

Machine Learning

Computer Sciences 760

Spring 2017

www.cs.wisc.edu/~dpage/cs760/

CS 760: Machine Learning

- Professor: David Page
 - email: page@biostat.wisc.edu, put “760” in subject for any email
 - office hours: 1pm-2pm TR in 1153 WID, starting tomorrow
 - other times by appointment in 3174 WID
- TAs:
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Monday, Wednesday and Friday?

- We'll have 30 lectures in all, just like a standard TR class
- Most weeks we'll just meet Mon and Wed
- Some weeks we'll meet on Friday
- This arrangement facilitates making up for days I'm out of town
- First three weeks we will meet MWF
- I will give 2 weeks' advance notice for other Fridays that the class meets

Class capacity



- Used to be limited to 30
- Demand has grown well over 200, hence now twice/year
- I've allowed 110 to register (room capacity)

Course emphases

- a variety of learning settings: supervised learning, unsupervised learning, reinforcement learning, active learning, etc.
- a broad toolbox of machine-learning methods: decision trees, nearest neighbor, Bayesian networks, SVMs, etc.
- some underlying theory: bias-variance tradeoff, PAC learning, mistake-bound theory, etc.
- experimental methodology for evaluating learning systems: cross validation, ROC and PR curves, hypothesis testing, etc.

Two major goals

1. Understand what a learning system should do
2. Understand how (and how well) existing systems work

Course requirements

- 5 homework assignments: 40%
- midterm exam (late in semester): 35%
- project (groups of 4-5): 25%

Homework 1

- Due in two weeks (2/1)
- Download Weka (it's free; you might already have access; if not, Google it)
- Create a data set of your choosing
 - At least 20 examples (data points)
 - At least 10 features (variables)
- Run decision trees, nearest neighbor, others if you want and submit a PDF report (1 page) at course moodle

Expected background

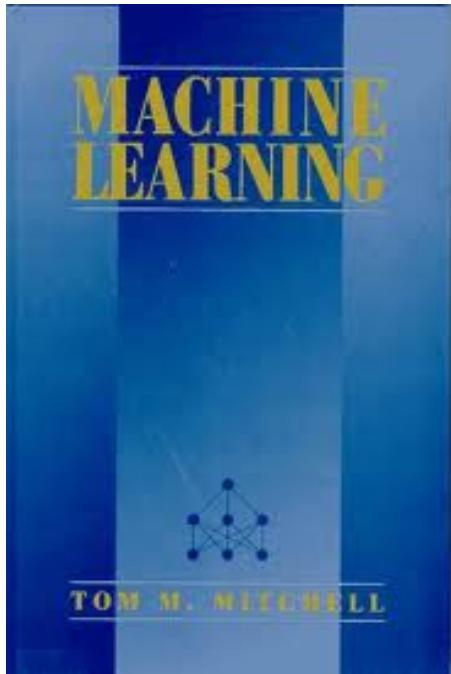
- CS 540 (Intro to Artificial Intelligence) or equivalent
 - search
 - first-order logic
 - unification
 - deduction
- reasonable programming skills
- basics of probability: but we'll review
- linear algebra
 - vectors and matrices
- calculus
 - partial derivatives

Programming languages

- for the programming assignments, you can use
 - C
 - C++
 - Java
 - Perl
 - Python
 - R
- programs must be callable from the command line and *must run on the CS lab machines (this is where they will be tested during grading!)*

Course readings

- *Machine Learning*. T. Mitchell. McGraw Hill, 1997.



- additional on-line articles, surveys, and chapters

What is machine learning?

- the study of algorithms that improve their performance P at some task T with experience E
- to have a well defined learning task, we must specify: $\langle T, P, E \rangle$

ML example: spam filtering

From fidelity <find-daily@littlesossuscamp.com>☆
Subject \$25k-life-policy-for-\$1-per-month
To Mark Craven☆
 Junk Mail

\$250,000 life insurance policy for around
\$10/month

From Dr. Sanusi Joseph <joseph@yahoo.com>☆
Subject AFTER A SERIOUS THOUGHT.....
Reply to sanusijoseph@yahoo.cn☆
To undisclosed-recipients: ☆
 Junk Mail

\$250,000 policy f
.click h
protect
\$250k p

Dear friend.

I decided to reach you directly and personally because i do not have anything against you, but your Nigerian partners.I am the director of wire transfer/telex department of the central bank of Nigeria,Some time in the past, my ministry here in Nigeria had some problems with some of our partners in the oil industry, so we had to help program to help protect our country's interest.

According to the information i have, your company has been receiving money from us for some time now, and we would give me a percentage of the money paid, instead of threats.i immediately accepted the position, and requested to be paid in full, and inherit the rest of the work, they started to work, they started to succeed. i was very happy, but i was breached of trust.

From breaking news <find-daily@illinoisccommittee.com>☆
Subject green-coffee-bean-study-results:-they-lost-17lbs-in-22-weeks
To Mark Craven☆
 Junk Mail

Is this email not displaying correctly?
[View it in your browser.](#)

green-coffee-bean-study-results:-they-lost-17lbs-in-22-weeks

Dr-Oz is calling this a "Miracle-In-A-Bottle".

The Fresh Green Bean Coffee Diet is being hailed a medical breakthrough in weight loss.

[READ FULL ARTICLE HERE](#)

From Nature News Alert <Nature_News@ealert.nature.com>☆
Subject Nature News highlights: 04 September 2012
To Mark Craven☆
 Junk Mail

Can't view this email? [Click here to view in your browser.](#)

04 September 2012

nature news alert
Your weekly update from *Nature*'s global news team.

 [get polished and published](#)
Is your paper ready for publication? AJE can help you get it published faster. Our editors and experts in editing and publishing can help you get your paper published faster. Visit [www.aje.com](#)

From "Yale, Steven H MD" <yale.steven@marshfieldclinic.org>☆
Subject FW: WGI Demonstration Project Final Report
To Mark Craven☆
 Junk Mail

Mark,

I will work on the draft for the report. I am still working on adjudicating cases within the MC system with post-hospitalization DVT and PE. I hope to have this done in the next two weeks.

