Kfold Cross-validation Model Valuation and Performance Metrics

1.Data Preparation: Splitting the dataset into training, validation, and test sets.

2.Model Fitting: Creating multiple models.
3.Model Evaluation: Nonlin | Would | Wall DL | Reg tree

- for Reg Problem: Mean Absolute error (MAE), Calculation of Mean Squared Error (MSE) and Root Mean Squared Error (RMSE) on the validation set for both models.
- for Classification Problem: Using confusion matrix, accuracy, precision, recall

(sensitivity), specificity, F1-score etc on the validation set.

4.Cross-Validation: Performing cross-validation on the training set.

Z.Final Model Selection and Evaluation: Applying the best model on the test set.

Hold CV cross validata Validation

KNN-(K) — how many neighbours

KMeens-(K) — how many clusters

Kfold -(K) — how many folds

- Mean Squared Error (MSE)
- MSE is a measure of the average of the squares of the errors—that is, the average squared difference between the estimated values and the actual value. It's a common measure of the estimation accuracy of a predictive model in regression tasks.

$$MSE = \frac{1}{n} \sum_{i=1}^{n} (Y_i - \hat{Y}_i)^2$$

- Root Mean Squared Error (RMSE)
- RMSE is the square root of the MSE. It's a widely used measure of the differences between values predicted by a model or an
 estimator and the values observed. The RMSE represents the sample standard deviation of the differences between predicted and
 observed values.

$$RMSE = \sqrt{MSE}$$

- Accuracy
- Most commonly used metrics for evaluating classification models. It measures the proportion of total correct predictions (both true positives and true negatives) out of all predictions made.
- Accuracy=Number of Correct Predictions / Total Number of Predictions

Or, using the terms of the confusion matrix:

- Accuracy= (TP + TN) / (TP + FP + FN + TN)
- Specificity
- Specificity measures the proportion of actual negatives that are correctly identified as such (e.g., the percentage of healthy people who are correctly identified as not having the condition, in the medical context). It's a key metric when the cost of false positives is high. Specificity=True Negatives (TN)/ (True Negatives (TN) + False Positives (FP))
- Recall (Sensitivity)
- Recall, also known as sensitivity, is the ratio of true positive predictions to the total actual positives. It answers the question: "Of all the actual positive instances, how many did we correctly classify as positive?"

Recall=True Positives (TP) / (True Positives (TP) + False Negatives (FN))

Precision

Precision is the ratio of true positive predictions to the total positive predictions (including both true
positives and false positives). It answers the question: "Of all instances classified as positive, how many
are actually positive?"

Precision=True Positives (TP)/(True Positives (TP) + False Positives (FP))

F1-Score

• The F1-score is the harmonic mean of precision and recall. It provides a single score that balances both the precision and recall. It's particularly useful when you need to balance both precision and recall, such as in imbalanced datasets.

F1-score=2×(Precision×Recall) / (Precision+Recall)

	True		
	Positive	Negative	Measures
Predicted class	True positive <i>TP</i>	False positive <i>FP</i>	Positive predictive value (PPV) TP TP+FP
Predicte Negative	False negative <i>FN</i>	True negative TN	Negative predictive value (NPV) TN FN+TN
Measures	Sensitivity TP TP+FN	Specificity <u>TN</u> FP+TN	Accuracy TP+TN TP+FP+FN+TN

<u> </u>		Actual Value		
		Positive	Negative	
Result Obtained	Positive	True Positive (1- β)	False Positive Type-I Error (α)	
	Negative	False Negative Type-II Error (β)	True Negative	

Predicted class

	positive
Positive (P)	T rue P ositive (TP)
True class	
Negative (N)	F alse P ositive (FP)
1	
	$PPV = \frac{TP}{TP + FP}$

$$PPV = \frac{TP}{TP + FP}$$
 $NPR = \frac{TN}{TN + FN}$ $FDR = \frac{FP}{TP + FP}$ $FOR = \frac{FN}{TN + FN}$

