# Classifying Malignant Tumors Through Image Characteristics: A Fuzzy Logic Based Approach

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## 1 Introduction

This paper will seek to utilize fuzzy logic to classify images of tumors as either benign or malignant. An approach that implements fuzzy logic rules based on image characteristics of a tumor has potential to be a far more desirable option for patients than the current standard of care if our results can reasonably approximate the current accuracy standards. We also compare these fuzzy results with results obtained from training a logistic regression classifier - a more widely practiced approach for classification in general. Kora et al. established a similar approach in prediction of the presence of cardiovascular disease in adults by creating fuzzy rules based on subjects' risk factors (Kora, Meenakshi, Swaraja, Rajani, & Islam, 2019), and we believe a similarly effective approach can be applied here.

## 2 Background

A benign tumor is one that is typically harmless and non-cancerous. It is constrained to a single area, and though it is possible for benign tumors to grow malignant, this is uncommon (What are Tumors?). Malignant tumors on the other hand are cancerous and can lead to tragic health outcomes if left untreated. Behind cardiovascular disease, cancer is the second leading cause of death among Americans (FastStats - Leading Causes of Death). To determine whether a cancer is benign or malignant, it is common to perform a biopsy operation (Fayed, 2020). Biopsies are not only invasive procedures that many patients would seek to avoid, they do not guarantee accurate results (Study Looks at Accuracy of Breast Biopsy Results). In pursuit of an alternative option for cancer diagnosis, we therefore seek to classify tumors based on x-ray images, a far cheaper and less invasive option for patients.

In traditional Boolean Logic, truth values of a statement are evaluated as either 1 or 0, (true or false). In fuzzy logic however, the truth value of a statement can be any number in the range of 0 to 1. We are interested in classifying various tumors by characteristics of their images such as "large",

for example, if a particular tumor has a mean radius greater than most other mean radii in the dataset. However, deciding the exact moment where a tumor ceases to be "medium" and becomes "large" can be quite hard to determine objectively. This makes fuzzy logic a desirable approach for our classification technique.

The first step in any fuzzy logic system (FLS) is to "fuzzify" the various input attributes into membership classes (Fuzzy Control Programming, 1997). For example, we may decide to create three fuzzy membership classes for the "mean radius" attribute like small, medium, and large. A membership class is typically depicted on a graph as a function of the measurement of an attribute on the x-axis, and the corresponding truth value from 0 to 1 for which that x value is a member of the class. These functions typically have trapezoidal or triangular shapes, though any shape that represents a function would be possible (Mendel, 1995). For our purposes, we have chosen trapezoidal functions for all fuzzy membership classes. Membership functions overlap with one another in such a way that it is often possible for any particular x value to be related to more than one membership class so long as the truth values for the membership of an x-value sum to 1 as will be demonstrated.

The next step after fuzzification is to create inference rules that we believe to be true. For example, we might observe that large tumors are often malignant and that medium sized ones that have a "rough" smoothness value are also malignant. We could represent these statements with the rules:

1. IF (radius is large) THEN tumor is malignant
2. IF (radius is medium) AND (smoothness is rough) THEN tumor is malignant

After we determine these rules, we now have fuzzy output classes. Much as in our fuzzy membership classes for our inputs, we now have fuzzy output membership classes in which, for example, a tumor may belong to both "benign" and "malignant" with nonzero values. A defuzzification process will convert these truth values from fuzzy to a "crisp" output value of either 0 or 1.

# 3 Methodology

Our data was obtained from the UCI Machine Learning Repository (Dua & Graff, 2019) and loaded into a pandas dataframe. This data contains information for 569 different images of potential breast cancer tumors. There are ten different attributes including radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension. Each tumor image has also been classified as either benign or malignant.

### 3.1 Fuzzification

Our most successful model ultimately came from using rules based off of the "mean radius" and "mean smoothness" features. The nature of creating fuzzy membership classes is rather arbitrary, and so we used our exploratory data analysis (EDA) on the dataset to inform how many fuzzy classes to create. We observed that the "mean radius" class had roughly four main divisions of sizes as can be seen in Figure 1. Figure 2 highlights three approximate divisions for "mean smoothness".

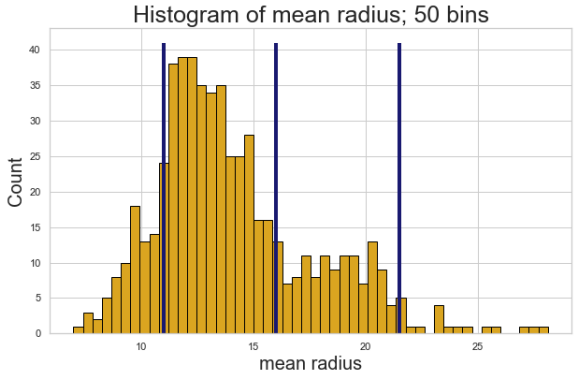


Figure 1: Approximate delineations of mean radius into four sub-classes.

