

Lecture 3: Model Evaluation

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Binary Classification

- **Binary** classification problem in Machine Learning (ML)
 - identifying if a certain patient has *some disease* using his *health record*
 - Credit versus No Credit (*using Decision Tree lecture 2*)
 - Class a versus Class b
- ML trained on a training set D_t tested on a test set D_{test} with

$$\emptyset = D_t \cap D_{test}$$

$$accuracy = \frac{\text{Correctly Classified}}{\text{All}} \quad \text{error rate} = 1 - accuracy$$

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Evaluating classification models

- Some types of mistakes that are worse than others
- We are choosing between two models A and B that diagnose a given infectious disease
 - positive if the disease present, negative if the disease not
 - present both models have the **same accuracy**, which model is better?
- model A's mistakes are all **false positives**
 - cases where the patient is not sick but the model *predicted disease*
- model B where all mistakes are **false negatives**
 - *contagious people are told they are healthy*

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Confusion Matrix

		true/actual/target		
		P	N	
predicted {	P	True Positives (TP)	False Positives (FP)	TP+FP
	N	False Negatives (FN)	True Negatives (TN)	FN+TN
		P=TP+FN	N=FP+TN	All=P+N

Recall/sensitivity

% of positive observations predicted as positive

$$Recall = \frac{TP}{P} = \frac{TP}{TP+FN}$$

Precision

% of positive observations among the observations predicted as positive

$$Precision = \frac{TP}{TP+FP}$$

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Precision and Recall

- A high recall value without a high precision does not give us any confidence about the quality of the binary classifier
 - High recall value by classifying all patterns as positive (the recall value will be one); however, the precision value will be very low

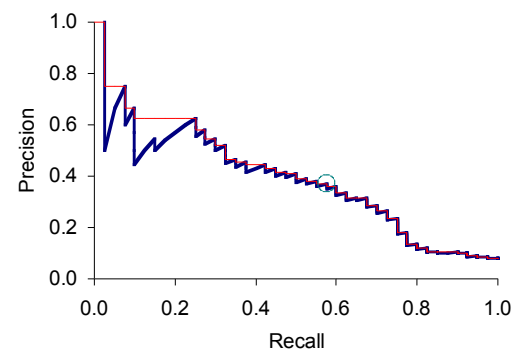
$$Recall = \frac{TP}{P} = \frac{TP}{TP+FN} = \frac{All}{All} = 1$$

- By classifying only one pattern correctly as positive, we obtain the maximal precision value of one but a low recall value.

$$Precision = \frac{TP}{TP+FP} = \frac{1}{1+0} = 1$$

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A precision-recall curve



Both values have to be simultaneously interpreted

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Balanced Measure

- Precision and Recall have to be simultaneously interpreted.
- We can combine both values with the *harmonic mean*

$$F = 2 \cdot \frac{\text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}}$$

- Both values are evenly weighted.
- This measure is also called the balanced measure.

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A combined measure: F

- Combined measure that assesses this tradeoff is F measure (weighted harmonic mean):

$$F = \frac{1}{\alpha \frac{1}{P} + (1-\alpha) \frac{1}{R}} = \frac{(\beta^2 + 1)PR}{\beta^2 P + R}$$

- However, usually use **balanced F_1 measure**
 - i.e., with $\beta = 1$ or $\alpha = \frac{1}{2}$
 - $P = \text{Precision}$, $R = \text{Recall}$

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ROC curve

- For binary classifier indicates the probability of two classes:
 $p(\text{positive})$ and $1 - p(\text{negative})$

