

EVML3

ML PERFORMANCE

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QUIZ TIME

- Individual, multiple-choice questions
- Online: <http://www.socrative.com> room **1PTGB6PY**
- Open book quiz, so books and slides can be consulted
- **HAN student number**, so NOT your name, nickname or anything else.
- Quiz starts exactly at class hour and takes 10 minutes.
- Be on time and have your equipment prepared.

CONTENTS

- Confusion matrix
- Evaluating classifiers
- Learning curves

VEROS COVID-19 DELIVERED:¹

Accuracy 97.9%

Sensitivity 95.2%

Specificity 99.5%



THE BOY WHO CRIED WOLF

"Wolf" is a **positive class**.

"No wolf" is a **negative class**

An Aesop's Fable ~620 BCE



Source: Sam Taplin

CONFUSION MATRIX

		ACTUAL	
PREDICTED			(Type I error)
		True Positive (TP) Reality: A wolf threatened. Shepherd said: "Wolf." Outcome: Shepherd is a hero.	False Positive (FP) Reality: No wolf threatened. Shepherd said: "Wolf." Outcome: Villagers are angry at shepherd for waking them up.
		False Negative (FN) Reality: A wolf threatened. Shepherd said: "No wolf." Outcome: The wolf ate all the sheep.	True Negative (TN) Reality: No wolf threatened. Shepherd said: "No wolf." Outcome: Everyone is fine.
			(Type II error)

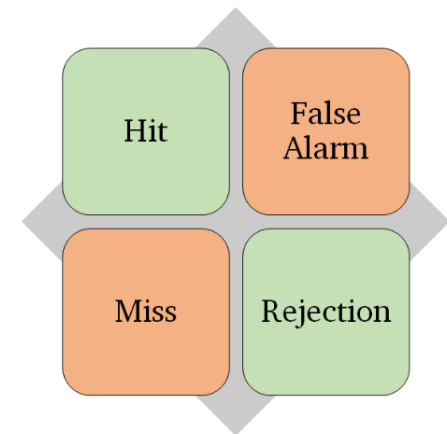
ACCURACY

- Fraction of predictions the model got right

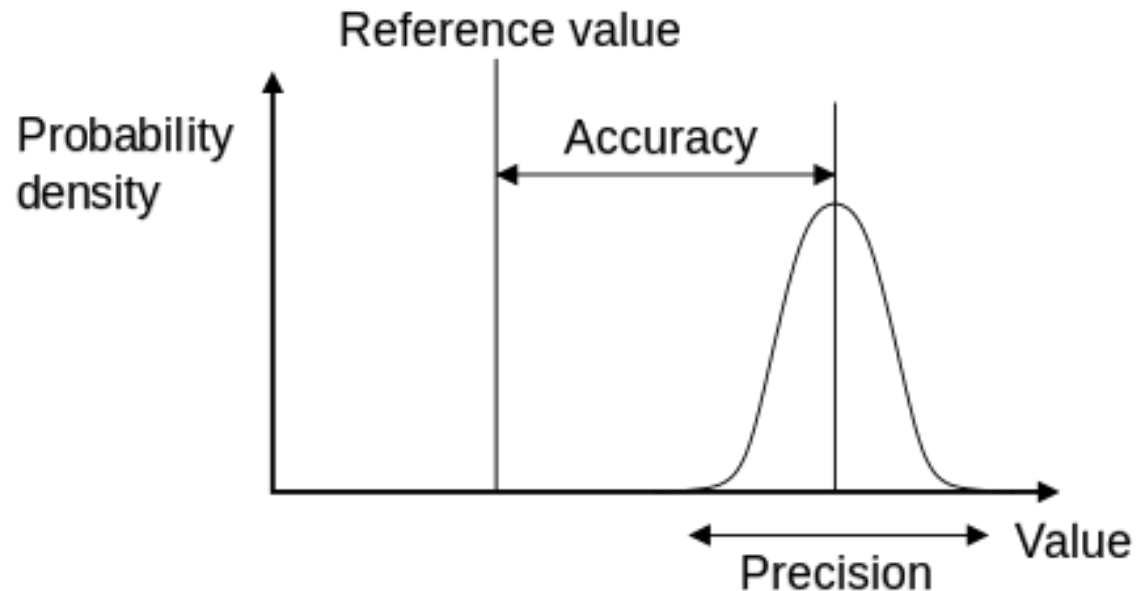
$$\text{Accuracy} = \frac{\text{Number of correct predictions}}{\text{Total number of predictions}}$$

- For binary classification

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



ACCURACY VS PRECISION



accuracy is closeness of the measurements to a specific value, while **precision** is the closeness of the measurements to each other.

PRECISION AND RECALL

- Precision, fraction of correct positive predictions

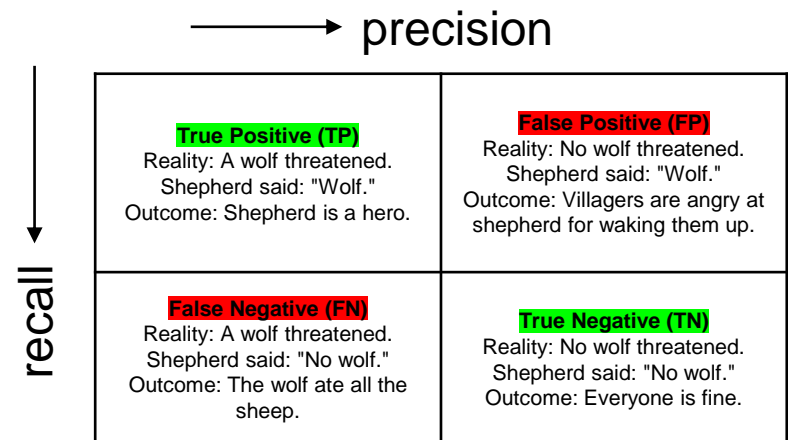
$$\Sigma \text{ True positive} / \Sigma \text{ Predicted condition positive}$$

