

CDS503: Machine Learning

Week 6: Designing Machine Learning Experiments

DR. JASY LIEW SUET YAN

SCHOOL OF COMPUTER SCIENCES
UNIVERSITI SAINS MALAYSIA (USM)

Outline

"Numbers have an important story to tell. They rely on you to give them a voice."—Stephen Few

- Designing machine learning experiments
- Model selection
- Bias-variance tradeoff
- ML diagnostic

ML Experiment Design

Frame the ML problem

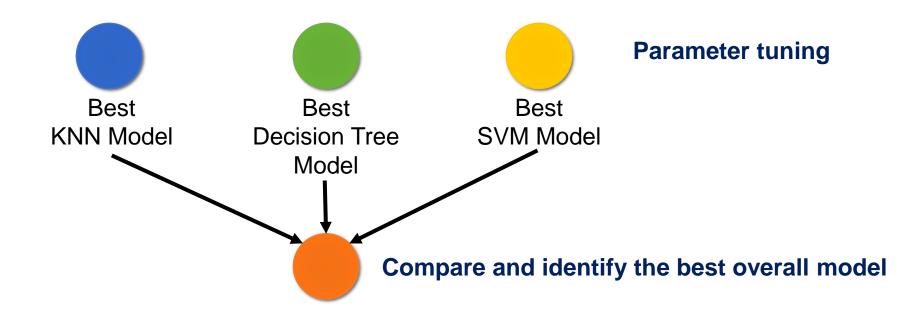
Prepare training/validation/test data

Plan and design ML experiments

- Select learning algorithm
- Tune parameters
- Select features
- Sample training and test data
- Test generalization error

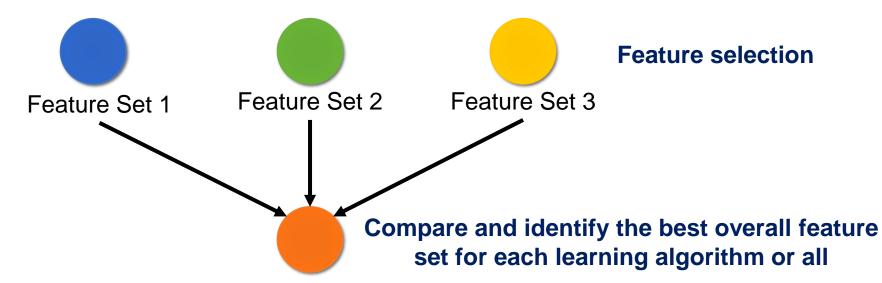
ML Experiment Design

 Example 1: Find the best parameter setting configuration for each learning algorithm. Compare the "best" model from each learning algorithm.



ML Experiment Design

Example 2: Find the best set of features across different learning algorithms. Do this "best" set of features consistently result in the best performance across different learning algorithms?



Data Description

Breast cancer data set: Medical data from 681 women (instances)
 who has potentially cancerous tumors (12 attributes)

Class attribute (1)

1: Tumor is malignant (238)

0: Tumor is benign (443)

Other attributes (2)

PID: Patient ID

Date: Diagnosis Date

Predictor attributes (9)

Adhes - marginal adhesion

BNucl - bare nuclei

Chrom - bland chromatin

Epith - epithelial cell size

Mitos – mitoses

NNucl - normal nucleoli

Thick - clump thickness

UShap - cell shape uniformity

USize - cell size uniformity

* A predictor is assigned the value 1 if it is normal and the value 10 if it is most abnormal

Prepare Data

Remove attributes. Not useful predictors.

	PID	Date	Adhes	BNucl	Chrom	Epith	Mitos	NNucl	Thick	UShape	USize	Class
	1	01/03/2007	1	1	3	2	1	1	5	1	1	0
	2	12/12/2005	5	10	3	7	1	2	5	4	4	0
	3	14/08/2016	1	2	3	2	1	1	3	1	1	0
	4	02/02/2001	1	4	3	3	1	7	6	8	8	0
t	5	14/11/2014	3	1	3	2	1	1	4	1	1	0
	6	22/09/2011	8	10	9	7	1	7	8	10	10	1
	7	18/05/2015	7	8	8	9	2	8	8	6	6	1
	8	27/04/2011	5	9	9	10	2	6	7	9	9	1
	9	19/02/2003	8	6	8	3	1	3	5	10	10	1
	10	25/07/2011	10	5	6	6	4	4	10	7	7	1