If $p(\text{positive}) \geq \text{threshold}$ then class positive

If $p(\text{positive}) < \text{threshold}$ then class negative

Usually the threshold is 0.5

- Niave Bayes, Perceptron, Logistic Regression
 - introduced later in the course

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ROC Curve

Receiver Operating Characteristic

Recall/sensitivity

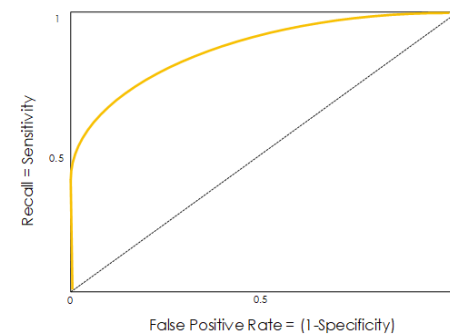
- % of positive observations predicted as positive

$$\text{Recall} = \frac{TP}{P} = \frac{TP}{TP + FN}$$

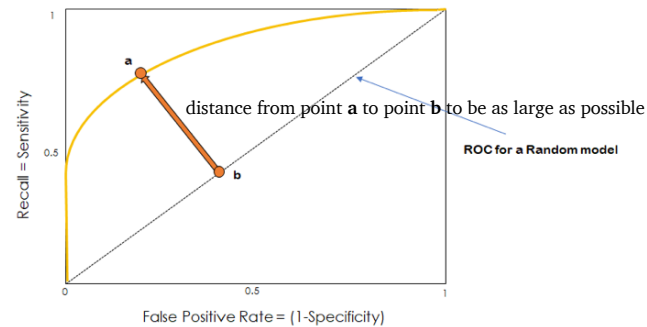
Fallout/specificity

- % of negative observations predicted as negative

$$\text{False Positive Rate} = \text{Specificity} = \frac{TN}{N} = \frac{TN}{TN + FP}$$



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- To plot the ROC curve, we must first calculate the *Recall* and the *Specificity* for **various thresholds**, and then plot them against each other
- The further away we are to the curve of the random model, the better

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Various thresholds for ROC curve

- Binary classifier indicates the probability of two classes:
 $p(\text{positive})$ and $1 - p(\text{negative})$

If $p(\text{positive}) \geq \text{threshold}$ then class positive

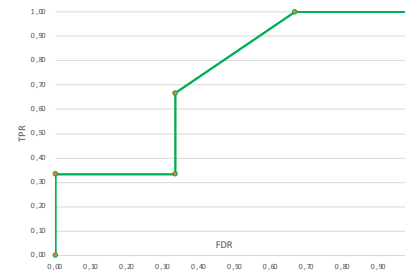
If $p(\text{positive}) < \text{threshold}$ then class negative

- Usually the threshold is 0.5
- To compute the ROC curve we chose **various thresholds** $\in [0,1]$
- We chose threshold=0, then threshold=0.1,..., threshold=0.9, threshold=1

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z is the true value and \hat{z} the classifier prediction

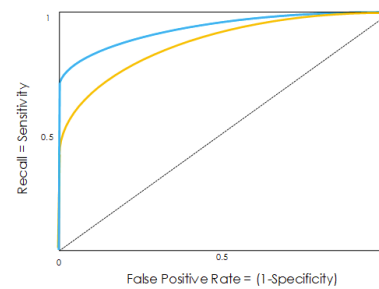
z	\hat{z}	0	>0.3	>0.4	>0.45	>0.6	>0.8
1	0.5	TP	TP	TP	FN	FN	FN
1	0.8	TP	TP	TP	TP	TP	FN
1	0.45	TP	TP	FN	FN	FN	FN
0	0.4	FP	FP	TN	TN	TN	TN
0	0.3	FP	TN	TN	TN	TN	TN
0	0.6	FP	FP	FP	FP	TN	TN
FPR=FP/N		1.00	0.67	0.33	0.33	0.00	0.00
TPR=TP/P		1.00	1.00	0.67	0.33	0.33	0.00



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AUC metric (Area Under the Curve)

- *ACU* quantifies in a **single metric** how well our model classifies the True and False data points.
- *AUC* goes from values of 0.5 (random classifier) to 1 (perfect classifier)



