Motivation and pre-requisites

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About this course

- This course covers the basic ideas behind machine learning/prediction
  - Study design - training vs. test sets
  - Conceptual issues - out of sample error, ROC curves
  - Practical implementation - the caret package
- What this course depends on
  - The Data Scientist's Toolbox
  - R Programming
- What would be useful
  - Exploratory analysis
  - Reporting Data and Reproducible Research
  - Regression models

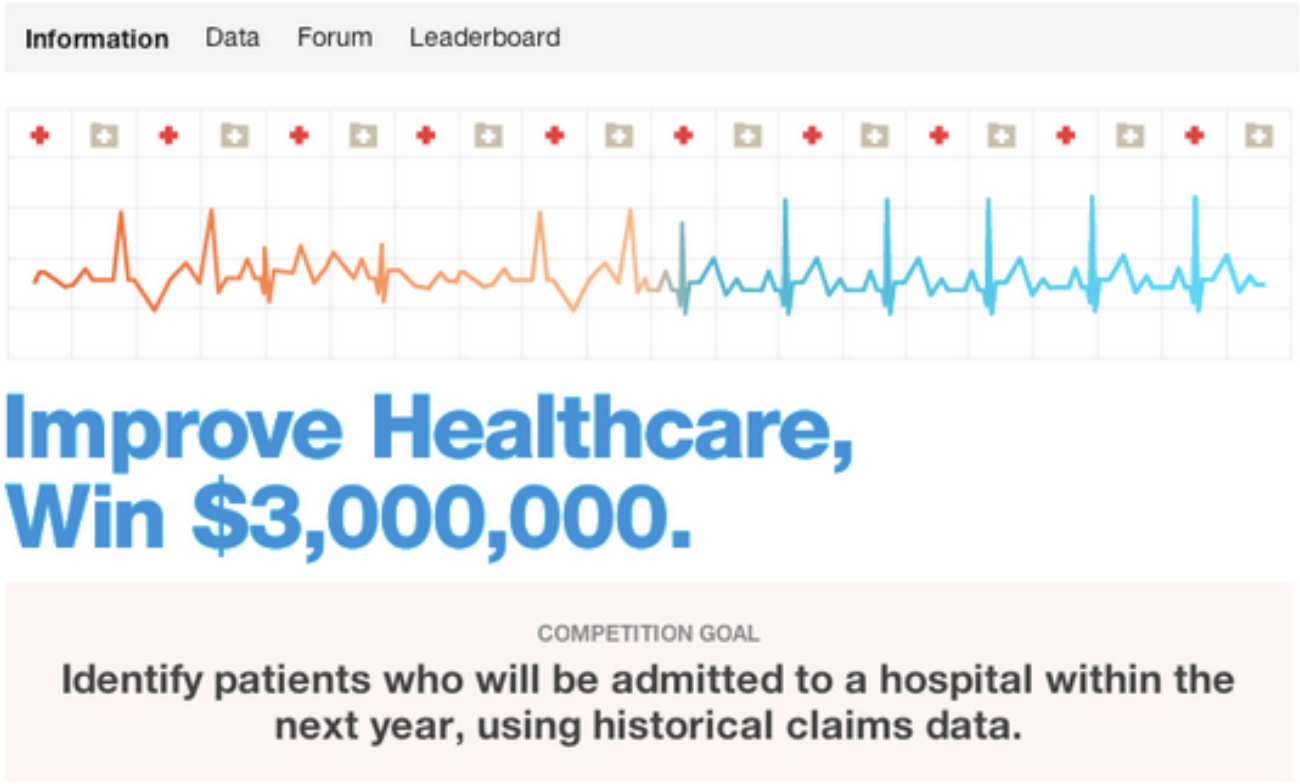
Who predicts?

- Local governments -> pension payments
- Google -> whether you will click on an ad
- Amazon -> what movies you will watch
- Insurance companies -> what your risk of death is
- Johns Hopkins -> who will succeed in their programs

Why predict? Glory!

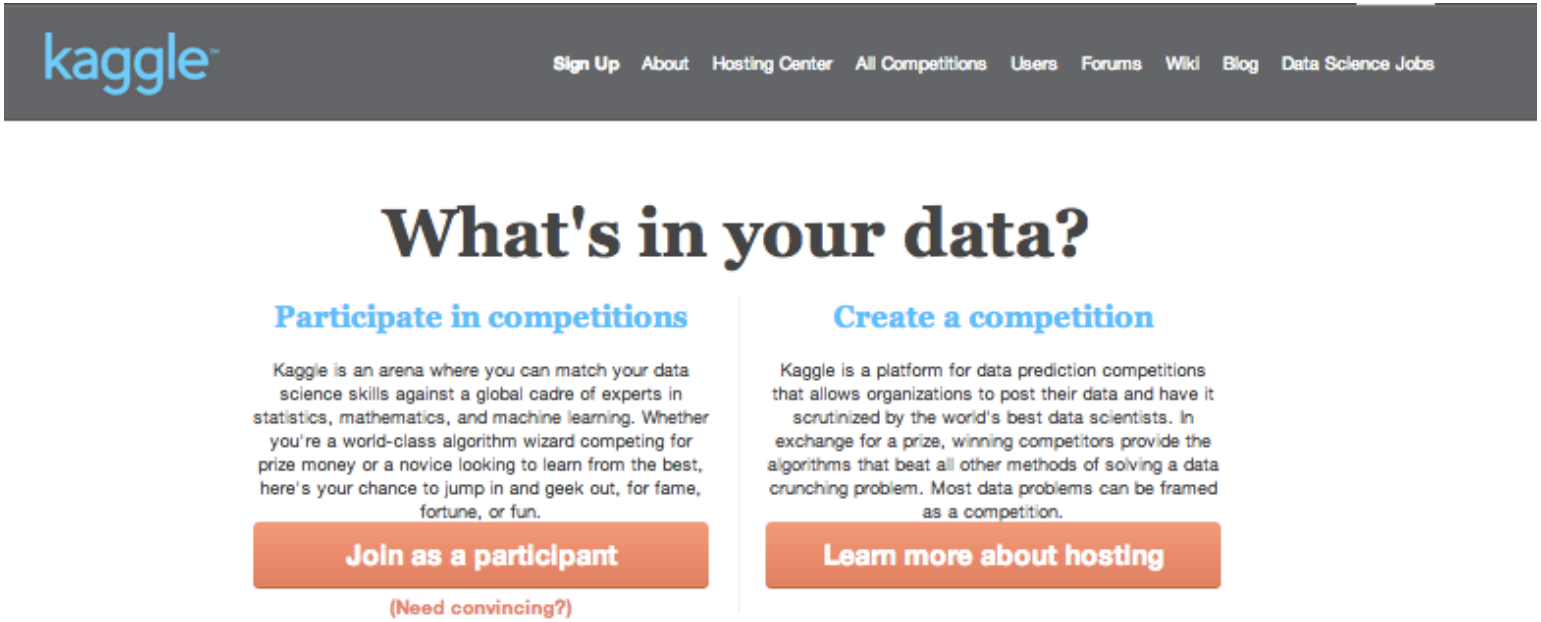
http://www.zimbio.com/photos/Chris+Volinsky

Why predict? Riches!



http://www.heritagehealthprize.com/c/hhp

Why predict? For sport!

