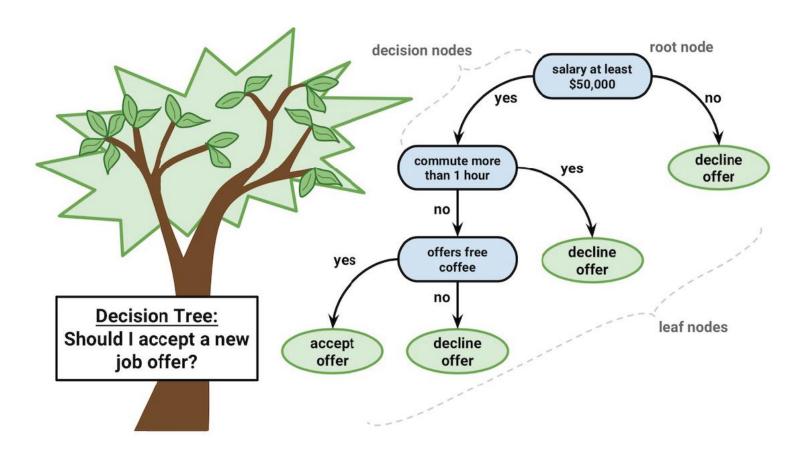
Memorization Method - part 2

Contents

- Decision Tree
- K-nearest neighbor
- Naïve Bayes

Decision Tree

Decision Tree Model



Before accepting a job offer, You may consider several conditions

Tree model organizes the conditions to make a decision

Conditions are organized from most significant condition to less significant ones

Loan Applications



considering:
amount of loan
purpose
credit history
income

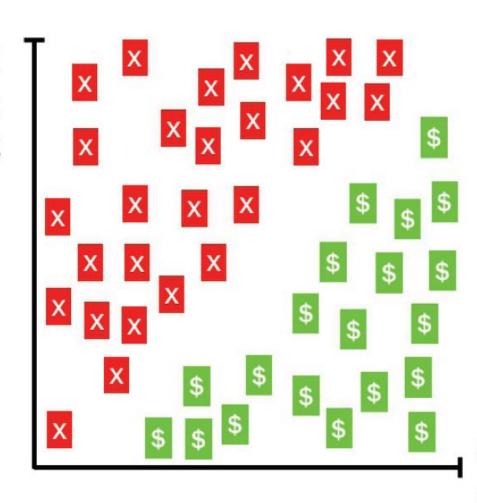
Decide: approve or decline

decision tree model is useful when deciding process is better to be interpretable and hence transparent

