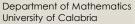
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Data Warehouse and Data Mining Module II – Data Mining

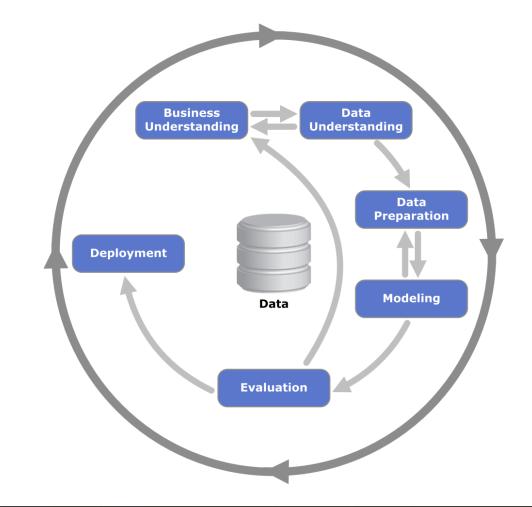
Evaluation

Ph.D. Ettore Ritacco

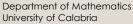




CRISP-DM Methodology

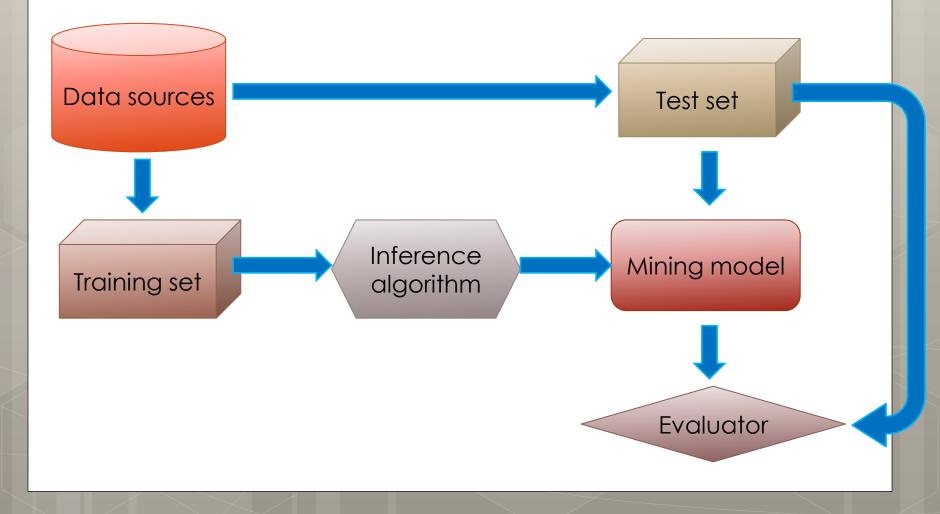


- Select a training set
- Build a mining model
- Choose a quality measure
- o Select a test set
- Apply the model on the test set
- Compute the value of the quality measure





A simple evaluation schema



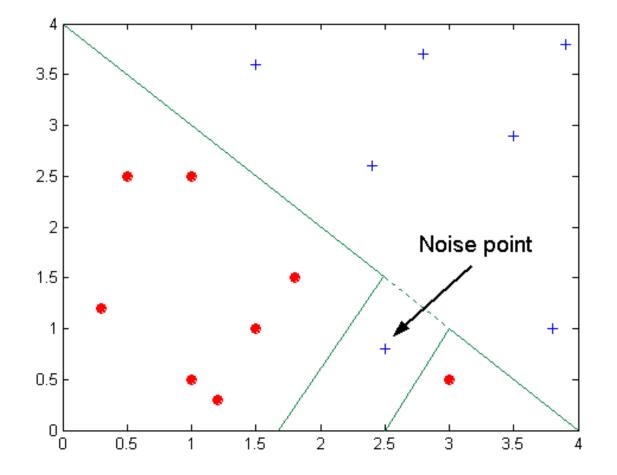
The fitting problem

• Beyond the data analysis issues, there are challenges even in the modeling and evaluate phases in the CRISP-DM Methodology

- Namely
 - Underfitting
 - The model is too simple: the evaluation will be poor on both the training and the evaluation set
 - Overfitting
 - The model is too complex, fitting as close as it can the training data, the evaluation will be good on the training set, but poor on the evaluation set

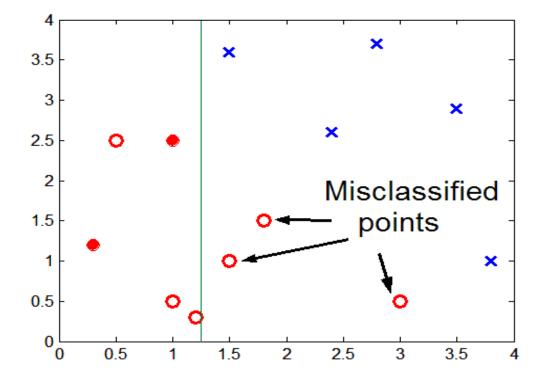


Overfitting (due to noise)





