

## **Evaluation and Experimentation**

- Evaluation Metrics
- Cross-Validation
- Significance Tests







### **Evaluation**

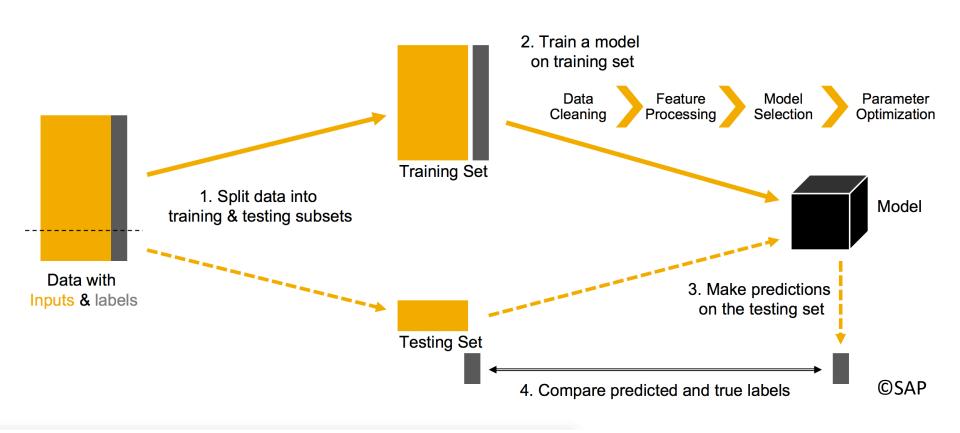
- Predictive analysis: training a model to make predictions on previously unseen data
- Evaluation: using previously unseen <u>labeled</u> data to estimate the quality of a model's predictions on new data
- Evaluation Metric: a measure that summarizes the quality of a model's predictions







## **Predictive Analysis**







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- There are many different metrics
- Different metrics make different assumptions about what end users care about
- Choosing the most appropriate metric is important!







## (1) accuracy

Accuracy: percentage of correct predictions

true

	pos	neg
pos	а	b
neg	С	d

$$\mathcal{A} = \frac{(a+d)}{(a+b+c+d)}$$











## **Evaluation Metrics** (1) accuracy

Accuracy: percentage of correct predictions

true

	pos	neut.	neg
pos	а	b	С
neut.	d	е	f
neg	g	h	i

$$\mathcal{A} = \frac{(a+e+i)}{(a+b+c+d+e+f+g+h+i)}$$













## **Evaluation Metrics** (1) accuracy

What assumption(s) does accuracy make?

#### true

	pos	neut.	neg
pos	а	b	С
neut.	d	е	f
neg	g	h	i

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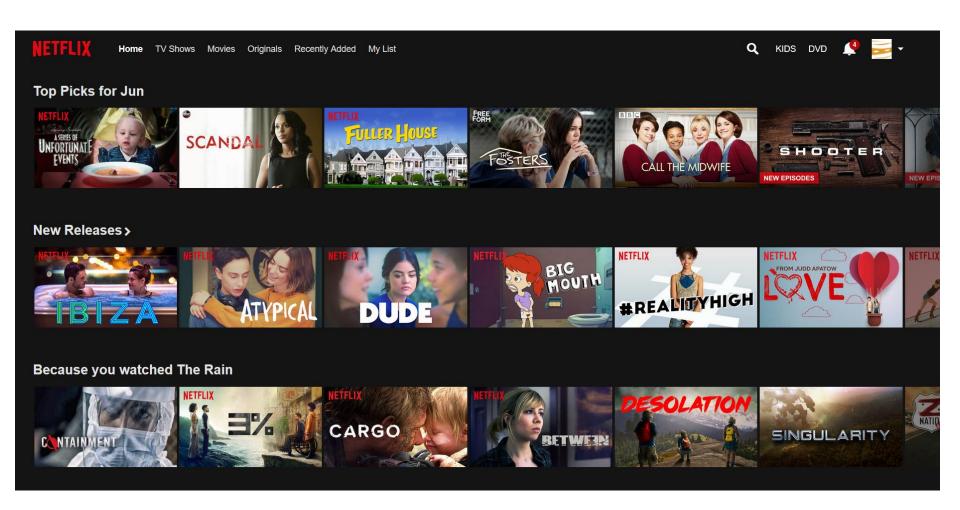








Content recommendation: relevant vs. non-relevant



Email spam filtering: spam vs. ham

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$\bowtie$ $\$	ei-sci@ei-sci.org	SCI-EI期刊检索、收录 (ICIEEE 2013) 邀请函 Thu 9/27/12 2:50 AM	<ul><li>Junk</li></ul>
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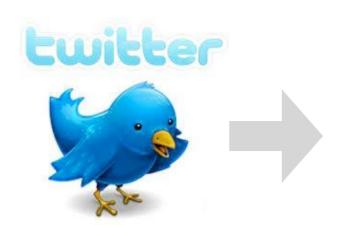




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Product reviews: positive vs. negative vs. neutral













Text-based Forecasting: buy vs. sell vs. hold









Health monitoring system: alarm vs. no alarm



# Evaluation Metrics (1) accuracy

- What assumption(s) does accuracy make?
- It assumes that all prediction errors are equally bad
- Oftentimes, we care more about one class than the others
- If so, the class of interest is usually the minority class
- We are looking for the "needles in the haystack"
- In this case, accuracy is not a good evaluation metric
- There are metrics that provide more insight into perclass performance

(2) precision and (3) recall

- For a given class C:
  - precision: the percentage of positive <u>predictions</u>
     that are truly positive
  - recall: the percentage of <u>true</u> positives that are correctly predicted positive







(2) precision and (3) recall

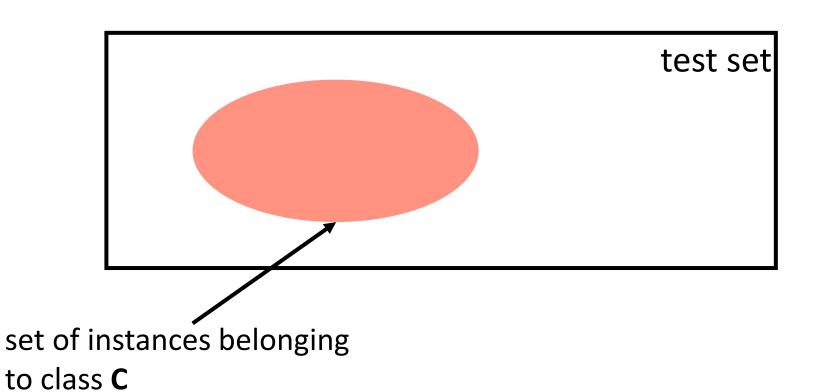
test set



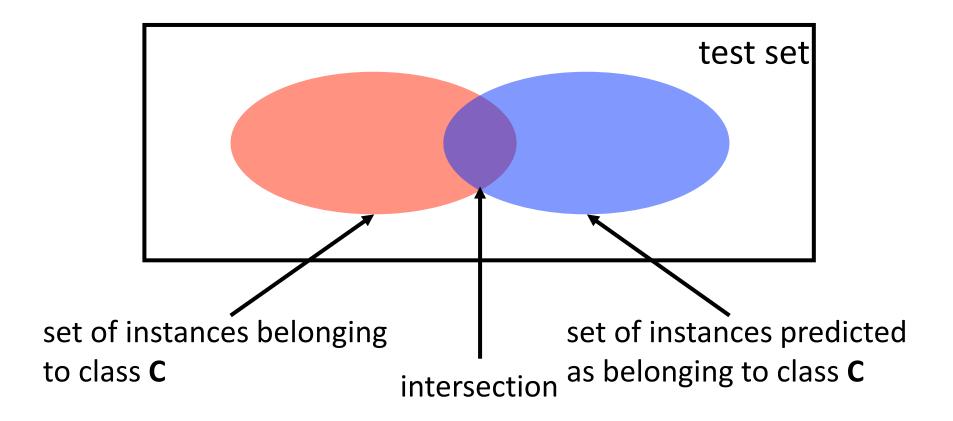




(2) precision and (3) recall

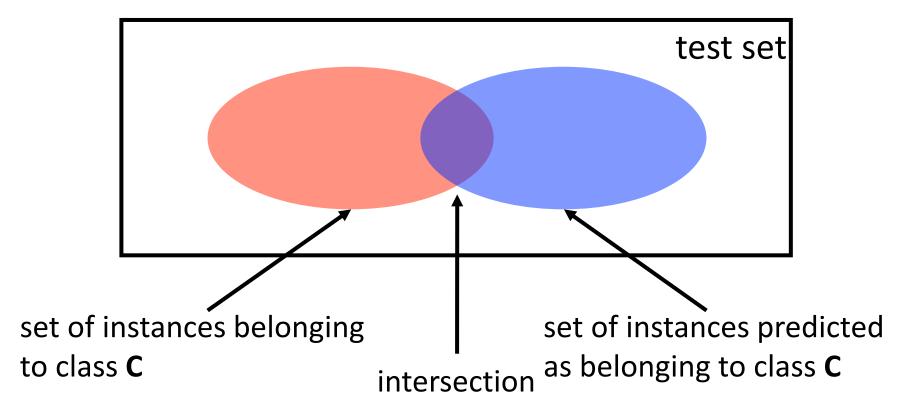


(2) precision and (3) recall



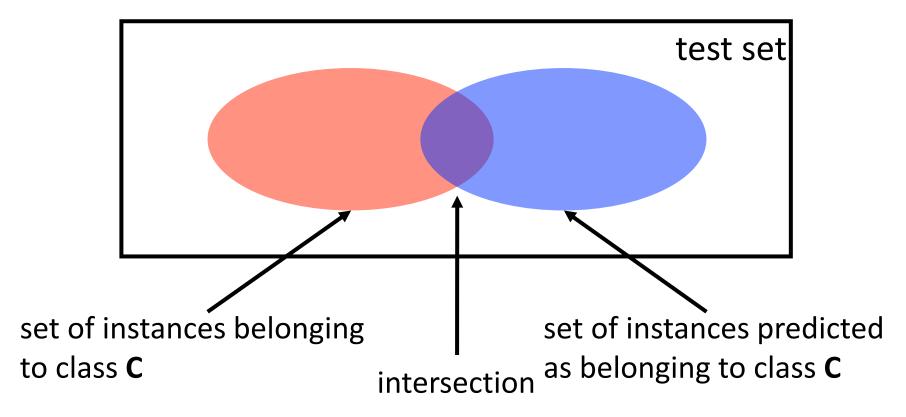
## (2) precision and (3) recall

 Precision (the percentage of positive predictions that are truly positive) = ?

