# Machine Learning 

## Lecture BigData Analytics

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## Outline

1 Introduction

2 Training

3 Classification \& Regression

4 Clustering

5 Association Rule Mining

1 Introduction

- Data Mining
- CRIP-DM

■ Terminology

## 2 Training

3 Classification \& Regression

4 Clustering

5 Association Rule Mining

## Data Mining (Knowledge Discovery) [35]

- Data mining: process of discovering patterns in large data sets
- (Semi-)Automatic analysis of large data to identify interesting patterns
- Using artificial intelligence, machine learning, statistics and databases


## Tasks / Problems

■ Anomaly detection: identify unusual data (relevant or error)
■ Association rule learning: identify relationships between variables
■ Classification: generalize known structures and apply them to new data
■ Clustering: discover and classify similar data into structures and groups
■ Regression: find a function to model data with the least error
■ Summarization: find a compact representation of the data

## Cross Industry Standard Process for Data Mining [39]

CRIP-DM is a commonly used methodology from data mining experts

## Phases

■ Business understanding: business objectives, requirements, constraints; converting the problem to a data mining problem

■ Data understanding: collecting initial data, exploration, assessing data quality, identify interesting subsets

■ Data preparation: creation of derived data from the raw data (data munging)

■ Modeling: modeling techniques are selected and applied to create models, assess model quality/validation

■ Evaluation (wrt business): check business requirements, review construction of the model(s), decide use

■ Deployment: applying the model for knowledge extraction;


Figure: Source:
Kenneth Jensen [38] creating a report, implementing repeatable data mining process

## Terminology [40]

■ Feature: measurable property of a phenomenon (explanatory variable)
■ Label: Outcome/property of interest that should be analyzed/predicted
■ Dependent variable

- Discrete in classification, continuous in regression

■ Online learning: update the model constantly while it is applied
■ Offline (batch) learning: learn from data (training phase), then apply
■ Supervised learning: feature and label are provided in the training
■ Unsupervised learning: no labels are provided, relevant structures must be identified by the algorithms
■ Reinforcement learning: algorithm tries to perform a goal while interacting with the environment

■ Humans use reinforcement, (semi)-supervised and unsupervised learning

## Strategy for Learning [40]

■ Goal: Learn properties of the population from a sample

- Data quality is usually suboptimal

■ Errornous samples (random noise, ambivalent data)

- Overfitting: a model describes noise in the sample instead of population properties

■ Robust algorithms reduce the chance of fitting noise

- How accurate is a specific model on the population?

■ Should we train a model on our data and check its accuracy on the same?
■ Good practice: split data into training and validation set
■ Training set: Build/train model from this data sample
■ Validation set: Check model accuracy on this set
■ Validate model accuracy via. k-fold cross validation ${ }^{1}$

[^0]
## Picking Training and Validation Sets

■ k-fold cross validation
■ Prevents cases in which we partition data suboptimally
1 Split data into k sets
2 For all permutations: train from k-1 sets, validate with remaining set
3 Compute average error metrics

Example with the iris data set

```
library(cvTools)
set.seed(123) # initialize random seed generator
data(iris)
# create 10 folds
f = cvFolds(nrow(iris), K=10, R=1, type="random")
# retrieve all sets
for (set in 1:10){
    validation = iris[ f$subsets[f$which == set] ,] # 135 elements
    training = iris[ f$subsets[f$which != set], ] # 15 elements
    # TODO Now build your model with training data and validate it
    # TODO Build error metrics for this repeat
}
# Output aggregated error metrics for all repeats
# Some packages perform the k-cross validation for you
```


## Classification: Supervised Learning

■ Goal: Identify/predict the class of previously unknown instances


Figure: Each class (flower type) is visualized in its own color

## Classification

■ k-nearest neighbor a simple supervised learning algorithm

- No training algorithm needed

■ Prediction: compute distance of new sample to k nearest samples
■ Majority of neighbors vote for new class
■ Confusion matrix: visualizes the performance of the classification

- Shows observation (row) and prediction class (column)

```
library(kknn)
m = kknn(Species ~ Sepal.Width + Petal.Length + Petal.Width + Sepal.Length, train=training, test=validation, k=3)
# Create a confusion matrix
table(validation$Species, m$fit)
    setosa versicolor virginica
    setosa 3 0 0
    versicolor 0 7 0
    virginica 
```