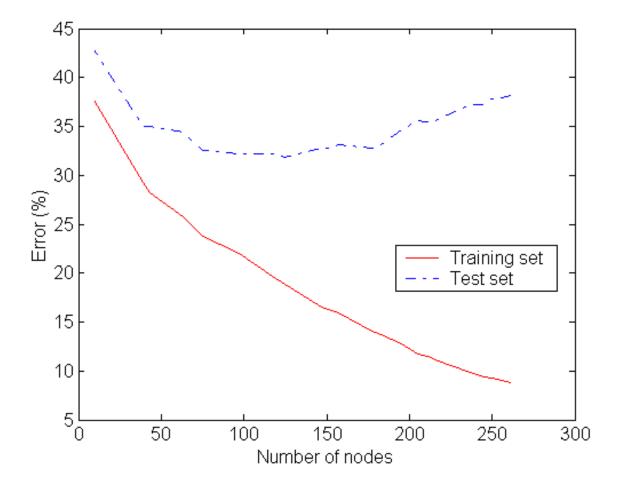
Overfitting (due to a too little dimension of the data set)



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Overfitting



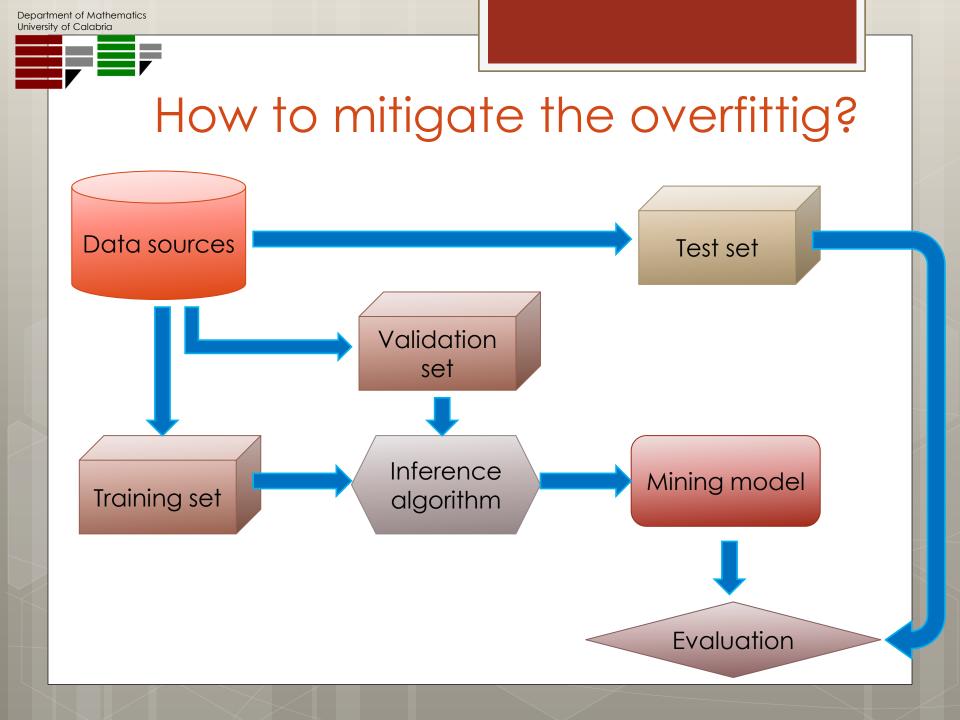
How to mitigate the overfittig?

• Prevention

- A good data preparation
- Avoiding
 - Feed the building phase with further data for improving the model's generality (e.g. online pruning)

• Recovery

• Manipulate the model after its creation (e.g. post pruning)



Is a model that achives 70% of global accuracy a "good" model?

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 - It dipends...

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 - It dipends...
- Is a model that achives 95% of global accuracy a "good" model?

- Is a model that achives 70% of global accuracy a "good" model?
 - It dipends...
- Is a model that achives 95% of global accuracy a "good" model?
 - It dipends...

- We can perform only comparative evaluations.
- A "null hypothesis" (in other words, a baseline) is needed.
- We can only say, given a statistic, if a model is better then another one, in terms of the chosen statistic.