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0 → 0, 3 → 3, 9 → 9, 0 → 0, 2 → 2, 1 → 1, 1 → 1, 3 → 3, 9 → 9
 4 → 4, 1 → 1, 2 → 2, 2 → 2, 1 → 1, 4 → 4, 8 → 8, 0 → 0, 4 → 4
 4 → 4, 7 → 7, 7 → 7, 2 → 2, 9 → 9, 6 → 6, 5 → 5, 5 → 5, 4 → 4
 8 → 8, 2 → 2, 5 → 5, 9 → 9, 5 → 5, 4 → 4, 1 → 1, 3 → 3, 7 → 7
 8 → 8, 0 → 0, 7 → 7, 4 → 4, 4 → 4, 7 → 7, 4 → 4, 7 → 7, 9 → 9
 8 → 8, 9 → 9, 9 → 9, 2 → 2, 2 → 2, 0 → 0, 1 → 1, 6 → 6, 5 → 5
 4 → 4, 4 → 4, 3 → 3, 9 → 9, 9 → 9, 1 → 1, 1 → 1, 5 → 5, 9 → 9
 2 → 2, 7 → 7, 0 → 0, 3 → 3, 4 → 4, 7 → 7, 5 → 5, 8 → 8, 7 → 7
 9 → 9, 0 → 0, 2 → 2, 8 → 8, 1 → 1, 2 → 2, 2 → 2, 7 → 7, 8 → 3

Example of MNIST digits represented by gray images of size 28 × 28

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		predicted class										
		0	1	2	3	4	5	6	7	8	9	
actual class	0	931	0	3	3	0	30	8	2	3	0	980
	1	0	1091	3	3	0	3	5	1	29	0	1135
	2	16	2	896	14	16	5	19	24	30	10	1032
	3	6	1	24	909	0	19	6	17	18	10	1010
	4	1	3	6	1	900	2	14	2	15	38	982
	5	15	3	8	57	6	728	18	8	39	10	892
	6	22	3	10	1	17	19	879	3	4	0	958
	7	4	15	28	6	8	0	0	925	4	38	1028
	8	11	6	14	29	10	28	11	17	832	16	974
	9	12	7	6	12	48	18	0	24	7	875	1009
		1018	1131	998	1035	1005	852	960	1023	981	997	

Confusion Matrix for 10 Classes (Error Matrix)

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Evaluating multiclass classifiers

- Most real-world classification problems have more than two classes
 - e.g. identifying risk groups, categorizing documents, recommending products
- Extend binary confusion matrices

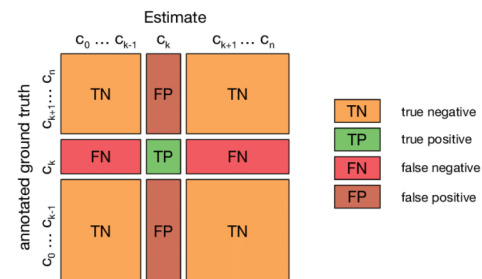
		<i>true/actual/target</i>		
		A	B	C
<i>predicted</i>	P	True A (TA)	False A (FA)	False A (FA)
	B	False B (FB)	True B (TB)	False B (FB)
	C	False C (FC)	False C (FC)	True C (TC)

- Accuracy is the % of observations along the diagonal

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Evaluating multiclass classifiers

- Recall/sensitivity, specificity and precision *per class*
 - the target class is seen as positive
 - the negative class is the **union** of the remaining classes



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Overfitting

- The training data contains information about the regularities in the mapping from input to output, but it also contains noise
- There is sampling error and a flexible architecture can model the sampling error really well
- However, we cannot tell which regularities are real and which are caused by sampling error

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- In general, we try to learn a function $f : \mathbb{R}^n \rightarrow \mathbb{R}^m$

$$\mathbf{y} = f(\mathbf{x})$$

- that is described by a sample of training data D_t of the labeled data set

$$D_t = \{(\mathbf{x}_1, \mathbf{y}_1), (\mathbf{x}_2, \mathbf{y}_2), \dots, (\mathbf{x}_N, \mathbf{y}_N)\}$$

- Labels can include multiple things like faces vs. non-faces or man-made objects vs. non-man-made objects