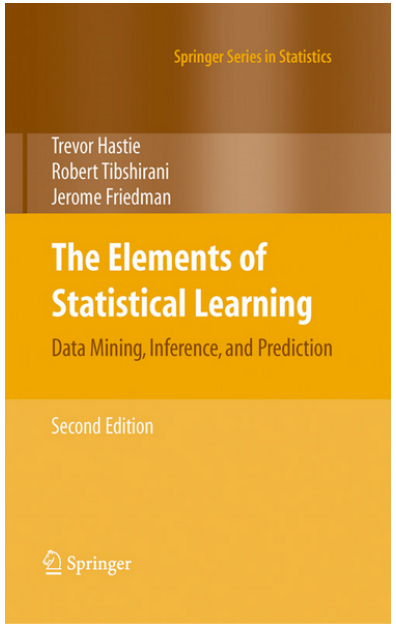


http://www.kaggle.com/

Why predict? To save lives!

http://www.oncotypedx.com/en-US/Home

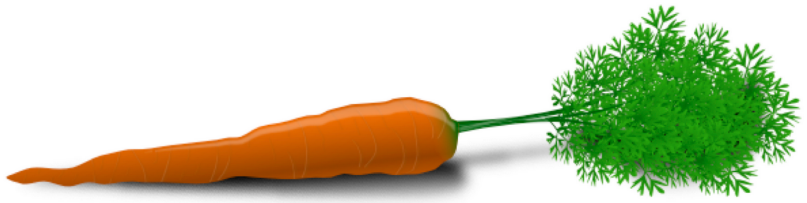
A useful (if a bit advanced) book



The elements of statistical learning

A useful package

the caret package



The **caret** package (short for *C*lassification *A*nd *RE*gression *T*raining) is a set of functions that attempt to streamline the process for creating predictive models. The package contains tools for:

Links

`train` Model List

Topics

- Main Page
- Data Sets
- Visualizations
- Pre-Processing

http://caret.r-forge.r-project.org/

Machine learning (more advanced material)

Stanford

Machine Learning

Andrew Ng

Taught In: English
Subtitles Available In: English

Sessions:
Oct 14th 2013 (10 weeks long)
Learn for Free

3,794 Tweet
12k +1
14k Like

https://www.coursera.org/course/ml

Even more resources

- List of machine learning resources on Quora
- List of machine learning resources from Science
- Advanced notes from MIT open courseware
- Advanced notes from CMU
- Kaggle - machine learning competitions

What is prediction?

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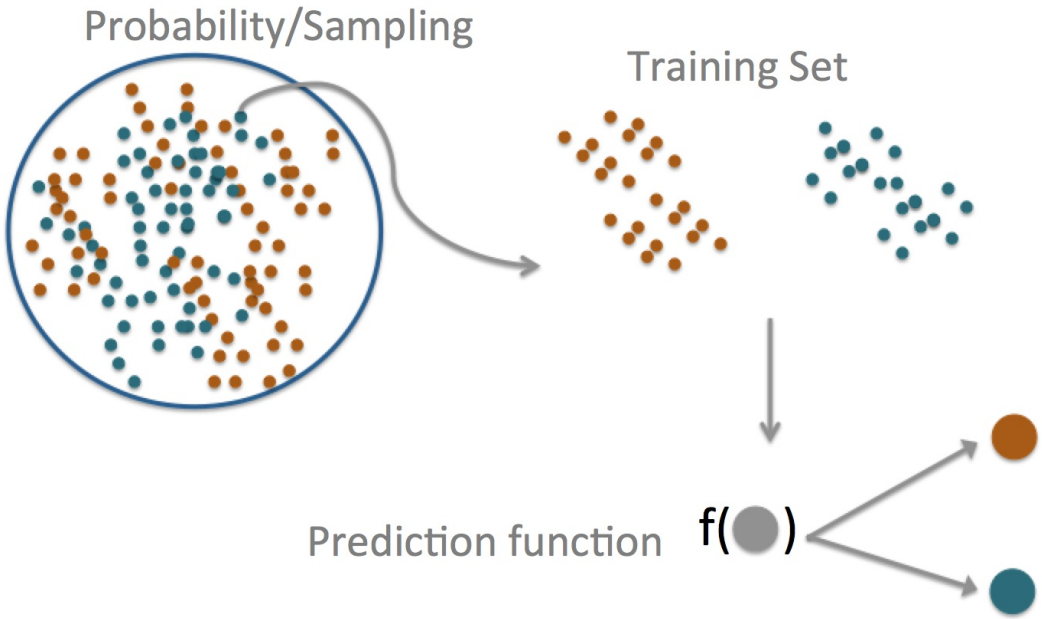
The central dogma of prediction



What can go wrong

BIG DATA

The Parable of Google Flu: Traps in Big Data Analysis

Large errors in flu prediction were largely avoidable, which offers lessons for the use of big data.

David Lazer,[1,2]* Ryan Kennedy,[1,3,4] Gary King,[3] Alessandro Vespignani[5,6,3]

In February 2013, Google Flu Trends (GFT) made headlines but not for a reason that Google executives or the creators of the flu tracking system would have hoped. *Nature* reported that GFT was predicting more than double the proportion of doctor visits for influenza-like illness (ILI) than the Centers for Disease Control and Prevention (CDC), which bases its estimates on surveillance reports from laboratories across the United States (*1*, *2*). This happened despite the fact that GFT was built to predict CDC reports. Given that GFT is often held up as an exemplary use of big data (*3*, *4*), what lessons can we draw from this error?

The problems we identify are not limited to GFT. Research on whether search or social media can

run ever since, with a few changes announced in October 2013 (*10*, *15*).

Although not widely reported until 2013, the new GFT has been persistently overestimating flu prevalence for a much longer time. GFT also missed by a very large margin in the 2011–2012 flu season and has missed high for 100 out of 108 weeks starting with August 2011 (see the graph). These errors are not randomly distributed. For example, last week's errors predict this week's errors (temporal autocorrelation), and the direction and magnitude of error varies with the time of year (seasonality). These patterns mean that GFT overlooks considerable information that could be extracted by traditional statistical methods.

http://www.sciencemag.org/content/343/6176/1203.full.pdf

Components of a predictor

question -> input data -> features -> algorithm -> parameters -> evaluation

SPAM Example

question -> input data -> features -> algorithm -> parameters -> evaluation

Start with a general question

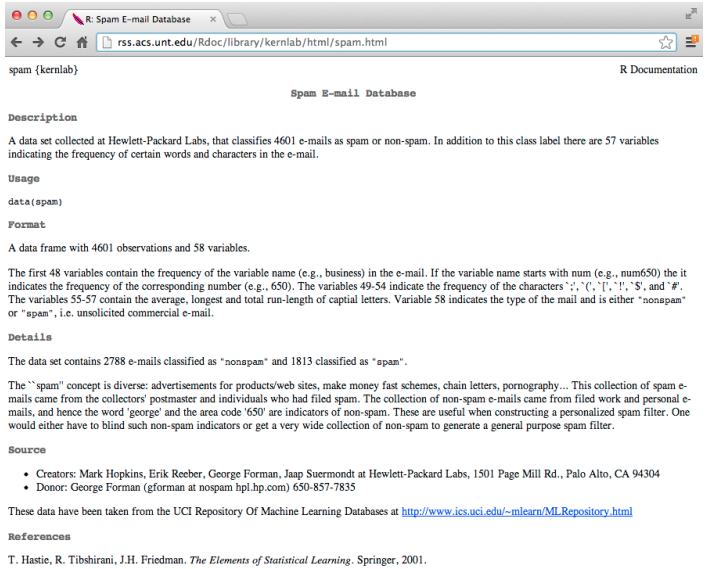
Can I automatically detect emails that are SPAM that are not?

Make it concrete

Can I use quantitative characteristics of the emails to classify them as SPAM/HAM?

SPAM Example

question -> input data -> features -> algorithm -> parameters -> evaluation



http://rss.acs.unt.edu/Rdoc/library/kernlab/html/spam.html

SPAM Example

question -> input data -> features -> algorithm -> parameters -> evaluation

Dear Jeff,

Can you send me your address so I can send you the invitation?