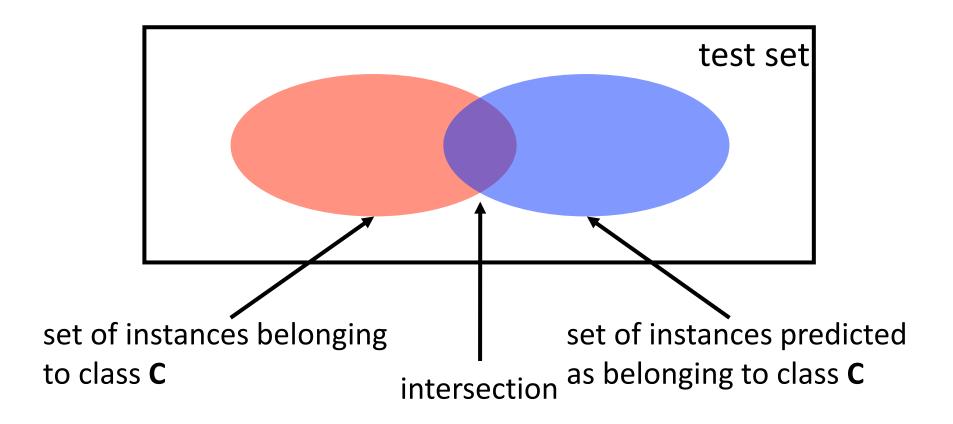


## (2) precision and (3) recall

 Recall (the percentage of <u>true</u> positives that are correctly predicted positive) = ?



(2) precision and (3) recall



(2) precision

true

predicted

	pos	neut.	neg
pos	а	b	С
neut.	d	е	f
neg	g	h	i

$$\mathcal{P}_{\text{positive}} = \frac{a}{a+b+a}$$

For a positive class, the percentage of correct predictions that are truly positive

## (3) recall

true

predicted

	pos	neut.	neg
pos	а	b	С
neut.	d	е	f
neg	g	h	i

$$\mathcal{R}_{\text{positive}} = \frac{a}{a+d+g}$$

For a positive class, the percentage of <u>true</u> positives that are correctly predicted positive

prevision vs. recall

#### true

	pos	neut.	neg
pos	а	b	С
neut.	d	е	f
neg	<b></b>	h	i











(4) f-measure

 F-measure: the harmonic (not arithmetic) mean of precision and recall

$$\mathcal{F} = \frac{2 \times \mathcal{P} \times \mathcal{R}}{\mathcal{P} + \mathcal{R}}$$

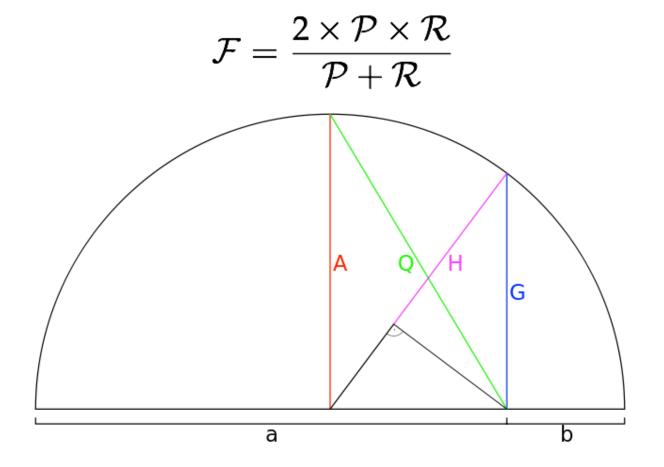






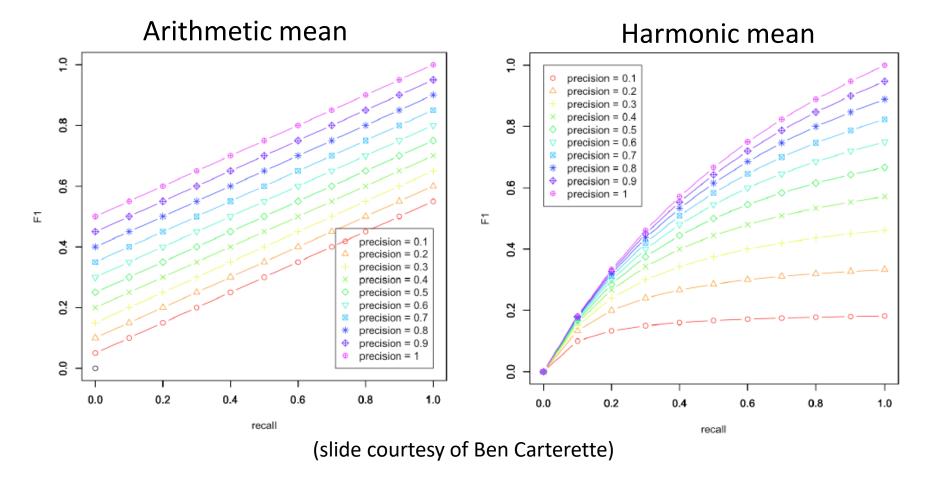
### (4) f-measure

 F-measure: the harmonic (not arithmetic) mean of precision and recall



## (4) f-measure

F-measure: the harmonic (not arithmetic) mean of precision and recall



(5) precision-recall curves

 F-measure: assumes that the "end users" care equally about precision and recall











- Most machine-learning algorithms provide a prediction confidence value
- The prediction confidence value can be used as a threshold in order to trade-off precision and recall







(5) precision-recall curves

- Remember Naive Bayes classification?
- Given instance D, predict positive (POS) if:

$$P(POS|D) \ge P(NEG|D)$$

Otherwise, predict negative (NEG)







# Evaluation Metrics (5) precision-recall curves

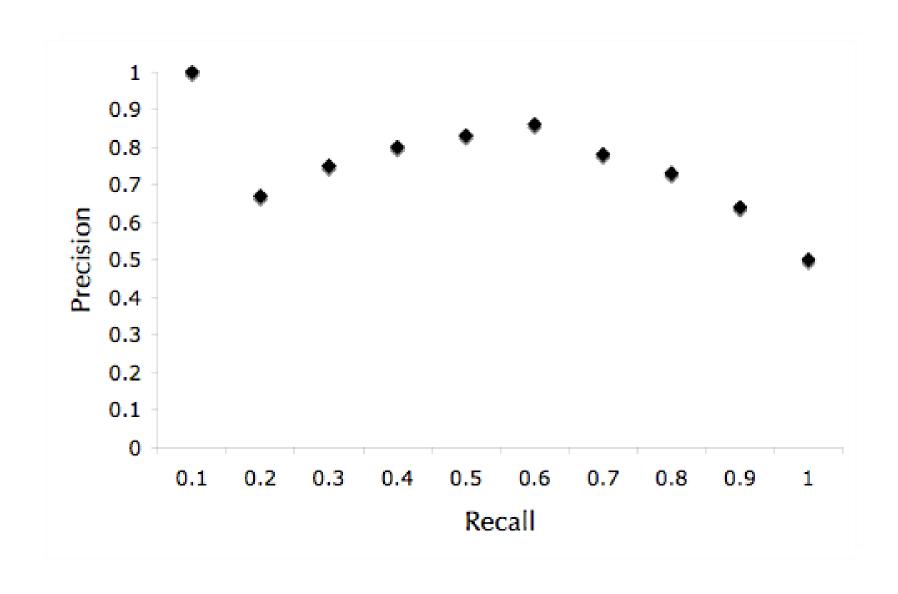
- Remember Naive Bayes classification?
- Given instance D, predict positive (POS) if:

$$P(POS|D) \ge P(NEG|D)$$

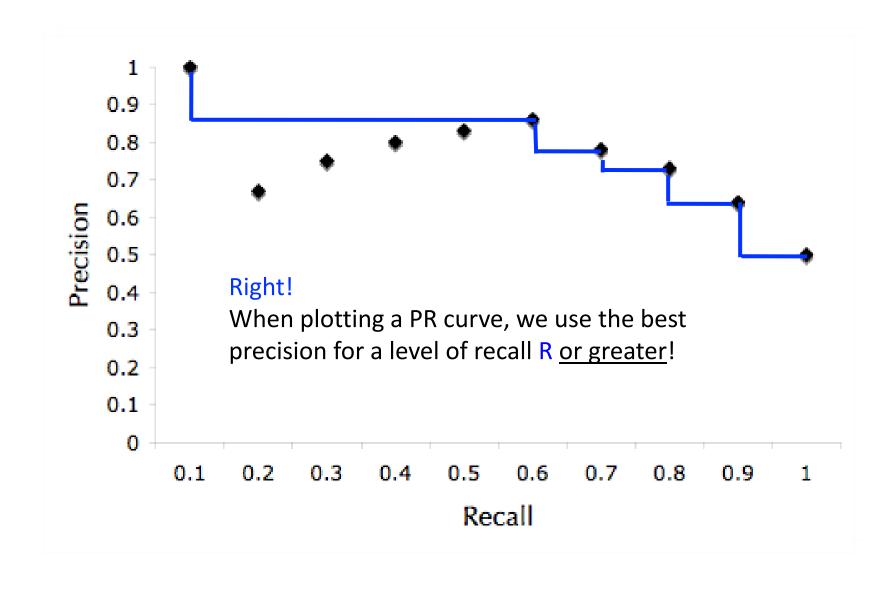
Otherwise, predict negative (NEG)