Divide and Conquer

requested loan amount

- x default
- s repaid

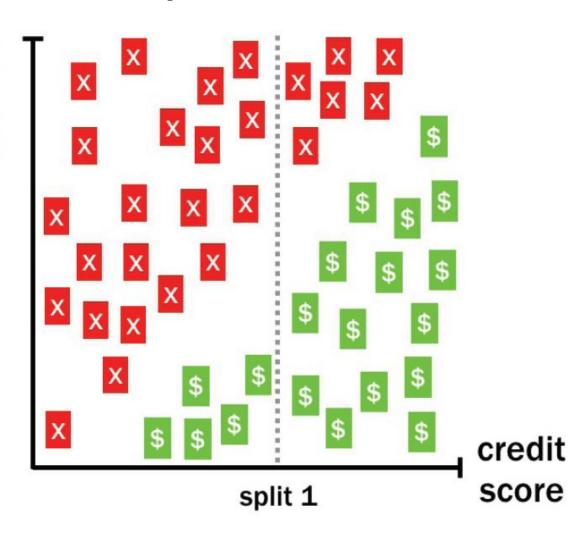


credit score

Divide and Conquer

requested loan amount

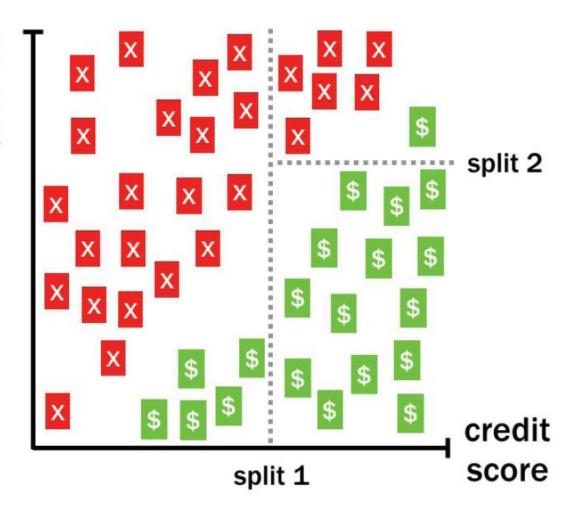
- x default
- \$ repaid



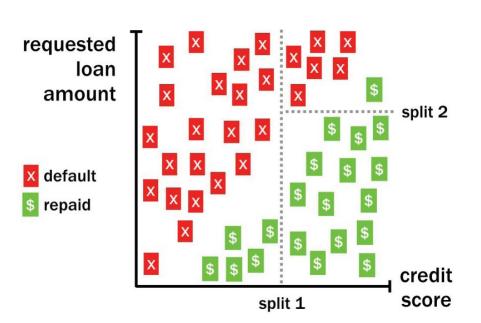
Divide and Conquer

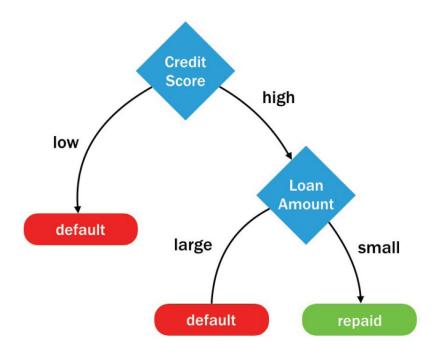
requested loan amount

- x default
- \$ repaid



The resulting tree





Building a simple decision tree

```
load(url('https://github.com/hbchoi/SampleData/blob/master/dtree data.RData?raw=true'))
str(loans)
## 'data.frame':
                    11312 obs. of 14 variables:
                        : Factor w/ 3 levels "HIGH", "LOW", "MEDIUM": 2 2 2 3 2 3 3 2 1 3 ...
    $ loan amount
## $ emp length
                        : Factor w/ 5 levels "< 2 years", "10+ years", ...: 2 1 4 3 1 1 3 2 2 1 ...
                        : Factor w/ 4 levels "MORTGAGE", "OTHER", ...: 4 4 4 3 4 4 4 1 4 4 ...
## $ home ownership
## $ income
                        : Factor w/ 3 levels "HIGH", "LOW", "MEDIUM": 2 2 3 3 2 2 1 1 1 3 ...
## $ loan purpose
                        : Factor w/ 14 levels "car", "credit card", ...: 2 1 1 12 10 3 10 7 3 7 ...
                        : Factor w/ 3 levels "AVERAGE", "HIGH", ...: 2 3 3 3 1 1 3 1 1 3 ...
   $ debt to income
                        : Factor w/ 3 levels "AVERAGE", "HIGH", ...: 1 1 3 1 1 1 1 2 1 1 ...
   $ credit score
                        : Factor w/ 2 levels "NO", "YES": 2 2 2 2 1 2 2 1 1 2 ...
   $ recent inquiry
##
                        : Factor w/ 3 levels "IN PAST 2 YEARS",..: 3 3 3 3 3 3 3 3 3 ...
## $ delinquent
                        : Factor w/ 3 levels "AVERAGE", "FEW", ...: 2 2 2 1 2 2 3 3 1 1 ...
## $ credit accounts
## $ bad public record : Factor w/ 2 levels "NO", "YES": 1 1 1 1 1 1 1 1 1 1 ...
   $ credit utilization: Factor w/ 3 levels "HIGH","LOW","MEDIUM": 1 2 1 3 3 1 3 2 1 3 ...
   $ past bankrupt
                        : Factor w/ 2 levels "NO", "YES": 1 1 1 1 1 1 1 1 1 1 ...
                        : Factor w/ 2 levels "default", "rapid": 2 1 2 1 1 1 1 2 1 1 ...
   $ outcome
```

The **loans** dataset contains 11,312 randomly-selected people who were applied for and later received loans from Lending Club, a US-based peer-to-peer lending company.

Building a simple decision tree

```
library(rpart)
loan model <- rpart(outcome ~ loan amount + credit score, data = loans, method = "class",</pre>
control = rpart.control(cp = 0))
# Examine the loan model object
loan model
## n= 11312
##
## node), split, n, loss, yval, (yprob)
         * denotes terminal node
##
##
##
   1) root 11312 5654 rapid (0.4998232 0.5001768)
##
      2) credit score=AVERAGE,LOW 9490 4437 default (0.5324552 0.4675448)
        4) credit score=LOW 1667 631 default (0.6214757 0.3785243) *
##
        5) credit score=AVERAGE 7823 3806 default (0.5134859 0.4865141)
##
         10) loan amount=HIGH 2472 1079 default (0.5635113 0.4364887) *
##
##
         11) loan amount=LOW, MEDIUM 5351 2624 rapid (0.4903756 0.5096244)
           22) loan amount=LOW 1810 874 default (0.5171271 0.4828729) *
##
           23) loan amount=MEDIUM 3541 1688 rapid (0.4767015 0.5232985) *
##
      3) credit score=HIGH 1822 601 rapid (0.3298573 0.6701427) *
##
```