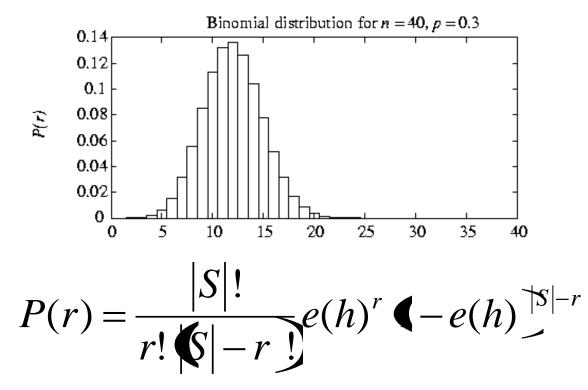
• The "true" error of a hypothesis h

$$e(h) = \Pr_{x \in D} \P \P \stackrel{\text{res}}{\to} h \P$$

• The error on our sample

$$e(h) = \frac{1}{|S|} \sum_{x \in S} \delta \langle \langle x \rangle \neq h \langle x \rangle$$

• The probability of *r* misclassifications is governed by a binomial distribution:

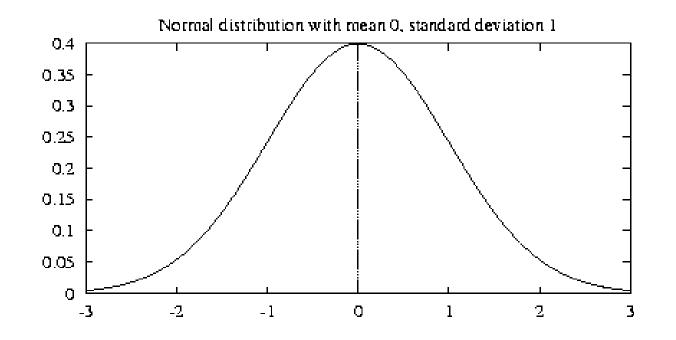


• If |S| is sufficient great (typically |S|>30) the binomial distribution can be approximated by a normal distribution

• Central limit theorem

How to evaluate a model?

• Normal distribution



- Normal distribution
 - Density $p(x) = \frac{1}{\sqrt{2\pi\sigma}} \exp\left(-\frac{\langle x \mu \rangle^2}{2\sigma^2}\right)$
 - Cumulative

$$P(a \le X \le b) = \int_a^b p(x) dx$$

- Expected Value
- Variance

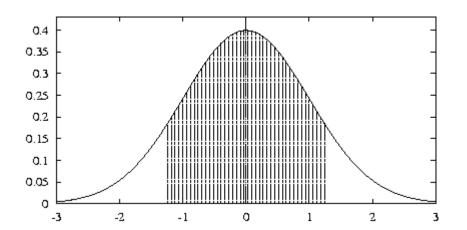
 $Var[X] = \sigma^2$

 $E[X] = \mu$

• Confidence Intervals

Given a probability
 α, we are interested
 in finding an interval
 [a, b] such that

 $P(a \le X \le b) = \alpha$



• In the normal case

 $P(\mu - z_n \sigma \le X \le \mu + z_n \sigma) = \gamma$

-	50%						
Z _N	0.67	1.00	1.28	1.64	1.96	2.33	2.58

• Consider two hypothesis *h* and *j*...

• ... and the random variable

d = e(h) - e(j)

• Choose z_n and consequently γ

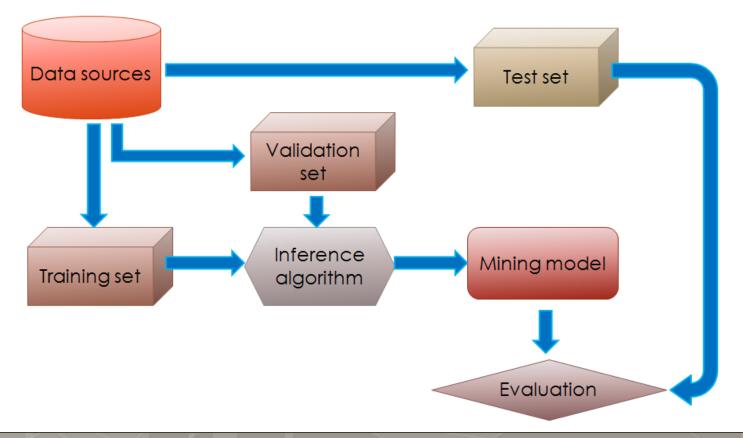
• Three cases:

$$d = e(h) - e(j)$$

- Zero is in the confidence interval of d• There is no statistical difference between h and j, with significance γ
- The confidence interval of d is under Zero
 e(h) is statistically lower than e(j), with significance γ
- The confidence interval of d is above Zero • e(h) is statistically higher than e(j), with significance γ

$$P(\mu - z_n \sigma \le X \le \mu + z_n \sigma) = \gamma$$

• Hold-out



• Hold-out

• Pros:

• Fast evaluation

• Cons:

• Only one experiment → low statistical relevance

• Repeated Hold-out with random sub-sampling

- Choose n
- ResultList = { }
- For 1 < i < n

• Random Sampling of (with or without replacement):

- Training set
- Validation set
- Test set
- Model = buildModel(Training set, Validation set)
- ResultList.add(evaluateModel(Model, Test set))
- Return avg(ResultList)

• Repeated Hold-out with random sub-sampling

• Pros:

• More statistical significance

• Cons:

• Slow evaluation

• Not all the tuples are involved in the training and evaluation phase

• *k*-fold Cross Validation

- Choose k
- Divide the whole dataset D in k folds (portion)
- ResultList = { }
- For 1 < i < k
 - Build Training set = $D \setminus fold_i$
 - Random sample the Validation Set from the Training Set
 - Training set = Training set \ Validation Set
 - Test set = $fold_i$
 - Model = buildModel(Training set, Validation set)
 - ResultList.add(evaluateModel(Model, Test set))
- Return avg(ResultList)

• k-fold Cross Validation

• Pros:

• Good statistical significance

- the greater is *k* the better the significance
 - If k = |D| Cross Validation is called leave-one-out evaluation

• Cons:

- Very slow evaluation
- The *k*-fold Cross Validation needs to be stratified:
 - Each fold has to keep the same statistical properties of the whole dataset

Evaluation Metrics

The focus is on the predictive quality of a model
instead of computational cost, scalability...

• Confusion Matrix

	Predicted class			
		Class = Yes	Class = No	
Actual class	Class = Yes	True Positive (TP)	False Negative (FN)	
	Class = No	False Positive (FP)	True Negative (TN)	



• Global Accuracy

$accuracy = \frac{TP + TN}{TP + FN + FP + TN}$

• Is a classifier, with a global accuracy equals to 99.9%, good?

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• To be continued...



Confusion Matrix

			sion matrix	1		Terminology and derivations from a confusion matrix true positive (TP) eqv. with hit true negative (TN) eqv. with correct rejection false positive (FP) eqv. with false alarm, Type I error false negative (FN)
		(as determined by "Gold standard")				eqv. with miss, Type II error
	Total population	Condition positive	Condition negative	Prevalence = Σ Condition positive Σ Total population		sensitivity or true positive rate (TPR) eqv. with hit rate, recall TPR = TP/P = TP/(TP + FN)
Test outcome	Test outcome positive	True positive	False positive (Type I error)	Positive predictive value (PPV, Precision) = Σ True positive Σ Test outcome positive	$\frac{\text{False discovery rate (FDR)}}{\Sigma \text{ False positive}}$ $\Sigma \text{ Test outcome positive}$	specificity (SPC) or true negative rate (TNR) SPC = TN/N = TN/(FP + TN) precision or positive predictive value (PPV) PPV = TP/(TP + FP)
	Test outcome negative	False negative (Type II error)	True negative	False omission rate (FOR) = Σ False negative Σ Test outcome negative	Negative predictive value (NPV) = Σ True negative Σ Test outcome negative	negative predictive value (NPV) NPV = TN/(TN + FN) fall-out or false positive rate (FPR) FPR = FP/N = FP/(FP + TN) false discovery rate (FDR)
	Positive likelihood ratio (LR+) = TPR/FPR	True positive rate (TPR, Sensitivity, Recall) = Σ True positive Σ Condition positive	False positive rate (FPR, Fall-out) = Σ False positive Σ Condition negative	$\frac{\text{Accuracy (ACC)} =}{\frac{\Sigma \text{ True positive } + \Sigma \text{ True negative}}{\Sigma \text{ Total population}}$		FDR = FP/(FP + TP) = 1 - PPV Miss Rate or False Negative Rate (FNR) FNR = FN/P = FN/(FN + TP)
	Negative likelihood ratio (LR-) = FNR/TNR	False negative rate (FNR) = Σ False negative Σ Condition positive	$\begin{tabular}{lllllllllllllllllllllllllllllllllll$		1	accuracy (ACC) ACC = (TP + TN)/(P + N) F1 score is the harmonic mean of precision and sensitivity E(t - 2)TD/(2)TD + ED + EN)
	Diagnostic odds ratio (DOR) = LR+/LR-					$F1 = 2TP/(2TP + FP + FN)$ Matthews correlation coefficient (MCC) $\frac{TP \times TN - FP \times FN}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}}$
						Informedness = Sensitivity + Specificity - 1

Markedness = Precision + NPV - 1

Sources: Fawcett (2006) and Powers (2011).^{[2][3]}