$$\text{precision} = \frac{TP}{TP + FP}$$

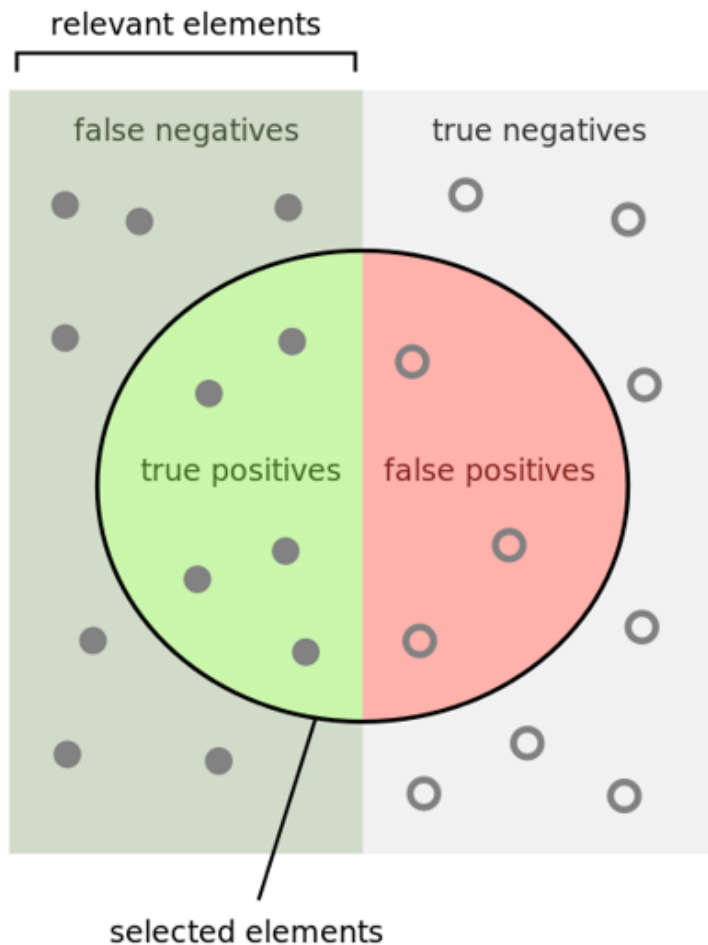
- Recall, probability of detection

$$\Sigma \text{ True positive} / \Sigma \text{ Condition positive}$$

$$\text{recall} = \frac{TP}{TP + FN}$$



PRECISION AND RECALL



How many selected items are relevant?

$$\text{Precision} = \frac{\text{true positives}}{\text{true positives} + \text{false positives}}$$

How many relevant items are selected?

$$\text{Recall} = \frac{\text{true positives}}{\text{true positives} + \text{false negatives}}$$

Recall = sensitivity = true positive rate (TPR)

SKLEARN CLASSIFICATION REPORT

```
>>> from sklearn.metrics import classification_report
>>> y_true = [0, 1, 2, 2, 2]
>>> y_pred = [0, 0, 2, 2, 1]
>>> target_names = ['class 0', 'class 1', 'class 2']
>>> print(classification_report(y_true, y_pred, target_names=target_names))
```

	precision	recall	f1-score	support
class 0	0.50	1.00	0.67	1
class 1	0.00	0.00	0.00	1
class 2	1.00	0.67	0.80	3
accuracy			0.60	5
macro avg	0.50	0.56	0.49	5
weighted avg	0.70	0.60	0.61	5

```
>>> y_pred = [1, 1, 0]
>>> y_true = [1, 1, 1]
>>> print(classification_report(y_true, y_pred, labels=[1, 2, 3]))
```

	precision	recall	f1-score	support
1	1.00	0.67	0.80	3
2	0.00	0.00	0.00	0
3	0.00	0.00	0.00	0
micro avg	1.00	0.67	0.80	3
macro avg	0.33	0.22	0.27	3
weighted avg	1.00	0.67	0.80	3

F1 SCORE

- To fully evaluate the effectiveness of a model, you must examine **both** precision and recall
- F1 score is the harmonic mean of precision and recall

$$F_1 = \frac{2}{\frac{1}{\text{precision}} + \frac{1}{\text{recall}}} = 2 \times \frac{\text{precision} \times \text{recall}}{\text{precision} + \text{recall}} = \frac{TP}{TP + \frac{FN + FP}{2}}$$

MANY METRICS

Source: https://en.wikipedia.org/wiki/Receiver_operating_characteristic

Predicted condition

veren. Alle tests van de deelnemende partijen zijn eerst beoordeeld door het RIVM. „We sturen tien monsters, vijf met SARS-CoV-2 in verschillende concentraties, drie met andere coronavirussen, en twee waar niets in zit. De labs weten niet wat waar in zit. Als hun uitslagen kloppen, is de test goed”, zegt Reusken.