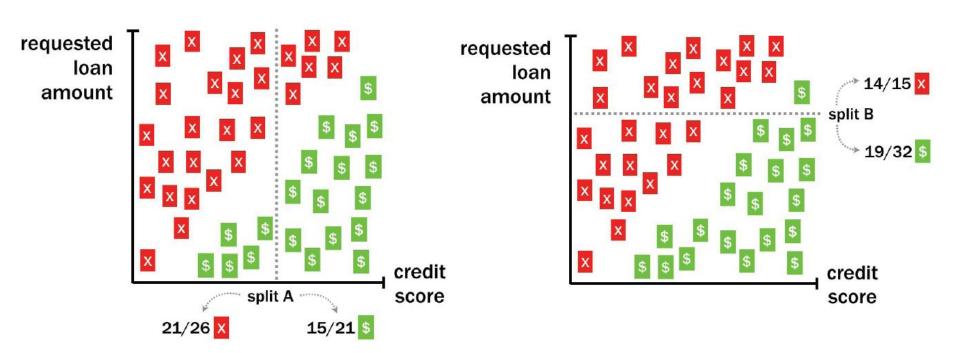
We will build a decision tree to try to learn patterns in the outcome of these loans (either repaid or default) based on the requested loan amount and credit score at the time of application.

Visualizing the Model

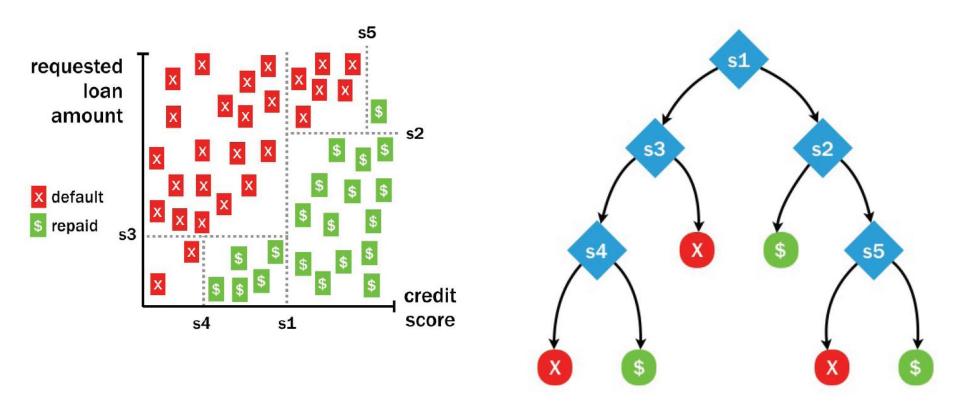
Load the rpart.plot package

```
library(rpart.plot)
# Plot the loan model with default settings
rpart.plot(loan model)
# Plot the loan_model with customized settings
rpart.plot(loan model, type = 3, box.palette = c("red", "green"), fallen.leaves = TRUE)
                                                                     credit_score = AVERAGE,LOW
                                  0.50
                                  100%
                                                                                                                   HIGH
                      yes -credit_score = AVERAGE,LOW - no
             default
                                                              credit_score = LOW
              0.47
                                                                                       AVFRAGE
         credit_score = LOW-
                        default
                         0.49
                                                                          loan_amount = HIGH
                         69%
                                                                                              LOW, MEDIUM
                    loan_amount = HIGH
                                   0.51
                                                                                      loan_amount = LOW
                              Ioan_amount = LOW
                                                                                                      MEDIUM
                                                                                                        rapid
  default
               default
                            default
                                         rapid
                                                      rapid
                                                                                0.44
                                                                                            0.48
                                                                                                        0.52
                                                                                                                   0.67
                                         0.52
                                                      0.67
   0.38
               0.44
                            0.48
                                                                     15%
   15%
```

Choosing where to split



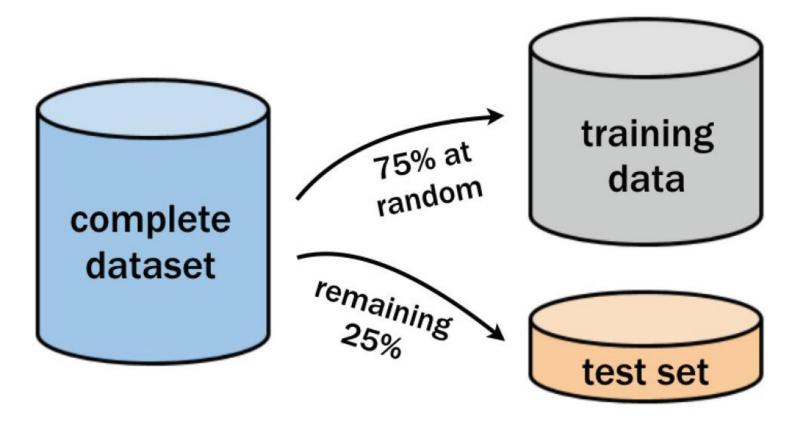
The problem of overfitting



Some over-grown decision trees capture errors that is too specific to the training dataset, which cannot be observed in general cases

Predicting very well on training data does not always guarantee that work well in the real world problem.

