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MACHINE LEARNING IN R Research Technologies

Machine Learning with R





- The Knowledge Discovery process takes 7 steps
 - Step 1: Understand your business goal and your data
 - Step 2: Select your data
 - Step 3: Prepare and process your data
 - Step 4: Transform your data
 - Step 5: Data mining
 - Step 6: Analyze, interpret the data and patterns
 - Step 7: Knowledge creation and presentation





- STEP 1: Understand your business goal and your data
 - Depending on your specific goal, the model you choose will be different
 - Exercise: For an electronics store, what type of factors lead to high return rate?



STEP 2: <u>Select your data</u>

- Figure out which data you need to solve your problem
- This is important since preprocessing is very time consuming, you want to focus on that data that you will actually use
- There will be problems when you get to this step (guaranteed!)
 - Incompatibilities in the databases or data files
 - Data may be incomplete
 - Data may be obscure
- Note: this step can also come later (again)
- Exercise: For the electronics store return rate problem, what data can we get (existing), could we create (start collecting)?



STEP 3: Prepare and process your data

- Very time consuming
- Data can come from legacy systems or external sources
- The data will need to be
 - Cleaned, integrated
 - Selected (again)
- There will be problems/issues
 - Incomplete: missing values or aggregates only
 - Noisy: missing, duplicated, erroneous or outliers
 - Inconsistent: birthday is 1 Jan 1993, 010193, 01-01-1993
 - Intentional: default values if not specified



STEP 3: Prepare and process your data

- Nominal -> name
 - For a person: name, SSN, age, education
 - Some numbers can be used for calculation like age; and some cannot, like SSN
 - Some values are ranked: Cancer stages 1,2,3,4
- Binary -> only two values
 - Boolean: True or False, organic or inorganic
 - Symmetric: if both values are equally important
 - Asymmetric: if one is more important use 1 for more important
- Numeric
 - Scale with units of equal size
 - Values can be +, -, or 0 (0 can be nothing or something like weight or temp)
- Ratio scale
 - All characteristics of interval + true zero
 - Able to compute mean, median, standard deviation etc



- STEP 4: Transform your data
 - Different type of transformations exist
 - Feature construction = applying mathematical formulas to existing data features
 - Feature subset selection = selecting which feature to use, which database columns to use
 - Aggregating data = sometimes, you will want to use only the average, or sum, or maximum, or minimum, or other groupings (per store, region, time unit)
 - Bin the data = breaking up continuous ranging in discrete segments (e.g. per month)



- STEP 5: Data mining
- Different models exist:
 - Pattern identification and description = link analysis, market basket analysis
 - E.g. People who buy soda, usually buy chips
 - E.g. People who visit website A, usually visit website B
 - Classification, prediction = supervised learning
 - E.g. if you work hard and you are smart -> you will get an A
 - Database segmentation, clustering = unsupervised learning:
 - E.g. documents covering the same topic (e.g., for similar documents, click here)
- For each model, you can choose a method to build your model
 - Classification: decision trees, neural networks
 - Prediction: linear regression
- For each method, you need to choose the algorithm
 - E.g. decision trees: ID3, C4.5, CART



- STEP 6: Analyze, interpret the data and patterns
 - Once the model is build -> learn the implications
 - Sometimes visualization can help
 - e.g. clusters of documents, outliers
- STEP 7: Knowledge creation and presentation
 - Use other resources to understand and interpret the end product
 - Tie back to original goal



Classification of Algorithms - Based on Technique

	Characteristics	Pro	Con
Statistical Techniques e.g. regression analysis	 usually involves numbers make strong assumptions about your model, e.g. normal distribution 	 elegant, theory based usually fast to train and test accurate tools available (SPSS, SAS, Minitab) results easy to understand 	 you need to know what to apply when need to be a good statistician (not an exact art :-))
Symbolic Learning e.g. decision trees (ID3)	 roots in Al decision trees, rules no assumptions made intuitive meaningful 	 very intuitive, easy to understand fast 	 not as accurate
Connectionist = Neural Networks FF/BP, SOM	 black box approach flexible powerful combination of specialty graphs (=the data structure) + statistics 	 general purpose, can be applied to many problems can be super accurate (can also be a problem) 	 black box approach no intuitive results slow to train
Evolutionary = Genetic Algorithms	 based on 'survival of the fittest' stochastic process 	 powerful for complex problems easy to implement relatively fast 	 problem representation (translation into GA) is hard to do
Heuristics/human based	 learn from experience rules of thumb sometimes translated into expert systems 	 human judgment, insight (will be compatible) 	 variation of performance memory limitations information overload problems