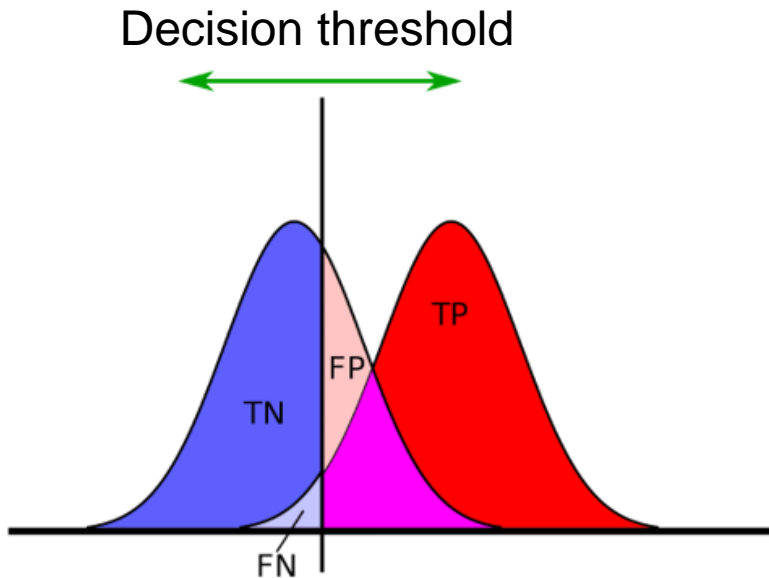
De testprestaties zullen per lab wat variëren: de specificiteit (de kans dat je een niet-ziek iemand ook als niet-ziek detecteert) en de sensitiviteit (de kans dat je een ziek iemand als ziek detecteert). De E-gen test is gevoeliger dan de RdRP-gen test, maar wat minder specifiek: naar schatting 99 tot 99,5 procent. Tests op meerdere genen zijn iets specifiek. Door de variatie ligt die specificiteit landelijk minimaal op 99,5 procent, zegt Reusken.

4 | Wat bepaalt hoeveel foute uitslagen een test geeft?

„De specificiteit hangt af van de test zelf

negative	Prevalence $= \frac{\sum \text{Condition positive}}{\sum \text{Total population}}$	Accuracy (ACC) = $\frac{\sum \text{True positive} + \sum \text{True negative}}{\sum \text{Total population}}$	
positive, error	Positive predictive value (PPV), Precision = $\frac{\sum \text{True positive}}{\sum \text{Predicted condition positive}}$	False discovery rate (FDR) = $\frac{\sum \text{False positive}}{\sum \text{Predicted condition positive}}$	
negative	False omission rate (FOR) = $\frac{\sum \text{False negative}}{\sum \text{Predicted condition negative}}$	Negative predictive value (NPV) = $\frac{\sum \text{True negative}}{\sum \text{Predicted condition negative}}$	
hit rate hit-out, false alarm positive negative	Positive likelihood ratio (LR+) $= \frac{\text{TPR}}{\text{FPR}}$	Diagnostic odds ratio (DOR) $= \frac{\text{LR+}}{\text{LR-}}$	F ₁ score = $2 \cdot \frac{\text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}}$
SPC), True (TNR) negative	Negative likelihood ratio (LR-) $= \frac{\text{FNR}}{\text{TNR}}$		

PRECISION/RECALL TRADE-OFF



TP	FP
FN	TN

$$\text{precision} = \frac{TP}{TP + FP} \quad \text{recall} = \frac{TP}{TP + FN}$$



Source: https://en.wikipedia.org/wiki/Tug_of_war#/media/File:Touwtrekken.jpg

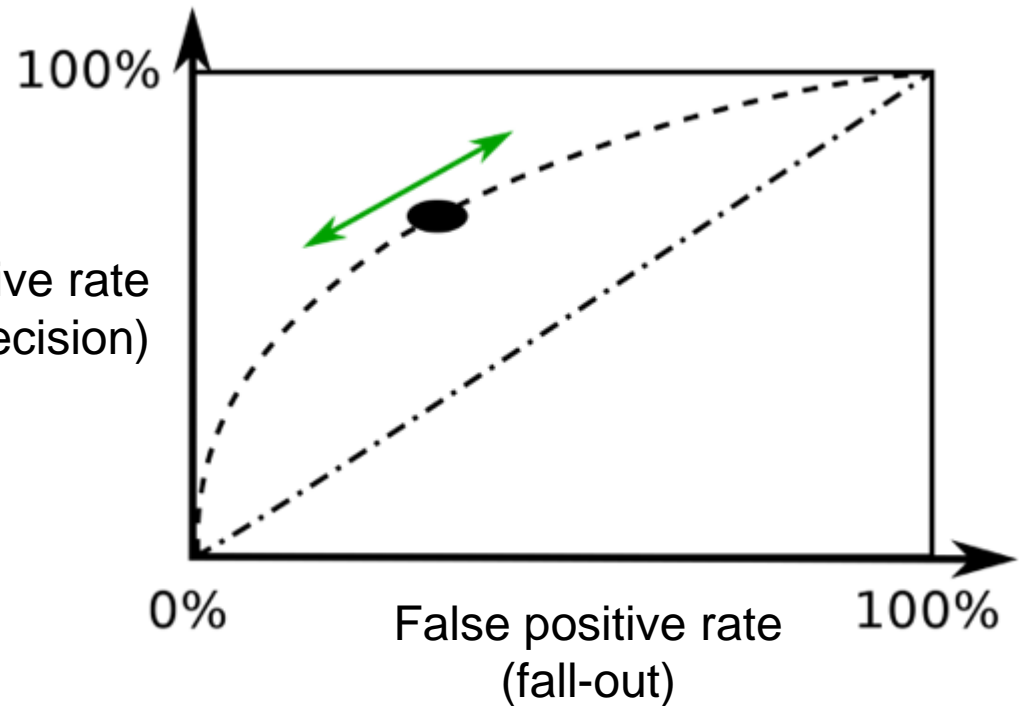
Source: https://en.wikipedia.org/wiki/Receiver_operating_characteristic#/media/File:ROC_curves.svg