Thanks,

Ben

SPAM Example

question -> input data -> features -> algorithm -> parameters -> evaluation

Dear Jeff,

Can you

send me your address so I can send you the invitation?

Thanks,

Ben

Frequency of you = 2/17 = 0.118

SPAM Example

question -> input data -> features -> algorithm -> parameters -> evaluation

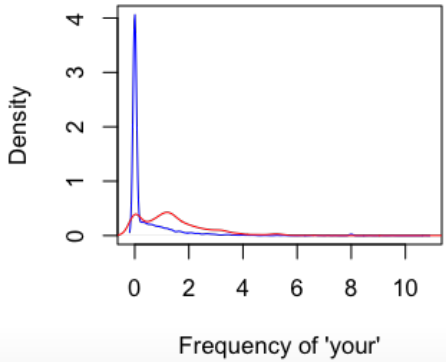
```
library(kernlab)
data(spam)
head(spam)
```

```
  make address  all num3d  our over remove internet order mail receive will people report addresses
1 0.00    0.64 0.64     0 0.32 0.00   0.00     0.00  0.00 0.00    0.00 0.64   0.00   0.00      0.00
2 0.21    0.28 0.50     0 0.14 0.28   0.21     0.07  0.00 0.94    0.21 0.79   0.65   0.21      0.14
3 0.06    0.00 0.71     0 1.23 0.19   0.19     0.12  0.64 0.25    0.38 0.45   0.12   0.00      1.75
4 0.00    0.00 0.00     0 0.63 0.00   0.31     0.63  0.31 0.63    0.31 0.31   0.31   0.00      0.00
5 0.00    0.00 0.00     0 0.63 0.00   0.31     0.63  0.31 0.63    0.31 0.31   0.31   0.00      0.00
6 0.00    0.00 0.00     0 1.85 0.00   0.00     1.85  0.00 0.00    0.00 0.00   0.00   0.00      0.00
  free business email  you credit your font num000 money hp hpl george num650 lab labs telnet
1 0.32     0.00  1.29 1.93   0.00 0.96    0   0.00  0.00  0   0      0      0   0    0      0
2 0.14     0.07  0.28 3.47   0.00 1.59    0   0.43  0.43  0   0      0      0   0    0      0
3 0.06     0.06  1.03 1.36   0.32 0.51    0   1.16  0.06  0   0      0      0   0    0      0
4 0.31     0.00  0.00 3.18   0.00 0.31    0   0.00  0.00  0   0      0      0   0    0      0
```

SPAM Example

question -> input data -> features -> algorithm -> parameters -> evaluation

```
plot(density(spam$your[spam$type=="nonspam"]),
     col="blue",main="",xlab="Frequency of 'your'")
lines(density(spam$your[spam$type=="spam"]),col="red")
```



SPAM Example

question -> input data -> features -> algorithm -> parameters -> evaluation

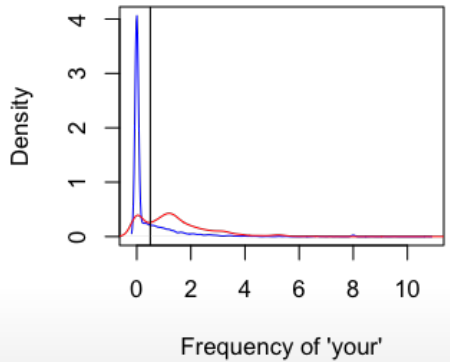
Our algorithm

- Find a value C.
- **frequency of 'your'** > **C** predict "spam"

SPAM Example

question -> input data -> features -> algorithm -> parameters -> evaluation

```
plot(density(spam$your[spam$type=="nonspam"]),
     col="blue",main="",xlab="Frequency of 'your'")
lines(density(spam$your[spam$type=="spam"]),col="red")
abline(v=0.5,col="black")
```



SPAM Example

question -> input data -> features -> algorithm -> parameters -> evaluation

```
prediction <- ifelse(spam$your > 0.5,"spam","nonspam")
table(prediction,spam$type)/length(spam$type)
```

```
prediction nonspam   spam
   nonspam  0.4590 0.1017
   spam     0.1469 0.2923
```

Accuracy≈ 0.459 + 0.292 = 0.751

Relative importance of steps

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Johns Hopkins Bloomberg School of Public Health

Relative order of importance

question > data > features > algorithms

An important point

> “The combination of some data and an aching desire for an answer does not ensure that a reasonable answer can be extracted from a given body of data.”
>
> John Tukey

Garbage in = Garbage out

question -> input data -> features -> algorithm -> parameters -> evaluation

1. May be easy (movie ratings -> new movie ratings)
2. May be harder (gene expression data -> disease)
3. Depends on what is a "good prediction".
4. Often more data > better models
5. The most important step!

Features matter!

question -> input data -> features -> algorithm -> parameters -> evaluation

Properties of good features

- Lead to data compression
- Retain relevant information
- Are created based on expert application knowledge

Common mistakes

- Trying to automate feature selection
- Not paying attention to data-specific quirks
- Throwing away information unnecessarily

May be automated with care

question -> input data -> features -> algorithm -> parameters -> evaluation

http://arxiv.org/pdf/1112.6209v5.pdf

Algorithms matter less than you'd think

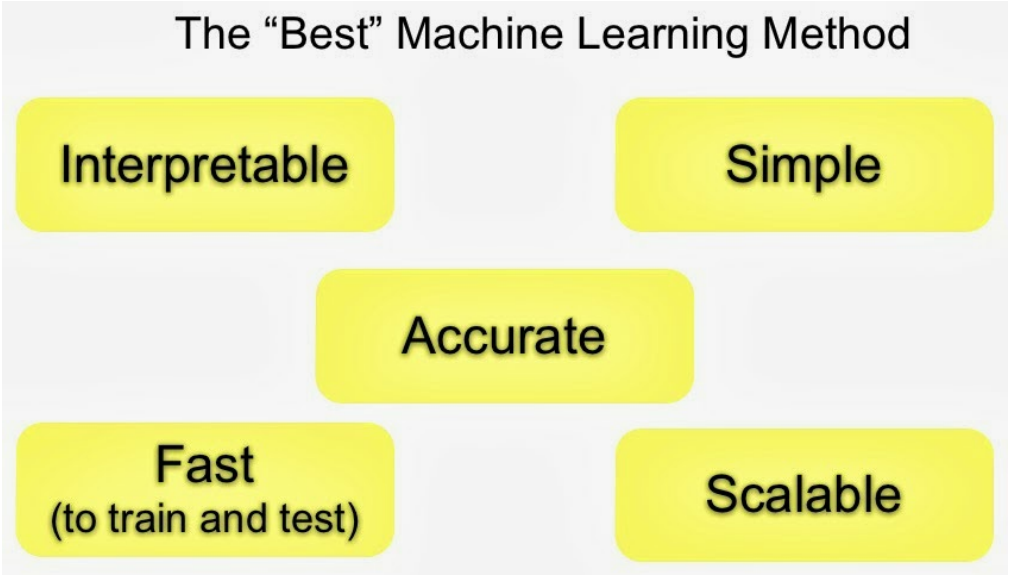
question -> input data -> features -> algorithm -> parameters -> evaluation

TABLE 1
Performance of linear discriminant analysis and the best result we found on ten randomly selected data sets

