



animal name: string hair: Boolean feathers: Boolean eggs: Boolean milk: Boolean airborne: Boolean aquatic: Boolean predator: Boolean toothed: Boolean backbone: Boolean breathes: Boolean venomous: Boolean fins: Boolean legs: {0,2,4,5,6,8} tail: Boolean domestic: Boolean catsize: Boolean type: {mammal, fish, bird, shellfish, insect, reptile, amphibian}

Zoo data

101 examples

aardvark,1,0,0,1,0,0,1,1,1,1,0,0,4,0,0,1,mammal antelope,1,0,0,1,0,0,1,1,1,1,0,0,4,1,0,1,mammal bass,0,0,1,0,0,1,1,1,1,0,0,1,0,1,0,1,0,fish bear,1,0,0,1,0,1,0,1,1,1,1,0,0,4,0,0,1,mammal boar,1,0,0,1,0,0,1,1,1,1,0,0,4,0,1,mammal buffalo,1,0,0,1,0,0,0,1,1,1,0,0,4,1,0,1,mammal calf,1,0,0,1,0,0,0,1,1,1,0,0,4,1,1,1,mammal carp,0,0,1,0,0,1,0,1,1,0,0,1,0,1,1,0,fish cartish,0,0,1,0,0,1,1,1,0,0,4,0,1,0,mammal chectah,1,0,0,1,0,0,1,1,1,0,0,4,1,0,1,mammal chectah,1,0,0,1,0,0,1,1,1,0,0,4,1,0,1,mammal chicken,0,1,1,0,1,0,0,1,1,1,0,0,4,1,0,1,mammal chicken,0,1,0,0,1,1,1,0,0,1,0,0,5,sh clam,0,0,1,0,0,1,1,1,0,0,1,0,1,0,0,fish crab,0,0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,shellfish crab,0,0,1,0,0,1,1,0,0,0,0,0,0,0,0,0,0,shellfish ...

Zoo example

aima-python> python
>>> from learning import *
>>> zoo
<DataSet(zoo): 101 examples, 18 attributes>
>>> dt = DecisionTreeLearner()
>>> dt.train(zoo)
>>> dt.predict(['shark',0,0,1,0,0,1,1,1,1,0,0,1,0,1,0,0])
'fish'
>>> dt.predict(['shark',0,0,0,0,0,1,1,1,1,0,0,1,0,1,0,0])
'mammal'

Evaluation methodology (1)

Standard methodology:

- 1. Collect large set of examples with correct classifications
- 2. Randomly divide collection into two disjoint sets: *training* and *test*
- 3. Apply learning algorithm to training set giving hypothesis H
- 4. Measure performance of H w.r.t. test set

Evaluation methodology (2)

- Important: keep the training and test sets disjoint!
- Study efficiency & robustness of algorithm: repeat steps 2-4 for different training sets & training set sizes
- On modifying algorithm, restart with step 1 to avoid evolving algorithm to work well on just this collection

Evaluation methodology (3)

Common variation on methodology:

- 1. Collect large set of examples with correct classifications
- 2. Randomly divide collection into two disjoint sets: *development* and *test*, and further divide development into *devtrain* and *devtest*
- 3. Apply learning algorithm to *devtrain* set giving hypothesis H
- 4. Measure performance of H w.r.t. *devtest* set
- 5. Modify approach, repeat 3-4 ad needed
- 6. Final test on *test* data

Zoo evaluation

train_and_test(learner, data, start, end) uses data[start:end] for test and the rest for train

```
>>> dtl = DecisionTreeLearner
```

>>> train_and_test(dtl(), zoo, 0, 10)

1.0

>>> train_and_test(dtl(), zoo, 90, 100)

0.800000000000000004

>>> train_and_test(dtl(), zoo, 90, 101)

0.81818181818181823

>>> train_and_test(dtl(), zoo, 80, 90)

0.900000000000000002

K-fold Cross Validation

- Problem: getting "ground truth" data can be expensive
- Problem: ideally need different test data each time we test
- Problem: experimentation is needed to find right "feature space" and parameters for ML algorithm
- Goal: minimize amount of training+test data needed
- Idea: split training data into K subsets, use K-1 for *training*, and one for *development testing*
- Common K values are 5 and 10

Zoo evaluation

cross_validation(learner, data, K, N) does N iterations, each time randomly selecting 1/K data points for test, rest for train

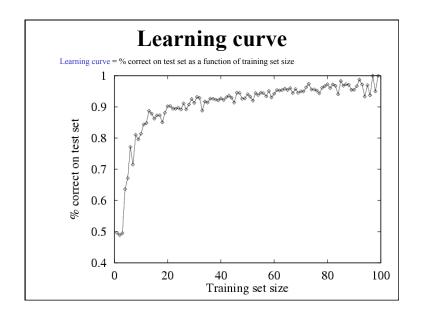
>>> cross_validation(dtl(), zoo, 10, 20)