Evaluating model performance



performance on train data >> perf. on test data performance on train data \approx perf. on test data

=> => high likely to be over-fitted less likely to be over-fitted

We should limit the **complexity** somehow to avoid **overfitting problem**

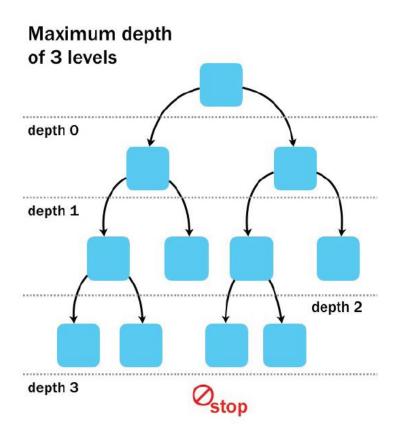
```
loan model <- rpart(outcome ~ ., data = loans train, method = "class", control = rpart.control(cp = 0))</pre>
# Make predictions on the training dataset
loans train$pred <- predict(loan model, loans train, type = 'class')</pre>
# Examine the confusion matrix
table(loans train$outcome, loans train$pred)
##
             default rapid
##
    default
               2932 1269
##
##
    rapid
               1084 3199
# Compute the accuracy on the training dataset
mean(loans train$outcome == loans train$pred)
## [1] 0.7226544
# Make predictions on the test dataset
loans test$pred <- predict(loan model, loans test, type = 'class')</pre>
# Examine the confusion matrix
                                                     Lending Club has additional information about
table(loans test$outcome, loans test$pred)
                                                     the applicants, such as home ownership status,
##
                                                     length of employment, loan purpose, and past
             default rapid
##
    default
                 821
                      632
##
                                                     bankruptcies, that may be useful for making
    rapid
                 546
                      829
##
                                                     more accurate predictions.
# Compute the accuracy on the test dataset
                                                     Using all of the available applicant data, we
mean(loans test$outcome == loans test$pred)
                                                     build a more sophisticated lending model using
## [1] 0.5834512
                                                     the training dataset and test the model on
loans train <- loans train[-15]</pre>
                                                     training and test datasets.
```

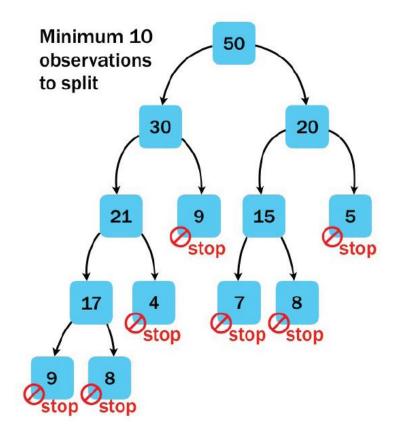
loans test <- loans test[-15]</pre>

Limiting Tree Model's Complexity

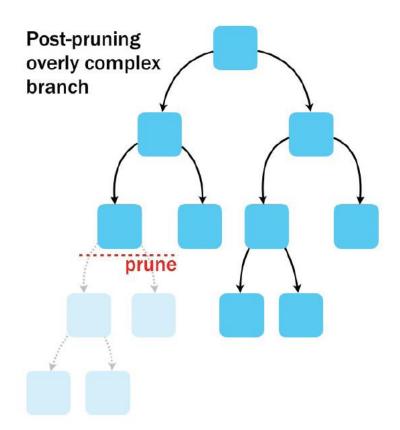
- Two Approaches
 - Pre-pruning
 - Restrict complexity before growing the model
 - Post-Pruning
 - Cut out two complex branches after having tree model

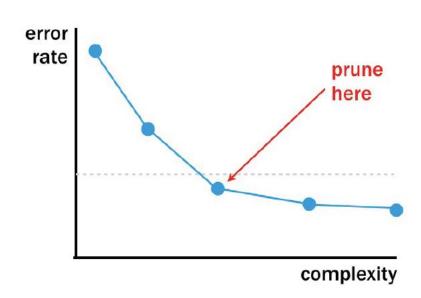
Pre-pruning





Post-pruning





Pre-pruning

```
# Grow a tree with maxdepth of 6
loan model <- rpart(outcome ~ ., data = loans train, method = "class",</pre>
control = rpart.control(cp = 0, maxdepth = 6))
# Compute the accuracy of the simpler tree
loans_test$pred <- predict(loan_model, loans_test, type = 'class')</pre>
mean(loans test$outcome == loans test$pred)
## [1] 0.5919378
# Grow a tree with minsplit of 500
loan model2 <- rpart(outcome ~ ., data = loans train, method =</pre>
"class", control = rpart.control(cp = 0, minsplit = 500))
# Compute the accuracy of the simpler tree
loans test$pred2 <- predict(loan_model2, loans_test, type = 'class')</pre>
mean(loans test$outcome == loans test$pred2)
## [1] 0.5922914
```