Thank you,
Steve

From Goran Nenadic <g.nenadic@manchester.ac.uk>☆
Subject [BioNLP] New paper on large-scale extraction and contextualisation of biomolecular events
To bionlp@lists.ccs.neu.edu☆
 Junk Mail

BioContext: an integrated text mining system for large-scale extraction and contextualisation of biomolecular events

Martin Gerner, Farzaneh Sarafraz, Casey M. Bergman, Goran Nenadic
<http://bioinformatics.oxfordjournals.org/content/early/2012/06/17/bioinformatics.bts332.abstract>

Abstract

Motivation: While the amount of data in biology is rapidly increasing, critical information for understanding biological events like phosphorylation or gene expression remains locked in the biomedical literature. Most current text mining approaches to extract information about biological events are focused on either limited-scale studies and/or abstracts, with data extracted lacking context and rarely available to support further research.

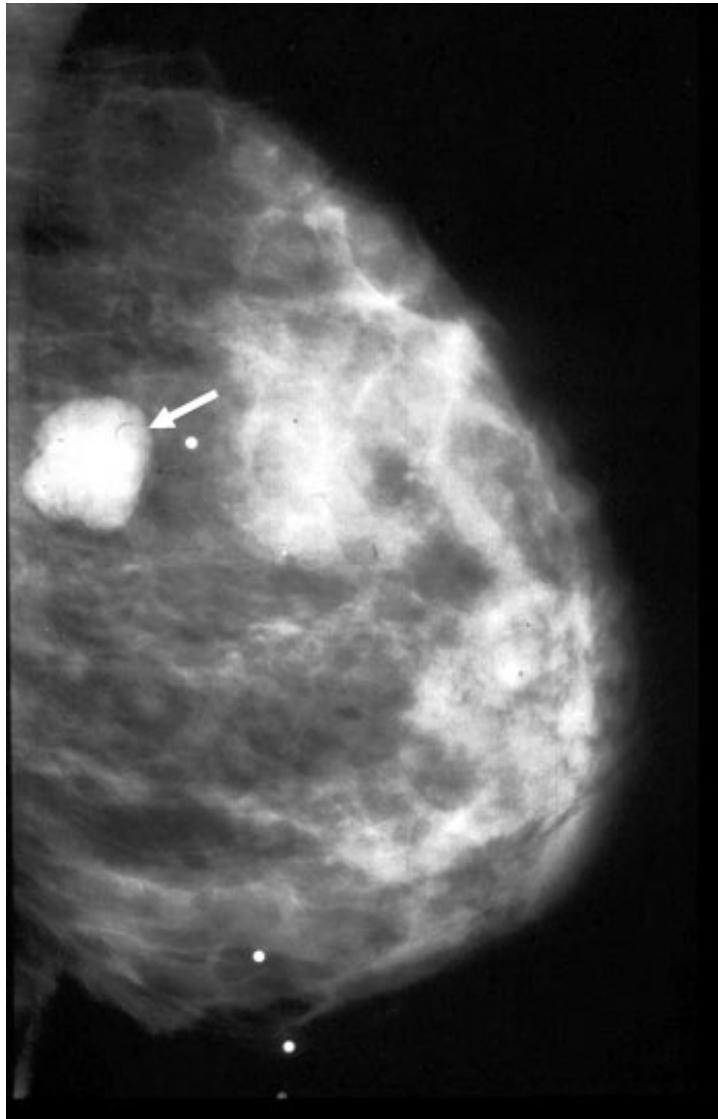
Results: Here we present BioContext, an integrated text mining system which extracts, extends and integrates results from a number of tools performing entity recognition, biomolecular event extraction and contextualisation. Application of our system to 10.9 million MEDLINE abstracts and 234,000 open-access full-text articles from PubMed Central

ML example: spam filtering

- T : given new mail message, classify as **spam** vs. other
- P : minimize misclassification costs
- E : previously classified (filed) messages

ML example: mammography

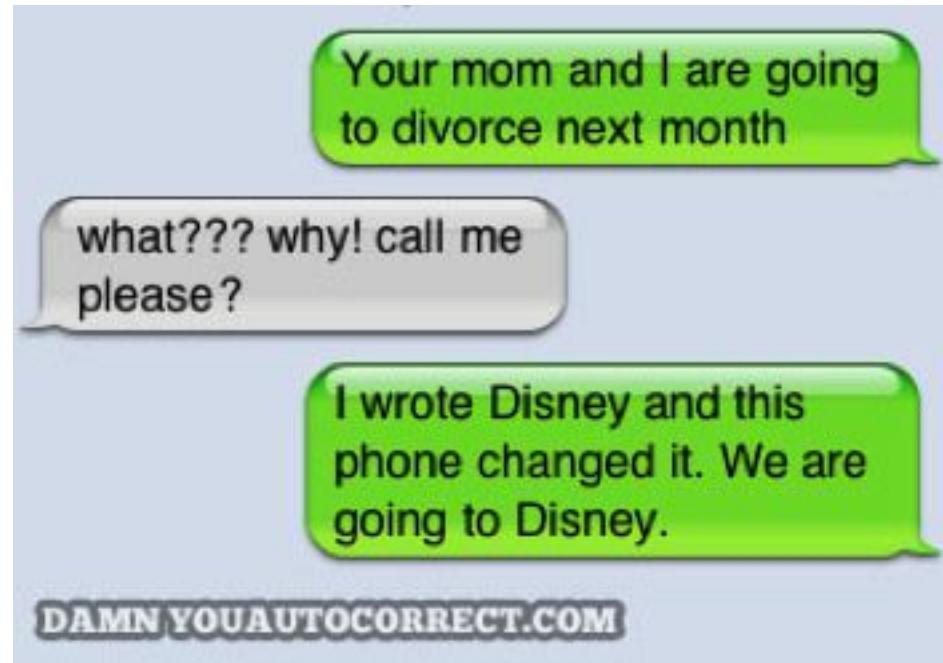
[Burnside et al., *Radiology* 2009]



ML example: mammography

- T : given new mammogram, classify as **benign** vs. **malignant**
- P : minimize misclassification costs
- E : previously encountered patient histories (mammograms + subsequent outcomes)