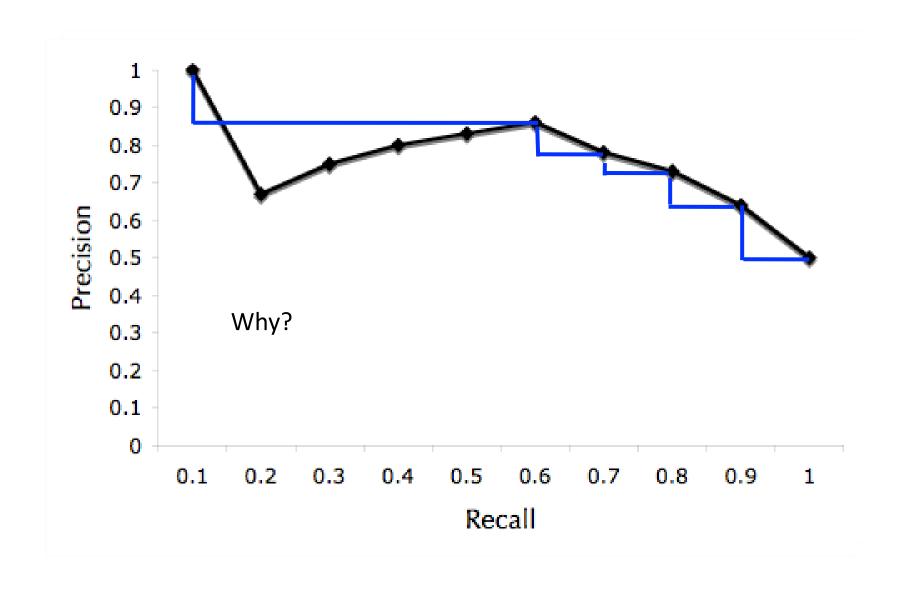
this value can be used as a threshold for classification into the POS class

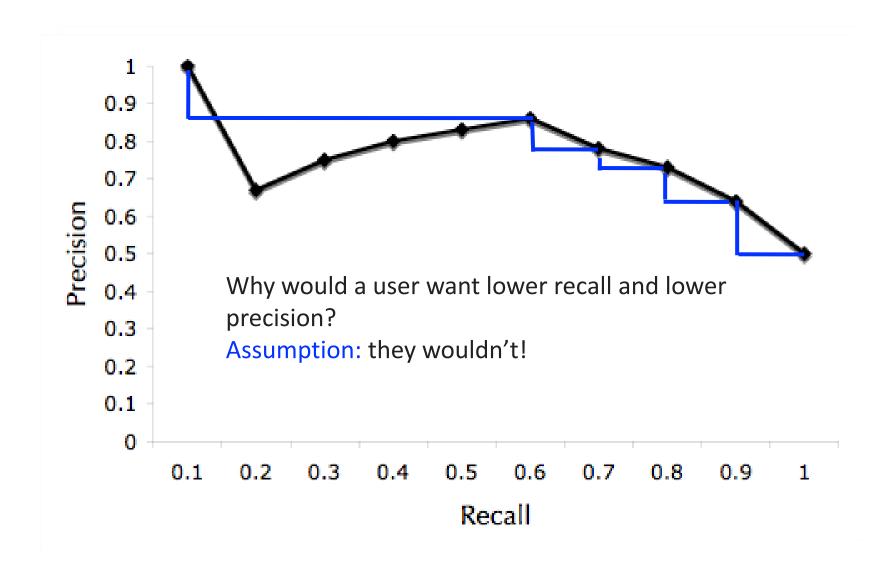
rank (K)	ranking	P(POS D)	P@K	R@K
1		0.99	1.00	0.10
2		0.87	0.50	0.10
3		0.84	0.67	0.20
4		0.83	0.75	0.30
5		0.77	0.80	0.40
6		0.63	0.83	0.50
7		0.58	0.86	0.60
8		0.57	0.75	0.60
9		0.56	0.78	0.70
10		0.34	0.70	0.70
11		0.33	0.73	0.80
12		0.25	0.67	0.80
13		0.21	0.62	0.80
14		0.15	0.64	0.90
15		0.14	0.60	0.90
16		0.14	0.56	0.90
17		0.12	0.53	0.90
18		0.08	0.50	0.90
19		0.01	0.47	0.90
20		0.01	0.50	1.00