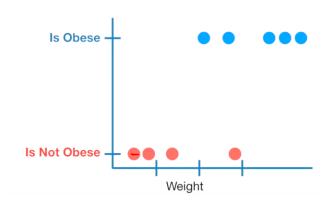
Row summary

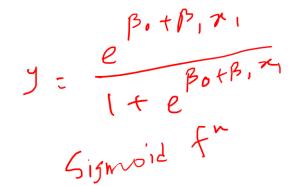
$$TPR = \frac{TP}{P} \quad FNR = \frac{FN}{P}$$

$$TNR = \frac{TN}{N}$$
 $FPR = \frac{FP}{N}$

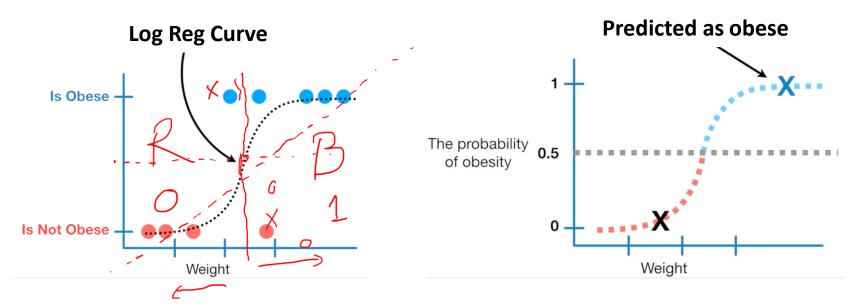
Column summary

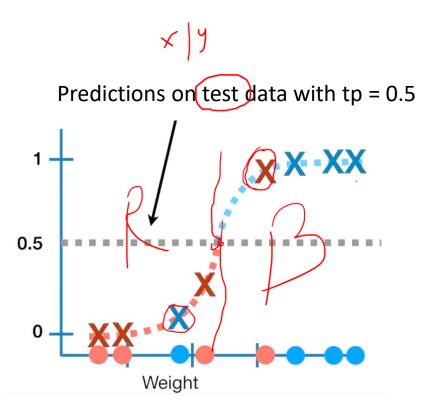
Log Reg training and Thresholds

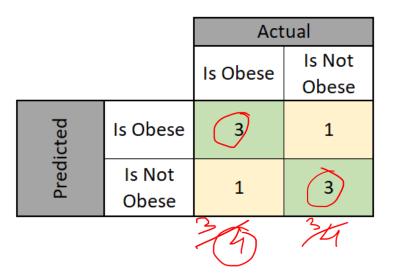




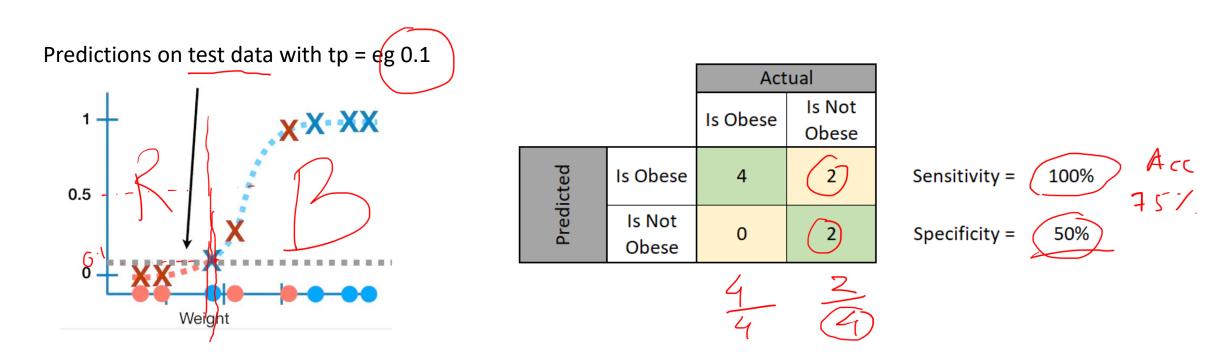








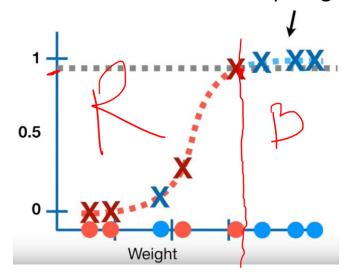




Think about an infectious disease. This is very important to correctly predict all the "yes" infected cases