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- After learning, the trained network can be seen as an hypothesis h that tries to represent the function f and it can be then used for mapping new examples
- The hypothesis h should represent the function f well on the training set. However, ideally, it should generalize from the training data set to unseen **future data points**.
- To try to make sure this is the case, we can validate on an unseen validation (or test set) data set D_v

$$D_v = \{(\mathbf{x}'_1, \mathbf{y}'_1), (\mathbf{x}'_2, \mathbf{y}'_2), \dots, (\mathbf{x}'_M, \mathbf{y}'_M)\} \quad \emptyset = D_t \cap D_v.$$

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Mean Squared Error (MSE)

- The validation of the model is done by comparing the hypothesis h outputs

$$\mathbf{o}_k = h(\mathbf{x}'_k)$$

- with the correct values \mathbf{y}'_k of the validation data set D_v by the mean squared error

$$MSE_{D_v}(h) = \sum_{k=1}^M \frac{1}{M} \|\mathbf{y}'_k - \mathbf{o}_k\|^2.$$

- The smaller the $MSE(D_v)$ the better the hypothesis h describing the function f

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- We can define the mean squared error for the training data set D_t

$$MSE_{D_t}(h) = \frac{1}{N} \cdot \sum_{k=1}^N \|\mathbf{y}_k - \mathbf{o}_k\|^2,$$

- usually

$$MSE_{D_v}(h) > MSE_{D_t}(h).$$

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- If we have two hypothesis h_1 and h_2 with

$$MSE_{D_t}(h_1) < MSE_{D_t}(h_2), \quad MSE_{D_v}(h_1) > MSE_{D_v}(h_2).$$

- then we say that the hypothesis h_1 overfits the training data set D_t
 - h_1 fits better the training examples than h_2 performs more poorly over examples it didn't learn.
- It seems as if h_1 learned D_t **by heart** and not the topological structure that describes the function f
- h_2 learned the corresponding structure and can **generalize**

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Cross-Validation

- Estimate the accuracy of a hypothesis induced by a supervised learning algorithm
- Predict the accuracy of a hypothesis over future unseen instances
- Select the optimal hypothesis from a given set of alternative hypotheses
 - Model selection
 - Feature selection
- Combining multiple classifiers (boosting)

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Holdout Method

- Partition data set $D = \{(v_1, y_1), \dots, (v_n, y_n)\}$ into *training* D_t and *validation* set $D_h = D \setminus D_t$



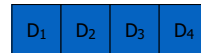
Problems:

- makes insufficient use of data
- training and validation set are correlated

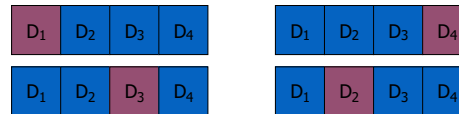
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Cross-Validation

- k -fold cross-validation splits the data set D into k mutually exclusive subsets D_1, D_2, \dots, D_k



- Train and test the learning algorithm k times, each time it is trained on $D \setminus D_i$ and tested on D_i

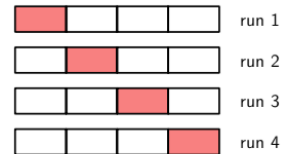


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Cross-Validation

- Uses all the data for training and testing
- Complete k -fold cross-validation splits the dataset of size m in all $(m \text{ over } m/k)$ possible ways (choosing m/k instances out of m)
- Leave n -out cross-validation sets n instances aside for testing and uses the remaining ones for training (leave one-out is equivalent to n -fold cross-validation)
- In stratified cross-validation, the folds are stratified so that they contain approximately the same proportion of labels as the original data set

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- One major drawback of cross-validation is that the number of training runs that must be performed is increased by a factor of k
- How to Evaluate cross-validation for different models (h_1, h_2, h_3)?
 - We will use t-statistics

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The logic of hypothesis testing

- Example: toss a coin ten times, observe eight heads. Is the coin fair (i.e., what is its long run behavior?) and what is your residual uncertainty?
- You say, "If the coin were fair, then eight or more heads is pretty unlikely, so I think the coin isn't fair."
- Like proof by contradiction: Assert the opposite (the coin is fair) show that the sample result (≥ 8 heads) has low probability p , **reject** the assertion, with residual uncertainty related to p .
- Estimate p with a *sampling distribution*.