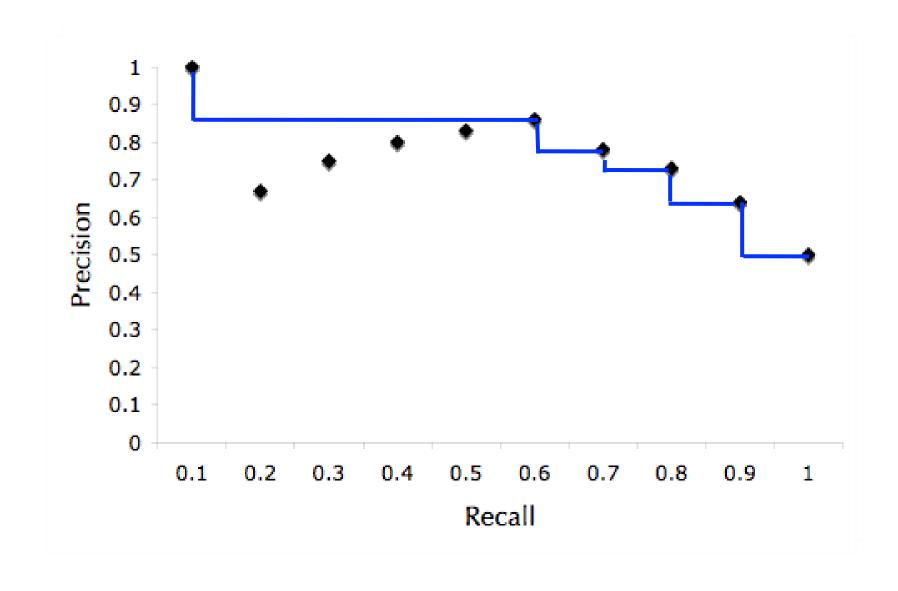


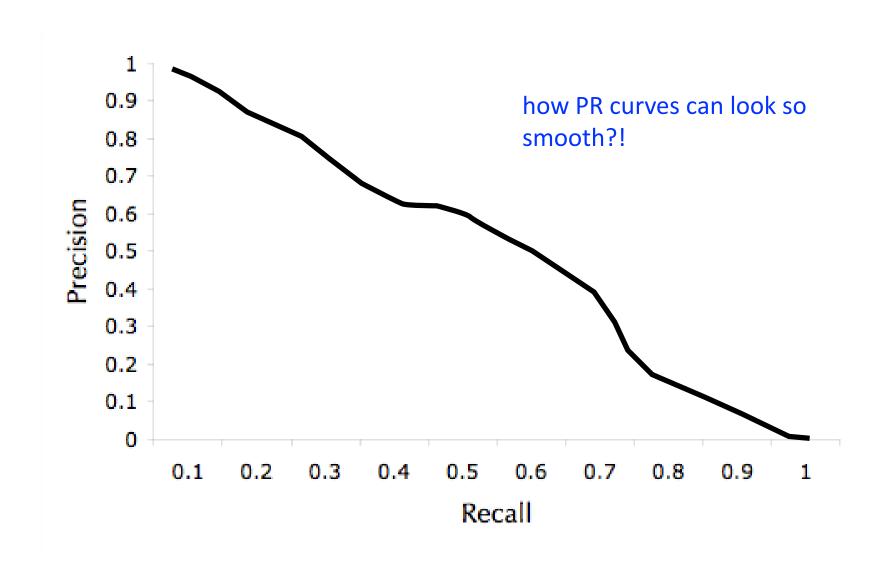


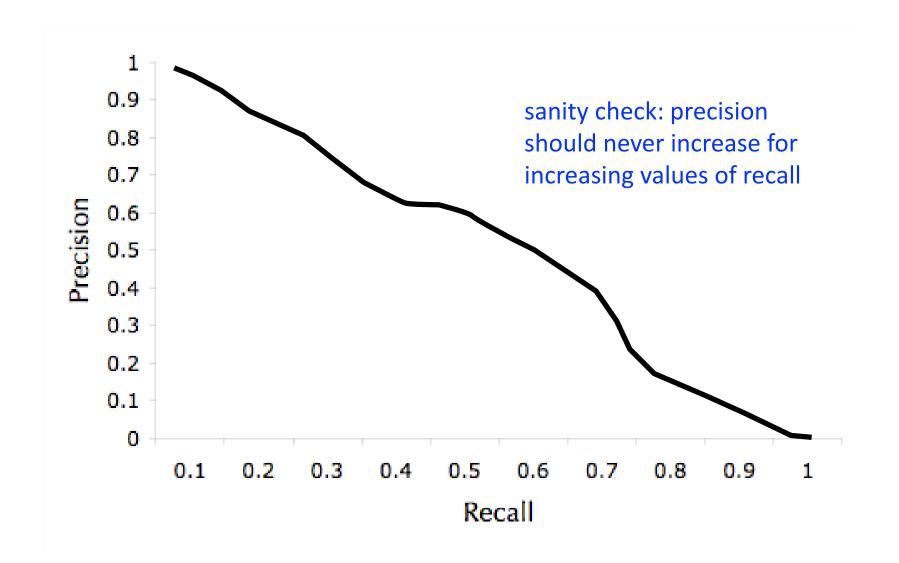


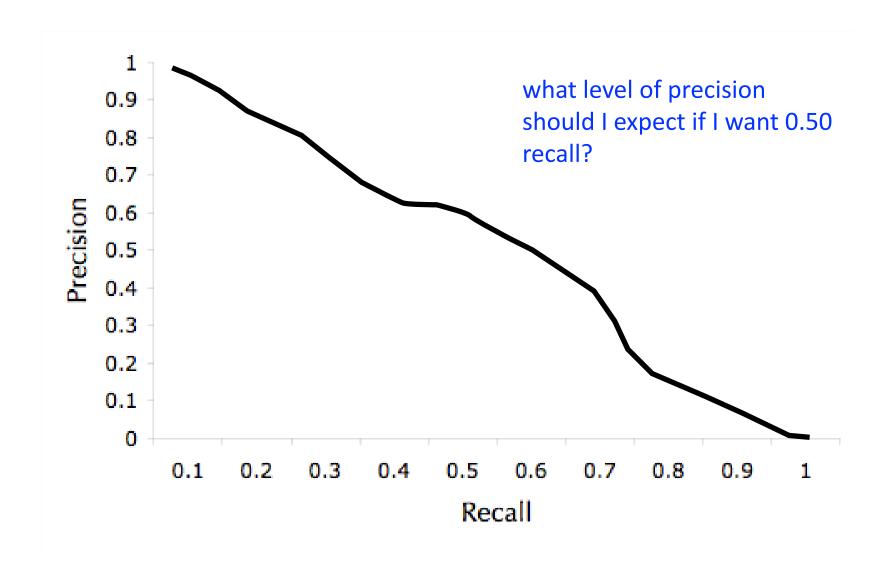


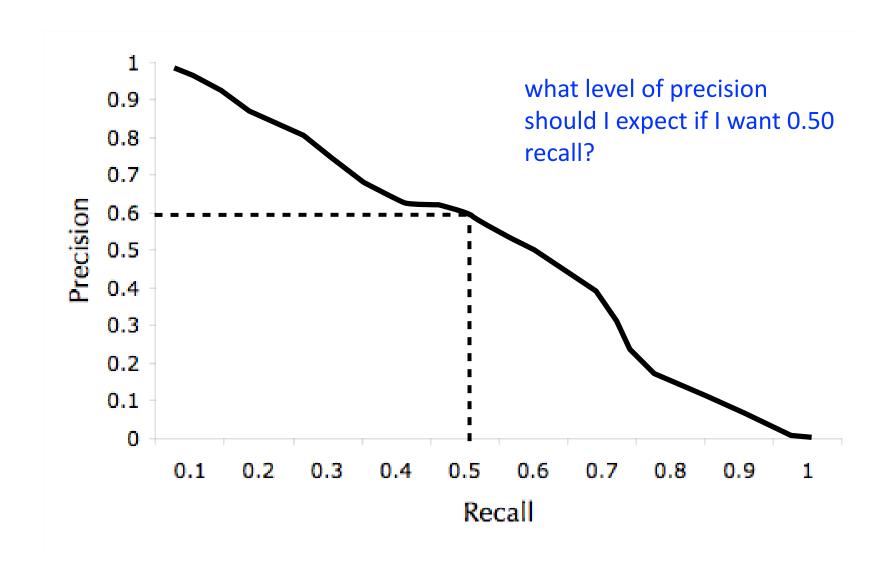


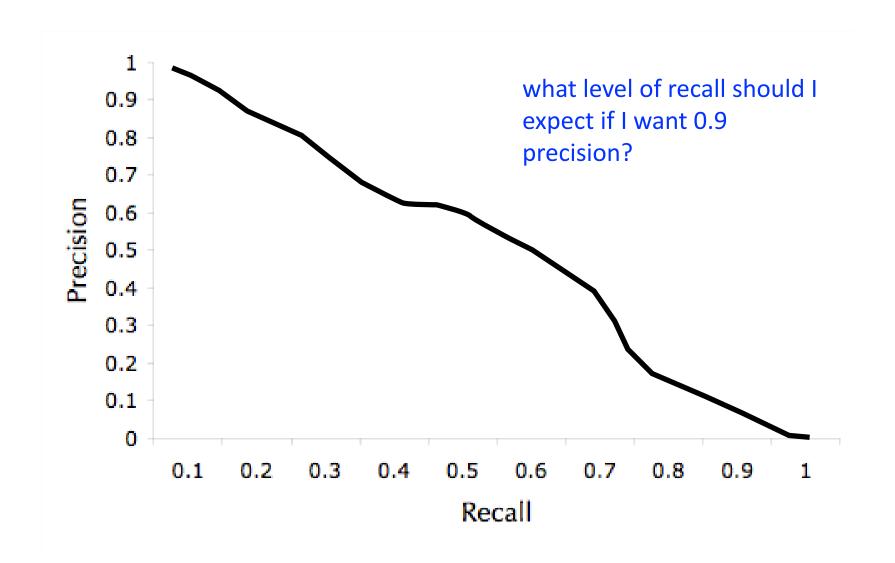


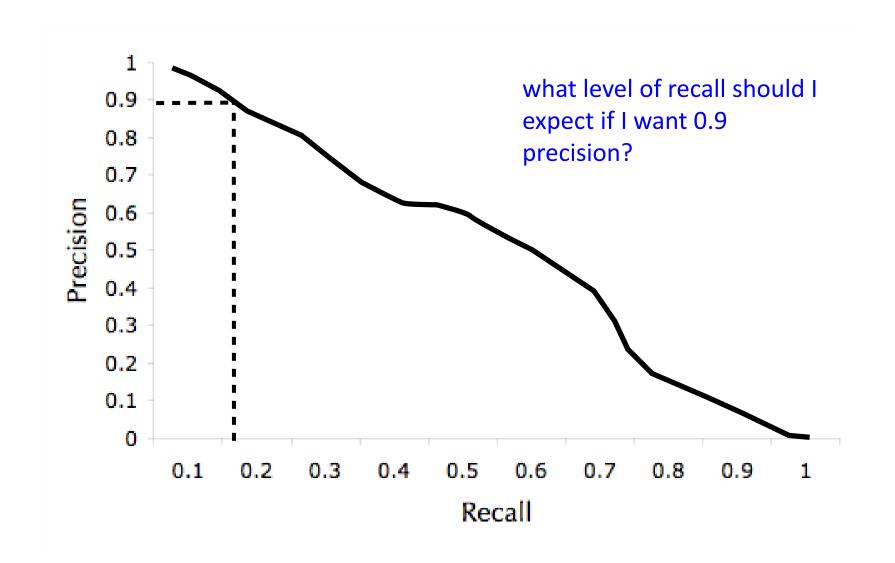


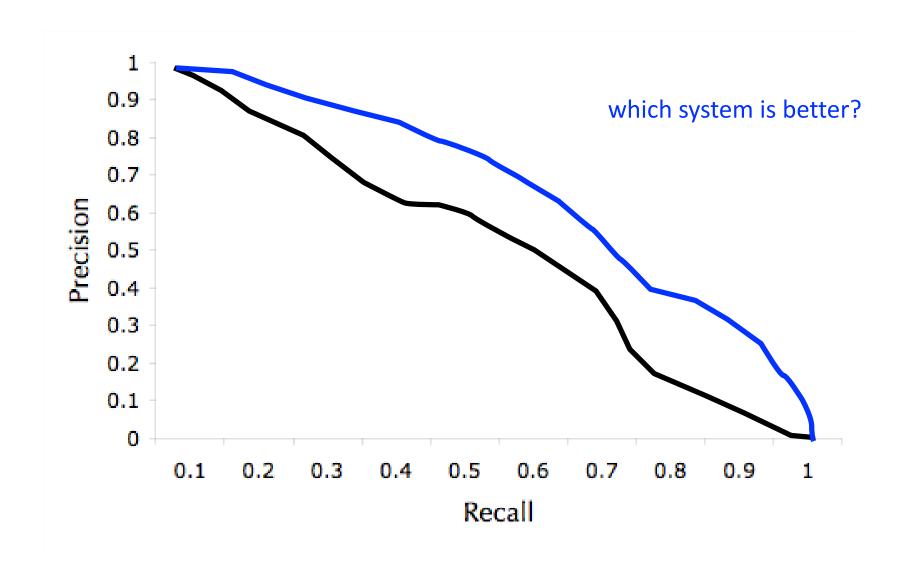


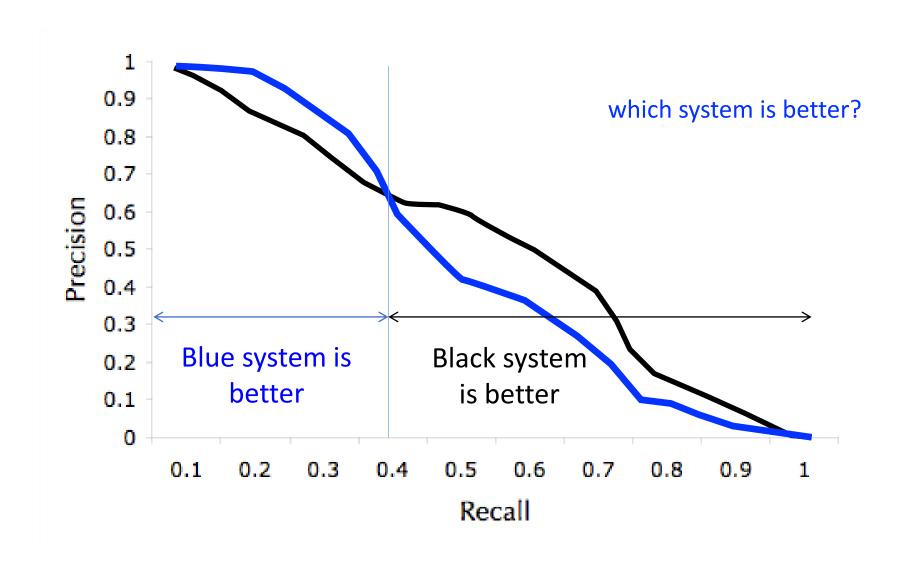


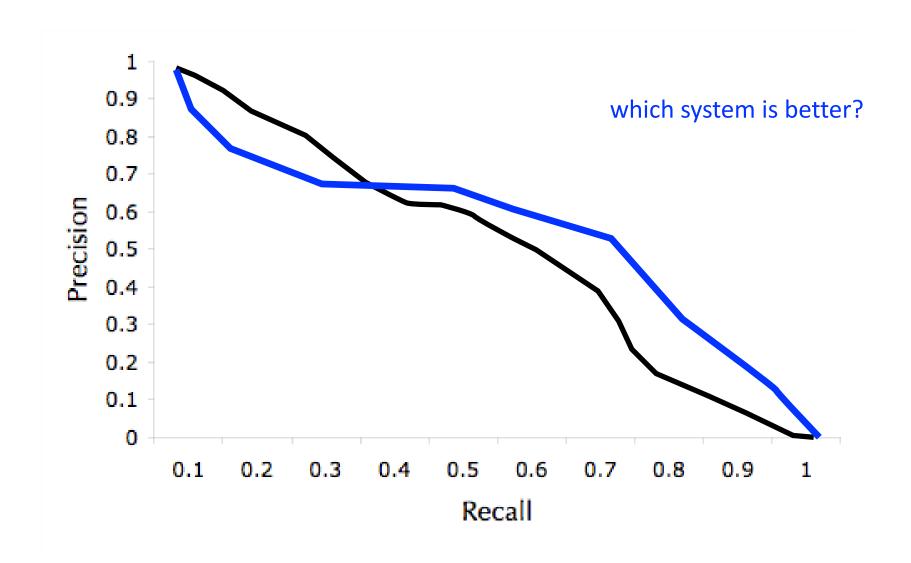


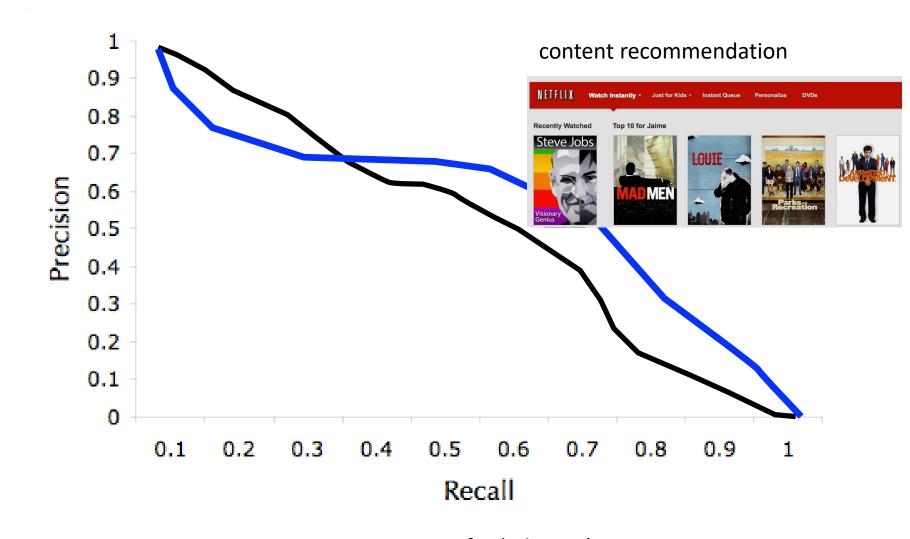




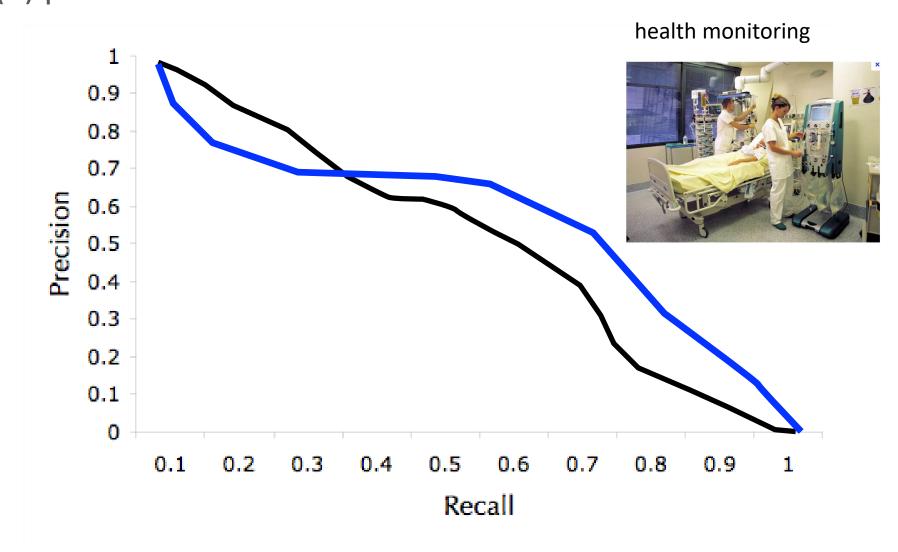








PR curves for 'relevant'



PR curves for 'alarm'

#### (5) precision-recall curves

- PR curves show different precision-recall operating points (or trade-off points)