## Decision Trees

■ Tree data structures, a node indicates an attribute and threshhold
■ Follow left edge if value is below threshold
■ Follow right edge if value is above
■ Leafs are decisions
■ Can separate data horizontally and vertically

- Classification trees (for classes) and regression trees for continuous vars
- Various algorithms to construct a tree

■ CART: Pick the attribute to maximize information gain of the split
■ Knowledge (decision rules) can be extracted from the tree

- Tree pruning: Recursively remove unlikely leafs (reduces overfitting)


Figure: Decision tree for the iris data set with observations and labels

## Decision Trees with R

■ Rpart package supports regression (method="anova")
■ and Classification (with 2 classes method="poisson" else "class")

- Control object defines requirements for splitting (e.g. observations per leaf, cost complexity (cp) factor)

```
library(rpart)
data(iris)
# Create a classification tree based on all inputs
m = rpart(Species ~ Sepal.Width + Petal.Length + Petal.Width + Sepal.Length, data=iris, method="class",
    control = rpart.control(minsplit=5, cp = 0.05)) # require a minimum number of 5 observations
summary(m) # print details of the tree
plot(m, compress=T, uniform=T, margin=0.7) # plot the tree
text(m, use.n=T, all=T) # add text to the tree, plot all nodes not only leafs
m = prune(m, cp=0.05) # prune the tree, won't change anything here
p = predict(m, iris[150,], type="class") # predict class of data in the data frame, here one value
# virginica
p = predict(m, iris[150,], type="prob") # predict probabilities
# setosa versicolor virginica
# 150 0 0.02173913 0.9782609
# confusion matrix
table(iris$Species, predict(m, iris, type="class"))
# setosa versicolor virginica
# setosa 50 0 0
# versicolor 0 49 1
# virginica 
```


## Regression Trees

- Regression trees predict numeric values

■ They usually optimize mean-squared error
■ Party package uses statistical stopping rules (no pruning needed)

```
# Create a regression tree for Sepal.Width which optimizes mean-squared error
m = rpart( Sepal.Width ~ Species + Petal.Length + Petal.Width + Sepal.Length, data=iris, method="anova")
plot(m, compress=T, uniform=T, margin=0.7) # plot the tree
text(m, use.n=T) # add text to the tree
library(party) # package for recursive partitioning using nonparametric regression
m = ctree( Sepal.Width ~ Species + Petal.Length + Petal.Width + Sepal.Length, data=iris)
```



Sepal.Lengt|Reablisength< 5.25


Figure: Regression tree for Sepal.Width


Fiqure: Rearession tree with party

## Clustering

■ Partition data into "similar" observations

- Allows prediction of class for new observations

■ Unsupervised learning strategy

- Clustering based on distance metrics to a center (usually euclidean)

■ Can identify regular (convex) shapes
■ k-means: k-clusters, start with a random center, iterative refinement
■ Hierarchical clustering: distance based methods
■ Usually based on $N^{2}$ distance matrix
■ Agglomerative (start with individual points) or divisive
■ Density based clustering uses proximity to cluster members
■ Can identify any shape
■ DBSCAN: requires the density parameter (eps)
■ OPTICS: nonparametric
■ Model-based: automatic selection of the model and clusters
■ Normalization of variable ranges is usually vital
■ One dimension with values in 0 to 1 is always dominated by one of 10 to 100

## Density-based Clustering

```
library(fpc) # for dbscan
# For illustration purpose, we cluster the 4D feature set only using two variables
# 2D plot coloring the species
plot(iris$Sepal.Width, iris$Sepal.Length, col=iris$Species)
# Create a 2D matrix as input for dbscan
d = cbind(iris$Sepal.Width, iris$Sepal.Length)
# try to identify classes, showplot illustrates the process
p = dbscan(d, eps=0.35, showplot=1)
```




Figure: Output of dbscan

## K-means Clustering



Figure: Real species
Figure: Kmeans in 4D

## Model Based Clustering

$\square$ Automatic selection of model and cluster number
■ Uses bayesian information criterion (BIC) and expectation-maximization

```
library(mclust)
m = Mclust(iris[,1:4]) # chooses a ellipsoidal model
```