(ovid: sonsility

Predictions on test data with tp = eg 0.9

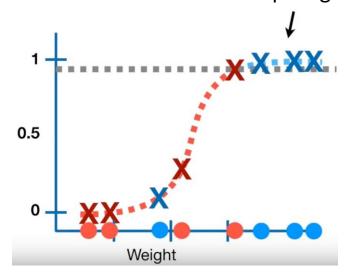


This is better than 0.5 for sure

		Actual		<u> </u>
		Is Obese	Is Not Obese	Acc
cted	Is Obese	3	0	Sensitivity = 75%
Predicted	Is Not Obese	1	4	Specificity = $\frac{75\%}{100\%}$ Acc
		3	94	

But which threshold is the best?

Predictions on test data with tp = eg 0.9



		Actual	
		Is Obese	Is Not Obese
Predicted	Is Obese	3	0
Pred	Is Not Obese	1	4

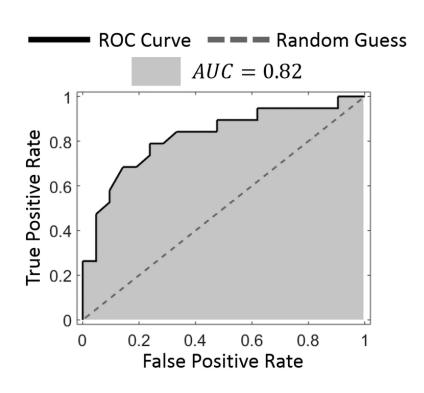
Sensitivity = 75%

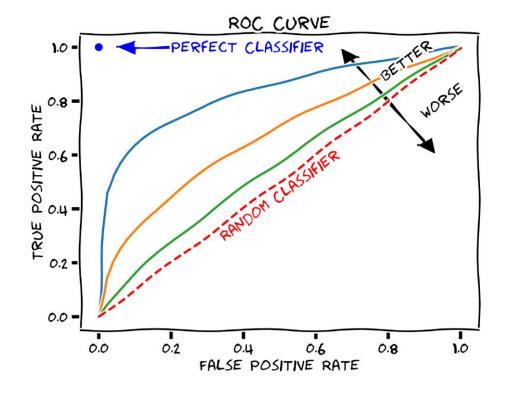
Specificity = 100%

This is better than 0.5 for sure

But which threshold is the best?

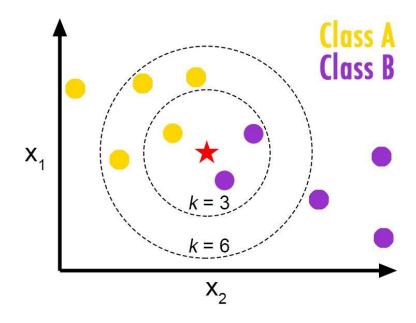
ROC (Receiver Operator Curve) Curve and AUC (Area Under Curve)