Data set	Best method e.r.	Lindisc e.r.	Default rule	Prop linear
Segmentation	0.0140	0.083	0.760	0.907
Pima	0.1979	0.221	0.350	0.848
House-votes16	0.0270	0.046	0.386	0.948
Vehicle	0.1450	0.216	0.750	0.883
Satimage	0.0850	0.160	0.758	0.889
Heart Cleveland	0.1410	0.141	0.560	1.000
Splice	0.0330	0.057	0.475	0.945
Waveform21	0.0035	0.004	0.667	0.999
Led7	0.2650	0.265	0.900	1.000
Breast Wisconsin	0.0260	0.038	0.345	0.963

http://arxiv.org/pdf/math/0606441.pdf

Issues to consider



http://strata.oreilly.com/2013/09/gaining-access-to-the-best-machine-learning-methods.html

Prediction is about accuracy tradeoffs

- Interpretability versus accuracy
- Speed versus accuracy
- Simplicity versus accuracy
- Scalability versus accuracy

Interpretability matters

if total cholesterol $\geq$160 **and** smoke **then** *10 year CHD risk* $\geq$ *5%*
else if smoke **and** systolic blood pressure$\geq$140 **then** *10 year CHD risk* $\geq$ *5%*
else *10 year CHD risk* $<$ *5%*

http://www.cs.cornell.edu/~chenhao/pub/mldg-0815.pdf

Scalability matters

Innovation
by Mike Masnick
Fri, Apr 13th 2012
12:07am

5

Why Netflix Never Implemented The Algorithm That Won The Netflix $1 Million Challenge

from the *times-change* dept

You probably recall all the excitement that went around when a group **finally won** the big Netflix $1 million prize in 2009, improving Netflix's recommendation algorithm by 10%. But what you might *not* know, is that **Netflix never implemented that solution itself.** Netflix recently put up a blog post **discussing some of the details of its recommendation system**, which (as an aside) explains why the winning entry never was used. First, they note that they *did* make use of an earlier bit of code that came out of the contest:

http://www.techdirt.com/blog/innovation/articles/20120409/03412518422/

http://techblog.netflix.com/2012/04/netflix-recommendations-beyond-5-stars.html

In sample and out of sample error

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In sample versus out of sample

In Sample Error: The error rate you get on the same data set you used to build your predictor. Sometimes called resubstitution error.

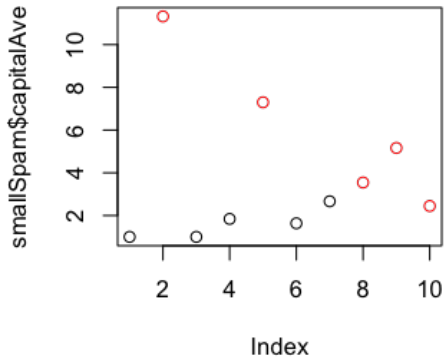
Out of Sample Error: The error rate you get on a new data set. Sometimes called generalization error.

Key ideas

1. Out of sample error is what you care about
2. In sample error $<$ out of sample error
3. The reason is overfitting
    - Matching your algorithm to the data you have

In sample versus out of sample errors

```
library(kernlab); data(spam); set.seed(333)
smallSpam <- spam[sample(dim(spam)[1],size=10),]
spamLabel <- (smallSpam$type=="spam")*1 + 1
plot(smallSpam$capitalAve,col=spamLabel)
```



Prediction rule 1

- capitalAve > 2.7 = "spam"
- capitalAve < 2.40 = "nonspam"
- capitalAve between 2.40 and 2.45 = "spam"
- capitalAve between 2.45 and 2.7 = "nonspam"

Apply Rule 1 to smallSpam

```
rule1 <- function(x){
  prediction <- rep(NA,length(x))
  prediction[x > 2.7] <- "spam"
  prediction[x < 2.40] <- "nonspam"
  prediction[(x >= 2.40 & x <= 2.45)] <- "spam"
  prediction[(x > 2.45 & x <= 2.70)] <- "nonspam"
  return(prediction)
}
table(rule1(smallSpam$capitalAve),smallSpam$type)
```

```
          nonspam spam
  nonspam       5    0
  spam          0    5
```

Prediction rule 2

- capitalAve > 2.40 = "spam"
- capitalAve ≤ 2.40 = "nonspam"

Apply Rule 2 to smallSpam

```
rule2 <- function(x){
  prediction <- rep(NA,length(x))
  prediction[x > 2.8] <- "spam"
  prediction[x <= 2.8] <- "nonspam"
  return(prediction)
}
table(rule2(smallSpam$capitalAve),smallSpam$type)
```

```
          nonspam spam
  nonspam       5    1
  spam          0    4
```

Apply to complete spam data

```
table(rule1(spam$capitalAve),spam$type)
```

```
         nonspam spam
  nonspam    2141  588
  spam        647 1225
```

```
table(rule2(spam$capitalAve),spam$type)
```

```
         nonspam spam
  nonspam    2224  642
  spam        564 1171
```

```
mean(rule1(spam$capitalAve)==spam$type)
```

Look at accuracy

```
sum(rule1(spam$capitalAve)==spam$type)
```

```
[1] 3366
```

```
sum(rule2(spam$capitalAve)==spam$type)
```

```
[1] 3395
```

What's going on?

Overfitting

- Data have two parts
  - Signal
  - Noise
- The goal of a predictor is to find signal
- You can always design a perfect in-sample predictor
- You capture both signal + noise when you do that
- Predictor won't perform as well on new samples

http://en.wikipedia.org/wiki/Overfitting

Prediction study design

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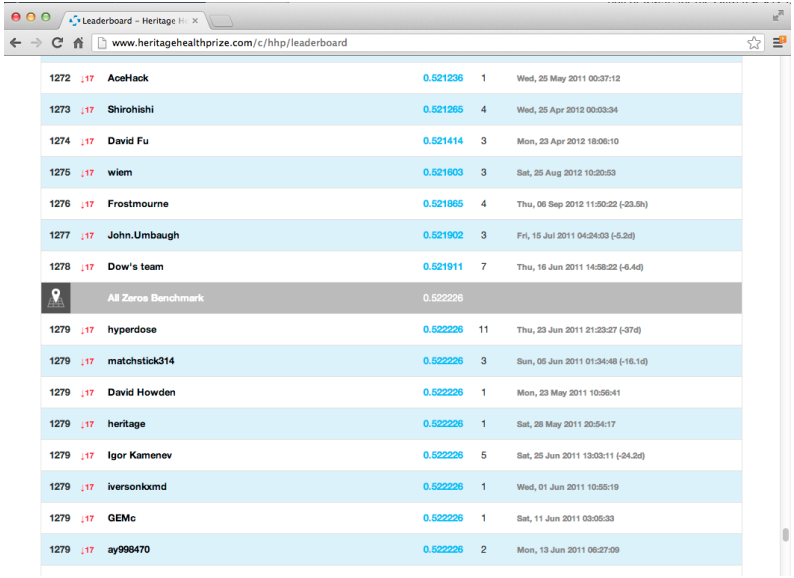
Prediction study design

1. Define your error rate
2. Split data into:
   - Training, Testing, Validation (optional)
3. On the training set pick features
   - Use cross-validation
4. On the training set pick prediction function
   - Use cross-validation
5. If no validation
   - Apply 1x to test set
6. If validation
   - Apply to test set and refine
   - Apply 1x to validation