ML example: predictive text input



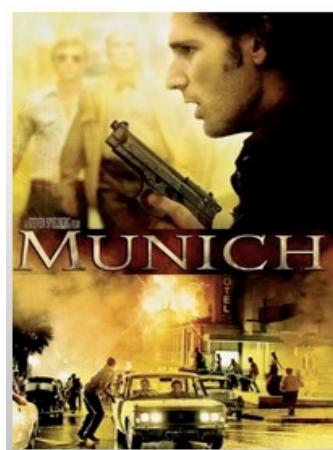
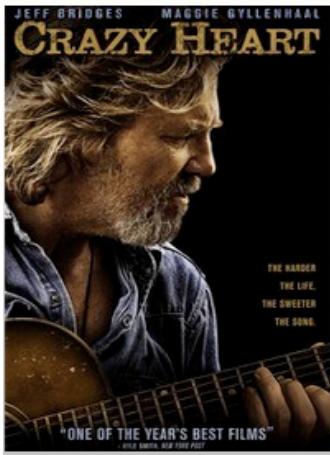
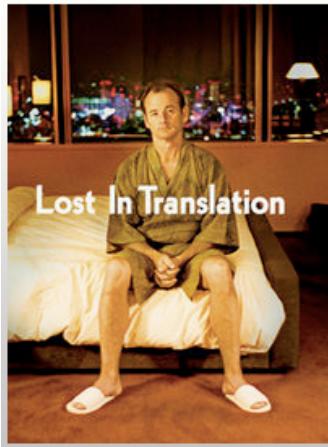
ML example: predictive text input

- T : given (partially) typed word, predict the word the user intended to type
- P : minimize misclassifications
- E : words previously typed by the user
(+ lexicon of common words + knowledge of keyboard layout)

domain knowledge



ML example: Netflix Prize



Who's watching?



David



chuck

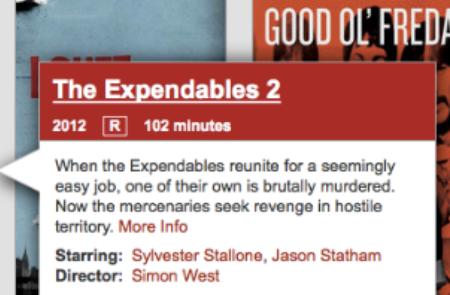


Skitzki



Add Profile

Top Picks for David



The Expendables 2

2012 R 102 minutes

When the Expendables reunite for a seemingly easy job, one of their own is brutally murdered. Now the mercenaries seek revenge in hostile territory. [More Info](#)

Starring: Sylvester Stallone, Jason Statham
Director: Simon West

Based on your interest in: Captain America: The First Avenger, Lockout and The Avengers

Our best guess for David



Not interested

+ My List

Random Picks



ML example: Netflix

- T : given a user/movie pair, predict the user's rating (1-5 stars) of the movie
- P : minimize difference between predicted and actual rating
- E : histories of previously rated movies (user, movie, rating triples)

Goals for this part of lecture

- define the supervised and unsupervised learning tasks
- consider how to represent instances as fixed-length feature vectors
- understand the concepts
 - instance (example)
 - feature (attribute)
 - feature space
 - feature types
 - supervised learning
 - classification (concept learning)
 - regression
 - i.i.d. assumption
 - generalization

Goals for the lecture (continued)

- understand the concepts
 - unsupervised learning
 - clustering
 - anomaly detection
 - dimensionality reduction

Can I eat this mushroom?



I don't know what type it is – I've never seen it before. Is it edible or poisonous?

Can I eat this mushroom?

suppose we're given examples of edible and poisonous mushrooms
(we'll refer to these as *training examples* or *training instances*)

edible



poisonous



can we learn a model that can be used to classify other mushrooms?

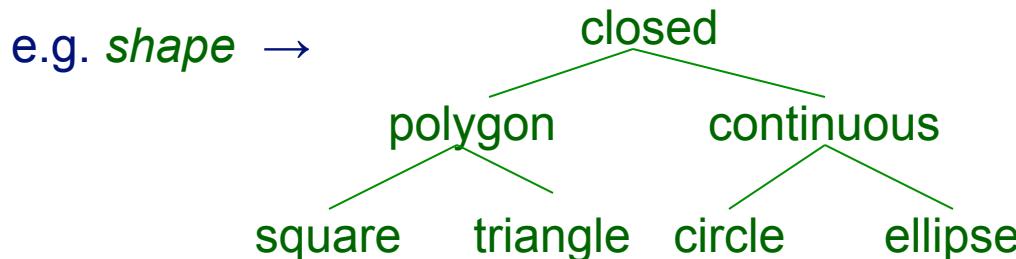
Representing instances using feature vectors

- we need some way to represent each instance
- one common way to do this: use a fixed-length vector to represent *features* (a.k.a. *attributes*) of each instance
- also represent *class label* of each instance

<i>cap-shape</i>	<i>cap-surface</i>	<i>cap-color</i>	<i>bruises</i>	<i>odor</i>	<i>Class</i>
$x_1 = \langle \text{bell}, \quad \text{fibrous}, \quad \text{gray}, \quad \text{false}, \quad \text{foul}, \dots \rangle$					$y_1 = \text{edible}$
$x_2 = \langle \text{convex}, \quad \text{scaly}, \quad \text{purple}, \quad \text{false}, \quad \text{musty}, \dots \rangle$					$y_2 = \text{poisonous}$
$x_3 = \langle \text{bell}, \quad \text{smooth}, \quad \text{red}, \quad \text{true}, \quad \text{musty}, \dots \rangle$					$y_3 = \text{edible}$
			\vdots		