ROC CURVE

- *probability of detection vs probability of false alarm at different decision thresholds.*



True positive rate
(precision)

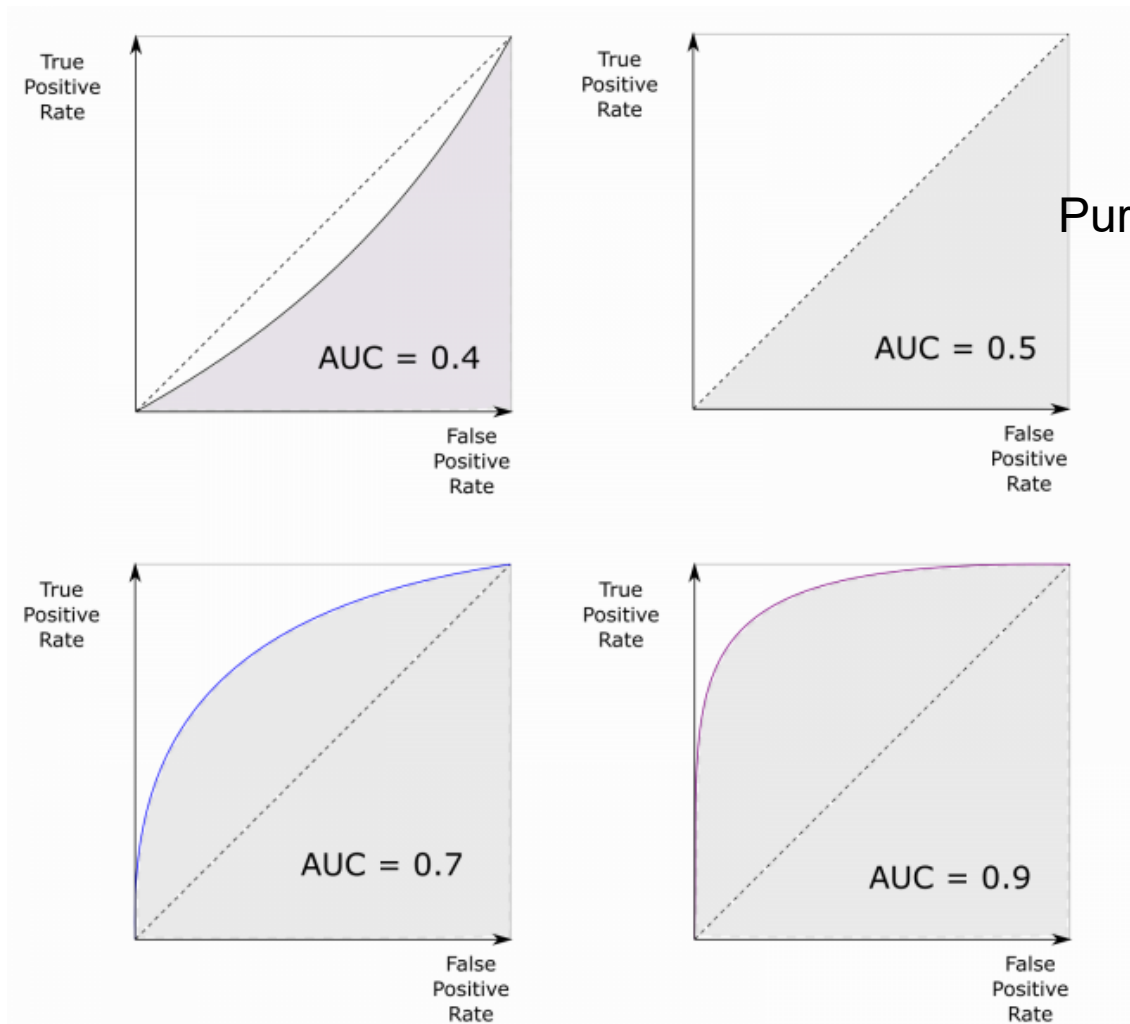


Source: https://en.wikipedia.org/wiki/Receiver_operating_characteristic#/media/File:ROC_curves.svg

COST OF CLASSIFICATION










- Sometimes false negatives don't hurt as much as false positives
Think of a poisonous mushroom detector....
- Use the ROC curve (receiver operating characteristics) to help balance the cost of classification

ROC AREA UNDER THE CURVE (AUC)



Purely random...

MULTICLASS CONFUSION MATRIX

		Predicted (what our model says))			
Actual (what the data says)	CLASSES	 A	 B	 C	Row totals
	 A	 5	2	3	10
	 B	2	 6	0	8
	 C	3	2	 2	7
	Column Totals	10	10	5	25