Classification of Algorithms - Based on Goal

Descriptive Models

- Link Analysis
 - Apriori algorithm
- Clustering models
 - Hierarchical: Prim's and Kruskal's
 - Partitioning: K-Means
 - Density-based: DBSCAN
 - Grid-based: Self-Organizing Map (SOM)

- Predictive Models
 - Classification (predict class)
 - Naïve Bayes
 - Decision Trees: ID3, C4.5
 - Ensemble Methods: Random Forest
 - Neural Networks: FF/BP
 - Support Vector Machines
 - Regression (predict number)
- Optimization Models
 - Evolutionary programming (parallel search)
 - Genetic Algorithm (GA)



Neural Networks Relation to Biology



Figure: Structure of a typical neuron



Neural Networks





Backpropagation – the math

Output Node Error =
$$\delta 2_j = o_j (1 - o_j) (y_j - o_j)$$

Hidden Node Error = $\delta 1_j = h_j (1 - h_j) \sum_{i=1}^C \delta 2_i \times w 2_{ji}$





Artificial Neural Networks



A single perceptron (or neuron) can be imagined as a Logistic Regression. An Artificial Neural Network is a group of multiple perceptrons at each layer. ANN can be used to solve problems related to:

- Tabular data
- Image data
- Text data



Recurrent Neural Networks



A looping constraint on the hidden layer of ANN turns it into RNN. Parameter sharing results in fewer parameters to train and so reduces cost RNN can be used for problems related to: Time series, Text or Audio data



Generative Adversarial Networks



A double network with a generator that tries to fool the discriminator.

Used to generate images but also used in large particle physics on the LHC to create results close to the simulations without the very high compute cost.



Convolutional Neural Networks



A filter extracts part of the visual data and creates a 3D array or convolution which are passed to the pooling layer which reduces unnecessary features. For image recognition, first layer detects gradients, second lines, third shapes etc CNN can be used for problems related to: Image processing, Computer vision, Speech recognition







Interactive Apps	RStudio Server	
Desktops	This app will launch RStudio Server, an IDE for R, on a UAz cluster.	
🖵 Interactive Desktop	Cluster	
GUIs	ElGato Cluster	
Abaqus GUI	RStudio Server version	
Ansys Workbench GUI	R 4.2.2	
Mathematica GUI	This defines the version of the application you want to use	
🛦 Matlab GUI	Run Time	0
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🛢 Jupyter Notebook	Enter the number of cores on a single node that the job is allowed to	use.
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	GPUs required	
	0	0

Enter number of gpus needed per node, if any.

PI Group

chrisreidy

Enter an HPC PI group to be charged for time used.



RStudio Server (638047)

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Created at: 2022-03-27 09:03:00 MST

Time Remaining: 1 hour and 59 minutes

Session ID: 6183a471-561b-498d-bd0b-06531ca63348

R Connect to RStudio Server



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		autamus-notes		3.7 KB	Sep 21, 2021, 9:52 AM	
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In this exercise, download package VIM and mice. The dataset 'sleep' is included in the package VIM. It comes from a study about the sleeping pattern of 62 mammals. It wants to identify the relationships between sleep, and some physical characteristics of mammals, such as brain and body weight, life span, gestation time, time sleeping, and predation and danger indices.

install package "VIM"
install.packages("VIM") # Hint: use multiple cores. It goes much faster
To use the package in an R session, we need to load it in an R session via
library()
library()

library(VIM)