Class attribute

Predictor attributes

Model Selection

Standard technique to evaluate a hypothesis

Adhes	BNucl	Chrom	Epith	Mitos	NNucl	Thick	UShape	USize	Class
1	1	3	2	1	1	5	1	1	0
5	10	3	7	1	2	5	4	4	0
1	2	3	2	1	1	3	1	1	0
1	4	3	3	1	7	6	8	8	0
3	1	3	2	1	1	4	1	1	0
8	10	9	7	1	7	8	10	10	1
7	8	8	9	2	8	8	6	6	1
5	9	9	10	2	6	7	9	9	1
8	6	8	3	1	3	5	10	10	1
10	5	6	6	4	4	10	7	7	1

Training set (70%)
Learn parameter
from training data
(hypothesis function)

Split dataset----

 Should be randomly sorted

Test set (30%) Compute test set error

Model Selection

Train / validation / test sets

Adhes	BNucl	Chrom	Epith	Mitos	NNucl	Thick	UShape	USize	Class	
1	1	3	2	1	1	5	1	1	0	
5	10	3	7	1	2	5	4	4	0	
1	2	3	2	1	1	3	1	1	0	
1	4	3	3	1	7	6	8	8	0	
3	1	3	2	1	1	4	1	1	0	
8	10	9	7	1	7	8	10	10	1	
7	8	8	9	2	8	8	6	6	1	
5	9	9	10	2	6	7	9	9	1	
8	6	8	3	1	3	5	10	10	1	
10	5	6	6	4	4	10	7	7	1	

Training set (60%)
Learn parameter
from training data
(hypothesis function)

Split dataset-

 Should be randomly ____
 sorted Validation set (20%)

Tune parameters (hyperparameters)

Test set (20%)

Compute test set error

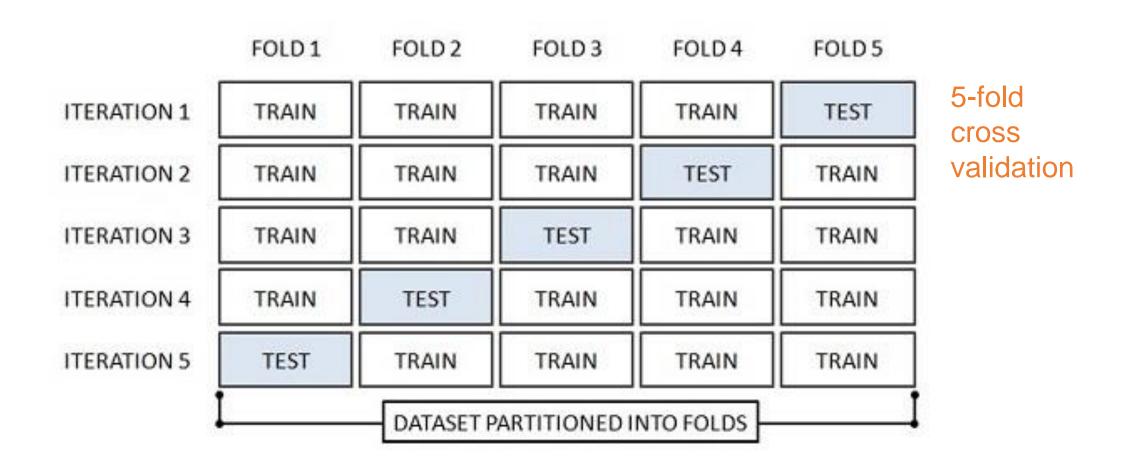
Model Selection

- Calculate 3 separate error values
 - Training error: Optimize the parameters in hypothesis function using training set
 - Validation error: Find the best hyperparameters with the least error using validation set
 - Test/Generalization error: Estimate the generalization error using the test set

Test Options

- Set up train and test sets
 - Percentage split: Splits the data and separates x% of the data for training and the rest for testing
 - Supplied test set: Prepare own external file as training set
 - **K-fold cross validation**: Data set is divided into *k* subsets. Each time, one of the *k* subsets is used as the test set and the other *k-1* subsets are put together to form a training set. Then the average error across all *k* trials is computed.