Diagonal numbers are rightly classified observations

Total number of observations/ records

#MLmuse
CLAIRVOYANT

Source: https://miro.medium.com/max/1400/1*jtoE1zEJaG0JvGIX3jOTFQ.png

SPLITTING DATA

- Slice data into three subsets: Training, validation and test data

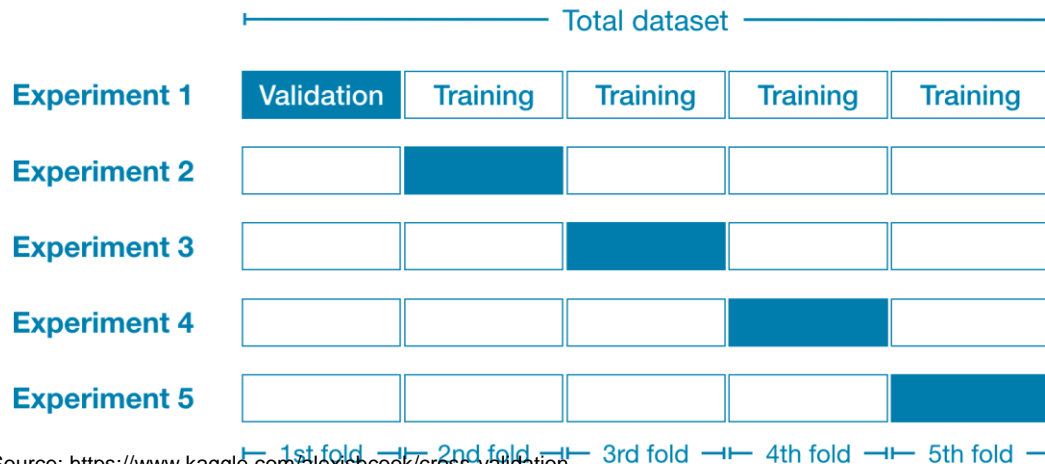


- Make sure that your subsets meet the following conditions:
 - Large enough to yield statistically meaningful results.
 - Representative of the data set as a whole.

E.g. don't pick a test set with different characteristics than the training set.

CROSS-VALIDATION

- Estimate of a model's generalization performance
- Break the data into folds



- For small datasets, where extra computational burden isn't a big deal, you should run cross-validation.

LEARNING CURVES

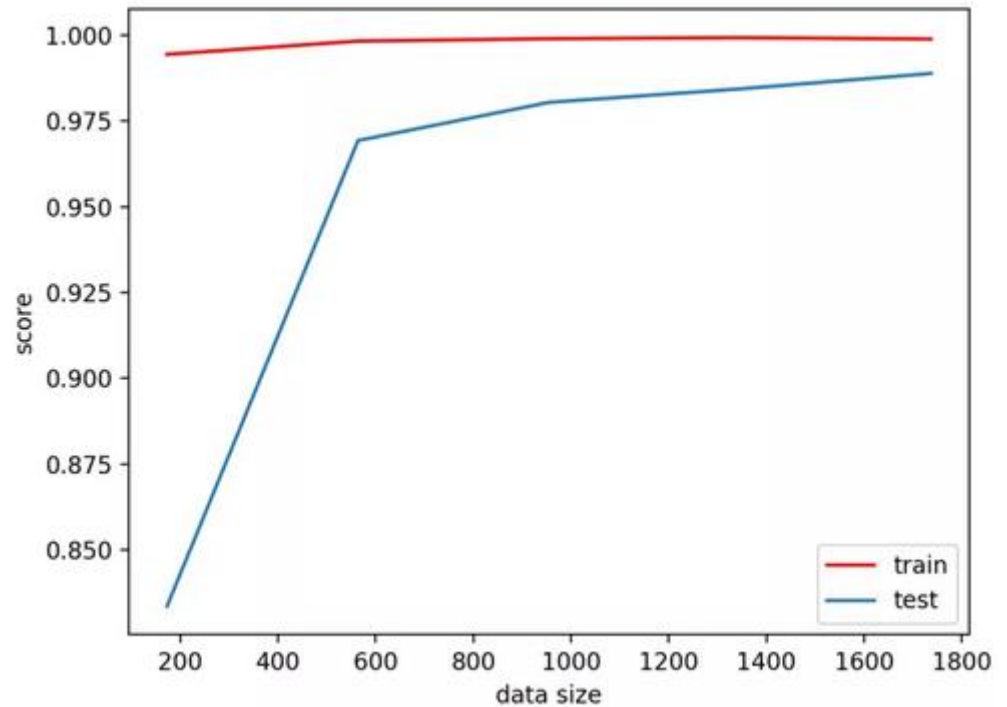
- A powerful diagnostic tool!

```
from sklearn.model_selection import learning_curve
from sklearn.svm import SVC
from sklearn.datasets import load_digits
from matplotlib import pyplot as plt
import numpy as np
```

```
X, y = load_digits(return_X_y=True)
estimator = SVC(gamma=0.001)
```