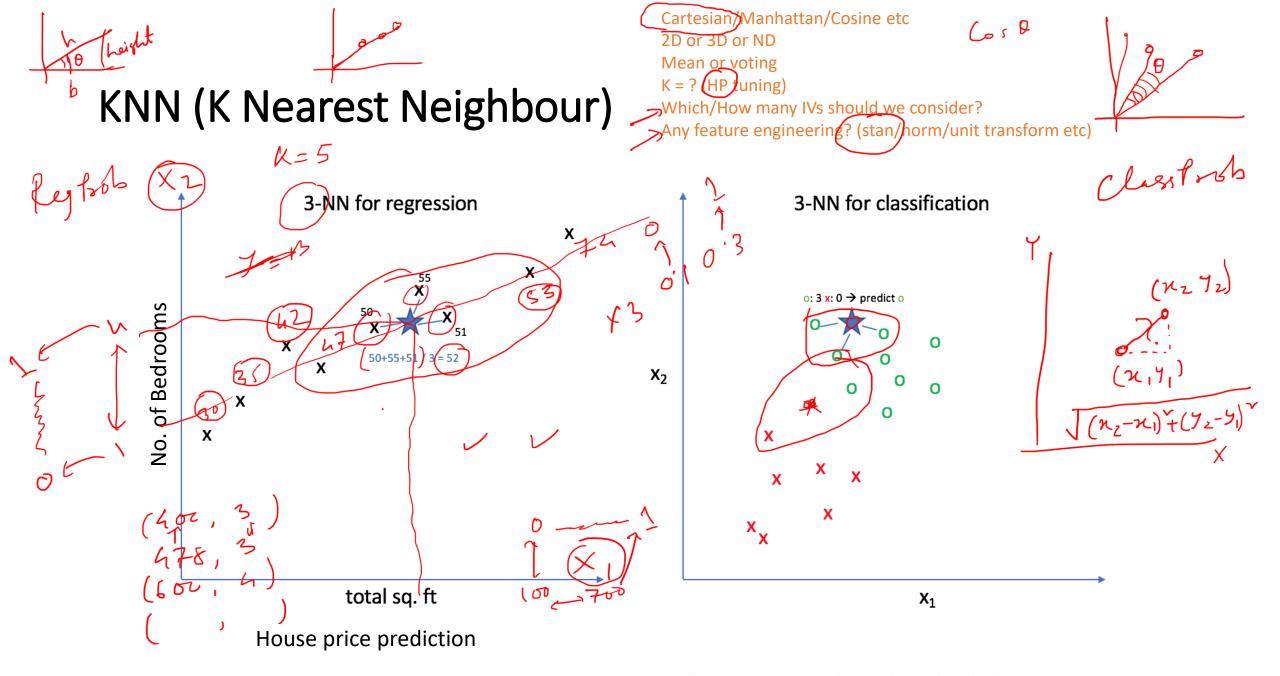




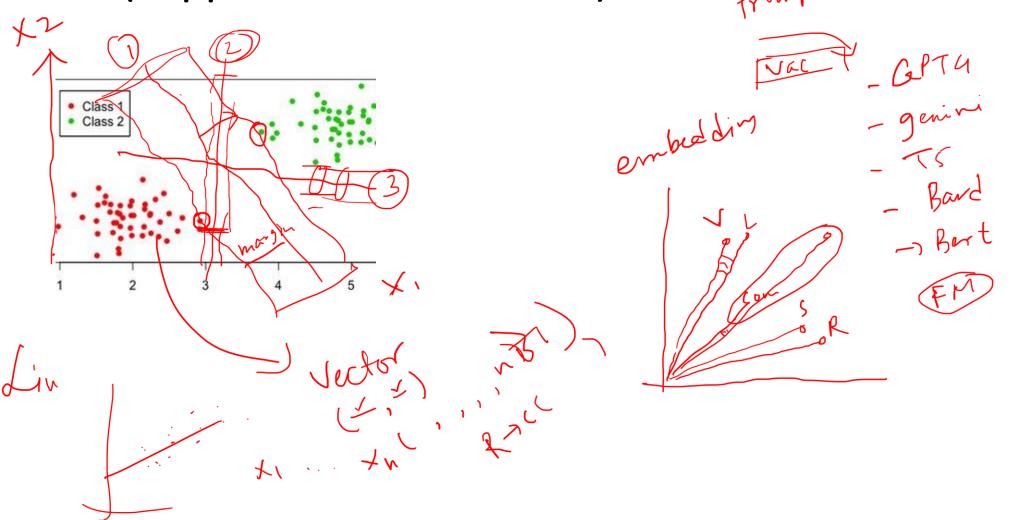
ROC (Receiver Operator Curve) Curve and Log Reg KNN/ AUC (Area Under Curve) o'0 5 Sensitivity 0 0.8 0.2 0.6 0.4 0.0

KNN (K Nearest Neighbour)