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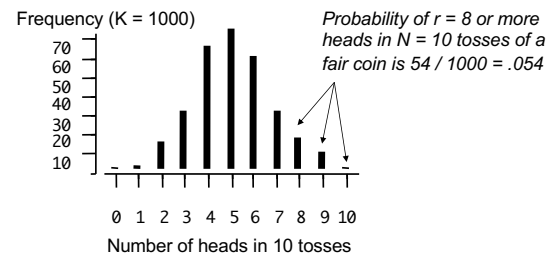
Probability of a sample result under a null hypothesis

- If the coin were fair ($p = .5$, the *null hypothesis*) what is the probability distribution of r , the number of heads, obtained in N tosses of a fair coin? Get it analytically or estimate it by simulation (on a computer):

- Loop K times
 - $r := 0$ // r is num.heads in N tosses
 - Loop N times // simulate the tosses
 - Generate a random $0 \leq x \leq 1.0$
 - If $x \geq p$ increment r // p is the probability of a head
 - Push r onto `sampling_distribution`
- Print `sampling_distribution`

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Sampling distributions



The estimation is constructed by *Monte Carlo sampling*.

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The t test

- Same logic as the Z test, but appropriate when **population standard deviation** is unknown, samples are small, etc.
- Sampling distribution is t, not normal, but approaches normal as samples size increases
- Test statistic has very similar form but probabilities of the test statistic are obtained by consulting tables of the t distribution, not the normal

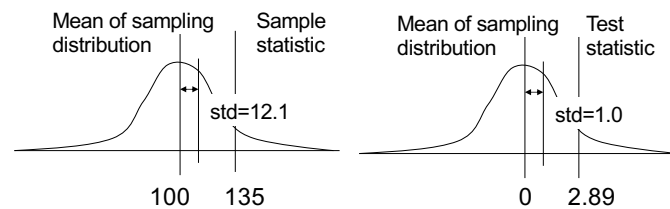
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The t test

Suppose $N = 5$ students have mean IQ = 135, std = 27

Estimate the standard deviation of sampling distribution using the sample standard deviation

$$t = \frac{\bar{x} - \mu}{\frac{s}{\sqrt{N}}} = \frac{135 - 100}{\frac{27}{\sqrt{5}}} = \frac{35}{12.1} = 2.89$$



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p Values

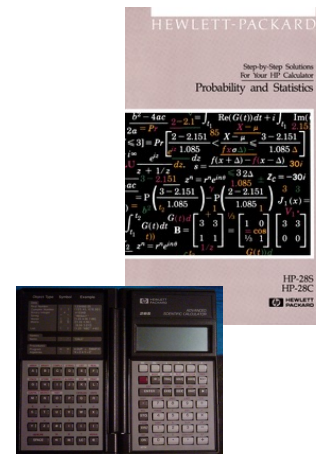
- We find the probabilities by looking them up in tables, or statistics packages provide them
 - The probability of obtaining a particular sample given the null hypothesis is called the p value
- Commonly we reject the H_0 when the probability of obtaining a *sample statistic* given the null hypothesis is low, say $p < 0.05$
- The null hypothesis is rejected but might be true

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Paired Sample t Test

- Given a set of paired observations
 - (from two normal populations)

A	B	$\delta = A - B$
x1	y1	x1-y1
x2	y2	x2-y2
x3	y3	x3-y3
x4	y4	x4-y4
x5	y5	x5-y5



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- Calculate the mean \bar{x}_δ and the standard deviation s_δ of the differences δ
- $H_0: \mu_\delta = 0$ (no difference)
- $H_0: \mu_\delta = k$ (difference is a constant)

$$t_\delta = \frac{\bar{x}_\delta - \mu_\delta}{\hat{\sigma}_\delta} \quad \hat{\sigma}_\delta = \frac{s_\delta}{\sqrt{N_\delta}}$$

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Paired sample t Test

- We have two rows of data
94, 86, 12, 90, 66, 40
10, 20, 22, 26, 6, 18
- Are the two rows significantly different?

$$\delta: 84, 66, -10, 64, 60, 22 \quad \frac{47.6667}{34.8119 / \sqrt{6}} = 3.3540$$

- For five degrees of freedom in t-student table between $p=0.01$ and $p=0.02$, which is less than 0.05, for this reason we have to reject H_0 ! The two rows are significantly different!