Load dataset "sleep", which comes within the package "VIM"
data(sleep, package ="VIM")

call function head() to get a feeling about data, or call sleep to see all values head(sleep)

download package "mice" and load it into R
install.packages("mice")
library(mice)



In R, we use "NA" stands for missing value; NaN(Not a Number) stands for an impossible value; And symbol "Inf" and "-Inf" stands for infinity and negative infinity respectively. In order to tell whether a value belongs to any case above, we use function is.na(), is.nan(), and is.infinite(). The return value of each function is Boolean

First, we need to know how many rows in "sleep" nrow(sleep) ## [1] 62 # We use complete.cases() or na.omit() to see tuples without missing value. sleep[complete.cases(sleep),] *# or try* na.omit(sleep) *# Count the number of rows without missing value* nrow(sleep[complete.cases(sleep),]) ## [1] 42 # To reverse the condition logic (rows containing one or more missing value), we use the exclamation mark highlighted in Red sleep[!complete.cases(sleep),] nrow(sleep[!complete.cases(sleep),]) ## [1] 20 OF ARIZONA

We tell R a Boolean value by inputting a TRUE or a FALSE. However, R can treat them as integer 1 or 0 respectively, which means information about missing value can be captured by using function sum() and mean().

Check how many observations contain missing value in column "Dream"
sum(is.na(sleep\$Dream))
[1] 12
About 19% of obs (observations) in column Dream contain missing value
mean(is.na(sleep\$Dream))
[1] 0.1935484
32% obs in data frame sleep containing one or more missing value
mean(!complete.cases(sleep))
[1] 0.3225806



Checking missing values is important, but little information about distribution and pattern can be observed via functions we called above. It will be a convenient alternative if we can see how the missing values distribute in datasets. To do so, we can use the function md.pattern() to generate a matrix that shows the pattern of missing value.

call function md.pattern(). Make sure you loaded package mice into R first md.pattern(sleep)

Body	yWgt	BrainWgt	Pred	Exp	Danger	Sleep	Span	Gest	Dream	NonD
	42	1	1	1	1	1 1	1	1	1	<u>1 0</u>
	2	1	1	1	1	1 1	0	1	1	<u>1 1</u>



Exercise: Visualization – aggr

Instead of seeing the sleep data in table via function md.pattern(), a visualization usually makes more sense to users. The package VIM provides several functions that visualize the pattern of missing values. Here we will apply aggr(), to our dataset.

call function aggr (), prop = FALSE convert percentage value into counts
aggr(sleep, prop = FALSE, numbers = TRUE)







Exercise: Visualization - marginplot

Function marginplot() returns a scatter chart, where we can observe the relationship between two variables.





Exercise: Visualization - boxplot

Load dataset mtcars into R and show relationship between mpg and # of cylinders



Exercise: Visualization – violin plot

A **violin plot** provides a comprehensive chart that combines information in box plot and density distribution.



Exercise: Visualization – scatter plot

Using mtcars again we apply dot plot to check how each observation is distributed in a given sample space.

plot(mpg ~ wt, data = mtcars)





Exercise: Visualization – violin plot

The outline of a violin chart indicates the density of distribution. The black bar at center tells the IQR of distribution.





Installing Packages

In the Mushroom dataset, there are 8123 observations belonging to 23 species of gilled mushrooms in the Agaricus and Lepiota Family. There are two types of mushroom in terms of edibility. If classes=e, the mushroom is edible, if classes=p, the mushroom is poisonous. We want to tell which mushrooms are edible from those poisonous by looking at some of their characteristics. Source: University of California Irvine

View working directory then set working directory

getwd()
setwd('/xdisk/chrisreidy/workshops')

• e1071 – This is the dataset we are going to use.

install.packages('e1071') library(e1071)