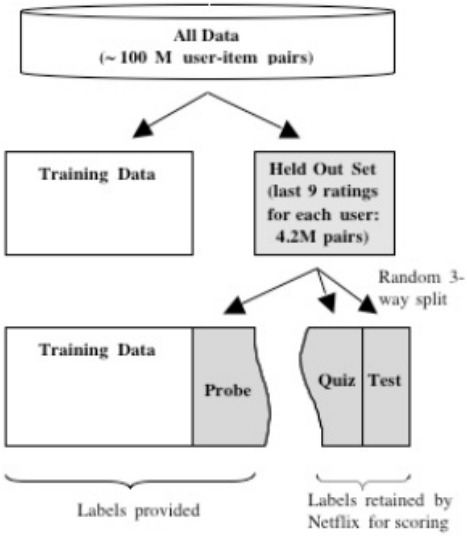
Know the benchmarks



1272	↓17	AceHack	0.521236	1	Wed, 25 May 2011 00:37:12
1273	↓17	Shirohishi	0.521265	4	Wed, 25 Apr 2012 00:03:34
1274	↓17	David Fu	0.521414	3	Mon, 23 Apr 2012 18:06:10
1275	↓17	wiem	0.521603	3	Sat, 25 Aug 2012 10:20:53
1276	↓17	Frostmourne	0.521865	4	Thu, 06 Sep 2012 11:50:22 (-23.5h)
1277	↓17	John.Umbaugh	0.521902	3	Fri, 15 Jul 2011 04:24:03 (-5.2d)
1278	↓17	Dow's team	0.521911	7	Thu, 16 Jun 2011 14:58:22 (-6.4d)
		All Zeros Benchmark	0.522226		
1279	↓17	hyperdose	0.522226	11	Thu, 23 Jun 2011 21:23:27 (-37d)
1279	↓17	matchstick314	0.522226	3	Sun, 05 Jun 2011 01:34:48 (-16.1d)
1279	↓17	David Howden	0.522226	1	Mon, 23 May 2011 10:56:41
1279	↓17	heritage	0.522226	1	Sat, 28 May 2011 20:54:17
1279	↓17	Igor Kamenev	0.522226	5	Sat, 25 Jun 2011 13:03:11 (-24.2d)
1279	↓17	iversonkxmd	0.522226	1	Wed, 01 Jun 2011 10:55:19
1279	↓17	GEMc	0.522226	1	Sat, 11 Jun 2011 03:05:33
1279	↓17	ay998470	0.522226	2	Mon, 13 Jun 2011 06:27:09

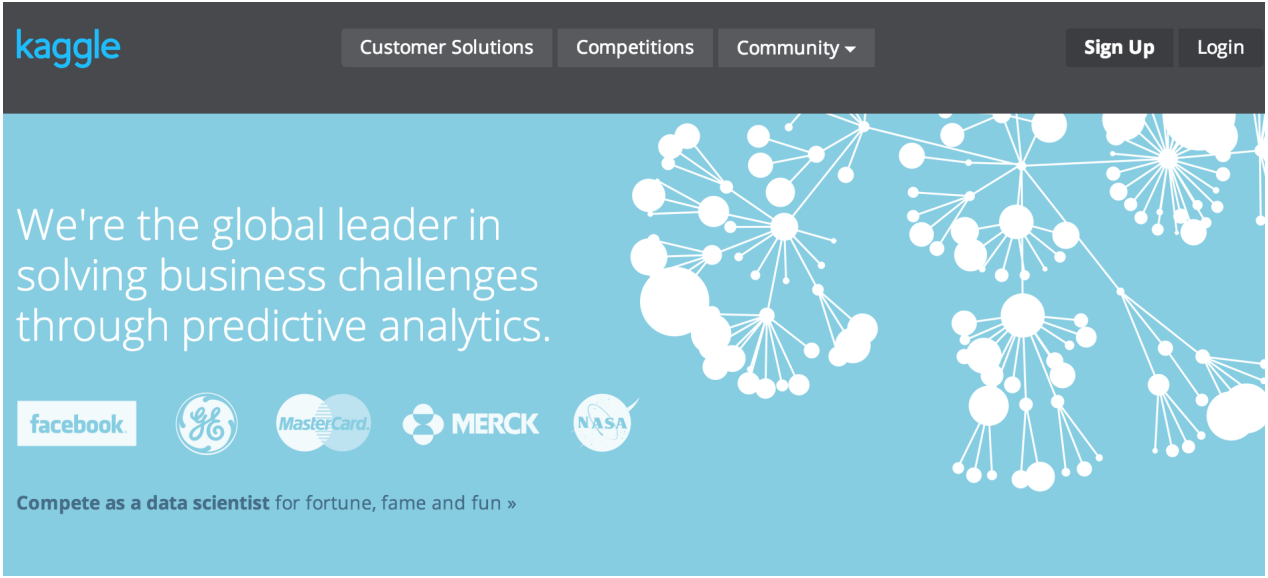
http://www.heritagehealthprize.com/c/hhp/leaderboard

Study design



http://www2.research.att.com/~volinsky/papers/ASAStatComp.pdf

Used by the professionals



http://www.kaggle.com/

Avoid small sample sizes

- Suppose you are predicting a binary outcome
  - Diseased/healthy
  - Click on ad/not click on ad
- One classifier is flipping a coin
- Probability of perfect classification is approximately:
  - $\left(\frac{1}{2}\right)^{\text{sample size}}$
  - n = 1 flipping coin 50% chance of 100% accuracy
  - n = 2 flipping coin 25% chance of 100% accuracy
  - n = 10 flipping coin 0.10% chance of 100% accuracy

Rules of thumb for prediction study design

- If you have a large sample size
  - 60% training
  - 20% test
  - 20% validation
- If you have a medium sample size
  - 60% training
  - 40% testing
- If you have a small sample size
  - Do cross validation
  - Report caveat of small sample size

Some principles to remember

- Set the test/validation set aside and *don't look at it*
- In general *randomly* sample training and test
- Your data sets must reflect structure of the problem
  - If predictions evolve with time split train/test in time chunks (called backtesting in finance)
- All subsets should reflect as much diversity as possible
  - Random assignment does this
  - You can also try to balance by features - but this is tricky

Types of errors

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Basic terms

In general, **Positive** = identified and **negative** = rejected. Therefore:

True positive = correctly identified

False positive = incorrectly identified

True negative = correctly rejected

False negative = incorrectly rejected

Medical testing example:

True positive = Sick people correctly diagnosed as sick

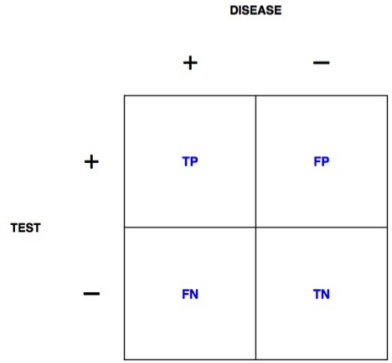
False positive= Healthy people incorrectly identified as sick

True negative = Healthy people correctly identified as healthy

False negative = Sick people incorrectly identified as healthy.

http://en.wikipedia.org/wiki/Sensitivity_and_specificity

Key quantities

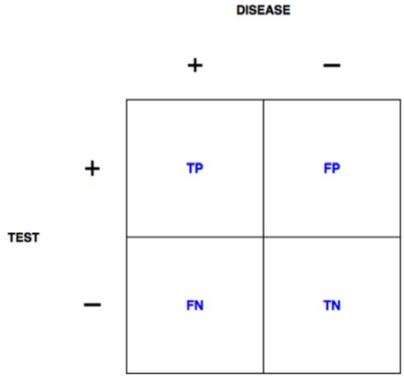


Sensitivity	→	Pr (positive test | disease)
Specificity	→	Pr (negative test | no disease)
Positive Predictive Value	→	Pr (disease | positive test)
Negative Predictive Value	→	Pr (no disease | negative test)
Accuracy	→	Pr (correct outcome)

http://en.wikipedia.org/wiki/Sensitivity_and_specificity

http://www.biostat.jhsph.edu/~iruczins/teaching/140.615/

Key quantities as fractions



Sensitivity	→	TP / (TP+FN)
Specificity	→	TN / (FP+TN)
Positive Predictive Value	→	TP / (TP+FP)
Negative Predictive Value	→	TN / (FN+TN)
Accuracy	→	(TP+TN) / (TP+FP+FN+TN)

