# Introduction to Machine Learning

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## Outline

# **Quick Review**

# **Model Complexity**

Bias - Variance Tradeoff

#### Performance

N-Fold Cross-Validation

## Features

Feature Engineering Feature Preprocessing

## **Nonlinear Models**

Naive Bayes

Arrhythmia Classification



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#### One should almost always prefer discriminative models over generative models, when possible

["On Discriminative vs. Generative classifiers", Andrew Ng and Michael Jordan, NIPS '01]



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Plots for various values



http://en.wikipedia.org/wiki/Normal\_distribution



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- One can simply compute the mean μ and variance σ<sup>2</sup> of these observations and approximate the distribution through N(μ, σ<sup>2</sup>)
- ... it's also incredibly simple, though it might look complicated



#### **The Bias - Variance Tradeoff**

$$\mathsf{MSE} = \frac{1}{n} \sum_{i} (\hat{y}_i - y_i)^2$$

The mean squared error of a classifier can be split as
 MSE = bias<sup>2</sup> + variance + noise [homework: research the math behind it<sup>1</sup>]



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To explain what the bias and variance are, assume that one trains the same model multiple times on the different subsets of data



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Represents a systematic error due to the model.



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Represents a systematic error due to the impact of data variability on the model



#### **Dartboard: Bias and Variance**



Dartboard analogy, Introduction to the Practice of Statistics, Moore & McCabe, 2002

Why do we say we trade one against the other in ML?



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- Higher dimensionality often implies higher variance and one could reduce it through principal component analysis or feature selection
- Ensemble methods are often used, bagging is used to reduce variance, while boosting to reduce bias [homework!]



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- Split the dataset into N subsets and use N-1 of those for training and one for testing
- Average the MSE accross all N trials



#### **Testing: N-Fold Cross-Validation**



Figure : 5-Fold Cross-Validation



- Advantage: makes best use of available data
- Disadvantage: very expensive computationally
- Leave-one-out (LOO): N = number of samples

scikit-learn already has everything you need <sup>2</sup>



<sup>2</sup> http://scikit-learn.org/stable/modules/cross\_validation.html

General workflow of supervised learning



- General workflow of supervised learning
- Statistics behind the data
- Types of models and some particular models
- Optimization criterias and kinds of error rates

How about getting the most out of the data we have?



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 Unfortunately, there's no recipe for this part and domain specific knowledge for designing features leads to huge improvements



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- Experimentally vary the subset of features you're using
- Let's look at a couple of problems and their features



## Feature Engineering: On-line Handwriting Recognition

Data: { $p_i = (x_i, y_i, t_i)$ } (two-dimensional points with time)

Two classes of features:



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Off-line matrix representation of the handwriting

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Data: { $p_i = (x_i, y_i, t_i)$ } (two-dimensional points with time)

Some of the first class features:

- [continous] normalized x, y coordinates
- [boolean] pen-up/pen-down
- [continous] cosine and sine of the writing direction
- [continous] average square distance to vicinity points
- [continous] length and aspect of trajectory
- [continous] angle of the straight line between vicinity ends

["Feature Selection for On-Line Handwriting Recognition of Whiteboard Notes", M. Liwicki and H. Bunke, '07]



Goal: identify one of the 16 types of arrhythmia Data: ecg images of patients (279 features)

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Types of features:

- Patient personal records
- Features extracted from ECG





["A Supervised Machine Learning Algorithm for Arrhythmia Analysis", H. A. Guvenir et al., '98]

Goal: identify one of the 16 types of arrhythmia Data: ecg images of patients

Some of the patient characteristics:

- [continous] age
- [boolean] sex
- [continous] height, weight

Some of the patient characteristics:

- [continous] average QRS duration in msec.
- [continous] average duration between onset of P and Q
- [continous] average width of Q, R, S waves
- [boolean] existence of notched R,P,T wave

["A Supervised Machine Learning Algorithm for Arrhythmia Analysis", H. A. Guvenir et al., '98]



Goal: predict which types of people are going to survive Data: passengers information