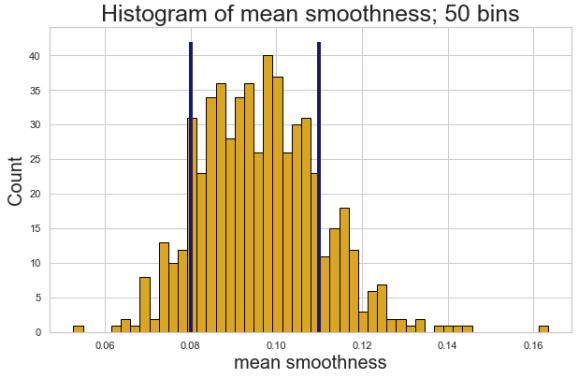


Figure 2: Approximate delineations of mean smoothness into three sub-classes.

Our python function *fuzzify* which will take in a feature from our dataset and a list of the names of fuzzy output classes that we have chosen. We then create divisions across an x-axis range from 0 to 1 which will represent the significant delineations for each trapezoidal shaped class. These shapes will all have equal lengths for the top of the trapezoid with diagonal sides that are each equal to $\frac{1}{2}$ the length of the top. Figure 3 shows the fuzzy membership classes for

"mean radius", where we have chosen to create 4 fuzzy classes named "Small", "Medium", "Large", and "X-Large".


Figure 3: The fuzzy membership classes for mean radius. The value of 17.99 belongs to 2 membership classes.

After creating the framework for the classes, the range is scaled horizontally from [0,1] to the appropriate range for our dataset feature of [min(feature range), max(feature range)]. For each tumor in our data, we then determine the fuzzy membership value of each class by determining where that feature value lies on the x-axis of our fuzzy membership class chart. Figure 3 shows that the value of 17.99 for a mean radius belongs roughly 0.27 to the fuzzy classes "Medium" and 0.73 to "Large".

After much experimentation with various inference rules, the "mean radius" and "mean smoothness" features were chosen. Note that one describes the size of the tumor whereas another describes the shape. These are the two main types of features we have, and picking one from each reduces any multicollinearity, (between "mean radius" and "mean area" for example). Figure 4 shows the fuzzy membership functions that were generated for "mean smoothness" class and how a value of 0.118 is mapped to just a single class with truth value 1.


Figure 4: The fuzzy membership classes for mean smoothness. The value 0.118 belongs only to the "medium" class.

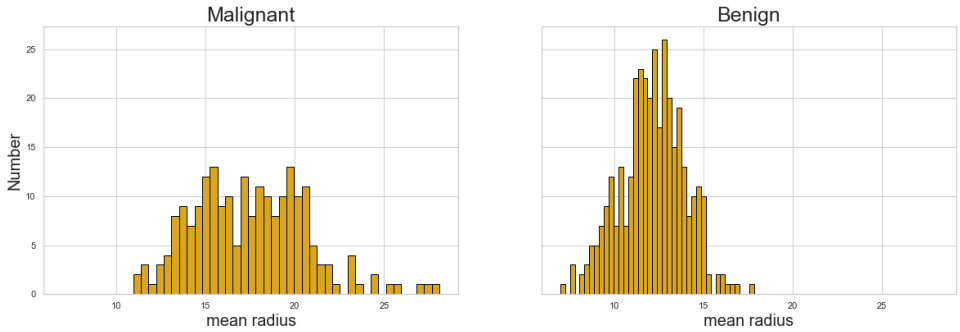


Figure 5: Histograms of tumors by mean radius, grouped by benign vs malignant.

## 3.2 Inference Rules

We now describe our final inference rules that were created for our FLS. Figures 5 and 6 show that we generally observed very few large tumors that were benign, and rougher images tended to correlate with malignancy. This led to the adoption of the following four rules:

**Rule 1**: IF (radius is X-large) THEN tumor is malignant
**Rule 2**: IF (radius is small) THEN tumor is benign
**Rule 3**: IF (radius is large OR medium) AND (smoothness is smooth) THEN tumor is benign
**Rule 4**: IF (radius is large OR medium) AND (smoothness is medium or rough) THEN tumor is malignant

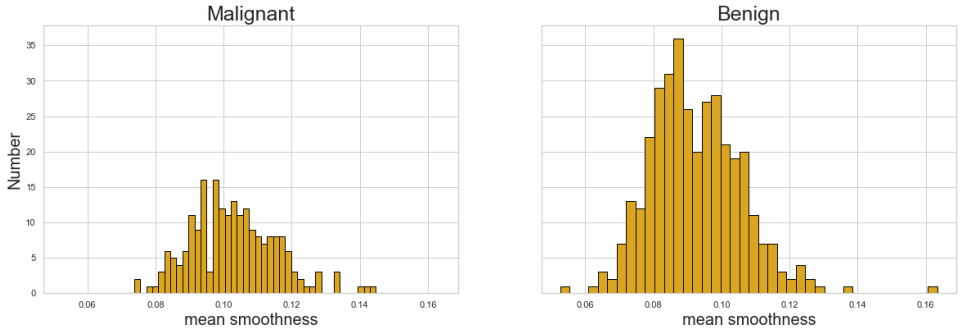


Figure 6: Histograms of tumors by mean smoothness, grouped by benign vs malignant.