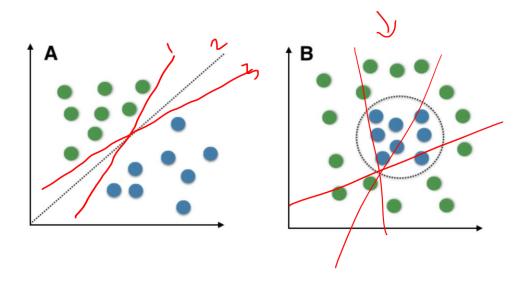


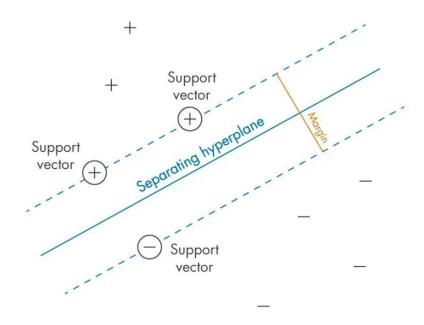


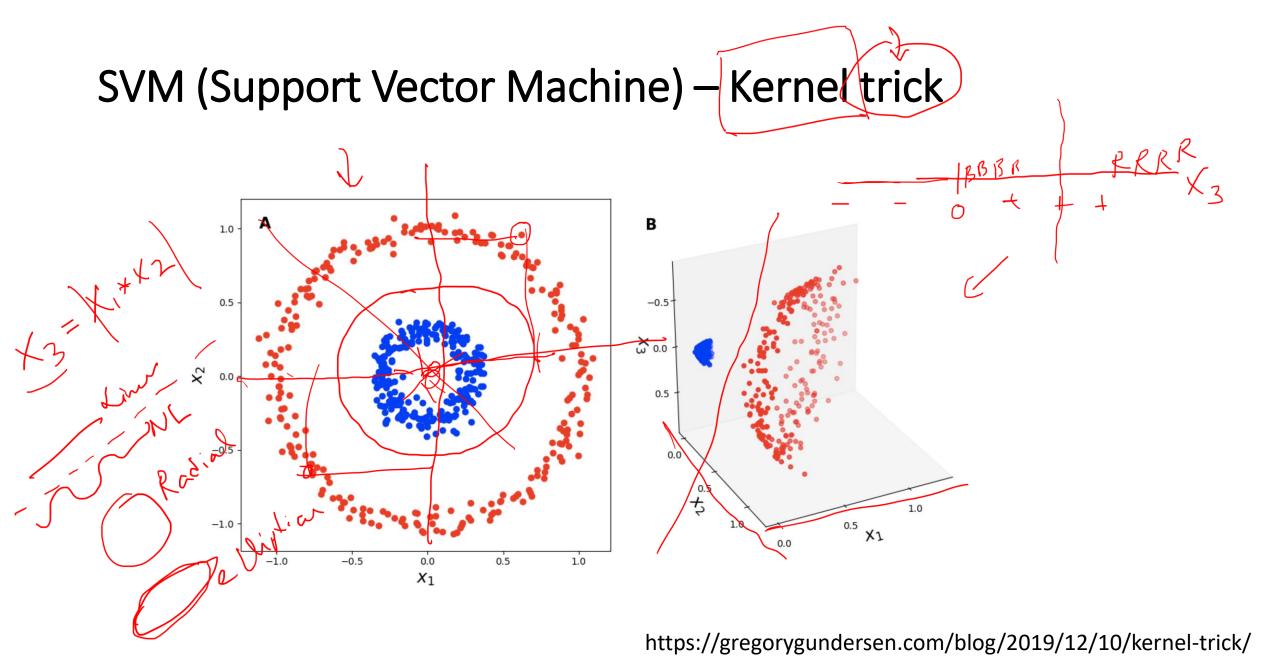
SVM (Support Vector Machine)



SVM (Support Vector Machine)