- How many false positives will I have to sift through for a desired level of recall?
- How many true positives will I have to miss for a desired level of precision?





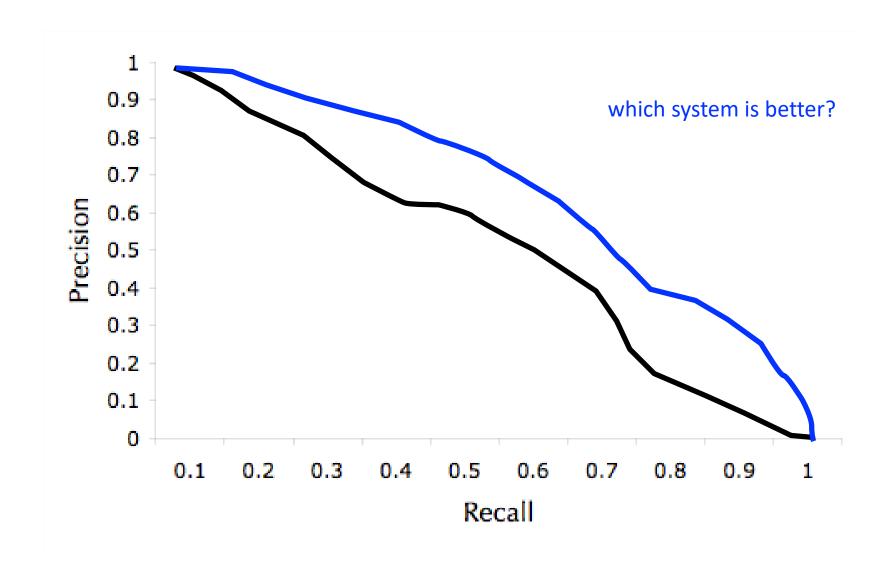


- In some situations we may want to summarize the quality of a PR curve using a single number
  - when comparing across lots of different models or feature representations
- Average precision: <u>proportional</u> (not equal) to the area under the PR curve







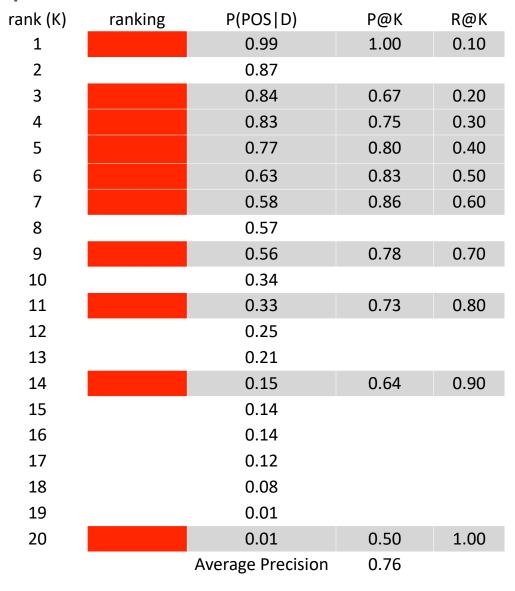


- Average Precision
  - 1. Sort instances by descending order of confidence value
  - 2. Go down the ranking, and measure P@K where recall increases
  - 3. Take the average of all P@K values where recall increases