http://www.biostat.jhsph.edu/~iruczins/teaching/140.615/

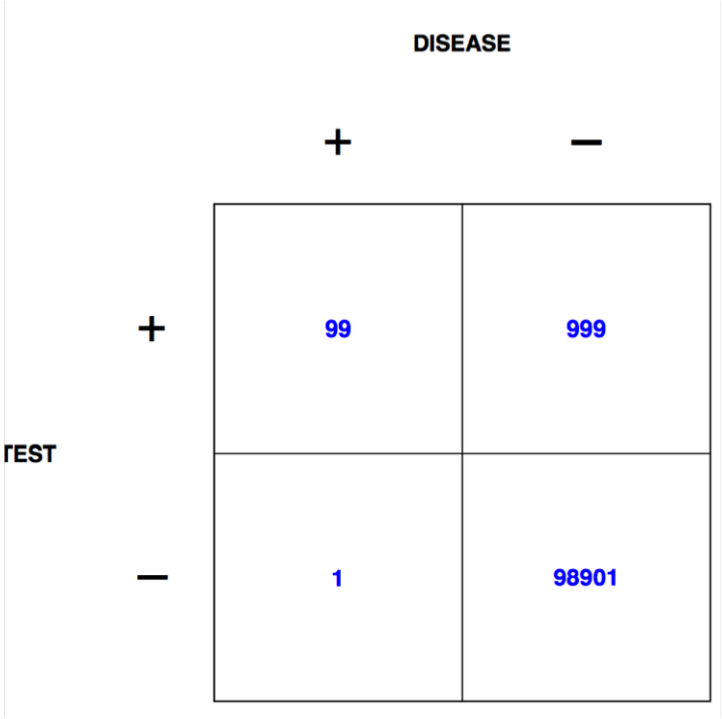
Screening tests

Assume that some disease has a 0.1% prevalence in the population. Assume we have a test kit for that disease that works with 99% sensitivity and 99% specificity. What is the probability of a person having the disease given the test result is positive, if we randomly select a subject from

- the general population?
- a high risk sub-population with 10% disease prevalence?

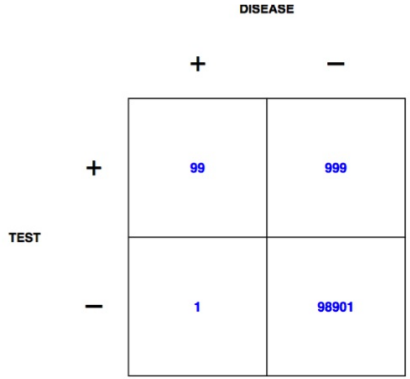
http://www.biostat.jhsph.edu/~iruczins/teaching/140.615/

General population



http://www.biostat.jhsph.edu/~iruczins/teaching/140.615/

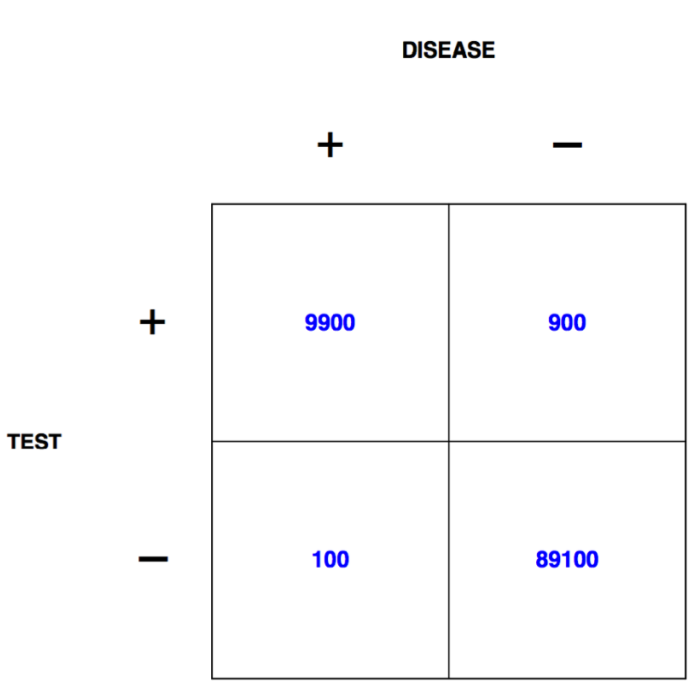
General population as fractions



Sensitivity	→	99 / (99+1) = 99%
Specificity	→	98901 / (999+98901) = 99%
Positive Predictive Value	→	99 / (99+999) ≈ 9%
Negative Predictive Value	→	98901 / (1+98901) > 99.9%
Accuracy	→	(99+98901) / 100000 = 99%

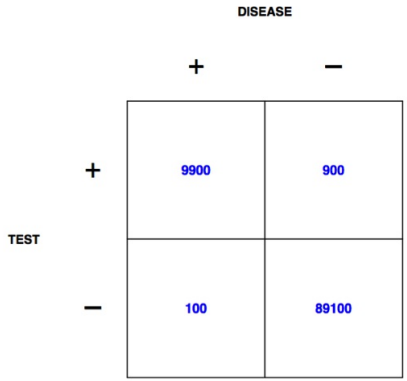
http://www.biostat.jhsph.edu/~iruczins/teaching/140.615/

At risk subpopulation



http://www.biostat.jhsph.edu/~iruczins/teaching/140.615/

At risk subpopulation as fraction



Sensitivity	→	9900 / (9900+100) = 99%
Specificity	→	89100 / (900+89100) = 99%
Positive Predictive Value	→	9900 / (9900+900) ≈ 92%
Negative Predictive Value	→	89100 / (100+89100) ≈ 99.9%
Accuracy	→	(9900+89100) / 100000 = 99%

http://www.biostat.jhsph.edu/~iruczins/teaching/140.615/

Key public health issue

Vast Study Casts Doubts on Value of Mammograms

By GINA KOLATA FEB. 11, 2014

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One of the largest and most meticulous studies of mammography ever done, involving 90,000 women and lasting a quarter-century, has added powerful new doubts about the value of the screening test for women of any age.

It found that the death rates from breast cancer and from all causes were the same in women who got mammograms and those who did not. And the screening had harms: One in five cancers found with mammography and treated was not a threat to the woman's health and did not need treatment such as chemotherapy, surgery or radiation.

The study, published Tuesday in The British Medical Journal, is one of the few rigorous

Nearly 75 percent of American women 40 and over say they had a mammogram in the past year. Damian Dovarganes/Associated Press

http://www.biostat.jhsph.edu/~iruczins/teaching/140.615/

Key public health issue

The New York Times

Business Day

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Looser Guidelines Issued on Prostate Screening

By ANDREW POLLACK
Published: May 3, 2013

In a major shift, the American Urological Association has pulled back its strong support of prostate cancer screening, saying that the testing should be considered primarily by men aged 55 to 69.

The association had staunchly defended the benefits of screening men with the prostate test, even after a government advisory committee, the United States Preventive Services Task Force, said in 2011 that healthy men should not be screened because far more men would be harmed by unnecessary prostate cancer treatments than would be saved from death.

