Ensembles and Model Evaluation

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Two parts to Models

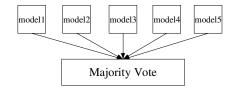
- Induction
 - Induce, Learn, Create, Make, Grow [a model]
- Inference
 - Infer, label, classify, deduce new examples with [a model]

Announcements

- Review Session
 - Tuesday, Nov 1st 4:30-5:30pm CS 1325
 - Come with quesions, no lecture prepared.
- Homework 3 due today
- Homework 2 returned today
 - Does NOT include the grade on the programming portion
 - still calculating that
 - Tournament is half over, we have the winners on the 7x7 standard board but still need to run on the previously "unseen" board

Two Heads are Better Than One

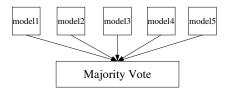
- induce N (say N=5) models from the training data
- Classify new examples by simple majority voting among the N models
- For the ensemble to mis-classify a new example, at least 3 of the 5 hypotheses have to mis-classify it.





Ensembles

- Assume
 - Each hypothesis, h, has error rate of p
 - The probability that a randomly chosen example is misclassified.
 - Errors made by each hypothesis are independent
- With 5 hypothesis, if p=0.10 then the ensemble will mis-classify with a rate less than 0.01

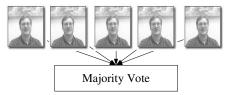


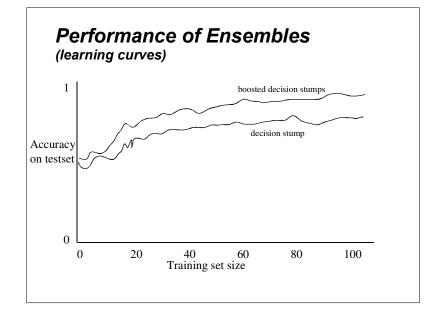
Boosting

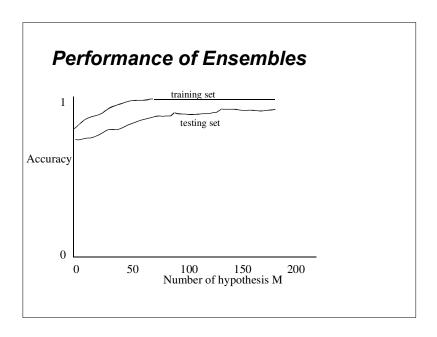
- Each example in training set is weighted
 - Initial weight is 1
- Induce a model on training set, using weights
- Change weights
 - increase weight of examples in training set that are misclassified
 - decrease weight of examples in training set that are correctly classified
- Repeat until you have M models
- Classify using a weighted vote of the M models
- Understand the general idea of Adaboost algorithm (figure 18.10)

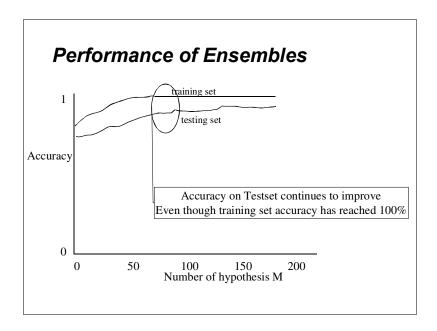
Getting Independence

- What if each model were trained the same, on the same training set?
 - Would the models have independent errors?
- Boosting is a method to help in creating models that are different, thus independent, in misclassification
- Different is Good! (at least when everybody else is wrong)



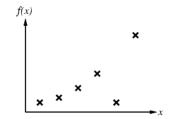






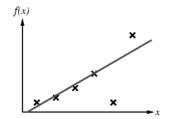
Inductive learning method

- Construct/adjust h to agree with f on training set
- (h is consistent if it agrees with f on all examples)
- E.g., curve fitting:



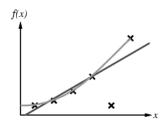
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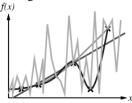
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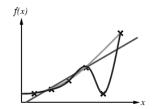
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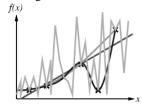
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Inductive learning method