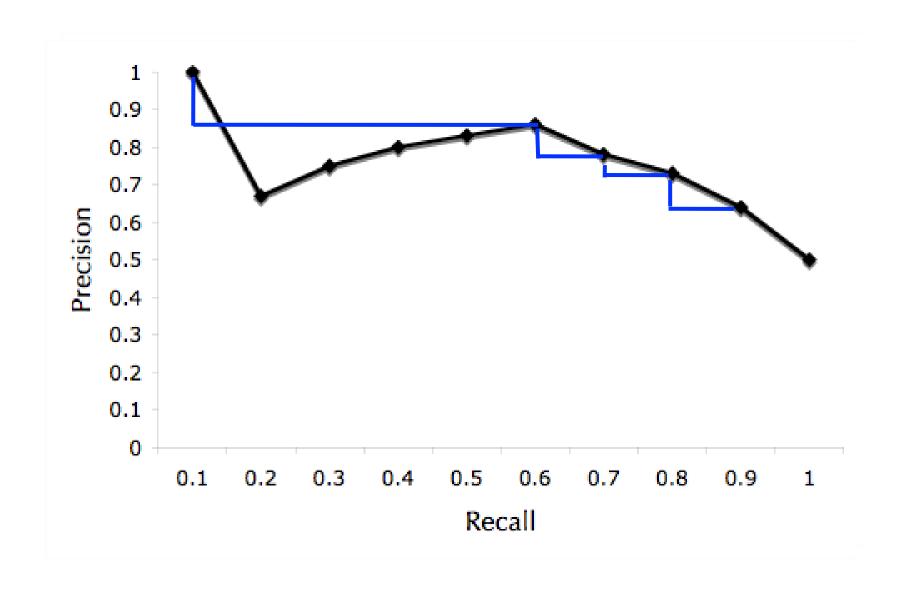
rank (K)	ranking	P(POS D)	P@K	R@K
1		0.99	1.00	0.10
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13		0.21		
14		0.15		
15		0.14		
16		0.14		
17		0.12		
18		0.08		
19		0.01		
20		0.01		
		Average Precision	1.00	

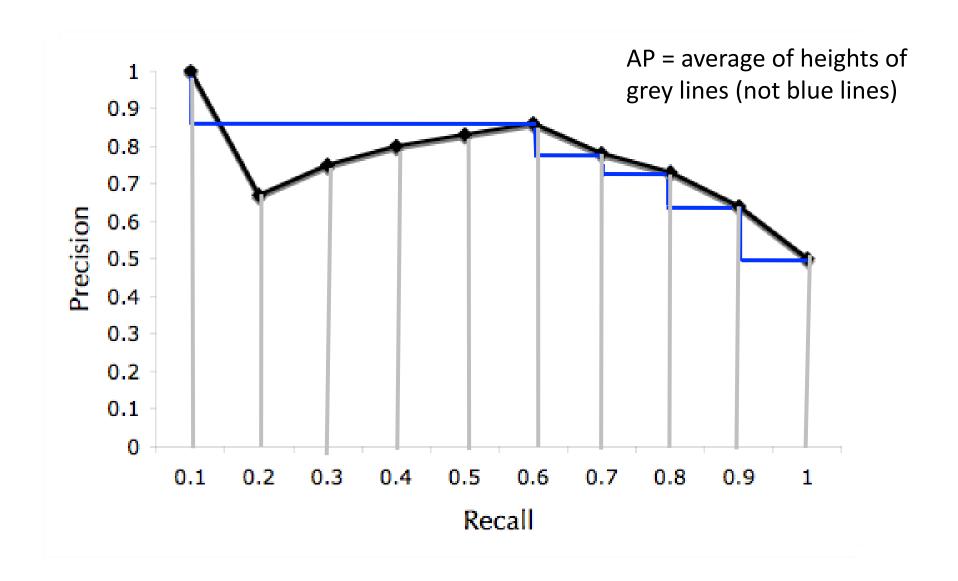
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19		0.01		
20		0.01		
		Average Precision	0.99	

(14)	1 *	D/DOC/D)	D.O.14	D 014
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17		0.12		
18		0.08		







- Average precision is proportional to the area under the PR curve
- It punishes high-confident mistakes more severely than low-confident mistakes







- Accuracy
- Precision
- Recall
- F-measure (or F1 measure)
- PR curves (not a metric, but rather a way to show different PR operating points)
- Average Precisions









## Evaluating numeric prediction

- Same strategies: independent test set, cross-validation, significance tests, etc.
- Difference: error measures
- Actual target values: a<sub>1</sub> a<sub>2</sub> ...a<sub>n</sub>
- Predicted target values:  $p_1 p_2 ... p_n$
- Most popular measure: mean-squared error

$$\frac{(p_1-a_1)^2 + \cdots + (p_n-a_n)^2}{n}$$

Easy to manipulate mathematically

## Other measures

The root mean-squared error :

$$\sqrt{\frac{(p_1-a_1)^2+\cdots+(p_n-a_n)^2}{n}}$$

 The mean absolute error is less sensitive to outliers than the mean-squared error:

$$\frac{|p_1-a_1|+\cdots+|p_n-a_n|}{n}$$

 Sometimes relative error values are more appropriate (e.g. 10% for an error of 50 when predicting 500)

#### Correlation coefficient

 Measures the statistical correlation between the predicted values and the actual values

$$\frac{S_{PA}}{\sqrt{S_P S_A}}, \text{ where } S_{PA} = \frac{\sum_i (p_i - \overline{p})(a_i - \overline{a})}{n-1}, S_P = \frac{\sum_i (p_i - \overline{p})^2}{n-1},$$

$$S_A = \frac{\sum_i (a_i - \overline{a})^2}{n-1} \text{ (here, } \overline{a} \text{ is the mean value over the test data)}$$

- Scale independent, between –1 and +1
- Good performance leads to large values!

(slide courtesy of Witten et al., 2017)

## **Evaluation and Experimentation**

- Evaluation Metrics
- Cross-Validation
- Significance Tests







#### N-fold cross-validation

- 1. divide the data into N sets of instances
- 2. use the union of N-1 sets to find the best parameter values
- 3. measure performance (using the best parameters) on the held-out set
- 4. do steps 2-3 N times
- 5. average performance across the N held-out sets













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• Split the data into N = 5 folds

12345

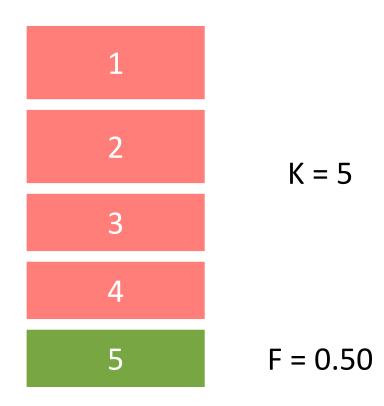








 For each fold, find the parameter value that maximizes performance on the union of N - 1 folds and test (using this parameter value) on the held-out fold.

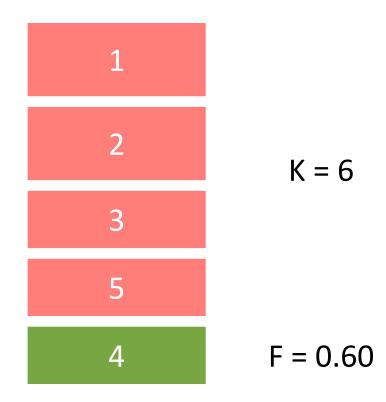








 For each fold, find the parameter value that maximizes performance on the union of N - 1 folds and test (using this parameter value) on the held-out fold.



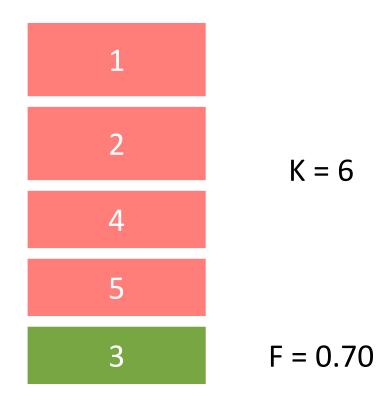




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 For each fold, find the parameter value that maximizes performance on the union of N - 1 folds and test (using this parameter value) on the held-out fold.



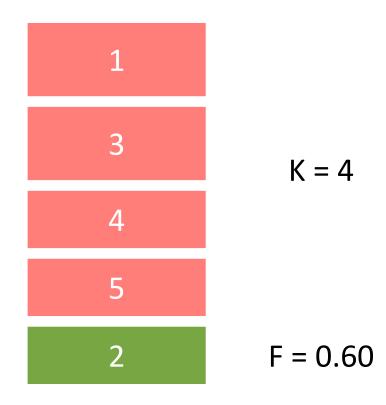








 For each fold, find the parameter value that maximizes performance on the union of N - 1 folds and test (using this parameter value) on the held-out fold.

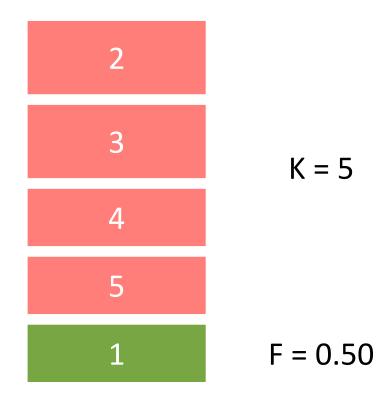








 For each fold, find the parameter value that maximizes performance on the union of N - 1 folds and test (using this parameter value) on the held-out fold.