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For continuous data

Mean squared error (MSE):

$$\frac{1}{n}\sum_{i=1}^{n}(\text{Prediction}_i - \text{Truth}_i)^2$$

Root mean squared error (RMSE):

$$\sqrt{\frac{1}{n}\sum_{i=1}^{n}(\text{Prediction}_i - \text{Truth}_i)^2}$$

Common error measures

1. Mean squared error (or root mean squared error)
   - Continuous data, sensitive to outliers
2. Median absolute deviation
   - Continuous data, often more robust
3. Sensitivity (recall)
   - If you want few missed positives
4. Specificity
   - If you want few negatives called positives
5. Accuracy
   - Weights false positives/negatives equally
6. Concordance
   - One example is kappa

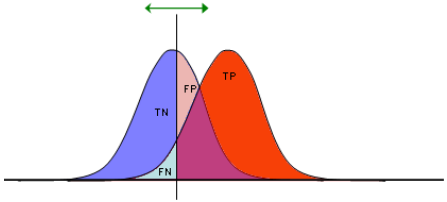
ROC curves

Jeffrey Leek
Johns Hopkins Bloomberg School of Public Health

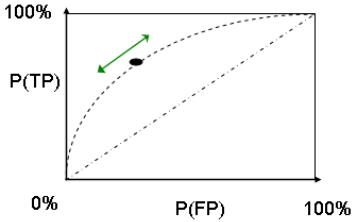
Why a curve?

- In binary classification you are predicting one of two categories
  - Alive/dead
  - Click on ad/don't click
- But your predictions are often quantitative
  - Probability of being alive
  - Prediction on a scale from 1 to 10
- The *cutoff* you choose gives different results

ROC curves

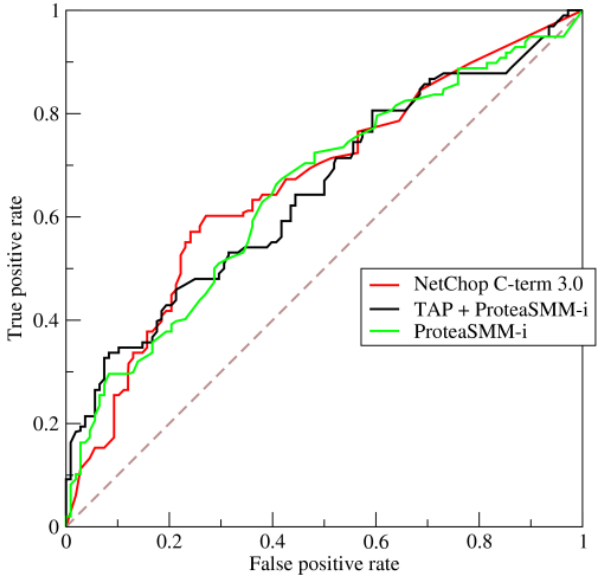


TP	FP
FN	TN
1	1



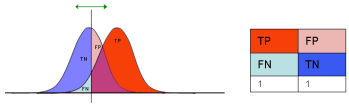
http://en.wikipedia.org/wiki/Receiver_operating_characteristic

An example

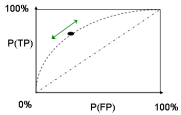


http://en.wikipedia.org/wiki/Receiver_operating_characteristic

Area under the curve



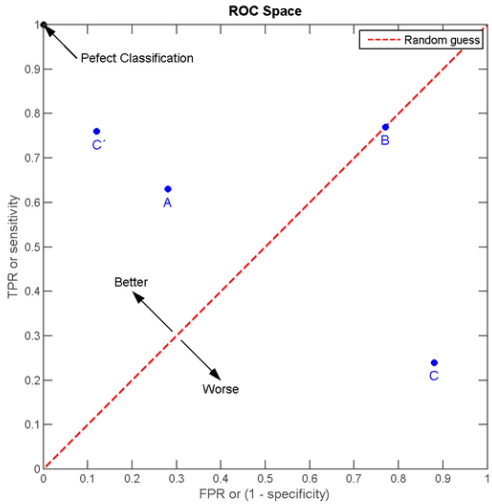
TP	FP
FN	TN
1	1



- AUC = 0.5: random guessing
- AUC = 1: perfect classifer
- In general AUC of above 0.8 considered "good"

http://en.wikipedia.org/wiki/Receiver_operating_characteristic

What is good?

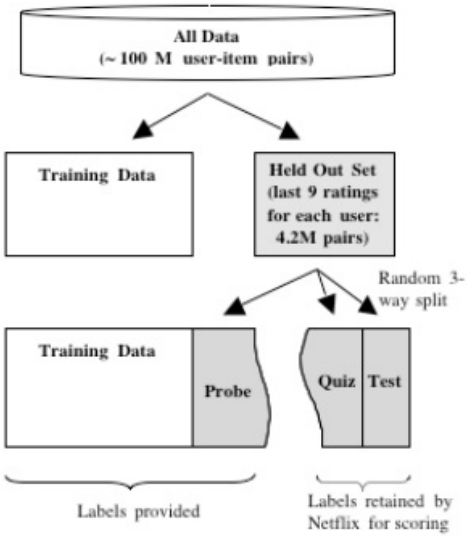


http://en.wikipedia.org/wiki/Receiver_operating_characteristic

Cross validation

Jeffrey Leek
Johns Hopkins Bloomberg School of Public Health

Study design



http://www2.research.att.com/~volinsky/papers/ASAStatComp.pdf

Key idea

1. Accuracy on the training set (resubstitution accuracy) is optimistic
2. A better estimate comes from an independent set (test set accuracy)
3. But we can't use the test set when building the model or it becomes part of the training set
4. So we estimate the test set accuracy with the training set.

Cross-validation

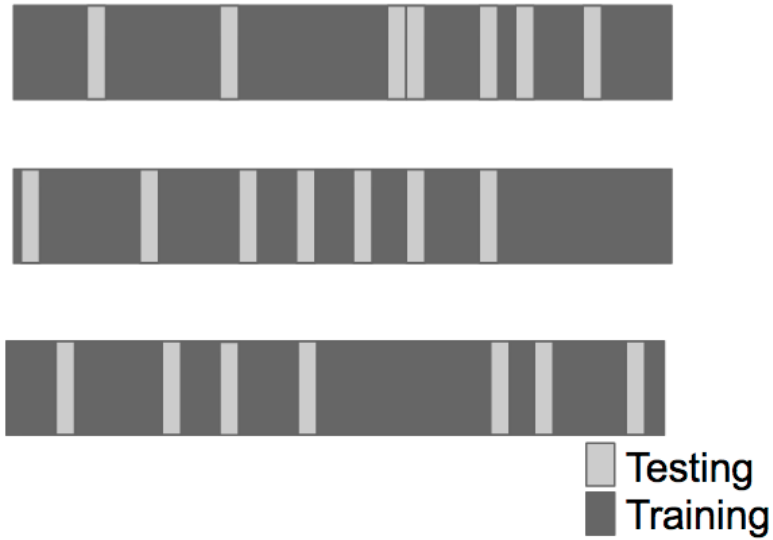
Approach:

1. Use the training set
2. Split it into training/test sets
3. Build a model on the training set
4. Evaluate on the test set
5. Repeat and average the estimated errors

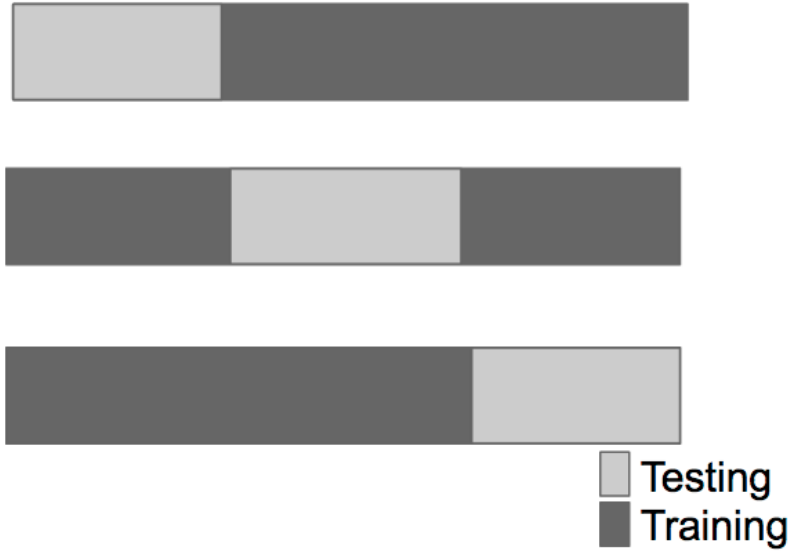
Used for:

1. Picking variables to include in a model
2. Picking the type of prediction function to use
3. Picking the parameters in the prediction function
4. Comparing different predictors

Random subsampling



K-fold



Leave one out

Considerations

- For time series data data must be used in "chunks"
- For k-fold cross validation
  - Larger k = less bias, more variance
  - Smaller k = more bias, less variance
- Random sampling must be done *without replacement*
- Random sampling with replacement is the *bootstrap*
  - Underestimates of the error
  - Can be corrected, but it is complicated (0.632 Bootstrap)
- If you cross-validate to pick predictors estimate you must estimate errors on independent data.