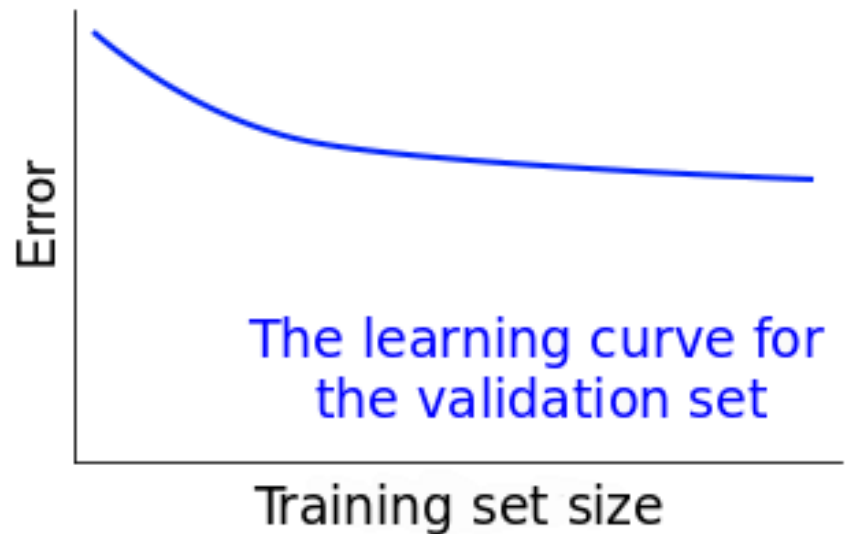
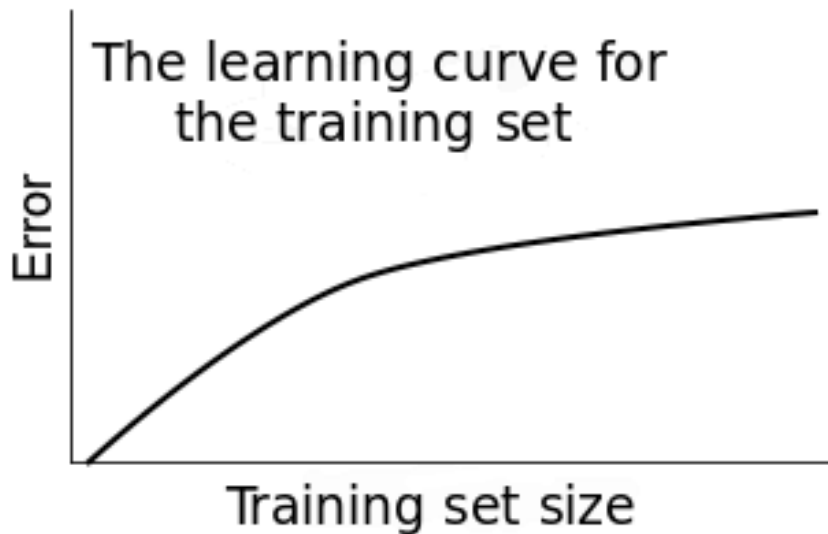
```
train_sizes, train_scores, test_scores, fit_times, _ = learning_curve(estimator, X, y, cv=30, return_times=True)
```

```
plt.plot([train_sizes, np.mean(train_scores, axis=1)])
```



LEARNING CURVES

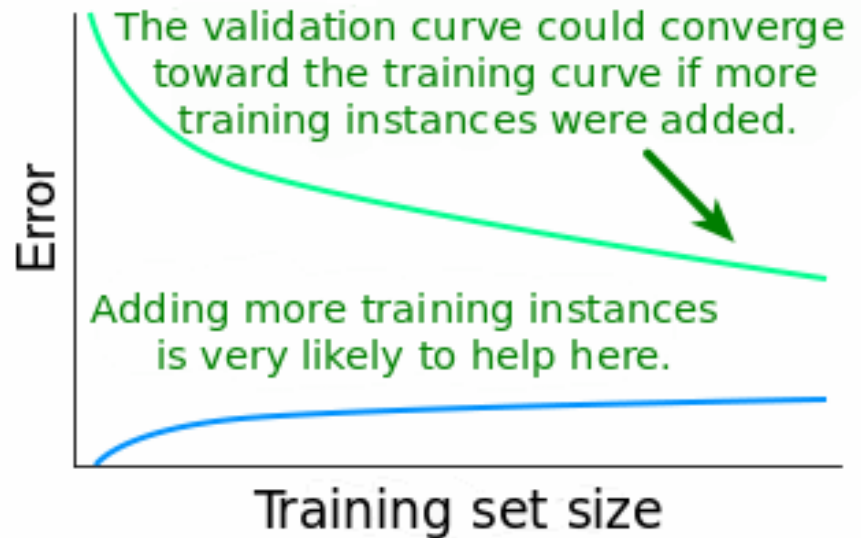
- Cost as a function of the training set size (or the training iteration)
- Examine evolution of train and validation learning curves



