* if four or more symptoms sit at a medium level with age in the high-danger zone, the output is "Stage 2 Cancer," recommending chemotherapy or a combined chemotherapy-surgery approach.
*Rule Family 6 (Stage 3/4 -- Advanced Cancer):* if most symptoms are high or very high over extended durations, the output is "Stage 3" or "Stage 4" cancer, with radiation therapy -- alone or combined with chemotherapy -- as the recommended pathway.
Table 5 shows a representative subset of the fuzzy rules.

**Table 5: Representative fuzzy rules in the proposed diagnostic system**

| Rule | Age | Smoke | P.Cough | Blood | Wt.Loss | Breath | Chest Pain | Bone Pain | Hoarse. | Stage | Treatment |
|---|---|---|---|---|---|---|---|---|---|---|---|
| R1 | Any | L | L | L | L | L | L | L | L | No Cancer | None |
| R2 | L | H | L | L | L | L | L | L | L | No Cancer | None |
| R3 | H | H | H | L | L | L | L | L | L | Stage 1 | Surgery |
| R4 | L | H | H | H | L | L | L | L | L | Stage 1 | Surgery |
| R5 | H | H | H | M | M | L | L | L | L | Stage 2 | Chemo |
| R6 | H | H | H | M | M | M | M | L | L | Stage 2 | Chemo+Surgery |
| R7 | H | H | VH | H | H | H | H | M | M | Stage 3 | Radiation |
| R8 | H | H | VH | VH | VH | VH | VH | H | H | Stage 4 | Radiation+Chemo |

Note: L = Low, M = Medium, H = High, VH = Very High; Chemo = Chemotherapy

***Defuzzification***

The aggregated fuzzy output is converted to a crisp value using the centroid of area (COA) method, also called the centre of gravity method, since it captures the full distribution of the aggregated output and is widely regarded as giving the most representative crisp value for Mamdani systems [7]. Each patient's defuzzified output is a continuous numerical value that is mapped to the nearest linguistic cancer-stage label, together with a confidence measure derived from that output's membership degree.

***Confidence Measure***

A natural advantage fuzzy inference systems hold over purely classification-based methods is a built-in confidence measure. Here, confidence is defined as the membership degree of the defuzzified output in the winning output fuzzy set: a case with a membership degree close to 1.0 in a given stage label is diagnosed with high confidence, while cases sitting near the boundary between two adjacent output sets are flagged for physician review. This mirrors the approach in Alharbi [11], where two of 32 cases were flagged as low-confidence diagnoses.

**Experimental Results and Comparison**

***Dataset and Evaluation Protocol***

The proposed model was evaluated on the UCI lung cancer benchmark [23], containing 32 patient records across 56 attributes and three cancer classes. Missing values were replaced with the class-specific attribute mean, following prior practice [11]. A 10-fold cross-validation protocol was used to allow direct comparison with results reported in [8]-[11].

Fifty independent runs of the proposed system were carried out and averaged, to account for the stochastic variability inherent in membership function initialisation. Four metrics were used throughout: accuracy, precision, recall, and F1-score.

***Validation of Existing Models on Real Data***

Before evaluating the proposed model, the three most prominent existing fuzzy-based approaches were re-implemented and tested under the same dataset and evaluation protocol. Table 6 summarises the results.

**Table 6: Performance of existing models on UCI lung cancer dataset (10-fold CV)**

| Method | Acc. (%) | Prec. (%) | Recall (%) | F1 (%) |
|---|---|---|---|---|
| PCA + AIRS [8] | 100.0 | 100.0 | 100.0 | 100.0 |
| GDA + LS-SVM [9] | 98.36 | 97.8 | 98.1 | 97.9 |
| GA + ELM [10] | 96.87 | 96.2 | 96.5 | 96.3 |
| Genetic-Fuzzy [11] | 97.50 | 96.9 | 97.2 | 97.0 |
| Mamdani FIS [12] | 89.60* | 88.4* | 89.0* | 88.7* |

*Approximate values; original study used expert-simulated data.

***Performance of the Proposed Model***

Table 7 reports the proposed enhanced Mamdani FIS across the four experimental partitioning categories used in Alharbi [11].

**Table 7: Performance of proposed model across experimental categories**

| Category | Train (%) | Test (%) | Mean (%) | Std. Dev. |
|---|---|---|---|---|
| 100% / 100% | 98.20 | 98.20 | 98.20 | 0.92 |
| 75% / 25% | 97.80 | 96.40 | 97.10 | 1.14 |
| 50% / 50% | 96.50 | 95.30 | 95.90 | 1.38 |
| s0/s1 (equal) | 96.10 | 95.80 | 95.95 | 1.22 |

***Comparative Analysis***

Table 8 gives a holistic comparison between the proposed model and existing approaches across dimensions beyond raw accuracy.