0.955000000000000007

leavelout(learner, data) does len(data) trials, each using one element for test, rest for train

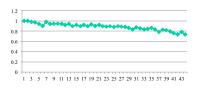
>>> leave1out(dtl(), zoo)

0.97029702970297027



Zoo

>>> learningcurve(DecisionTreeLearner(), zoo)
[(2, 1.0), (4, 1.0), (6, 0.983333333333333), (8,
0.974999999999999), (10, 0.9400000000000000), (12,
0.90833333333333331), (14, 0.98571428571428577), (16,
0.9375), (18, 0.9499999999999), (20,
0.944999999999995), ... (86, 0.78255813953488373), (88,
0.7363636363636363644), (90, 0.70777777777777795)]



Iris Data

- Three classes: Iris Setosa, Iris Versicolour, Iris Virginica
- Four features: sepal length and width, petal length and width
- 150 data elements (50 of each)

aima-python> more data/iris.csv

5.1,3.5,1.4,0.2,setosa

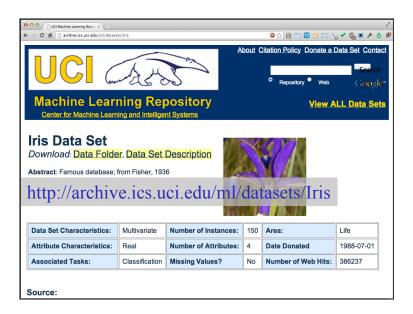
4.9,3.0,1.4,0.2,setosa

4.7,3.2,1.3,0.2,setosa

4.6,3.1,1.5,0.2,setosa

5.0,3.6,1.4,0.2,setosa

http://code.google.com/p/aima-data/source/browse/trunk/iris.csv



Comparing ML Approaches

- The effectiveness of ML algorithms varies depending on the problem, data and features used
- You may have institutions, but run experiments
- Average accuracy (% correct) is a standard metric >>> compare([DecisionTreeLearner, NaiveBayesLearner, NearestNeighborLearner], datasets=[iris, zoo], k=10, trials=5)

iris zoo

DecisionTree 0.86 0.94

NaiveBayes 0.92 0.92

NearestNeighbor 0.85 0.96

Confusion Matrix (1)

- A <u>confusion matrix</u> can be a better way to show results
- For binary classifiers it's simple and is related to <u>type I and type II errors</u> (i.e., false positives and false negatives)
- There may be different costs for each kind of error
- So we need to understand their frequencies

predicted			
a/c	C	~C	
С	True positive	False negative	
~C	False positive	True negative	

Confusion Matrix (2)

- For multi-way classifiers, a confusion matrix is even more useful
- It lets you focus in on where the errors are

ored		

		Cat	Dog	rabbit
actual	Cat	5	3	0
	Dog	2	3	1
	Rabbit	0	2	11

Accuracy, Error Rate, Sensitivity and Specificity

	A\P	С	¬C	
	С	TP	FN	P
1	¬C	FP	TN	N
1		Ρ'	N'	All

- Classifier Accuracy, or recognition rate: percentage of test set tuples that are correctly classified
 - Accuracy = (TP + TN)/AII
- Error rate: 1 accuracy, or Error rate = (FP + FN)/All

- Class Imbalance Problem:
 - One class may be rare, e.g. fraud, or HIV-positive
 - Significant majority of the negative class and minority of the positive class
 - Sensitivity: True Positive recognition rate
 - Sensitivity = TP/P
 - Specificity: True Negative recognition rate
 - Specificity = TN/N

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Precision and Recall

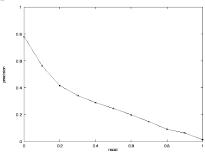
- Information retrieval uses <u>precision and recall</u> to characterize retrieval effectiveness
 - Precision: exactness what % of tuples that the classifier labeled as positive are actually positive
- -Recall: completeness what % of positive tuples did the classifier label as positive?

$$precision \ = \ \frac{TP}{TP+FP}$$

$$recall = \frac{TP}{TP + FN}$$

Precision and Recall

- In general, increasing one causes the other to decrease
- Studying the precision recall curve is informative



Precision and Recall If one system's curve is always above the other, it's better Output Description and Recall If one system's curve is always above the other, it's better

F measure

The F measure combines the two into a useful single metric $F = \frac{2 \times precision \times recall}{precision + recall}$

Actual\Predicted class	cancer = yes	cancer = no	Total	Recognition(%)
cancer = yes	90	210	300	30.00 (sensitivity
cancer = no	140	9560	9700	98.56 (specificity)
Total	220	0770	10000	06 40 (accuracy)