Standard feature types

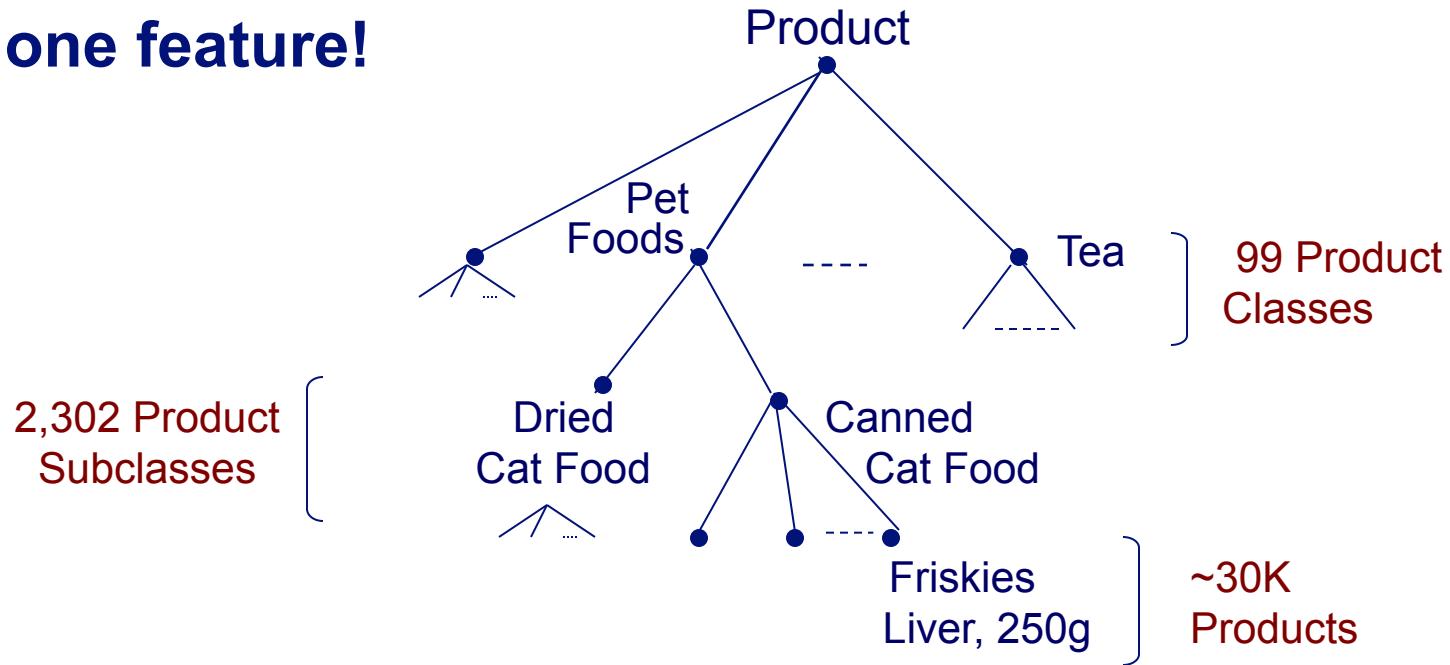
- *nominal* (including Boolean)
 - no ordering among possible values
e.g. `color` $\in \{\text{red}, \text{blue}, \text{green}\}$ (vs. `color = 1000` Hertz)
- *linear (or ordinal)*
 - possible values of the feature are totally ordered
e.g. `size` $\in \{\text{small}, \text{medium}, \text{large}\}$ ← discrete
`weight` $\in [0\dots 500]$ ← continuous
- *hierarchical*
 - possible values are partially ordered in an ISA hierarchy



Feature hierarchy example

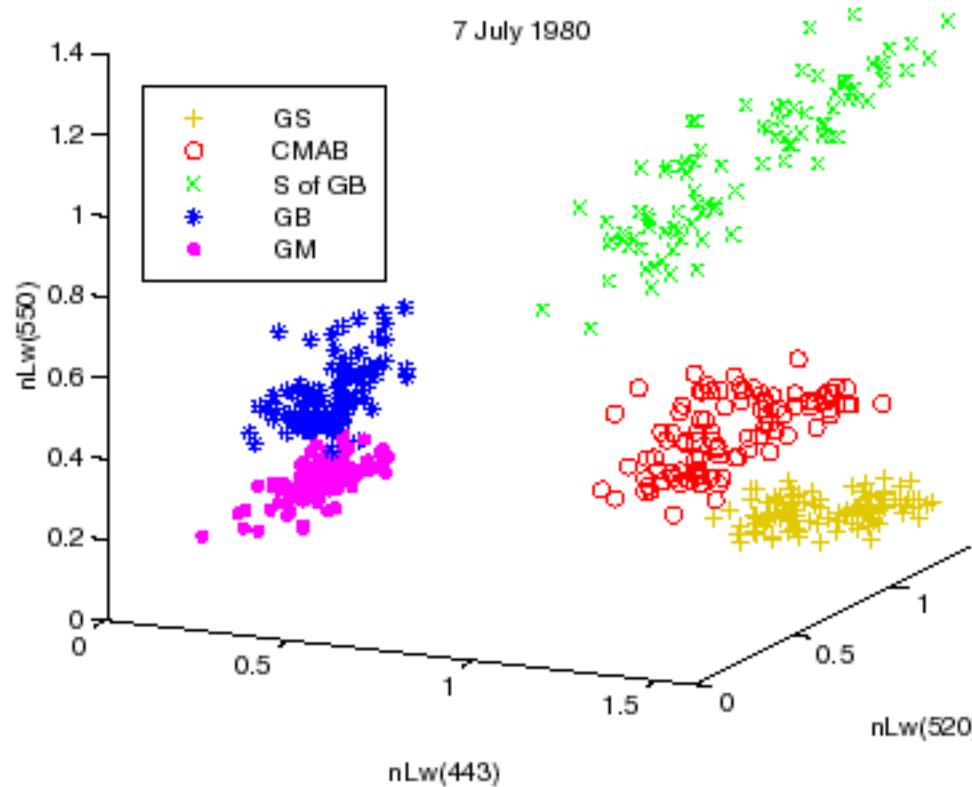
Lawrence et al., *Data Mining and Knowledge Discovery* 5(1-2), 2001

Structure of one feature!