Cross Validation



Confusion Matrix

N = 10	Predic	Total		
		1	0	
Actual Class	1: Malignant	3 (TP)	2 (FN)	5
	0: Benign	1 (FP)	4 (TN)	5
То	4	6	10	

1: Malignant (Positive Class)

0: Benign (Negative Class)

True Positives (TP): Actual class of the data point was TRUE and the predicted is also TRUE (positive class)

Ex: The case where a tumor is malignant and the model classifying the tumor as malignant

True Negatives (TN): Actual class of the data point was FALSE and the predicted is also FALSE (negative class)

Ex: The case where the tumor is benign and the model classifying the tumor as benign

False Positives (FP): Actual class of the data point was FALSE and the predicted is TRUE.

Ex: A tumor being benign and the model classifying the tumor as malignant

False Negatives (FN): Actual class of the data point was TRUE and the predicted is FALSE.

Ex: Tumor is malignant and the model classifying the tumor as benign

Accuracy

Good measure when the classes in the data are nearly balanced.

Malignant = 5

Benign = 5

N = 10	Predic	Total		
		1	0	
Actual Class	1: Malignant	3 (TP)	2 (FN)	5
	0: Benign	1 (FP)	4 (TN)	5
То	4	6	10	

Accuracy =
$$\frac{TP+TN}{TP+TN+FP+FN}$$
 = $\frac{(3+4)/(3+4+1+2)}{(3+4+1+2)}$ = $\frac{7}{10}$ = 0.7

Accuracy

Accuracy is 80% even though the classifier assigned all 10 instances as BENIGN (0)
Malignant = 2
Benign = 8

* NEVER be used as a measure when classes in the data are a majority of one class

N = 10	Predic	Total		
		1	0	
Actual Class	1: Malignant	0 (TP)	2 (FN)	2
	0: Benign	0 (FP)	8 (TN)	8
То	0	10	10	

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

Accuracy
=
$$(0 + 8) / (0 + 8 + 0 + 2)$$

= $8 / 10$
= 0.8

Precision

- Measures how good is the model at whatever it predicted
 - Example: Proportion of tumors predicted as malignant, which are actually malignant

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

N = 10	Predic	Total		
		1	0	
Actual Class	1: Malignant	0 (TP)	2 (FN)	2
	0: Benign	1 (FP)	7 (TN)	8
То	1	9	10	

Precision	
= 0 / (0 +	1
= 0 / 1	
= 0	

Recall

- Measures how good is the model at picking the correct items
 - Example: Proportion of actual malignant tumors being predicted by the algorithm as being malignant

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

Recall	
= 0 / (0 + 2))
= 0 / 2	
= 0	

N = 10	Predic	Total		
		1	0	
Actual Class	1: Malignant	0 (TP)	2 (FN)	2
	0: Benign	1 (FP)	7 (TN)	8
То	1	9	10	

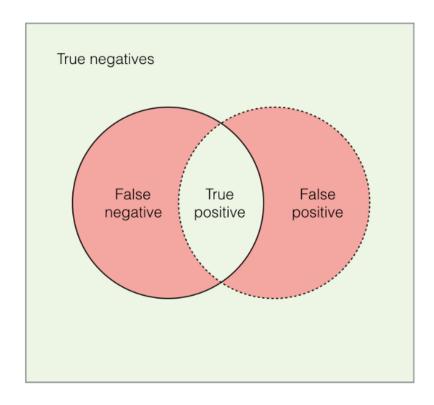
F-Measure (F1)

- Harmonic mean of precision and recall
- A single score that represents both precision and recall

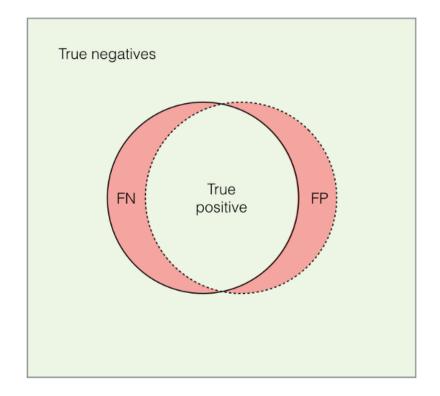
$$F1 = \frac{2 * Precision * Recall}{Precision + Recall}$$

```
Say precision = 0.4, recall = 0.7
F1 = (2 * 0.4 * 0.7) / (0.4 + 0.7)
= 0.56 / 1.1
= 0.51
```