Post-pruning

```
# Grow an overly complex tree
loan model <- rpart(outcome ~ ., data = loans train, method = "class", control =
rpart.control(cp = 0))
                                                           size of tree
                                                1 6 18 36 54 89 155 262 373 440
# Examine the complexity plot
                                                plotcp(loan_model)
                                         K-val Relative Error
                                            0
                                            ത
                                            O
                                            8
                                                Inf 0.004 0.0014 0.00069 0.00034 8.7e-05
# Prune the tree
                                                              cp
loan model pruned <- prune(loan model, cp = 0.0014)</pre>
# Compute the accuracy of the pruned tree
loans_test$pred <- predict(loan_model_pruned, loans_test, type = 'class')</pre>
mean(loans test$outcome == loans test$pred)
## [1] 0.6007779
```

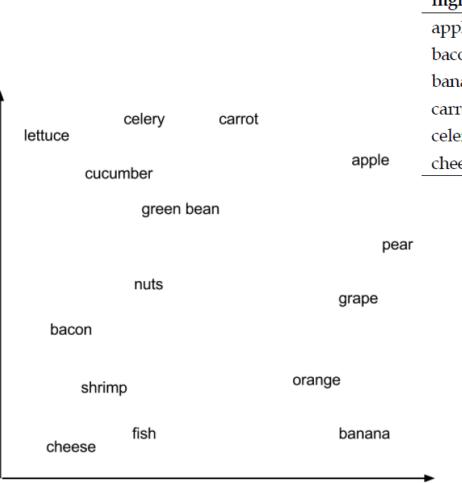
Ref.

- rpart manual: https://cran.r-project.org/web/packages/rpart/rpart.pdf
- An Introduction to Recursive Partitioning Using the RPART Routines:
 https://cran.r-project.org/web/packages/rpart/vignettes/longintro.pdf
- Plotting rpart trees with the rpart.plot package:
 http://www.milbo.org/rpart-plot/prp.pdf

k Nearest Neighbors

how crunchy the food is

k-Nearest Neighbors (kNN)



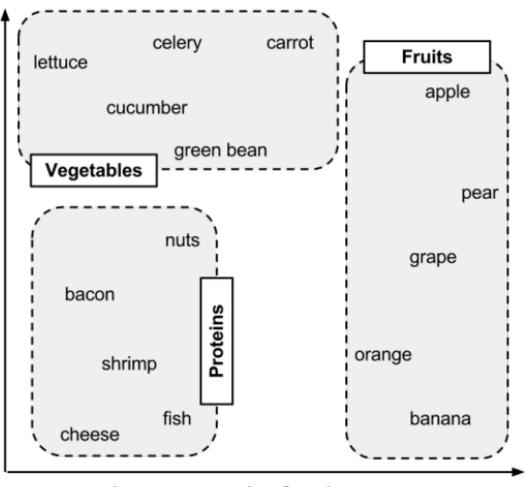
ingredient	sweetness	crunchiness	food type
apple	10	9	fruit
bacon	1	4	protein
banana	10	1	fruit
carrot	7	10	vegetable
celery	3	10	vegetable
cheese	1	1	protein

Similar Foods are located near to each other geographically

how sweet the food tastes

how crunchy the food is

k-Nearest Neighbors (kNN)



Similar Foods are located near to each other geographically

how sweet the food tastes

k-Nearest Neighbors (kNN)

celery carrot Fruits lettuce apple cucumber how crunchy the food is green bean Vegetables pear nuts grape bacon Proteins tomato orange shrimp fish banana cheese

Then what is tomato?

Tomato is close to green bean, nuts, orange, and graph

1 Veg, 1 Protein, 2 Fruits

We may consider tomato belongs to Fruits class

how sweet the food tastes

k-Nearest Neighbors (kNN)

celery carrot Fruits lettuce apple cucumber how crunchy the food is green bean Vegetables pear nuts grape bacon Proteins tomato orange shrimp fish banana cheese

how sweet the food tastes

In kNN method, we decide according to most similar examples = nearest neighbors

Majority class would be our answer

The portion could be estimated probability

How many neighbors do we need to consider?

k -> # of neighbor to be consider
for classification (or regression)

Measuring similarity with distance

distance between object p and q

Euclidean distance

$$\sqrt{(p_1-q_1)^2+(p_2-q_2)^2+\cdots+(p_d-q_d)^2}$$

 $p_1, p_2, ..., p_d$ and $q_1, q_2, ..., q_d$ are feature sets of p and q

Other distance measures:

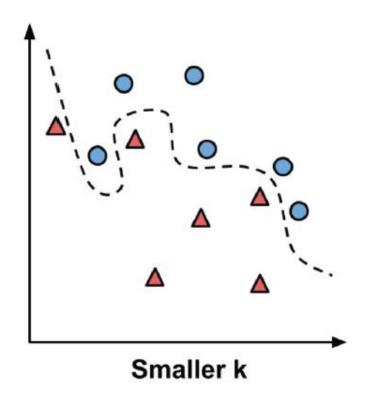
Manhattan distance, Cosign Similarity, Minkowski, ...