Feature space

we can think of each instance as representing a point in a d -dimensional feature space where d is the number of features



example: optical properties of oceans in three spectral bands
[Traykovski and Sosik, *Ocean Optics XIV Conference Proceedings*, 1998]

Another view of the feature-vector representation: a single database table

	feature 1	feature 2	...	feature d	class
instance 1	0.0	small		red	true
instance 2	9.3	medium		red	false
instance 3	8.2	small		blue	false
...					
instance n	5.7	medium		green	true

Representation Caveat

- Feature vector format has proved very “workable”
- But much real world data doesn’t arrive in neatly aligned feature vectors
 - Sequences: events in time, genomes, books
 - Graphs: social networks, logistics, comms
 - Relational databases: patient’s health data distributed over many tables

ML example: Stock Forecasting



ML example: Stock Forecasting

- T : given a stock, predict the value tomorrow/next week/next month
 - P : minimize difference between predicted and actual value
 - E : histories of this stock, other stocks
-
- Alternatives in specification:
 - T: given NYSE, choose an investment strategy
 - P: maximize profit
 - E: might also include background information about companies

ML example: Personalized Medicine

Demographics

ID	Year of Birth	Gender
P1	3.10.1946	M

Diagnoses

ID	Date	Diagnosis	Sign/Symptom
P1	6.2.2011	Atrial fibrillation	Discomfort

The Electronic Health Record (EHR)

Demographics

ID	Year of Birth	Gender
P1	1946.03.10	M

Diagnoses

ID	Date	Diagnosis	Sign/Symptom
P1	7.3.2011	Atrial fibrillation	Dizziness, Nausea

The Electronic Health Record (EHR)

Demographics

ID	Year of Birth	Gender
P1	1946.03.10	M

Diagnoses

ID	Date	Diagnosis	Sign/Symptom
P1	2.29.2012	Stroke	Schizophasia

The Electronic Health Record (EHR)

Demographics

ID	Year of Birth	Gender
P1	1946.03.10	M

Diagnoses

ID	Date	Diagnosis	Sign/Symptom
P1	6.2.2011	Atrial fibrillation	Discomfort
P1	7.3.2011	Atrial fibrillation	Dizziness, Nausea
P1	2.29.2012	Stroke	Schizophasia

Electronic Health Record (EHR)

Patient ID	Gender	Birthdate
P1	M	3/22/1963

Demographics

Patient ID	Date	Physician	Symptoms	Diagnosis
P1	1/1/2001	Smith	palpitations	hypoglycemic
P1	2/1/2001	Jones	fever, aches	influenza

Diagnoses

Patient ID	Date	Lab Test	Result
P1	1/1/2001	blood glucose	42
P1	1/9/2001	blood glucose	45

Lab Results

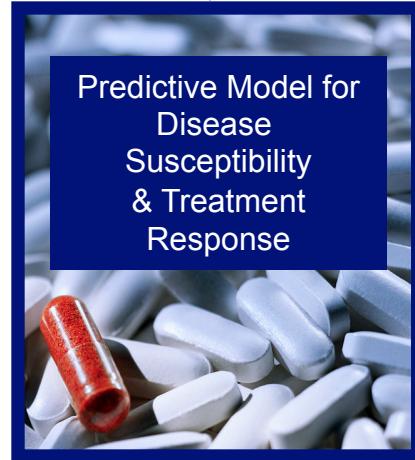
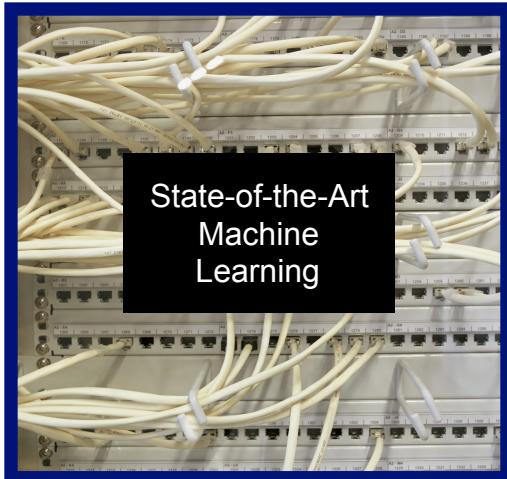
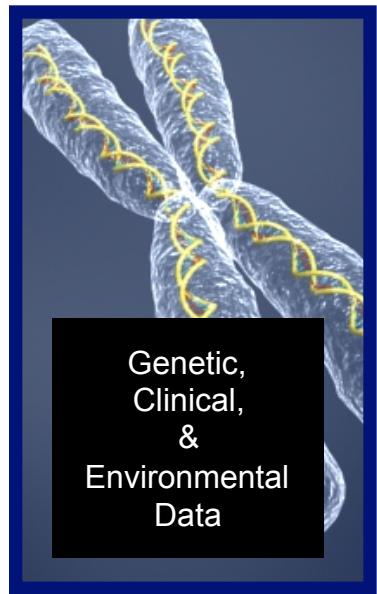
Patient ID	Date	Observation	Result
P1	1/1/2001	Height	5'11
P2	1/9/2001	BMI	34.5

Vitals

Medications

Patient ID	Date Prescribed	Date Filled	Physician	Medication	Dose	Duration
P1	5/17/1998	5/18/1998	Jones	Prilosec	10mg	3 months

Precision Medicine



ML example: Precision Medicine

- T : given a patient and disease diagnosis, choose best treatment
- P : cure disease
- E : treatment and outcomes for other patients with same disease
(+ electronic health records (EHRs) + genome sequences)
- Alternatives in specification:
 - T: given a patient, choose lifestyle and treatment plan
 - P: maximize patient health as measured by survey questions
 - E: might also include answers to questionnaire about lifestyle

Back to Feature Vectors

	feature 1	feature 2	...	feature d	class
instance 1	0.0	small		red	true
instance 2	9.3	medium		red	false
instance 3	8.2	small		blue	false
...					
instance n	5.7	medium		green	true

The supervised learning task

problem setting

- set of possible instances: X
- unknown *target function*: $f : X \rightarrow Y$
- set of *models* (a.k.a. *hypotheses*): $H = \{h \mid h : X \rightarrow Y\}$

given

- training set of instances of unknown target function f
 $(x_1, y_1), (x_2, y_2) \dots (x_n, y_n)$

output

- model $h \in H$ that best approximates target function

The supervised learning task

- when y is discrete, we term this a *classification* task (or *concept learning*)
- when y is continuous, it is a *regression* task
- later in the semester, we will consider tasks in which each y is more structured object (e.g. a *sequence* of discrete labels)

i.i.d. instances

- we often assume that training instances are *independent and identically distributed* (i.i.d.) – sampled independently from the same unknown distribution
- later in the course we'll consider cases where this assumption does not hold
 - cases where sets of instances have dependencies
 - instances sampled from the same medical image
 - instances from time series
 - etc.
 - cases where the learner can select which instances are labeled for training
 - *active learning*
 - the target function changes over time (*concept drift*)

Generalization

- The primary objective in supervised learning is to find a model that *generalizes* – one that accurately predicts y for previously unseen x

Can I eat this mushroom that
was not in my training set?