- Construct/adjust h to agree with f on training set
- (*h* is consistent if it agrees with *f* on all examples)
- E.g., curve fitting:



 Ockham's razor: prefer the simplest hypothesis consistent with data

Model Evaluation

- Given two models:
 - how do you decide which one is better for a given task (on a given dataset)?
 - Accuracy
 - Accuracy with cross-validation
 - Confusion Matrix
 - Recall, Precision

Reducing the Error in the Estimation

- N-Fold Cross Validation
 - For a given dataset split into N disjoint subsets

 Dataset

 Set 1 | Set 2 | Set 3 | Set 4 | Set 5

- Train on N-1 of the sets and test the accuracy of the left out set
- Do this for each combination of train/test split (N possible ways)
- Report the average accuracy of the N test set accuracies along with error bars (standard deviation)

Model Evaluation

- Accuracy (inversely error rate)
 - What is the probability of labeling some new example correctly?
- Estimating Accuracy
 - Fraction of examples in some previously unseen dataset that are labeled correctly
 - Why is this just an estimate?

The dataset may not be representative sample i.e. it is too easy or too hard

N-Fold Cross Validation

• Model 1

0.78 0.72 0.77 0.73 0.80

Which Model would you choose? why?

average accuracy: 0.76standard deviation: 0.03

• Model 2

0.62 0.88 0.70 0.81 0.77

average accuracy: 0.76standard deviation: 0.10

• Standard Deviation

 $s = \sqrt{\text{var}} = \sqrt{\frac{\sum (X - \overline{X})^2}{N - 1}}$

 The standard deviation is defined as the average amount by which scores in a distribution differ from the mean

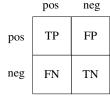
Confusion Matrix

- Imagine a model that predicts if a tumor is malignant or benign:
 - Is it just as bad to
 - incorrectly predict that a person has cancer when they don't
 - incorrectly predict that a person doesn't have cancer when they do
- When evaluating models we want to know what kind of errors they made – Create a Confusion Matrix of the models on the test set

Confusion Matrix

Actual

Predicted



TP – True Positives FP – False Positives FN – False Negatives TN – True Negatives

Confusion Matrix

Model 1 Actual

Model 2 Actual

		pos	neg
Predicted	pos	700	0
	neg	300	1000

pos neg
1000 300
neg 0 700

What is the accuracy of the two models? Which model would you want diagnosing if your tumor were malignant or benign?

Predicted

Skewed Data

- Hypothetical Dataset
 - Negatives 500,000 examples
 - Positives 100 examples
- Lots of real data is like this. Imagine The tumor scenario. Most people don't have cancer.
- Suppose you create a model that always guesses negative. What will your accuracy on the dataset be? 99.99% Wow, what a great model!
- But we want to get the positive examples right.
- Two metrics are commonly used when working with skewed data: precision and recall

Precision and Recall

- Recall What fraction of the positive examples did your model find (predict positive) Recall=
- Precision What fraction of the predicted positive examples were actually positive Precision=

Actual

Predicted

pos neg TP FP pos TN FN

Precision and Recall

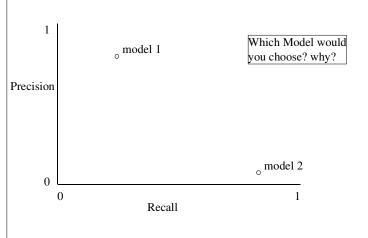
- Recall What fraction of the positive examples did your model find (predict positive) Recall= TP/(TP+FN)
- Precision What fraction of the predicted positive examples were actually positive Precision= TP/(TP+FP) Actual

pos

Predicted

TP FP pos FN TN

Recall and Precision "Space"



Conclusion

- Ensembles
- Ockam's Razor
- Accuracy
- N-Fold Cross Validation
- Confusion Matrix
- Recall and Precision