Preprocessing

Save Mushroom.csv under your working directory. The null value in mushroom dataset is denoted by question mark.

```
# read in csv file mushroom.csv. Note the question mark
represents null value
mushroom <- read.csv("Mushroom.csv", na.strings = "?")
summary(mushroom)</pre>
```

check completion
nrow(mushroom[!complete.cases(mushroom),])
[1] 2480



Preprocessing

Naive Bayes is an algorithm that depends on probability. To predict a conditional probability, we have to figure out the prior probability of each predictive variables. Therefore, a dataset with null value will raise risk for our prediction

we can retain observations that do not contain NA(null) value
mushroom = mushroom[complete.cases(mushroom),]



Training and testing sets

Next, we will create train and test sets of the data. We will fit the model with the training set, and use the test set to evaluate the model. We will do a 70/30 split (70% will be training data).

```
# 70% of original data will be used for training
sample_size <- floor(0.7 * nrow(mushroom))
# randomly select index of observations for training
training_index <- sample(nrow(mushroom), size = sample_size,
replace = FALSE)
train <- mushroom[training_index,]
test <- mushroom[-training_index,]</pre>
```



Fitting and Model Performance

There is a Naive Bayes classifier in the e1071 package, loaded into our current session already via function library (e1071). Fit the model to the training data.

note the period coming after tilde. It means all the other variables in that dataset will be predictive variable mushroom.model <- naiveBayes(classes ~ . , data = train) # We can explore the detail conditional probabilities for each variables by calling the object mushroom.model itself. mushroom.model



Fitting and Model Performance

After fitting, run the test data through the model to get the predicted class for each observation.

The result of prediction, a vector, will be attached to test set labelled as "class". The return of prediction is a vector including predicted type of mushroom mushroom.predict <- predict(mushroom.model, test, type = "class")</pre>



Fitting and Model Performance

Show the performance of the model.

pick actual value and predicted value together in a dataframe called results results <- data.frame(actual = test[,'classes'], predicted = mushroom.predict) # We can get a popular matrix called confusion matrix table(results) # columns indicate the number of mushrooms in actual type; likewise, rows indicate the number those in predicted type. predicted actual edible poisonous edible TN=1067 FP= 2 poisonous FN= 46 TP=580



Installing Packages

For this example, we need to install package ISLR. The data we will use is a built-in dataset of ISLR called College Data Set. It has several features of a college and a categorical column indicating whether or not the School is Public or Private.

- ISLR This is the dataset we are going to use.
- caTools We will use the caTools package to randomly split the data into a training set and test set.
- neuralnet This package contains the function about neural network neuralnetwork().

install.packages('ISLR')
install.packages('caTools')
install.packages('neuralnet')



Loading Data

Install package ISLR, which is a dataset package and contains data we will use - College.

library(ISLR)					
	Private	Apps	Accept	Enroll	Top10perc
Abilene Christian University	Yes	1660	1232	721	23
Adelphi University	Yes	2186	1924	512	16
Top	25perc F	.Under	grad P.L	Jndergi	rad Outstate
Abilene Christian University	52	2885	537	7	7440
Adelphi University	29	2683	1227	7	12280
Room.Board Books Personal PhD Terminal					
Abilene Christian University	3300	450	2200	70	78
Adelphi University	6450	750	1500	29	30
S.F.Ratio per	rc.alumn	i Exper	nd Grad.	Rate	



Preprocessing

It is important to normalize data before training a neural network on it. The neural network may have difficulty converging before the maximum number of iterations allowed if the data is not normalized. There are a lot of different methods for normalization of data.

Normally it is better to scale the data from 0 to 1, or -1 to 1. We can specify the center and scale as additional arguments in the scale() function. For example:

Create Vector of Column Max and Min Values maxs <- apply(College[,2:18], 2, max) mins <- apply(College[,2:18], 2, min)

Use scale() and convert the resulting matrix to a data frame scaled.data <- as.data.frame(scale(College[,2:18], center = mins, scale = maxs - mins))



Preprocessing - continued

Check out results
print(head(scaled.data,2))