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 Average the performance across held-out folds

1	F = 0.50
2	F = 0.60
3	F = 0.70
4	F = 0.60
5	F = 0.50



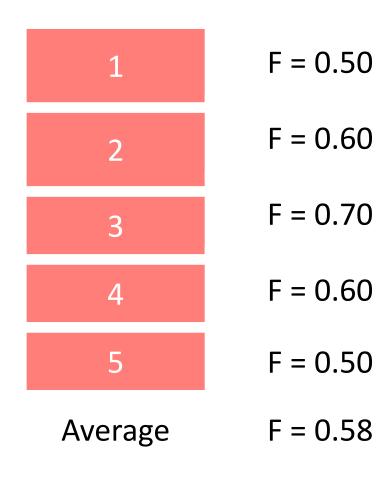
**Average** 





F = 0.58

 Average the performance across held-out folds



Advantages and Disadvantages?

#### N-Fold Cross-Validation

- Advantage
  - multiple rounds of generalization performance.
- Disadvantage
  - ultimately, we'll tune parameters on the whole dataset and send our system into the world.
  - a model trained on 100% of the data should perform better than one trained on 80%.
  - thus, we may be underestimating the model's performance!









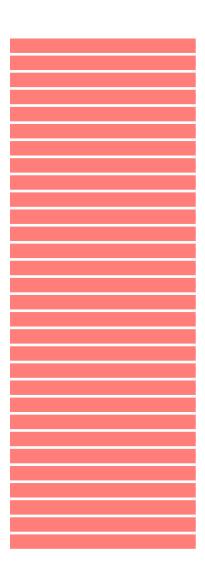




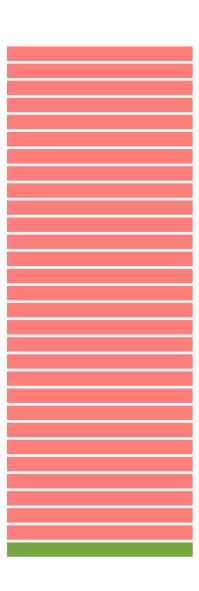
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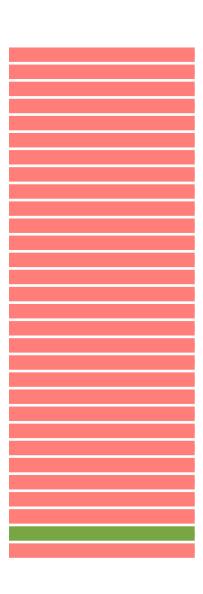
 Split the data into N folds of 1 instance each



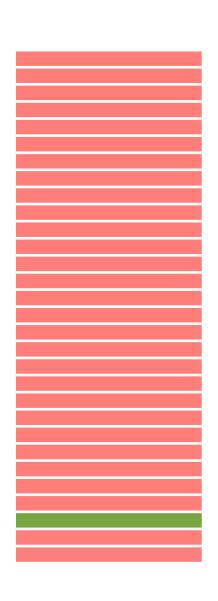
 For each instance, find the parameter value that maximize performance on for the other instances and and test (using this parameter value) on the held-out instance.



 For each instance, find the parameter value that maximize performance on for the other instances and and test (using this parameter value) on the held-out instance.



- For each instance, find the parameter value that maximize performance on for the other instances and and test (using this parameter value) on the held-out instance.
- And so on ...
- Finally, average the performance for each heldout instance



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- And so on ...
- Finally, average the performance for each heldout instance

Advantages and Disadvantages?

#### Advantages

- multiple rounds of generalization performance.
- each training fold is as similar as possible to the one we will ultimately use to tune parameters before sending the system out into the world.

#### Disadvantage

- our estimate of generalization performance may be artificially high
- we are likely to try lots of different things and pick the one with the best "generalization" performance
- still indirectly over-training to the dataset (sigh...)

### **Evaluation and Experimentation**

- Evaluation Metrics
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### **Comparing Systems**

•	Train and test both
	systems using 10-fold
	cross validation

- Use the same folds for both systems
- Compare the difference in average performance across held-out folds

Fold	System A	System B
1	0.2	0.5
2	0.3	0.3
3	0.1	0.1
4	0.4	0.4
5	1	1
6	0.8	0.9
7	0.3	0.1
8	0.1	0.2
9	0	0.5
10	0.9	0.8
Average	0.41	0.48
	Difference	0.07

## Significance Tests motivation

- Why would it be risky to conclude that System B is better System A?
- Put differently, what is it that we're trying to achieve?







## Significance Tests motivation

- In theory: that the average performance of System B is greater than the average performance of System A for all possible test sets.
- However, we don't have all test sets. We have a sample
- And, this sample may favor one system vs. the other!







## Significance Tests definition

 A significance test is a statistical tool that allows us to determine whether a difference in performance reflects a true pattern or just random chance







## Significance Tests ingredients

- Test statistic: a measure used to judge the two systems (e.g., the difference between their average F-measure)
- Null hypothesis: no "true" difference between the two systems
- P-value: take the value of the observed test statistic and compute the probability of observing a statistical summary (e.g., sample mean difference between two compared groups) that is large (or larger) <u>under the null hypothesis</u>







## Significance Tests ingredients

- If the p-value is large, we cannot reject the null hypothesis
- That is, we cannot claim that one system is better than the other
- If the p-value is small (p<0.05), we can reject the null hypothesis
- That is, the observed test-statistic is not due to random chance







#### **Comparing Systems**

P-value: the probability
 of observing a difference
 equal to or greater than
 0.07 under the null
 hypothesis (i.e., the
 systems are actually
 equal).

Fold	System A	System B
1	0.2	0.5
2	0.3	0.3
3	0.1	0.1
4	0.4	0.4
5	1	1
6	0.8	0.9
7	0.3	0.1
8	0.1	0.2
9	0	0.5
10	0.9	0.8
Average	0.41	0.48
	Difference	0.07

# Fisher's Randomization Test procedure

- Inputs: counter = 0, N = 100,000
- Repeat N times:

**Step 1:** for each fold, flip a coin and if it lands 'heads', flip the result between System A and B

**Step 2:** see whether the test statistic is equal to or greater than the one observed and, if so, increment counter

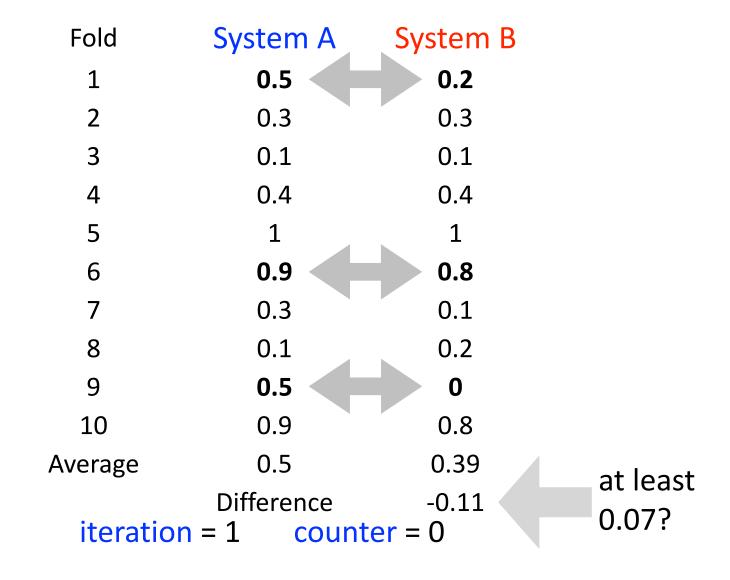
Output: counter / N

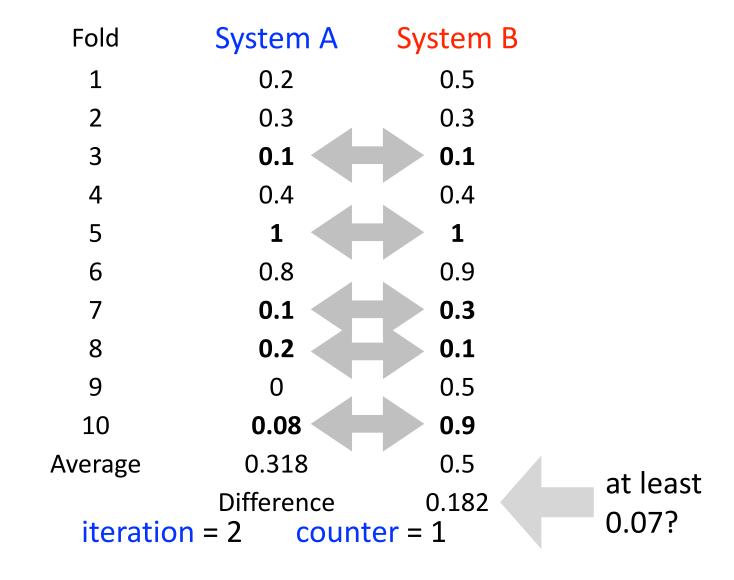


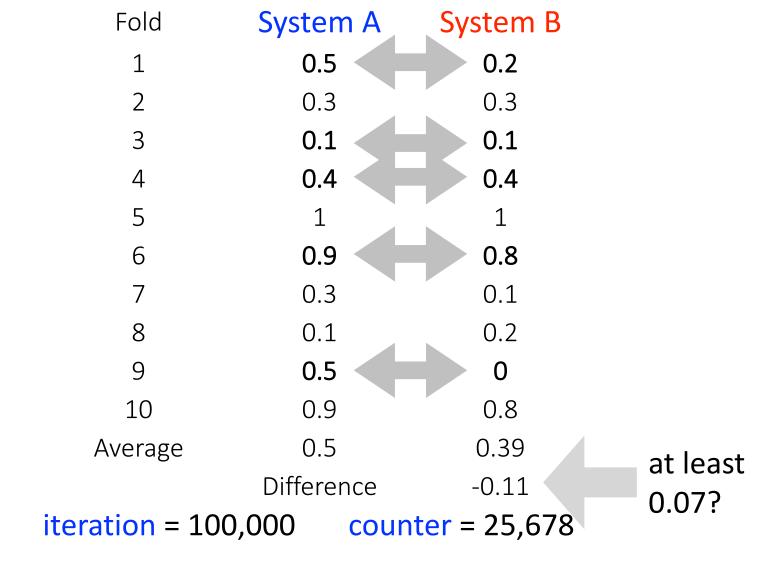




Fold	System A	System B
1	0.2	0.5
2	0.3	0.3
3	0.1	0.1
4	0.4	0.4
5	1	1
6	0.8	0.9
7	0.3	0.1
8	0.1	0.2
9	0	0.5
10	0.9	0.8
Average	0.41	0.48
	Difference	0.07