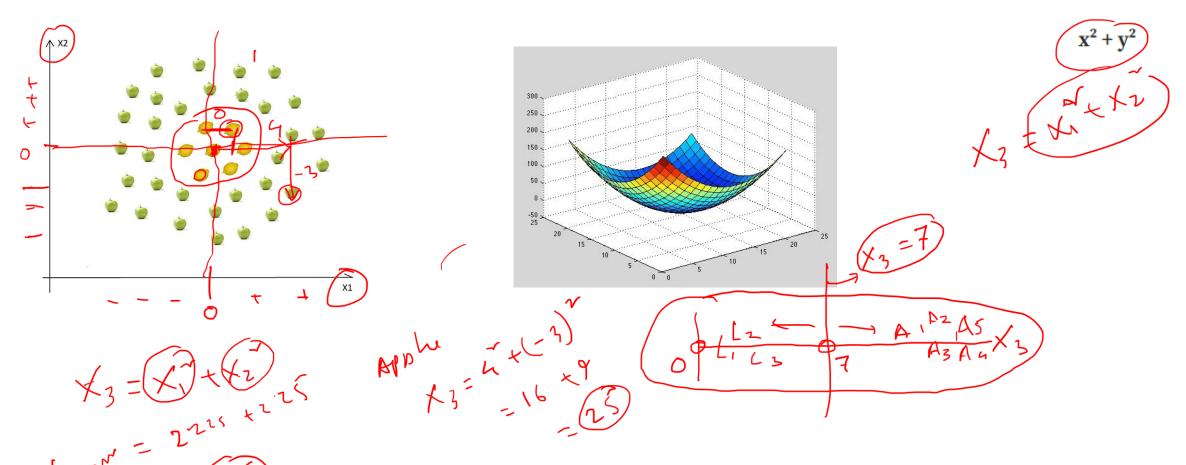




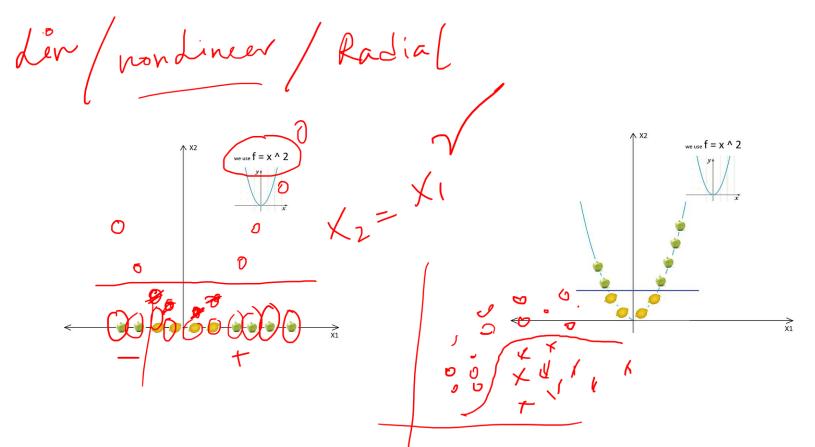
SVM (Support Vector Machine) – Kernel trick