Model representations

throughout the semester, we will consider a broad range of representations for learned models, including

- decision trees
- neural networks
- support vector machines
- Bayesian networks
- logic clauses
- ensembles of the above
- etc.

Mushroom features (from the UCI Machine Learning Repository)

sunken is one possible value of the *cap-shape* feature

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

A learned decision tree

```
odor = a: e (400.0)
```

```
odor = c: p (192.0)
```

```
odor = f: p (2160.0)
```

```
odor = l: e (400.0)
```

```
odor = m: p (36.0)
```

```
odor = n
```

```
    spore-print-color = b: e (48.0)
```

```
    spore-print-color = h: e (48.0)
```

```
    spore-print-color = k: e (1296.0)
```

```
    spore-print-color = n: e (1344.0)
```

```
    spore-print-color = o: e (48.0)
```

```
    spore-print-color = r: p (72.0)
```

```
    spore-print-color = u: e (0.0)
```

```
    spore-print-color = w
```

```
        gill-size = b: e (528.0)
```

```
        gill-size = n
```

```
            gill-spacing = c: p (32.0)
```

```
            gill-spacing = d: e (0.0)
```

```
            gill-spacing = w
```

```
                population = a: e (0.0)
```

```
                population = c: p (16.0)
```

```
                population = n: e (0.0)
```

```
                population = s: e (0.0)
```

```
                population = v: e (48.0)
```

```
                population = y: e (0.0)
```

```
            spore-print-color = y: e (48.0)
```

```
odor = p: p (256.0)
```

```
odor = s: p (576.0)
```

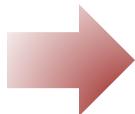
```
odor = y: p (576.0)
```

if odor=almond, predict edible

if odor=none \wedge
spore-print-color=white \wedge
gill-size=narrow \wedge
gill-spacing=crowded,
predict poisonous

Classification with a learned decision tree

once we have a learned model, we can use it to classify previously unseen instances



$x = \langle \text{bell, fibrous, brown, false, foul, ...} \rangle$

```
odor = a: e (400.0)
odor = c: p (192.0)
odor = f: p (2160.0)
odor = l: e (400.0)
odor = m: p (36.0)
odor = n
    spore-print-color = b: e (48.0)
    spore-print-color = h: e (48.0)
    spore-print-color = k: e (1296.0)
    spore-print-color = n: e (1344.0)
    spore-print-color = o: e (48.0)
    spore-print-color = r: p (72.0)
    spore-print-color = u: e (0.0)
    spore-print-color = w
        gill-size = b: e (528.0)
        gill-size = n
            gill-spacing = c: p (32.0)
            gill-spacing = d: e (0.0)
            gill-spacing = w
                population = a: e (0.0)
                population = c: p (16.0)
                population = n: e (0.0)
                population = s: e (0.0)
                population = v: e (48.0)
                population = y: e (0.0)
                spore-print-color = y: e (48.0)
odor = p: p (256.0)
odor = s: p (576.0)
odor = y: p (576.0)
```