Some of the features:

- [continous] passenger class
- [boolean] sex
- [continous] age
- [continous] number of siblings/spouses aboard
- [continous] number of parents/children aboard
- [continous] ticket number
- [continous] port of embarkation

Check it out at: http://www.kaggle.com/c/titanic-gettingStarted



# What particular problems are you interested in?



 Preprocessing is an important step in helping the model get the most out of the data

Luckily, scikit-learn implements a lot of these methods <sup>3</sup>



<sup>3</sup>http://scikit-learn.org/stable/modules/preprocessing.html

- The dataset might have missing or corrupted values, especially in the case where features were extracted manually by experts or through crowd-sourcing
- Solution 1: replace missing values with mean, median or the most frequent values
- Solution 2: first cluster entries together through similarity between known features, and then complete missing ones



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## Feature Prepocessing: Rescaling and Normalization

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- Models might be sensible to these simple dimensionality variations
- Think of linear models, regularization and the impact of feature dimensionality on the weights
- Common approach is to normalize features to have zero mean and unit variance, thus following N(0,1), regardless whether they are actually normally distributed



#### **Feature Prepocessing: Correlations**

 Correlations between features [how do you identify them?] are subtle and can impact the performance of the underlying model



1:25

["Feature Selection for On-Line Handwriting Recognition of Whiteboard Notes" M. Liwicki and H.



## **Principal Component Analysis: Overview**

- Simple unsupervised model for dimensionality reduction
- Build new K-dimensional of uncorrelated features





## Principal Component Analysis: Understanding Data

- Simple model to start and understand better the data
- Simple to implement, and available in scikit-learn



First centered Olivetti faces

Eigenfaces - RandomizedPCA - Train time 1.6s



• Eigenfaces - 4096 features (64 x 64)  $\rightarrow$  16 features



http://scikit-learn.org/0.13/modules/decomposition.html

- The input-output mapping function can be nonlinear
- Through nonlinear models one can learn this mapping
- Through nonlinear models, such as deep learning, one might also project data in a new higher-order feature spaces



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Recall Bayes Rule

$$P(y|x) = \frac{P(y)P(x|y)}{P(x)}$$

Terminology

Posterior =  $\frac{\text{Prior x Likelihood}}{\text{Evidence}}$ 



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- The prior P(y) can either be modeled from train data (counts), or if there's a known distribution of the class labels, it can be directly used
- Consider  $x = (x_1, x_2, ..., x_n)$ , then the likelihood is  $P(x|y) = P(x_1, x_2, ..., x_n|y) =$   $P(x_1|y)P(x_2, x_3, ..., x_n|y, x_1) =$   $P(x_1|y)P(x_2|y, x_1)P(x_3, ..., x_n|y, x_1, x_2) =$  $P(x_1|y)P(x_2|y, x_1)P(x_3|y, x_1, x_2)...P(x_n|y, x_1, ..., x_{n-1})$



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- ► Back to our original problem  $P(y|x_1,...,x_n) \propto P(y) \prod_i P(x_i|y)$



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- Mathematically,  $P(x_i|y, x_1, ..., x_{i-1}) = P(x_i|y)$
- ► Back to our original problem  $P(y|x_1,...,x_n) \propto P(y) \prod_i P(x_i|y)$
- ► So what about P(x<sub>i</sub>|y)?



► Think about spam classification of a document (words  $w_i$ ):  $P(y = spam | w_1, ..., w_n) \propto P(y = spam) \prod_i P(w_i | y = spam)$ 



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• How can we compute  $P(w_i|y = spam)$  from training set?



- In the case of continous features, the probability is often modeled using a normal distribution
- The mean and variance are computed from the feature values found in the training data

$$P(x_i = v | y) = rac{1}{\sqrt{2\pi\sigma_{x_i,y}^2}} \exp^{-rac{(v - \mu_{x_i,y})^2}{2\sigma_{x_i,y}^2}}$$



Questions?



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Next: classifying arrhythmia patterns using naive bayes