Enroll Apps Accept Abilene Christian University 0.03288692646 0.04417701272 0.10791253736 Adelphi University 0.04384229271 0.07053088583 0.07503539405 Top10perc Top25perc F.Undergrad Abilene Christian University 0.2315789474 0.4725274725 0.08716353479 Adelphi University 0.1578947368 0.2197802198 0.08075165058 P.Undergrad Outstate Room.Board Abilene Christian University 0.02454774445 0.2634297521 0.2395964691 Adelphi University 0.05614838562 0.5134297521 0.7361286255 Books Personal PhD Abilene Christian University 0.1577540107 0.2977099237 0.6526315789 Adelphi University 0.2914438503 0.1908396947 0.2210526316 Terminal S.F.Ratio perc.alumni Abilene Christian University 0.71052631579 0.4182305630 0.1875 Adelphi University 0.07894736842 0.2600536193 0.2500 HE UNIVERSITY

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Train and Test Split

Let us now split our data into a training set and a test set. We will run our neural network on the training set and then see how well it performed on the test set.

We will use the caTools package to randomly split the data into a training set and test set.

```
# Convert Private column from Yes/No to 1/0
Private = as.numeric(College$Private)-1
data = cbind(Private, scaled.data)
```

library(caTools)
set.seed(101) # sets random numbers

Create Split (any column is fine)
split = sample.split(data\$Private, SplitRatio = 0.70)

Split based off split Boolean Vector
train = subset(data, split == TRUE)
test = subset(data, split == FALSE)



Neural Network Function

Before we actually call the function, we need to create a formula to insert into the machine learning model. The neuralnetwork() function won't accept the typical decimal R format for a formula involving all features (e.g. y \sim .). However, we can use a simple script to create the expanded formula and save us some typing:

```
feats <- names(scaled.data)

# Concatenate strings

f <- paste(feats,collapse=' + ')

f <- paste('Private ~', f)

# Convert to formula

f <- as.formula(f)

f

## Private ~ Apps + Accept + Enroll + Top10perc + Top25perc + F.Undergrad +

## P.Undergrad + Outstate + Room.Board + Books + Personal +

## PhD + Terminal + S.F.Ratio + perc.alumni + Expend + Grad.Rate
```

```
library(neuralnet)
nn <- neuralnet(f, train, hidden = c(10,10,10), linear.output = FALSE)</pre>
```





Predictions and Evaluations

Now let's see how well we performed! We use the compute() function with the test data (just the features) to create predicted values. This returns a list from which we can call net.result

Compute Predictions off Test Set
predicted.nn.values <- compute(nn, test[2:18])</pre>

Check out net.result
print(head(predicted.nn.values\$net.result))

	[,1]
Adrian College	1
Alfred University	1
Allegheny College	1
Allentown Coll. of St. Francis de Sales	1
Alma College	1
Amherst College	1





Predictions and Evaluations

Notice we still have results between 0 and 1 that are more like probabilities of belonging to each class. We'll use sapply() to round these off to either 0 or 1 class so we can evaluate them against the test labels.

Now let's create a simple confusion matrix:

table(test\$Priva	ate, predicted.nn.	values\$net.result)
Actual No Actual Yes	Predicted No TN = 55 FN = 6	Predicted Yes FP = 9 TP = 163



Visualize

We can visualize the Neural Network by using the plot(nn) command. The black lines represent the weighted vectors between the neurons. The blue line represents the bias added. Unfortunately, even though the model is clearly a very powerful predictor, it is not easy to directly interpret the weights. This means that we usually have to treat Neural Network models more like black boxes.







Exercise: Accuracy Terminology

	Predicted No	Predicted Yes
Actual No	TN = 55	FP = 9
Actual Yes	FN = 6	TP = 163

Starting with the confusion matrix:

- True Positive is bottom right cell divided by sum of bottom row
- TP is also called Sensitivity or Recall or "did I correctly predict positive?"
- True Negative is top left divided by sum of top row; also called Specificity
- FP <- 1 TN
- FN <- 1 TP : Percent of observations in negative class
- Precision is True Positive / Total Positive
- F <- 2 * precision * recall / (precision + recall) aka balanced mean
- Receiver Operating Characteristic Curve (ROC) measures Sensitivity (TP) to Specificity (TN). Visually, closer to right angle is better than diagonal.