Figure: Model-based classification


Figure: BIC

## Association Rule Mining [44]

- Discover interesting relations in correlated facts and extract rules

■ Identify frequent item sets "likes HR, likes BigData"
■ Example association rule: "likes HR, likes BigData $\Rightarrow$ likes NTHR"
■ Data are individual transactions, e.g. purchases, with items
■ Items $I=i_{1}, \ldots, i_{n}$
■ Transactions $T=t_{1}, \ldots, t_{n}$
■ Each $t_{i}$ is a subset of $I$, e.g. items bought together in a market basket
■ Several algorithms exist e.g. APRIORI, RELIM

- Relevance of rules is defined by support and confidence

■ Assume $X \Rightarrow Y$ be an association rule, $X, Y$ are item-sets
■ supp( $X$ ): number of transactions which contains item-set $X$
$■ \operatorname{conf}(X \Rightarrow Y)=\operatorname{supp}(X \cup Y) / \operatorname{supp}(X)$ : fraction of transactions which contain $X$ and $Y$. Indicates if the rule is good

## Titanic Dataset Shows if People Survived



Class

## Association Analysis with Python Using Pyming²

```
from pymining import itemmining, assocrules
import csv
with open('titanic2.csv', 'r') as csvfile:
    reader = csv.reader(csvfile)
    data = [ r for r in reader ]
# apply relim algorithm
r = itemmining.get_relim_input(data)
# find frequent items (more than 1000 instances)
itemsets = itemmining.relim(r, min_support=1000)
# {frozenset(['No']): 1490, frozenset(['Male', 'Adult', 'No']): 1329, frozenset(['Adult', 'No']): 1438, frozenset(['Adult']):
    \hookrightarrow2092, frozenset(['Male', 'Adult']): 1667, frozenset(['Male', 'No']): 1364, frozenset(['Male']): 1731}
# mine the association rules
r = itemmining.get_relim_input(data)
itemsets = itemmining.relim(r, min_support=1)
rules = assocrules.mine_assoc_rules(itemsets, min_support=2, min_confidence=0.7)
# [((['Adult', 'No']), (['Male']), 1329, 0.9242002781641169), ((['No']), (['Male', 'Adult']), 1329, 0.8919463087248322), ...
# identify only survival-relevant rules with two or one items/attributes
relevant = [ (p, "Yes" in c,supp,conf) for p, c, supp, conf in rules if (c == frozenset(['No']) or c == frozenset(['Yes']))
    4 and len(p) <= 2]
relevant.sort(key=lambda x : x[1]) # sort based on the survival
for p, c, supp, conf in relevant:
    print(("%d,%.2f: %s <= %s" % (supp, conf, c, p)).replace("frozenset",""))
#1329,0.80: False <= (['Male', 'Adult'])
#476,0.76: False <= (['Adult', '3rd'])
#154,0.86: False <= (['Male', '2nd'])
#422,0.83: False <= (['Male', '3rd'])
#344,0.73: True <= (['Female'])
#316,0.74: True <= (['Adult', 'Female'])
#6,1.00: True <= (['1st', 'Child'])
#24,1.00: True <= (['2nd', 'Child'])
```


## ${ }^{2}$ https://github.com/bartdag/pymining

## Machine Learning with Python

■ Recommended package: scikit-learn ${ }^{3}$
■ Provides classification, regression, clustering, dimensionality reduction
■ Supports via model selection and preprocessing
Example: Decision tree

```
from sklearn.datasets import load_iris
from sklearn import tree
iris = load_iris()
m = tree.DecisionTreeClassifier()
m = m.fit(iris.data, iris.target)
# export the tree for graphviz
with open("iris.dot", 'w') as f:
    tree.export_graphviz(m, out_file=f)
# To plot run: dot -Tpdf iris.dot
```



Figure: Sklearn decision tree

[^1]
## Bibliography


[^0]:    ${ }^{1}$ Leave-one-out cross validation builds model with all elements except one

[^1]:    ${ }^{3}$ http://scikit-learn.org/stable/

