**Mushroom Data Classification**

**CS5950: Machine Learning**

**Final Project**

**By Chris Carlson, Colin MacCreery, and Ben Mechling**

**MUSHROOM DATA**

The mushroom data was obtained from a UCI data repository (<https://archive.ics.uci.edu/ml/datasets/Mushroom>). The data set has 8124 rows and a total of 23 columns. All of the data is categorical. Each value is a single letter representing a value specific to a given attribute (column). The first column “class” indicates whether the mushroom is considered to be poisonous (p) or edible (e). The number of possible values for each attribute varies. The table below shows the possible of each attribute and symbol used to represent it. The largest number of possible values is 12.

|  |  |
| --- | --- |
| **Attribute** | **Values** |
| class | edible=e, poisonous=p |
| cap.shape | bell=b,conical=c,convex=x,flat=f,knobbed=k,sunken=s |
| cap.surface | fibrous=f,grooves=g,scaly=y,smooth=s |
| cap.color | brown=n,buff=b,cinnamon=c,gray=g,green=r,  pink=p,purple=u,red=e,white=w,yellow=y |
| bruises | bruises=t,no=f |
| odor | almond=a,anise=l,creosote=c,fishy=y,foul=f,  musty=m,none=n,pungent=p,spicy=s |
| gill.attachment | attached=a,descending=d,free=f,notched=n |
| gill.spacing | close=c,crowded=w,distant=d |
| gill.size | broad=b,narrow=n |
| gill.color | black=k,brown=n,buff=b,chocolate=h,gray=g,green=r,orange=o,pink=p,purple=u,red=e,  white=w,yellow=y |
| stalk.shape | enlarging=e,tapering=t |
| stalk.root | bulbous=b,club=c,cup=u,equal=e,  rhizomorphs=z,rooted=r,missing=? |
| stalk.surface.above.ring | fibrous=f,scaly=y,silky=k,smooth=s |
| stalk.surface.below.ring | fibrous=f,scaly=y,silky=k,smooth=s |
| stalk.color.above.ring | brown=n,buff=b,cinnamon=c,gray=g,orange=o,  pink=p,red=e,white=w,yellow=y |
| stalk.color.below.ring | brown=n,buff=b,cinnamon=c,gray=g,orange=o,  pink=p,red=e,white=w,yellow=y |
| veil.type | partial=p,universal=u |
| veil.color | brown=n,orange=o,white=w,yellow=y |
| ring.number | none=n,one=o,two=t |
| ring.type | cobwebby=c,evanescent=e,flaring=f,large=l,  none=n,pendant=p,sheathing=s,zone=z |
| spore.print.color | black=k,brown=n,buff=b,chocolate=h,green=r,  orange=o,purple=u,white=w,yellow=y |
| population | abundant=a,clustered=c,numerous=n,  scattered=s,several=v,solitary=y |
| habitat | grasses=g,leaves=l,meadows=m,paths=p,  urban=u,waste=w,woods=d |

**Data Observations**

The attributes values for mushrooms tend to be heavily grouped by the class, making classification somewhat easy.

Class

The number of elements in each class (edible, poisonous) is roughly equal.

|  |  |
| --- | --- |
| **Edible** | **Poisonous** |
| 4208 | 3916 |

Odor

The odor class is the most distinctive attribute. The table below shows the frequency of each value in the feature for each class over the entire data set. Not all the features were this segregated, but some clear division were found in other features as well.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Class** | **a** | **c** | **f** | **l** | **m** | **n (none)** | **p** | **s** | | | | **y** |
| **Edible** | 400 | 0 | 0 | 400 | 0 | 3408 | 0 | 0 | | | | 0 |
| **Poisonous** | 0 | 192 | 2160 | 0 | 36 | 120 | 256 | 576 | | | | 576 |

Veil Type

The veil type attribute is supposed to have two possible values, but in the data only one value exists. All 8124 rows have value “p” (partial). For Bayesian and regression models this column was excluded from the data.

**CLASSIFICATION**

**Directly Available Methods**

Since the data is entirely categorical, numerical methods cannot be directly applied. Methods that can be directly applied are **naive Bayesian classification** (NBC), **classification trees**, and **random forests**.

**Indirect Methods**

While implementing a Bayesian classifier, it was observed that the naive Bayesian approach computes a numeric probability estimate value for each element of a test vector. If a dataset was created using these estimates, then numeric methods could be applied as well. Using an estimate of the log-likelihood that the vector is edible given the value of the feature, numeric training and test sets were built. **Linear discriminate analysis** (LDA), **quadratic discriminate analysis** (QDA), and **logistic regression** (Log.Reg.) were applied.

**Naive Bayesian Classification**

*By Ben Mechling*

The naïve Bayesian classifier computes an estimate probability that a test vector belongs to a class for each class. In the mushroom data there are only two classes: edible and poisonous. The estimate probabilities are computed using a modified form of Bayes theorm. Bayes' theorem is stated as products.

p(c|v) = p(v|c) \* p(c) / p(v)

As is commonly done for classification, the form is converted to sums of logs and the denominator p(v) is discarded.

log(p(c|v)) = log (p(c)) + sum(log(p(v\_i|c)))

To find probabilities in a formal sense, the number of occurrences is divided by the total number of elements.

p(x) = freq(x)/n

log(p(x)) = log(freq(x)) - log(n)

For this application, however, the size of the set only scales the results. Experimentally, probability estimates were better by ignoring the -log(n) term in computations.

estimate(c|v) = log(freq(c)) + sum(log(freq(v\_i|c)))

Thus, the estimate value use in the implementation uses log frequencies rather than proper probabilities.