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Paired sample t-test

Partition Index	Partition Size	Test	Measure	Value
1	125	Classification	True Positive	79
2	125	Classification	True Positive	79
3	125	Classification	True Positive	72
4	125	Classification	True Positive	80
5	125	Classification	True Positive	75
6	125	Classification	True Positive	81
7	125	Classification	True Positive	64
8	125	Classification	True Positive	72
classifier A			Average	75.25
			Standard Deviation	5.3794

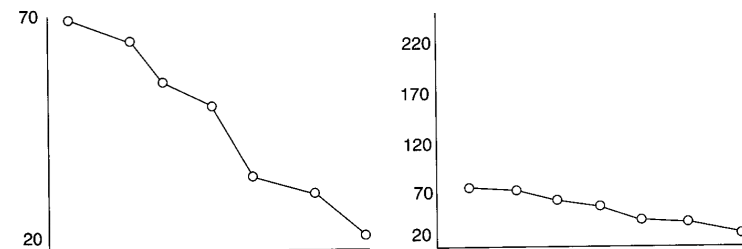
Partition Index	Partition Size	Test	Measure	Value
1	125	Classification	True Positive	63
2	125	Classification	True Positive	55
3	125	Classification	True Positive	70
4	125	Classification	True Positive	58
5	125	Classification	True Positive	67
6	125	Classification	True Positive	70
7	125	Classification	True Positive	55
8	125	Classification	True Positive	61
classifier C			Average	62.375
			Standard Deviation	5.7866

Partition Index	Partition Size	Test	Measure	Value
1	125	Classification	True Positive	75
2	125	Classification	True Positive	73
3	125	Classification	True Positive	80
4	125	Classification	True Positive	71
5	125	Classification	True Positive	75
6	125	Classification	True Positive	80
7	125	Classification	True Positive	67
8	125	Classification	True Positive	77
classifier B			Average	74.75
			Standard Deviation	4.1458

using Cross Validation, determine if the classifier A, B, C are significantly different
Compare (A,B), (A,C), (B,C)

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Confidence Intervals



- Just looking at a figure representing the mean values, we can not see if the differences are significant

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Confidence Intervals (σ known)

- Standard error from the standard deviation

$$\sigma_{\bar{x}} = \frac{\sigma_{Population}}{\sqrt{N}}$$

- 95 Percent confidence interval for normal distribution is about the mean

$$\bar{x} \pm 1.96 \cdot \sigma_{\bar{x}}$$

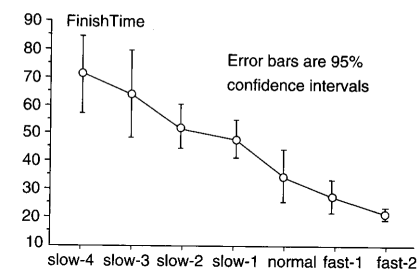
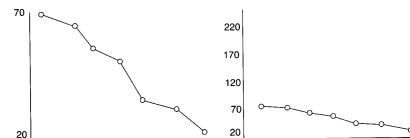
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Confidence interval when (σ unknown)

- Standard error from the sample standard deviation
- 95 Percent confidence interval for t distribution ($t_{0.025}$ from a table) is

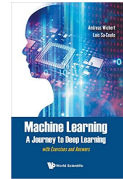
$$\bar{x} \pm t_{0.025} \cdot \hat{\sigma}_{\bar{x}}$$

$$\hat{\sigma}_{\bar{x}} = \frac{s}{\sqrt{N}}$$



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Literature



- Machine Learning - A Journey to Deep Learning, A. Wichert, Luis Sa-Couto, World Scientific, 2021
 - Chapter 8