# Fisher's Randomization Test procedure

- Inputs: counter = 0, N = 100,000
- Repeat N times:

**Step 1:** for each query, flip a coin and if it lands 'heads', flip the result between System A and B

**Step 2:** see whether the test statistic is equal to or greater than the one observed and, if so, increment counter

• Output: counter / N = (25,678/100,000) = 0.25678







- Under the null hypothesis, the probability of observing a value of the test statistic of 0.07 or greater is about 0.26.
- Because p > 0.05, we cannot confidently say that the value of the test statistic is <u>not</u> due to random chance.
- A difference between the average F-measure values of 0.07 is not significant







## Fisher's Randomization Test procedure

- Inputs: counter = 0, N = 100,000
- Repeat N times:

**Step 1:** for each query, flip a coin and if it lands 'heads', flip the result between System A and B

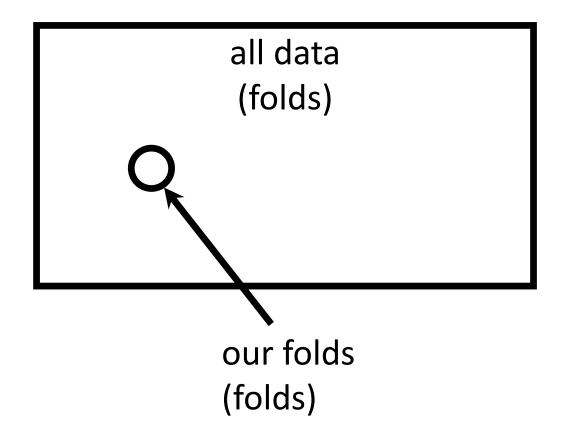
**Step 2:** see whether the test statistic is equal to or greater than the one observed and, if so, increment counter

• Output: counter / N = (25,678/100,00) = 0.25678

This is a one-tailed test (B > A). We can modify it to be a two-tailed test (|B| > A)

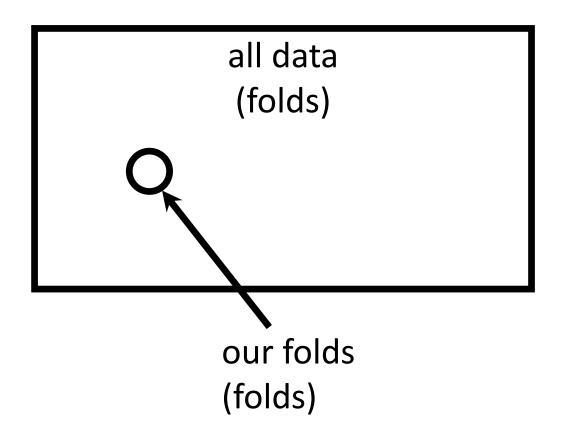
## Bootstrap-Shift Test motivation

Our sample is a representative sample of all data



## Bootstrap-Shift Test motivation

 If we sample (with replacement) from our sample, we can generate a new representative sample of all data



- **Inputs:** Array  $T = \{\}$ , N = 100,000
- Repeat N times:
- **Step 1:** sample 10 folds (with replacement) from our set of 10 folds (called a subsample)
- **Step 2:** compute test statistic associated with new sample and add to T
- Step 3: compute <u>average</u> of numbers in T
- Step 4: reduce every number in T by <u>average</u> and put in T'
- Output: % of numbers in T' greater than or equal to the observed test statistic

- **Inputs:** Array  $T = \{\}$ , N = 100,000
- Repeat N times:

**Step 1:** sample 10 folds (with replacement) from our set of 10 folds (called a subsample)

**Step 2:** compute test statistic associated with new sample and add to T

- Step 3: compute <u>average</u> of numbers in T
- Step 4: reduce every number in T by <u>average</u> and put in T'
- Output: % of numbers in T greater than or equal to the observed test statistic

Fold	System A	System B
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2	0.3	0.3
3	0.1	0.1
4	0.4	0.4
5	1	1
6	0.8	0.9
7	0.3	0.1
8	0.1	0.2
9	0	0.5
10	0.9	0.8
Average	0.41	0.48
	Difference	0.07

Fold	System A	System B	sample
1	0.2	0.5	0
2	0.3	0.3	1
3	0.1	0.1	2
4	0.4	0.4	2
5	1	1	0
6	0.8	0.9	1
7	0.3	0.1	1
8	0.1	0.2	1
9	O	0.5	2
10	0.9	0.8	0

iteration = 1

Fold	System A	System I	В	
2	0.3	0.3		
3	0.1	0.1		
3	0.1	0.1		
4	0.4	0.4		
4	0.4	0.4		
6	0.8	0.9		
7	0.3	0.1		
8	0.1	0.2		
9	0	0.5		
9	0	0.5		
Average	0.25	0.35		$T = \{0.10\}$
	Difference iteration	<b>0.1</b> on = 1		, (0.10)

sample	System B	System A	Fold
0	0.5	0.2	1
0	0.3	0.3	2
3	0.1	0.1	3
2	0.4	0.4	4
0	1	1	5
1	0.9	0.8	6
1	0.1	0.3	7
1	0.2	0.1	8
1	0.5	0	9
1	0.8	0.9	10

 $T = \{0.10\}$ 

iteration = 2

Fold	System A	System	В	
3	0.1	0.1		
3	0.1	0.1		
3	0.1	0.1		
4	0.4	0.4		
4	0.4	0.4		
6	0.8	0.9		
7	0.3	0.1		
8	0.1	0.2		
9	0	0.5		
10	0.9	0.8		
Average	0.32	0.36		$T = \{0.10,$
	Difference	0.04		0.04}
	iteratio	n = 2		

Fold	System A	System B	
1	0.2	0.5	
1	0.2	0.5	
4	0.4	0.4	
4	0.4	0.4	
4	0.4	0.4	
6	0.8	0.9	
7	0.3	0.1	
8	0.1	0.2	
8	0.1	0.2	
10	0.9	0.8	$T = \{0.10,$
Average	0.38	0.44	0.04,
	Difference	0.06	,
	iteration =	100,000	0.06}

- **Inputs:** Array T = {}, N = 100,000
- Repeat N times:
- **Step 1:** sample 10 folds (with replacement) from our set of 10 folds (called a subsample)
- **Step 2:** compute test statistic associated with new sample and add to T
- Step 3: compute <u>average</u> of numbers in T
- Step 4: reduce every number in T by <u>average</u> and put in T'
- Output: % of numbers in T' greater than or equal to the observed test statistic

• For the purpose of this example, let's assume N = 10.

Average = 0.12

- **Inputs:** Array T = {}, N = 100,000
- Repeat N times:
- **Step 1:** sample 10 folds (with replacement) from our set of 10 folds (called a subsample)
- **Step 2:** compute test statistic associated with new sample and add to T
- Step 3: compute average of numbers in T
- Step 4: reduce every number in T by <u>average</u>
- Output: % of numbers in T' greater than or equal to the observed test statistic

• Output: (3/10) = 0.30

```
T = \{0.10,
                                           T' = \{-0.02,
    0.04,
                                                -0.08,
    0.21,
                                                0.09,
    0.20,
                                                0.08,
    0.13,
                                                0.01,
    0.09,
                                                -0.03,
    0.22,
                                                0.10,
                Step 3
                                      Step 4
    0.07,
                                               -0.05,
                                                -0.09,
    0.03,
    0.11}
                                                -0.01}
```

Average = 0.12

• For the purpose of this example, let's assume N = 10.

$$T = \{0.10, & T' = \{-0.02, \\ 0.04, & -0.08, \\ 0.21, & 0.09, \\ 0.20, & two-tailed test. & 0.01, \\ 0.09, & -0.03, \\ 0.022, & 0.10, \\ 0.07, & Step 3 & Step 4 & -0.05, \\ 0.03, & -0.09, \\ 0.11\}$$

Average = 0.12

# Significance Tests summary

- Significance tests help us determine whether the outcome of an experiment signals a "true" trend
- The null hypothesis is that the observed outcome is due to random chance (sample bias, error, etc.)
- There are many types of tests
- Parametric tests: assume a particular distribution for the test statistic under the null hypothesis
- Non-parametric tests: make no assumptions about the test statistic distribution under the null hypothesis
- The randomization and bootstrap-shift tests make no assumptions, are robust, and easy to understand

### Any Questions?







### **Exploratory Analysis: Clustering**

**Next Class** 