What data should you use?

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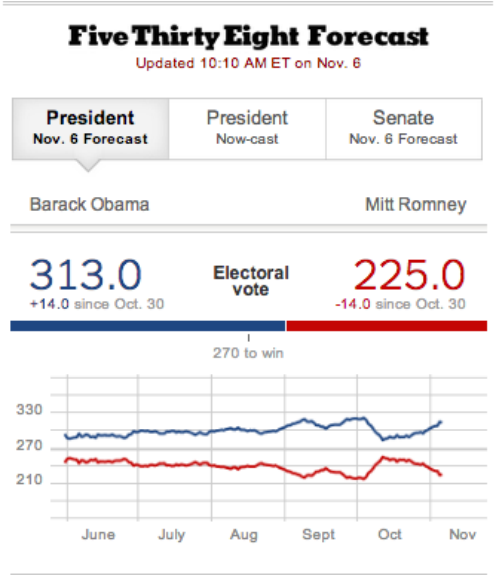
Johns Hopkins Bloomberg School of Public Health

A succcessful predictor



fivethirtyeight.com

Polling data

http://www.gallup.com/

Weighting the data

6.06.2010

Pollster Ratings v4.0: Methodology

by Nate Silver

Rating pollsters is at the core of FiveThirtyEight's mission, and forms the backbone of our forecasting models. But, it has been two years since we last revised our ratings. Here, at last, is an update. We have both substantially increased the amount of data that we are evaluating, and significantly refined our methodology.

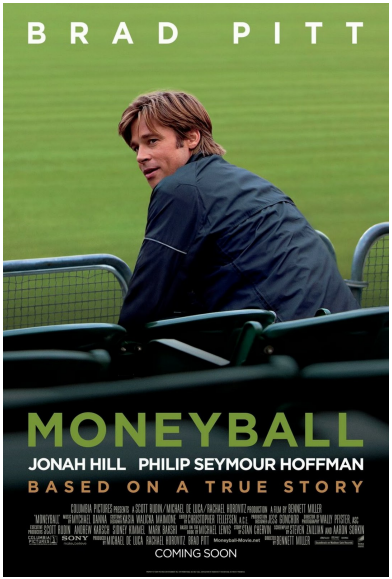
http://www.fivethirtyeight.com/2010/06/pollster-ratings-v40-methodology.html

Key idea

To predict X use data related to X

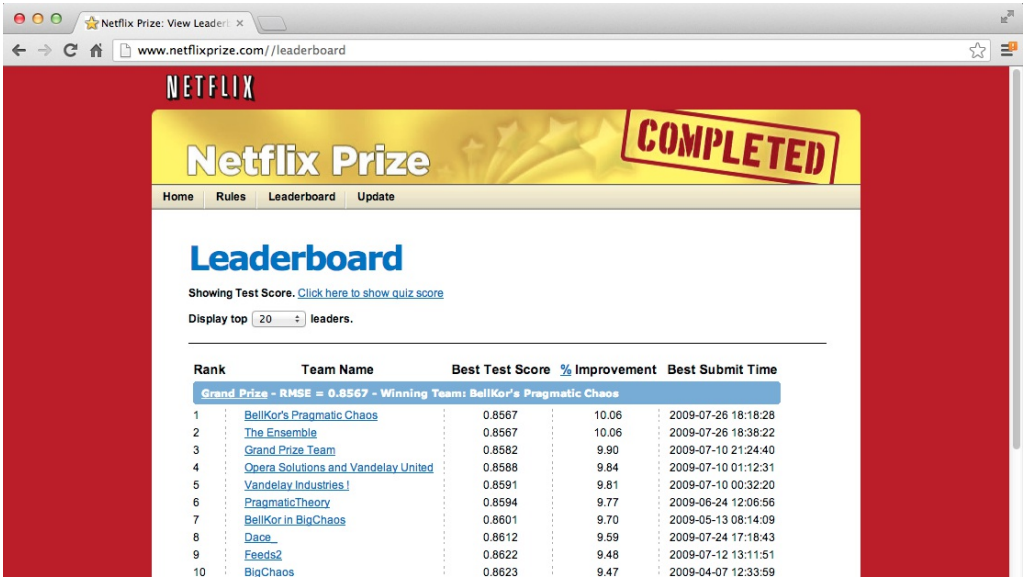
Key idea

To predict player performance use data about player performance



Key idea

To predict movie preferences use data about movie preferences



Key idea

To predict hospitalizations use data about hospitalizations

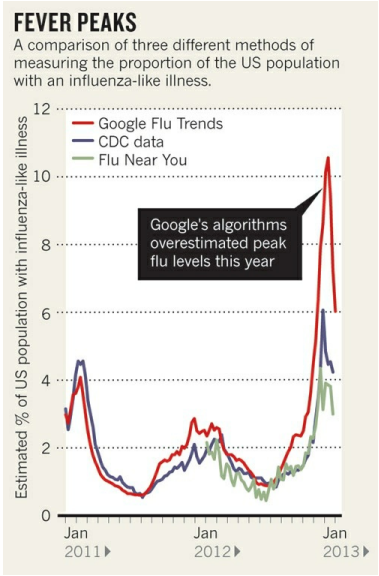
Not a hard rule

To predict flu outbreaks use Google searches

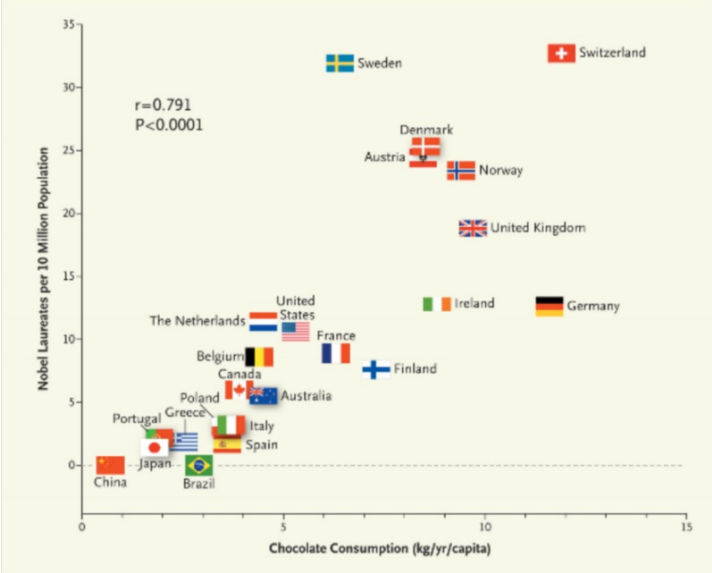
http://www.google.org/flutrends/

Looser connection = harder prediction

Data properties matter



Unrelated data is the most common mistake



http://www.nejm.org/doi/full/10.1056/NEJMon1211064