The freq(v\_i|c) value of is the number of occurrences of the given feature value in a given class. A heuristic was used to replace log(freq(v\_i|c)) the value never occurred in class c. Naturally the arithmetic results in negative infinity, which is difficult to use in computation. In such cases, the -log(freq(v\_i)), the negative log frequency over all classes used as a more reasonable penalty. With this approach if the edible class never have value v\_i, but the number of occurrences was large and all poisonous, a large penalty would be given to the estimate probability of the test being edible. On the other hand, if the number of occurrences was small and all were poisonous, Then a smaller penalty was given.

*For the mushroom data, features values had a tendency exclusively used by one class. For Bayesian classification, the experimental results improved when the penalty was large. Some of the best results were found for a penalty of -log(freq(v\_i)) \* 100. It is believed large penalties push that results strongly to one side or the other and the because the data is very segregated this strong push tends to be accurate. In the general scope of this assignment, the \* 100 multiplier was not used.*

Results

Using 5-fold cross validation NBC gave the following results.

|  |  |  |
| --- | --- | --- |
|  | Actual Edible | Actual Poisonous |
| Predicted Edible | 4206 | 78 |
| Predicted Poisonous | 0 | 3838 |

Using the heavily weighted penalties as described above better results can be found.

|  |  |  |
| --- | --- | --- |
|  | Actual Edible | Actual Poisonous |
| Predicted Edible | 4206 | 3 |
| Predicted Poisonous | 2 | 3913 |

**Indirect Numerical Classification**

*By Ben Mechling*

The computation process for NBC computes sum(log(freq(v\_i|c))) for each class. Effectively the NBC model has two training data sets: one set with edible mushrooms and one set with poisonous mushrooms. In order to run numerical methods, a single numerical training data needed to be created. Thus for a given value v\_i a single and useful number was needed. In experimentation, the best form found was a subtraction to the two values.

numericalData(v\_i) = freq(v\_i|edible) – freq(v\_i|poisonous)

This form seemed theoretically reasonable given the form for the odds' of a value.

odds(x) = p(x)/(1-p(x))

logit(x) = log(odds) = log(p(x)) – log(1-p(x))

For this implementation, proper probabilities were not used, thus 1-p(x) is not a good estimate. The estimate of p(poisonous) should reasonable inverse for p(edible).

estimate logit(v\_i) = log(edible) – log(poisonous)

For practical use, the value will be positive if the data supports edible and negative if the data supports poisonous.

For each training set of original data, version of the mushroom data was created as numerical data. From this numerical data, train and test data sets were partitioned in the same manner as the original data. Using the standard R modeling functions on the training data, LDA, QDA, and logistic regression models were built and predictions were made over the numerical test data.

Results

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|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Regular Penalty | Actually Edible | Actually Poisonous | Heavy  Penalty | Actually Edible | Actually Poisonous |
| Predicted Edible | 4206 | 78 | Predicted Edible | 4206 | 3 |
| Predicted Poisonous | 0 | 3838 | Predicted Poisonous | 2 | 3913 |

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**Decision Tree Classification**

*By Chris Carlson*

The Decision tree classifier was constructed in R using the ‘rpart’ package. Due to the nature of the data the decision tree classifier was a simple and effective classifier to build. As mentioned in the introduction, the data can be split using only two feature vectors, odor and spore-print-color, with excellent results. The sample plot shown below is representative of the trees rpart builds. In fact, without imposing additional constraints, the rpart package always splits this data on these two features regardless of how the data subsets are arranged.



**Random Forest Classification**

*By Chris Carlson*

The Random Forest classifier was produced using the r package called ‘randomForest’. The results of random forest classification were much better than the simple decision tree, which is expected. Typical test error rates for random forest models were less than 0.01, which is the second best result we achieved - the best being logistic regression on Bayesian probabilities. The random forest classifier was tested with as many as 500 trees and as few as 150 trees, and the number of variables available per split was also adjusted from between 3 up to 8. Overall adjusting these characteristics didn’t affect test error rates significantly. Shown below are confusion matrices produced by the random forest algorithm in a typical k-folds cross validation.



**CROSS VALIDATION**

**K-Folds Cross Validation**

K-Folds Cross Validation was used for all model types, though the specific implementation differs between the tree based approaches and the Bayesian approaches. For the Bayesian approaches cross validation was computed precisely according to the method description; the data is dived into k equal size subsets, and for k iterations one section of the data is held out as testing data, and the remaining data is used to build a model which is subsequently tested on the test data. The results for each iteration are reported individually and an average across iterations is reported. For the decision tree methods cross validation was implemented slightly differently; in this approach a tree-model was generated for each of the folds individually, and each of these models was tested on the test data. The results of each model were averaged to determine the test error for each fold.