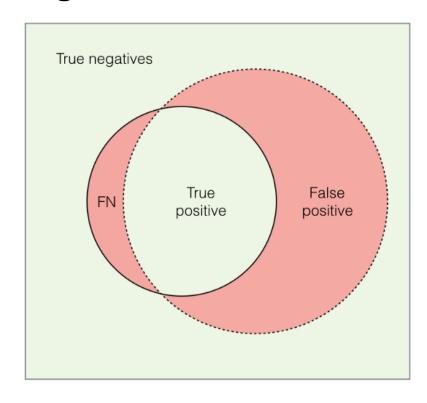
Low Recall, Low Precision



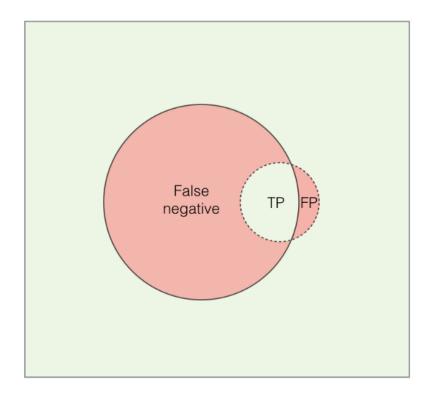
High Recall, High Precision



High Recall, Low Precision



Low Recall, High Precision



 Suppose we want to predict cancer only if very confident (avoid false positives)

Higher precision, lower recall

 Suppose we want to avoid missing too many cases of cancer (avoid false negatives)

Higher recall, lower precision

Confusion Matrix (Multiclass Classification)

	precision	recall	f1-score
0	1.00	1.00	1.00
1	1.00	0.94	0.97
2	0.92	1.00	0.96

For each class

Macro F1

$$= (1.00 + 0.97 + 0.96) / 3$$

= 0.98

accuracy			0.98
macro avg	0.97	0.98	0.98
eighted avg	0.98	0.98	0.98

Weighted F1

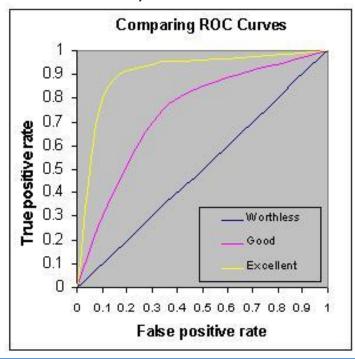
= 0.98

Average across all classes

- Macro avg: Equal weights assigned to each class
- Weighted avg = Assign weights to each class based on number of samples

Area Under ROC

- ROC: Receiver Operating Characteristic
- Represent model's ability to discriminate between positive and negative classes (for binary classification)



ROC area of 1.0 represents a model that made all predictions perfectly ROC area of 0.5 represents a model as good as random

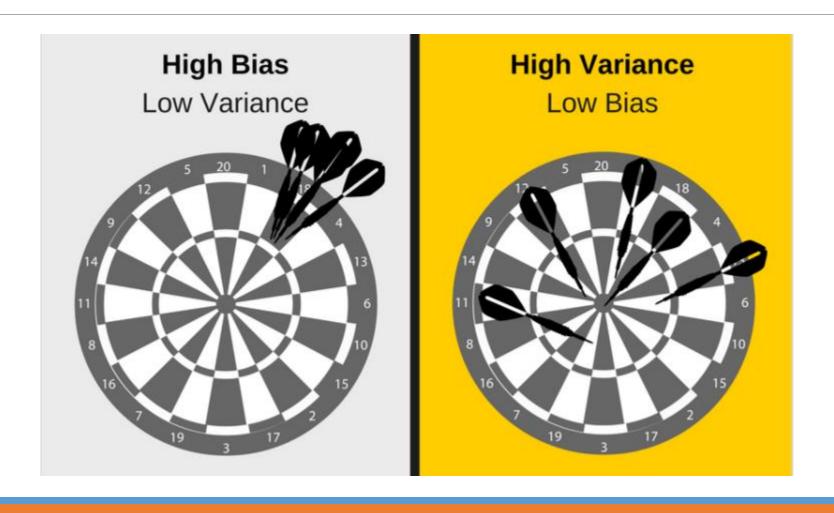
- X-axis: 1 specificity (false positive rate = FP/(FP+TN))
- Y-axis: sensitivity (true positive rate = TP/(TP+FN))

Bias

- How removed a model's predictions are from correctness
- Occurs when an algorithm has limited flexibility to learn the true signal from a data set

Variance

- Degree to which these predictions vary between model iterations
- Refers to algorithm's sensitivity to specific sets of training data



High bias, low variance algorithms train models that are consistent, but inaccurate on average.