$y = \text{edible or poisonous?}$

Unsupervised learning

in unsupervised learning, we're given a set of instances, without y 's

$x_1, x_2 \dots x_n$

goal: discover interesting regularities that characterize the instances

common unsupervised learning tasks

- *clustering*
- *anomaly detection*
- *dimensionality reduction*

Clustering

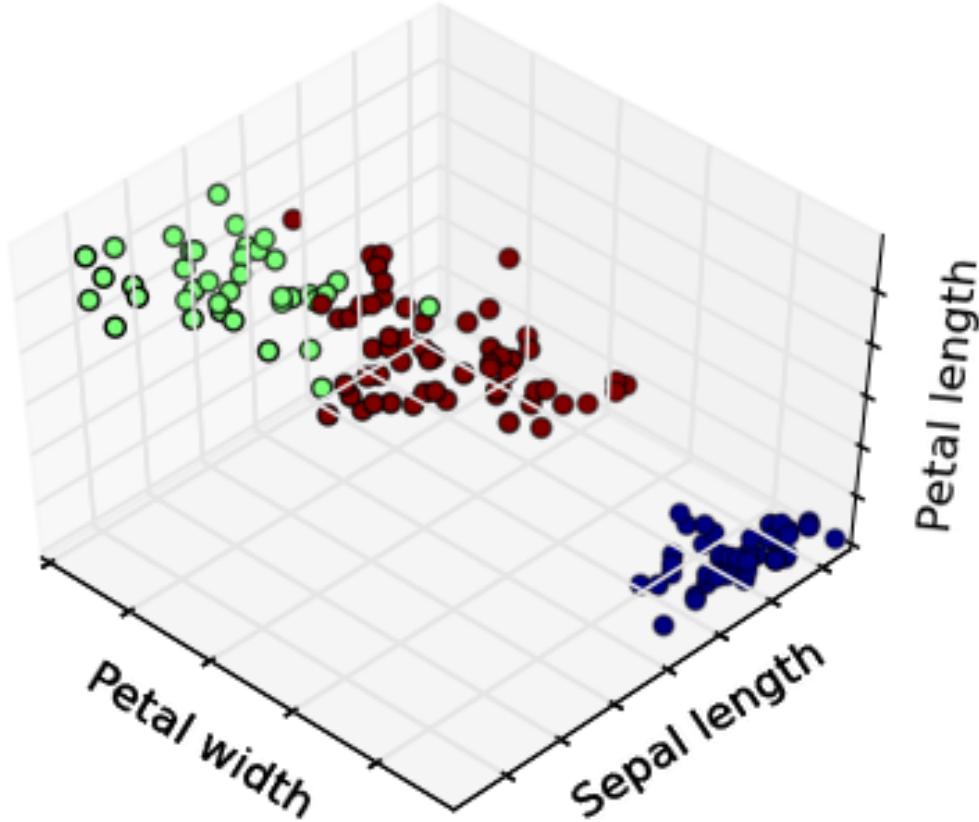
given

- training set of instances $x_1, x_2 \dots x_n$

output

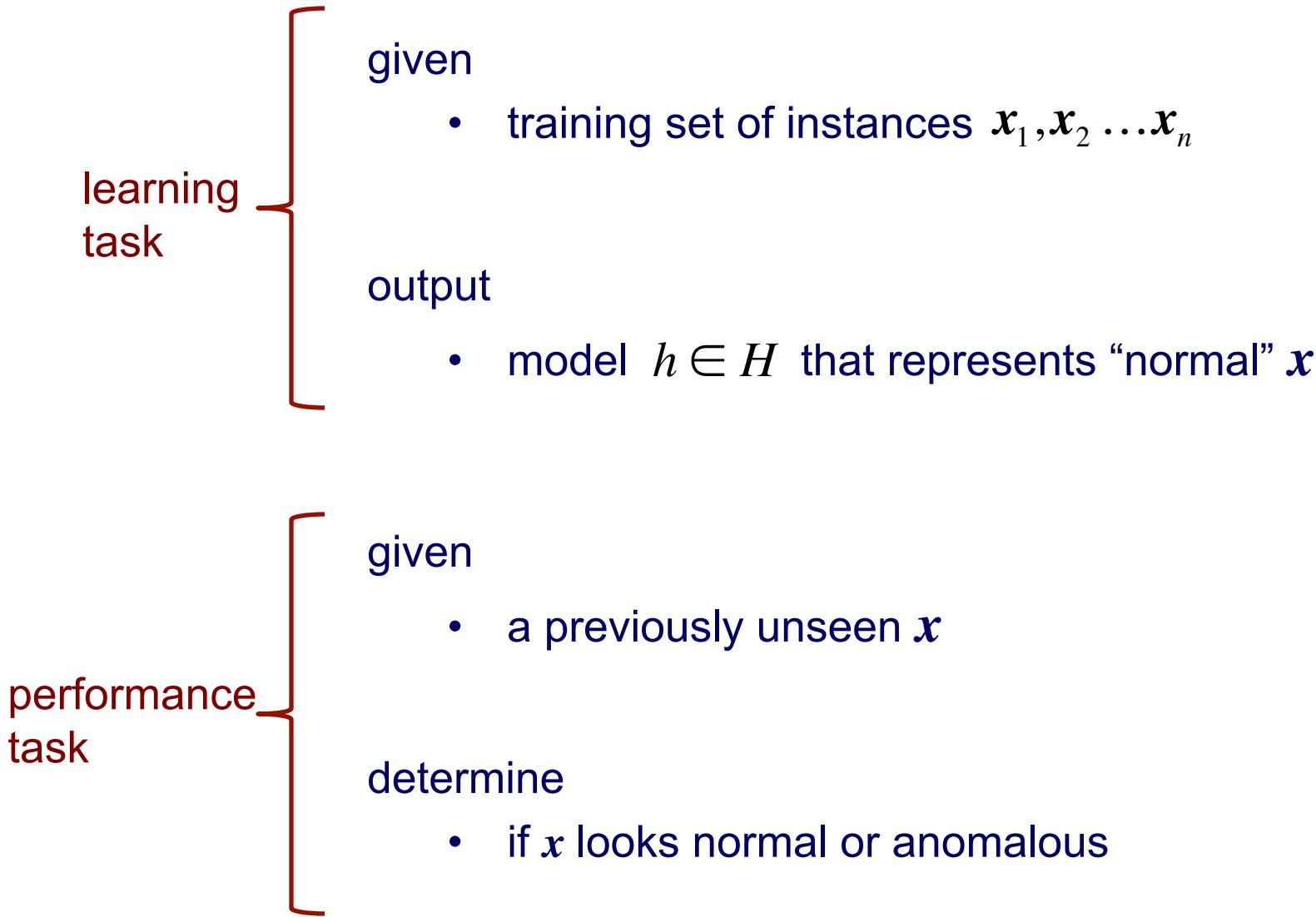
- model $h \in H$ that divides the training set into clusters such that there is intra-cluster similarity and inter-cluster dissimilarity