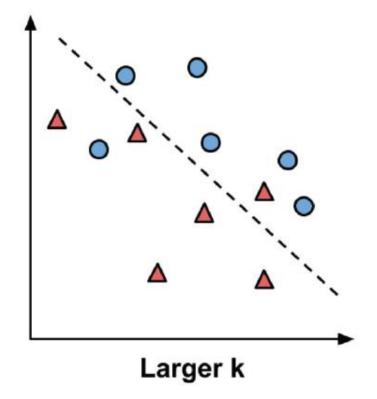
Applying nearest neighbors in R

```
library(class)
pred <- knn(training data, testing data, training labels)</pre>
```

Choosing k

Bigger 'k' is not always better





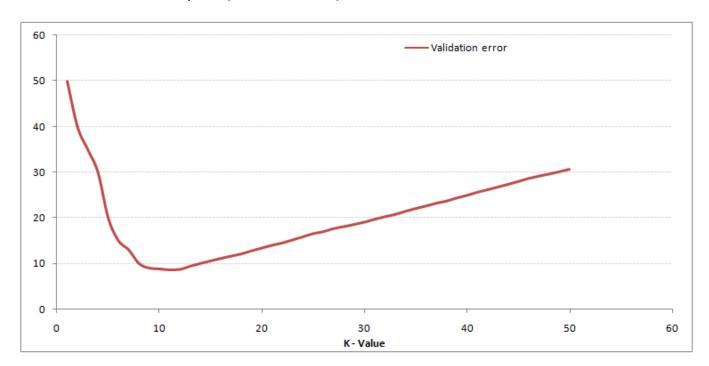
Choosing k

There is no right k for all the problems

You may try different k to find the best

Suggesting square root of # of training examples, empirically

When a certain class is very rare, larger k would be better to see sufficient number of example (about 10?) in each class



kNN – example

- Diagnosing Breast Cancer with KNN
- "Breast Cancer Wisconsin Diagnostic" dataset from the *UCI Machine Learning Repository*
 - 30 numeric measurements comprise the mean, standard error,
 and worst (that is, largest) value for 10 different characteristics
 of the digitized cell nuclei.

Radius

Texture

Perimeter

Area

Smoothness

Compactness

Concavity

Concave points

Symmetry

Fractal dimension

Loading Data

```
wbcd <- read.csv("https://github.com/hbchoi/SampleData/raw/master/wisc bc data.csv",</pre>
stringsAsFactors = F)
str(wbcd)
## 'data.frame': 569 obs. of 32 variables:
## $ id
                      : int 87139402 8910251 905520 868871 9012568 906539 925291
87880 862989 89827 ...
                             "B" "B" "B" "B" ...
   $ diagnosis
                      : chr
## $ radius mean : num 12.3 10.6 11 11.3 15.2 ...
## $ texture mean : num 12.4 18.9 16.8 13.4 13.2 ...
   $ perimeter mean : num 78.8 69.3 70.9 73 97.7 ...
                      : num 464 346 373 385 712 ...
##
   $ area mean
   $ points worst
                      : num 0.0939 0.0793 0.0743 0.0861 0.0818 ...
##
   $ symmetry worst : num 0.283 0.294 0.3 0.21 0.249 ...
##
   $ dimension worst
                             0.0677 0.0759 0.0788 0.0678 0.0677 ...
                      : num
```

Data Preparation

Var. ID is not helpful to determine the type of tumor, hence remove it

```
# removing ID variable
wbcd <- wbcd[,-1]

table(wbcd$diagnosis)

##
## B M
## 357 212

# changing value for clear interpretation
wbcd$diagnosis <- ifelse(wbcd$diagnosis == 'B', 'Benign', 'Malignant')</pre>
```

Normalization

Var. in larger scale contributes more to the distance than Var. in smaller scale e.g. area_mean has bigger effect on Euclidean distance than smoothness_mean

Having all variables in same scale is important preprocessing for kNN

- normalization

```
summary(wbcd[c("radius_mean", "area_mean", "smoothness_mean")])
```

```
radius mean
                                 smoothness mean
##
                    area mean
   Min. : 6.981
                  Min. : 143.5 Min.
                                        :0.05263
##
##
   1st Qu.:11.700
                  1st Qu.: 420.3
                                 1st Qu.:0.08637
##
   Median :13.370
                  Median: 551.1 Median: 0.09587
##
   Mean :14.127
                  Mean: 654.9 Mean
                                       :0.09636
                  3rd Qu.: 782.7
   3rd Qu.:15.780
                                 3rd Qu.:0.10530
##
   Max. :28.110
                  Max. :2501.0
                                 Max. :0.16340
##
```