### 3.3 Defuzzification

After creating our inferences rules, we can apply them and defuzzify the results. Our function *defuzzify* accomplishes this by considering the effect that each rule contributes to the membership of each fuzzy output class. For example, by Rule 1 we first find the truth value that each entry belongs to class "Fuzzy mean radius class: X-Large". The effect from this rule is then combined with the effect from Rule 4 which also states a rule for our tumor being malignant. After weighting the effects from each of these rules equally, this value is then considered the output for the fuzzy malignant class. A similar procedure is applied for the rules stating the effect of the fuzzy benign output class, (note that here our truth values no longer need to sum to 1). We then take the simple majority between these two fuzzy output classes as the final crisp output, (with any ties being counted as benign as there are more benign than malignant tumors in our dataset).

## 4 Results

To evaluate our model, we compared it to a common logistic regression package *LogisticRegression* from the *sklearn* library in Python. We split the data into a random partition of training size 60% and test size of 40%. The classifier was then trained on a selected feature set evaluated by precision, sensitivity, and specificity. We used the Bootstrap method to repeat this process 100 times and determine the average values across each metric. We found no set of features on which to train our logistic regressor that provided a significantly better result than our set of features used for our fuzzy rules: "mean radius" and "mean smoothness".

For our fuzzy model, note that due to the nature of fuzzy logic we are unable to truly create a training set as a subset of our data - because the rules are created somewhat arbitrarily by a human there is no tractable way to "train" the data across 100 bootstrap samples. We can, however, test our model against the same partitions of data that were used in our standard logistic regression model and determine bootstrap average precision, sensitivity, and specificity values. This ensures that metrics compared between each model can be reliably compared.

Our results as compared to our logistic regressor are summarized in Table 1. We see that the standard logistic regression model provided a significantly better precision value over our fuzzy model. However, our fuzzy based system provided a moderate improvement in sensitivity and a slight improvement in specificity relative to the logistic model.

Table 2 highlights how our model compares to various forms of biopsies (Eisenberg , 2010). Our model cannot reach the accuracy as reported from the most painful and expensive biopsy procedures, however, our model is nearly comparable to a freehand biopsy procedure. This procedure is a less commonly practiced form where no ultrasound or x-ray equipment is used.

| | Precision | Sensitivity | Specificity |
|---|---|---|---|
| Log Regression | 0.8747 | 0.7921 | 0.8838 |
| Fuzzy Model | 0.7232 | 0.8332 | 0.8919 |

Table 1: Mean bootstrap sample results.

| | |
|---|---|
| Surgical Biopsy | 0.98 - 0.99 |
| Ultrasound-guided Biopsy | 0.97 - 0.99 |
| Freehand Biopsy | $\sim 0.86$ |
| Fuzzy Model | 0.8332 |

Table 2: Sensitivity values for various means of predicting breast cancer.

# 5 Discussion

We see that while a standard logistic regression approach provides better precision than our fuzzy model, we argue that the metric we are most concerned with is sensitivity. A low sensitivity value relative to precision implies a high number of false negatives. When dealing with a life-threatening condition such as breast cancer, we believe that patients would be better served if doctors erred on the side of caution when diagnosing. There is very often a trade-off between precision and sensitivity, and here we are interested in ensuring that as many people that actually have a malignant tumor are correctly informed as such as the risks of letting a cancer go untreated are more harmful than leading some patients to believe they have a malignant tumor when indeed their tumor is actually benign. Therefore, we argue that not only can a fuzzy-based system provide a reasonable approach to classification in general, but may very well provide more favorable results as compared to a more well established logistic regression model.

One limitation to our approach is the possibility for our fuzzy model to be over-fitting our data. As discussed, the nature of creating fuzzy rules makes it infeasible to create standard train/test sets, nevertheless, our fuzzy rules are broad enough that we deem it unlikely for our model to be over-fitting.

Improvements in our FLS could come from more exhaustive combinations of features, such as incorporating "mean concavity". Additionally, the effect of creating more fuzzy sub-classes for each feature could be explored. Finally, the shape of the fuzzy sub-classes could also be modified in an attempt to improve results: both modifying the ratios of each side of the trapezoid or exploring other shapes altogether have potential to improve our model.

# 6 Conclusion

We have demonstrated the efficacy of leveraging fuzzy logic on classification of breast cancer tumors as benign or malignant based solely on their images. While this technique does not yet eliminate the need for most common forms of

biopsy procedures, we present this as a viable alternative to a more commonly used logistic regression approach that is worth further investigation with even more nuanced and advanced fuzzy rules.

# 7 References


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