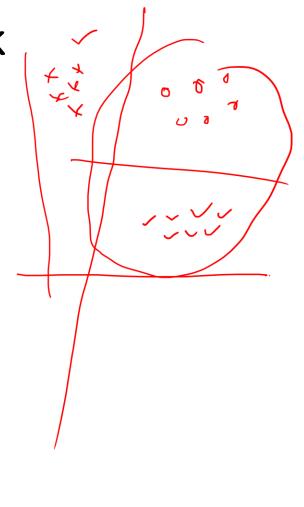


https://towardsdatascience.com/svm-and-kernel-svm-fed02bef1200

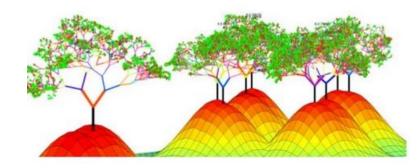


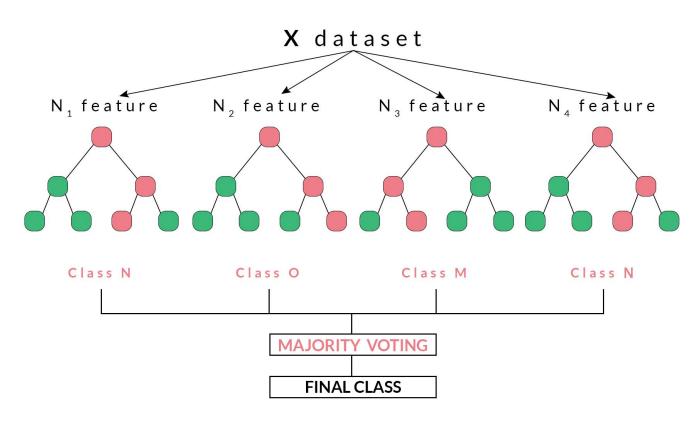
SVM (Support Vector Machine) – Kernel trick



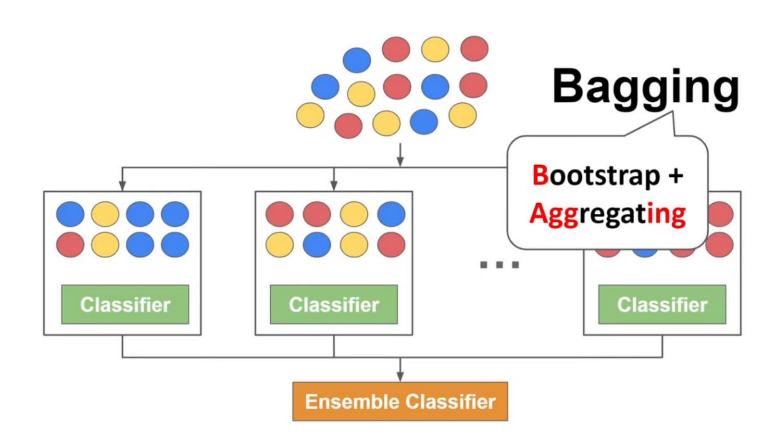


Random Forest

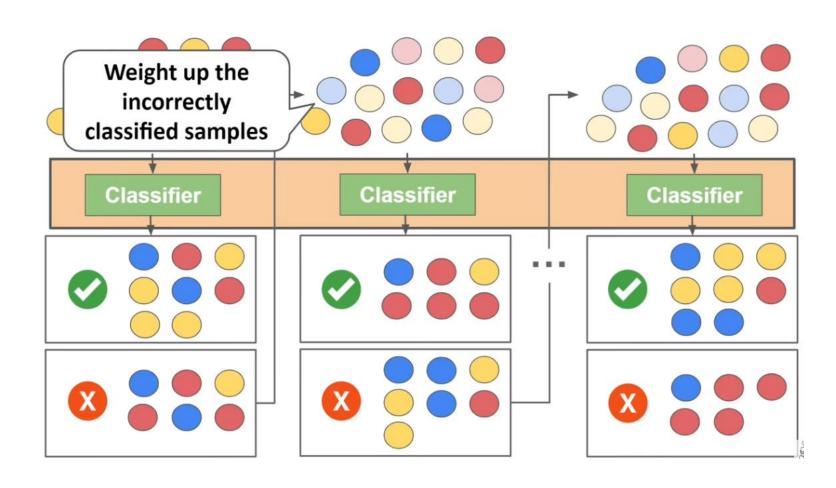




Bagging



Boosting



Regularization: Lasso vs Ridge vs Elastic

minimize
$$\left\{ \sum_{i=1}^{n} \left(y_i - \beta_0 - \sum_{j=1}^{p} \beta_j x_{ij} \right)^2 \right\} \quad \text{subject to} \quad \sum_{j=1}^{p} |\beta_j| \le s$$

$$(6.8)$$

and

minimize
$$\left\{ \sum_{i=1}^{n} \left(y_i - \beta_0 - \sum_{j=1}^{p} \beta_j x_{ij} \right)^2 \right\} \quad \text{subject to} \quad \sum_{j=1}^{p} \beta_j^2 \le s,$$

$$(6.9)$$