min-max normalization

setting the scale of variables to 0~1

0 for minimum value, 1 for maximum value minmax norm <- function(x) {</pre> (x-min(x))/(max(x)-min(x))wbcd norm <- sapply(wbcd[,-1], minmax norm)</pre> summary(wbcd_norm[,c("radius_mean", "area_mean", "smoothness_mean")]) radius mean area_mean smoothness mean ## Min. :0.0000 Min. :0.0000 Min. :0.0000 ## 1st Qu.:0.2233 1st Qu.:0.3046 1st Qu.:0.1174 ## Median :0.3024 Median :0.1729 Median :0.3904 ## ## Mean :0.3382 Mean :0.2169 Mean :0.3948 ## 3rd Qu.:0.4164 3rd Qu.:0.2711 3rd Qu.:0.4755 ## Max. :1.0000 Max. :1.0000 Max. :1.0000

kNN – split test and training data

```
# split data into train and test set
dim(wbcd norm)
## [1] 569 30
wbcd_train <- wbcd_norm[1:469, ]</pre>
wbcd_test <- wbcd_norm[470:569, ]</pre>
wbcd train label <- wbcd[1:469, 1]
wbcd test label <- wbcd[470:569, 1]
# choosing proper k
sqrt(nrow(wbcd train))
## [1] 21.65641
```

kNN – Making Prediction

library(class)

```
wbcd test pred <- knn(train = wbcd_train, test = wbcd_test, cl = wbcd_train_label,
k = 21
wbcd test pred
    [1] Benign
                Malignant Benign Benign
                                             Malignant Benign
                                                                Malignant
##
    [8] Benign Malignant Benign
                                                      Malignant Malignant
##
                                    Malignant Benign
   [15] Benign Benign
                          Malignant Benign
                                             Malignant Benign
                                                                Malignant
##
    [22] Malignant Malignant Malignant Benign
                                             Benign
                                                       Benign
                                                                Benign
##
   [29] Malignant Malignant Malignant Malignant Malignant Malignant Benign
##
   [36] Benign
                 Benign
                           Benign
                                    Benign
                                             Malignant Malignant Benign
##
   [43] Malignant Malignant Benign Malignant Malignant Malignant Malignant
##
##
   [50] Malignant Malignant Benign
                                    Benign
                                             Benign
                                                       Benign
                                                                Benign
   [57] Benign
                 Benign
                           Malignant Benign
                                             Benign
                                                       Benign
                                                                Benign
##
   [64] Benign
               Malignant Malignant Benign
                                             Benign
                                                       Benign
                                                                Benign
##
                                    Benign
   [71] Benign
               Malignant Benign
                                             Malignant Malignant Benign
##
   [78] Benign Benign Malignant Benign
                                             Benign
                                                       Benign
                                                                Malignant
##
   [85] Benign
                 Benign Malignant Benign
                                             Benign
                                                       Benign
                                                                Benign
##
   [92] Malignant Benign
##
                           Benign
                                    Benign
                                             Benign
                                                       Benign
                                                                Malignant
   [99] Benign
                 Malignant
## Levels: Benign Malignant
```

Performance

```
#accuracy
mean(wbcd_test_label == wbcd_test_pred)
## [1] 0.98
#confusion matrix
cmat <- table(wbcd_test_label, wbcd_test_pred)</pre>
cmat
##
                  wbcd test pred
## wbcd test label Benign Malignant
##
         Benign
                        61
         Malignant
                                  37
##
#precision
cmat[2,2] / sum(cmat[,2])
## [1] 1
#recall
cmat[2,2] / sum(cmat[2,])
## [1] 0.9487179
 We hope to avoid false negative rather than false positive.
 How can?
```

kNN – Probabilistic Interpretation

```
wbcd test pred <- knn(train = wbcd train, test = wbcd test, cl = wbcd train label, k =
21, prob = TRUE)
head(wbcd test pred)
## [1] Benign
                Benign Benign
                                  Benign Malignant Benign
## Levels: Benign Malignant
head(attributes(wbcd test pred)$prob)
## [1] 1.000000 0.952381 0.952381 0.952381 1.000000
                                                          1.000000
     P(Benign) P(Benign) P(Benign) P(Malignant) P(Benign)
# converting all Prob to P(Malignant)
wbcd test pred prob <- ifelse(wbcd test pred == 'Malignant',
                             attributes(wbcd test pred)$prob,
                             1-attributes(wbcd test pred)$prob)
head(wbcd test pred prob)
## [1] 0.00000000 0.04761905 0.04761905 0.04761905 1.00000000 0.00000000
```