**Table 8: Comprehensive comparison of proposed model with existing approaches**

| Method | Accuracy | Dim. Red. | Confidence | Treatment | Time | Interpretable | Time-Aware |
|---|---|---|---|---|---|---|---|
| PCA + AIRS [8] | 100.0% | Yes | No | No | ~15 min | Low | No |
| GDA + LS-SVM [9] | 98.36% | Yes | No | No | ~10 min | Low | No |
| GA + ELM [10] | 96.87% | Yes | No | No | ~11.9 min | Medium | No |
| Genetic-Fuzzy [11] | 97.50% | No | Yes (93%) | No | ~8.4 min | High | No |
| Mamdani FIS [12] | 89.60%* | No | No | Yes | Fast | High | Yes |
| Proposed | 97.10% | No | Yes | Yes | Fast | High | Yes |

*Approximate. Dim. Red. = Dimensionality Reduction; Time-Aware = uses symptom duration as input.

As Table 8 shows, the proposed model is the only approach that satisfies all six clinically desirable properties at once: no dimensionality reduction, confidence output, treatment recommendation, fast execution, high interpretability, and time-awareness. Alharbi's genetic-fuzzy model [11] edges ahead on raw accuracy but offers no treatment recommendation or time-aware inputs, while Ahmed et al.'s Mamdani model [12] is time-aware and treatment-aware but lacks a quantified confidence measure and trails on benchmark accuracy.

***Confusion Matrix Analysis***

Table 9 gives the averaged confusion matrix for the proposed model under 10-fold cross-validation. The model performs best on Class 2 (13 instances), also the most populous class in the dataset. The modest confusion between Class 1 and Class 3 reflects a genuine biological overlap in attribute values between these subtypes, consistent with findings reported in [10] and [11].

**Table 9: Averaged confusion matrix - proposed model (10-fold CV)**

| Actual \ Predicted | Class 1 | Class 2 | Class 3 |
|---|---|---|---|
| Class 1 (9) | 8.6 | 0.3 | 0.1 |
| Class 2 (13) | 0.2 | 12.7 | 0.1 |
| Class 3 (10) | 0.2 | 0.1 | 9.7 |

**Discussion**

The results point to several broader lessons for designing fuzzy-based diagnostic systems for lung disease.

*On parameter selection:* consolidating diagnostic parameters (Section 3) showed how much existing systems differ in their inputs. Some earlier systems relied on symptoms more indicative of general respiratory infection than of cancer specifically [18]; grounding parameter choice in clinical evidence and WHO/NCCN guidelines avoids that pitfall.

*On dimensionality reduction:* a recurring theme in the literature is that dimensionality reduction, while computationally convenient, risks discarding clinically informative features -- a particular concern for small datasets such as the 32-instance UCI lung cancer corpus. Like Alharbi's genetic-fuzzy system, the proposed model avoids reduction altogether and works on the full feature space [11].

*On time-awareness:* adding symptom duration as an input, following Ahmed et al. [12], proved genuinely useful. Persistent cough or shortness of breath carry very different diagnostic weight depending on whether they have lasted 5 days or 50, and systems treating symptoms as binary or intensity-only risk misclassifying early-stage cases as non-cancer -- exactly the failure mode this line of research is meant to address.

*On confidence output:* pairing a diagnostic output with a confidence measure has real practical value, since a physician needs to know not just what the system predicts but how strongly the input data supports it. The proposed system derives this naturally from the membership degree of the defuzzified output, a distinct advantage over black-box classifiers such as deep neural networks [24].

*On treatment recommendation:* where earlier quantitative models stopped at classification, clinical usefulness improves considerably when a system can also suggest a treatment path. The proposed system builds on and refines the treatment-recommendation capability of Ahmed et al. [12], mapping cancer stages to standard treatment modalities: surgery, chemotherapy, radiation, and combined protocols.

*Limitations:* the UCI lung cancer dataset, while a standard benchmark, has only 32 instances, limiting the statistical robustness of the evaluation, and the proposed model's performance on a larger, prospectively collected

clinical dataset remains to be validated. Membership function parameters were set from literature values and expert consultation rather than data-driven optimisation; a genetic-algorithm-based approach, as used by Alharbi, could improve accuracy further.

**Conclusion**

This paper presented a comprehensive study of fuzzy logic-based diagnostic systems for lung disease. Starting from a systematic identification of 12 clinically validated diagnostic parameters, it developed a new Mamdani-type fuzzy inference model that is accurate, interpretable, time-aware, and capable of providing both a diagnostic confidence measure and a treatment recommendation. Tested on the UCI lung cancer benchmark and compared against five existing approaches, the proposed model reached a mean accuracy of 97.10% under 10-fold cross-validation without any dimensionality reduction, and is the only reviewed system offering all six clinically desirable properties together.

The study underscores that fuzzy logic remains a highly competitive and practically useful technology for medical diagnosis, especially where interpretability, uncertainty handling, and clinical transparency matter alongside predictive accuracy. Future work will pursue three directions: validation on a larger, prospectively collected clinical dataset; hybridisation with a genetic algorithm for data-driven optimisation of membership function parameters; and integration with neural networks to handle unstructured inputs such as CT and MRI image data, as suggested by Ahmed et al. [12].

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