Source: <https://www.dataquest.io/blog/learning-curves-machine-learning/>

LEARNING CURVES

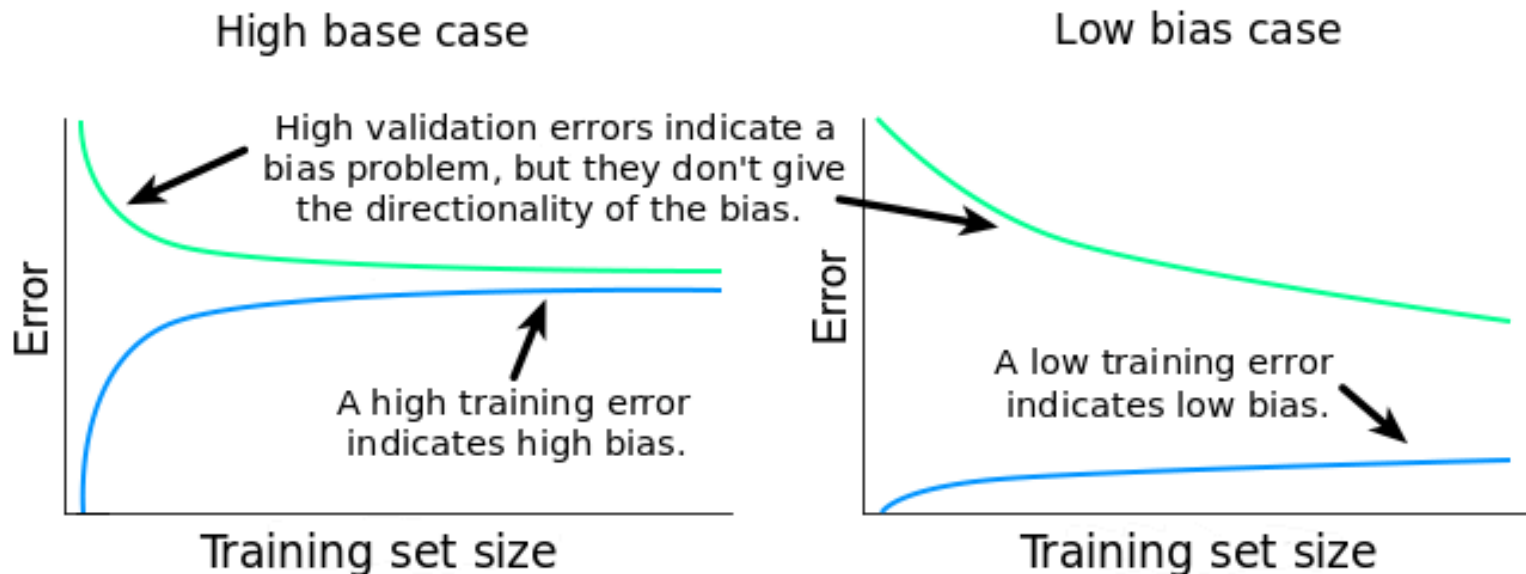
- Convergence of curves



Source: <https://www.dataquest.io/blog/learning-curves-machine-learning/>

BIAS PROBLEM

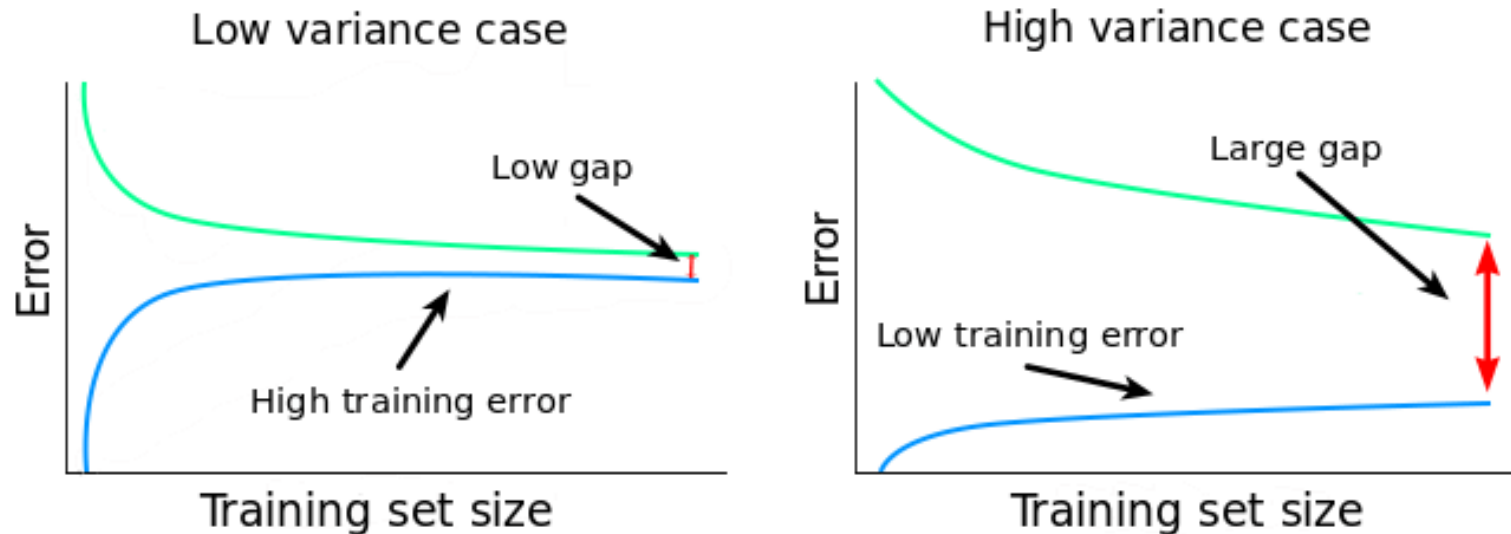
- High validation error indicates a prediction bias problem
- Underfitting usually gives high bias



Source: <https://www.dataquest.io/blog/learning-curves-machine-learning/>

VARIANCE PROBLEM

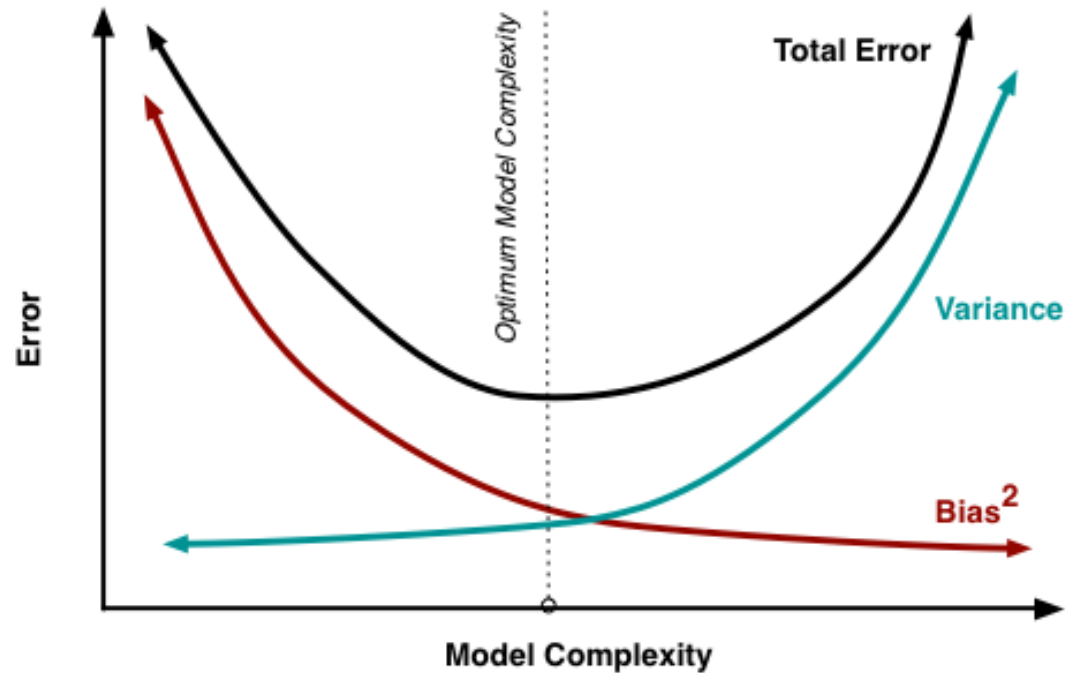
- Low gap indicates low prediction variance
- Overfitting usually gives high variance