Clustering example

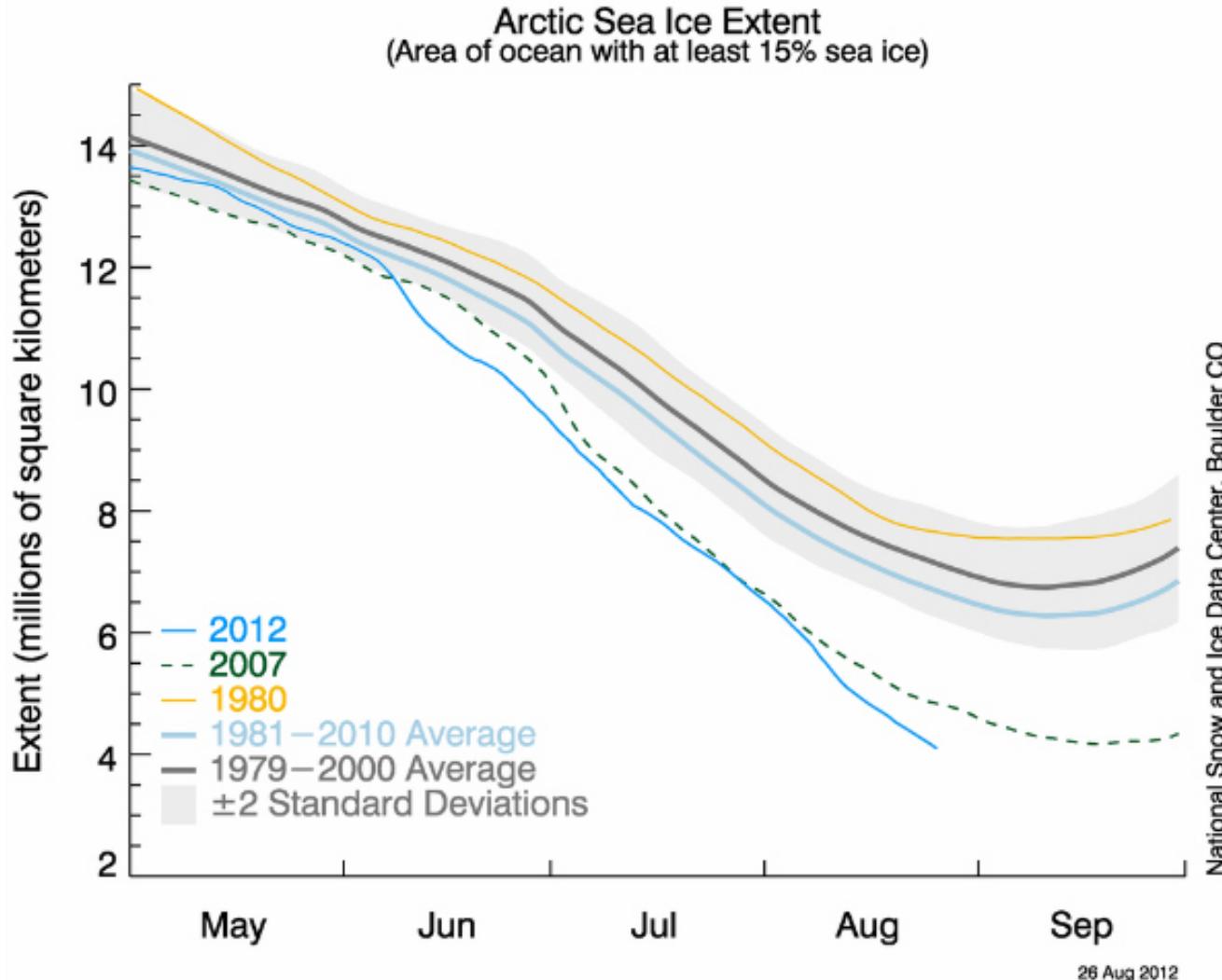


Clustering irises using three different features (the colors represent clusters identified by the algorithm, not y 's provided as input)

Anomaly detection



Anomaly detection example



Does the data for 2012 look anomalous?

Dimensionality reduction

given

- training set of instances $\mathbf{x}_1, \mathbf{x}_2 \dots \mathbf{x}_n$

output

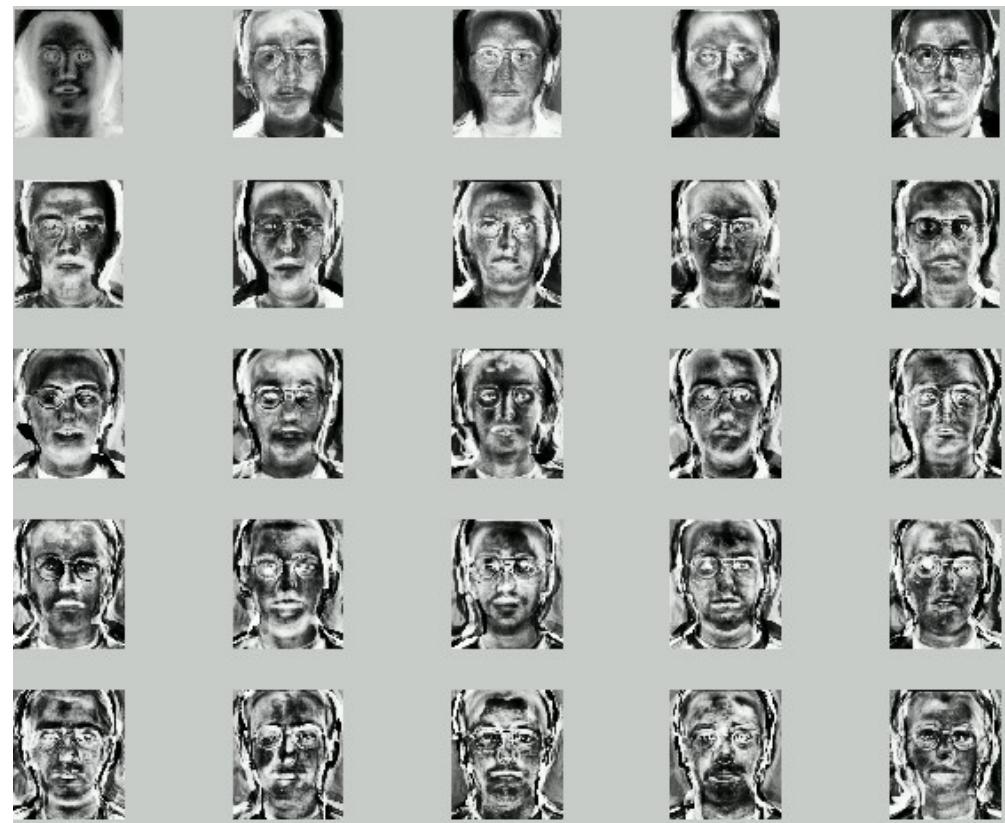
- model $h \in H$ that represents each \mathbf{x} with a lower-dimension feature vector while still preserving key properties of the data

Dimensionality reduction example



We can represent a face using all of the pixels in a given image

More effective method (for many tasks): represent each face as a linear combination of *eigenfaces*



Dimensionality reduction example

represent each face as a linear combination of *eigenfaces*

$$\text{face} = \alpha_{1,1} \times \text{eigenface}_1 + \alpha_{1,2} \times \text{eigenface}_2 + \dots + \alpha_{1,20} \times \text{eigenface}_{20}$$

$$x_1 = \langle \alpha_{1,1}, \alpha_{1,2}, \dots, \alpha_{1,20} \rangle$$

$$\text{face} = \alpha_{2,1} \times \text{eigenface}_1 + \alpha_{2,2} \times \text{eigenface}_2 + \dots + \alpha_{2,20} \times \text{eigenface}_{20}$$

$$x_2 = \langle \alpha_{2,1}, \alpha_{2,2}, \dots, \alpha_{2,20} \rangle$$

of features is now 20 instead of # of pixels in images

Other learning tasks

later in the semester we'll cover other learning tasks that are not strictly supervised or unsupervised

- *reinforcement learning*
- *semi-supervised learning*
- etc.