High variance, low bias algorithms train models that are accurate *on average*, but inconsistent.

But why is there a tradeoff?

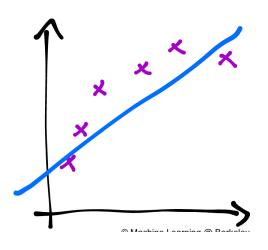
Low variance algos tend to be **less complex**, with simple or rigid underlying structure.

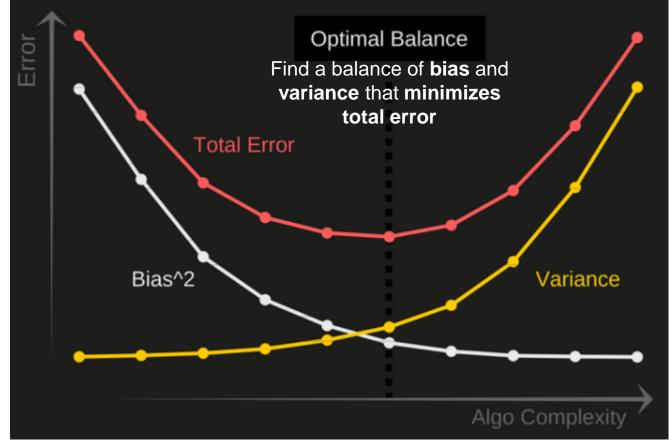
- e.g. Regression
- e.g. Naive Bayes
- Linear algos
- Parametric algos

Low bias algos tend to be **more complex**, with flexible underlying structure.

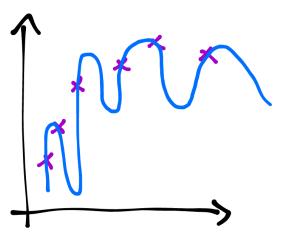
- e.g. Decision trees
- e.g. Nearest neighbors
- Non-linear algos
- Non-parametric algos

Algorithms that are not complex enough (high BIAS) produce UNDERFIT models that cannot learn the signal from data





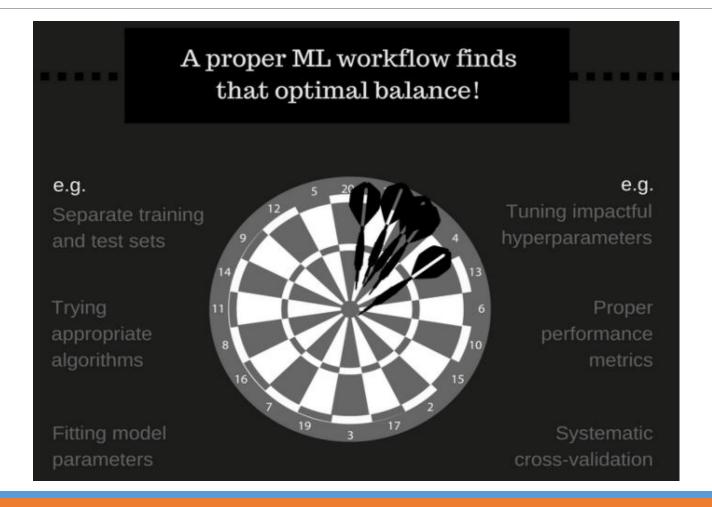
Algorithms that are too complex (high VARIANCE) produce OVERFIT models that memorize noise instead of the signal



Separate training and test sets

Trying appropriate algorithms

Fitting model parameters



Tuning impactful hyperparameter

Proper performance metrics

Systematic crossvalidation

ML Diagnostic

- A test to gain insight what is or is not working with a learning algorithm
- Gain guidance as to how best to improve the performance of the learning algorithm (deciding what to try next)
- Perform error analysis
 - Manually examine misclassified instances
 - Use a single real number performance metric based on validation set

ML Diagnostic

- Choosing what to try next
 - Get more training data
 - Try smaller sets of features
 - Try getting additional features
 - Try adding polynomial features (increase the complexity of hypothesis function)

ML Diagnostic

Choosing what to try next

Get more training data	Fixes high variance
Try smaller sets of features	Fixes high variance
Try getting additional features	Fixes high bias
Try adding polynomial features	Fixes high bias