Source: <https://www.dataquest.io/blog/learning-curves-machine-learning/>

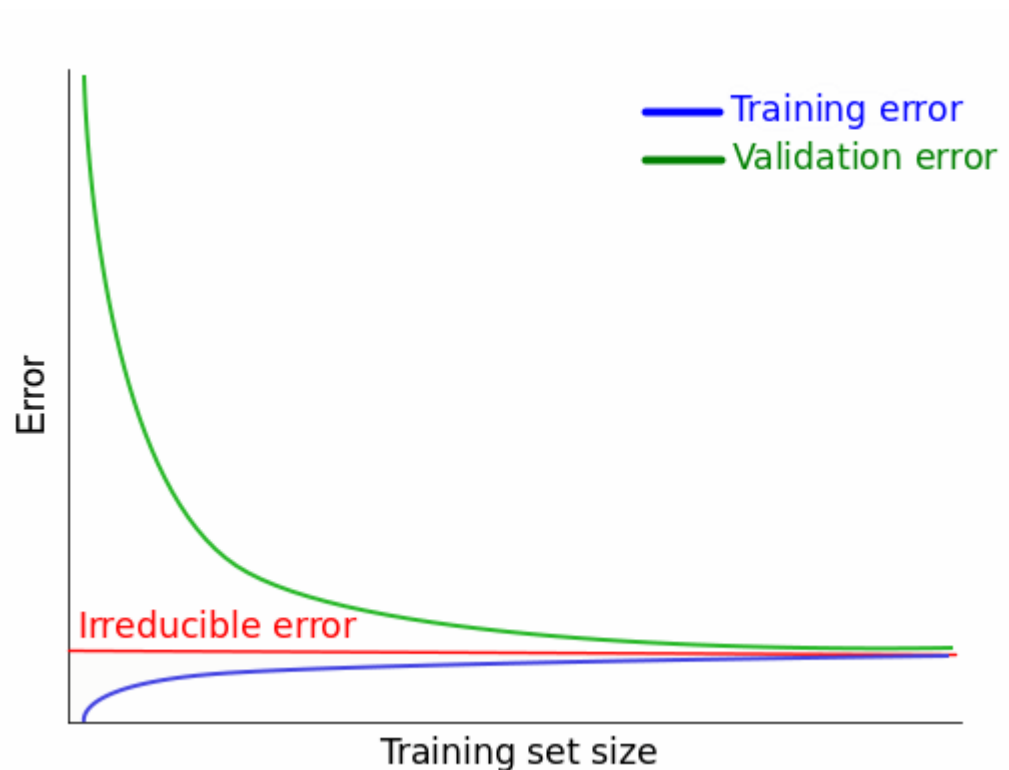
PREDICTION BIAS–VARIANCE TRADEOFF

- Central problem in supervised learning



IRREDUCIBLE ERROR

- Noise
- Cannot be predicted
- Loss cannot be reduced
- Outliers



MORE ON PREDICTION BIAS

- Average of predictions \approx average of labels in test set
- A significant difference shows there is bias
- Possible causes:
 - Underfitting, e.g. incomplete feature set, overly strong regularization
 - Biased training samples
 - (Noisy data set)

QUESTION

- We know that on average, 1% of all emails are spam.
- My spam filter predicts that 20% of my incoming mail is spam.

What can we say about my spam filter?

COMPUTING CROSS-VALIDATED METRICS

- Predefined scoring parameters

Scoring	Function	Comment
Classification		
'accuracy'	<code>metrics.accuracy_score</code>	
'balanced_accuracy'	<code>metrics.balanced_accuracy_score</code>	
'average_precision'	<code>metrics.average_precision_score</code>	
'neg_brier_score'	<code>metrics.brier_score_loss</code>	
'f1'	<code>metrics.f1_score</code>	for binary targets
'f1_micro'	<code>metrics.f1_score</code>	micro-averaged
'f1_macro'	<code>metrics.f1_score</code>	macro-averaged
'f1_weighted'	<code>metrics.f1_score</code>	weighted average
'f1_samples'	<code>metrics.f1_score</code>	by multilabel sample
'neg_log_loss'	<code>metrics.log_loss</code>	requires <code>predict_proba</code> support
'precision' etc.	<code>metrics.precision_score</code>	suffixes apply as with 'f1'
'recall' etc.	<code>metrics.recall_score</code>	suffixes apply as with 'f1'
'jaccard' etc.	<code>metrics.jaccard_score</code>	suffixes apply as with 'f1'
'roc_auc'	<code>metrics.roc_auc_score</code>	
'roc_auc_ovr'	<code>metrics.roc_auc_score</code>	

See: https://scikit-learn.org/stable/modules/model_evaluation.html