ROC curve and AUC

```
library(ROCR)
plot(performance(prediction(wbcd_test_pred_prob, wbcd_test_label == 'Malignant'),
'tpr', 'fpr'))
calAUC <- function(predCol, targetCol){</pre>
  perf <- performance(prediction(predCol, targetCol), 'auc')</pre>
  as.numeric(perf@y.values)
# AUC for our kNN
calAUC(wbcd test pred prob, wbcd test label == 'Malignant')
## [1] 0.9964271
                                     \infty
                                 True positive rate
                                     0
                                     9.0
                                     4.
                                     Ŋ
                                     0
                                     0.0
                                        0.0
                                               0.2
                                                      0.4
                                                             0.6
                                                                    8.0
                                                                           1.0
                                                    False positive rate
```

Adjusting Threshold

```
# set Lower threshold
threshold <- 0.1
wbcd test pred new <- ifelse(wbcd test pred prob > threshold,
                              'Malignant', 'Benign')
cmat <- table(wbcd test label, wbcd test pred new)</pre>
cmat
##
                  wbcd test pred new
## wbcd_test_label Benign Malignant
         Benign
##
                       54
         Malignant
                        0
                                  39
##
#accuracy
mean(wbcd test_label == wbcd_test_pred_new)
## [1] 0.93
#precision
cmat[2,2] / sum(cmat[,2])
## [1] 0.8478261
                                           Accuracy is lower,
#recall
cmat[2,2] / sum(cmat[2,])
                                           but zero false negative!
## [1] 1
```

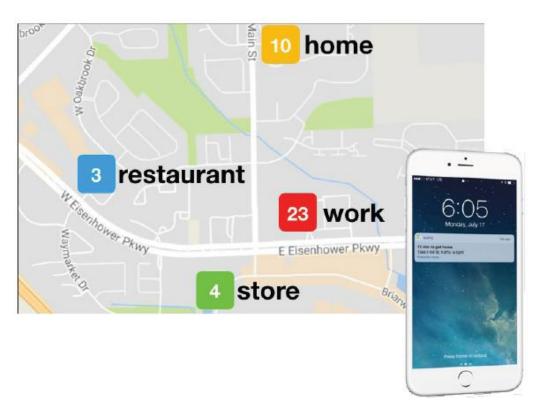
One more Thing

Euclidean distance makes sense only when input variables are numeric

-> Non-numeric Variables need to be converted to numeric, i.e. *dummy coding*

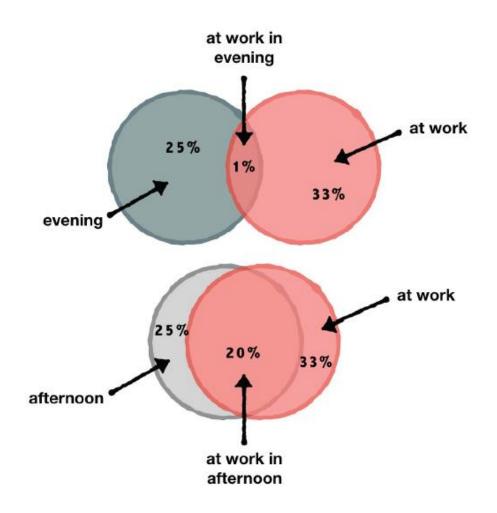
```
##
                                     blood type.A blood type.AB blood type.B blood type.O skin color.black
sample df
                                ## 1
                                ## 2
     blood type skin color age
##
                                ## 3
## 1
                     black 22
                                ## 4
                     white
                           35
## 2
                                ## 5
                                                                                                          1
                    yellow
                            21
## 3
                                     skin color.red skin color.white skin color.yellow
                       red
                            26
## 4
              0
                                ## 1
                     black 70
## 5
             AB
                                ## 2
                                ## 3
                                ## 4
                                ## 5
         dummy encoding
```

Estimating probability



The **probability** of A is denoted P(A)

Joint probability and independent events



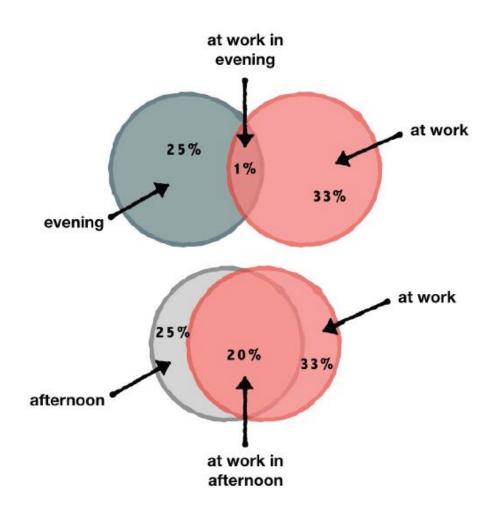
The **joint probability** of events A and B is denoted P(A and B)

- P(work and evening) = 1%
- P(work and afternoon) = 20%

Event A and B are **independent**-> occurring A does not affect P(B)
and vice versa
P(evening) = 25%
p(weekend) = 28.5%

then P(evening and weekend) = P(evening) x p(weekend) = 7.1%

Conditional probability and dependent events



The conditional probability of events A and B is denoted **P(A | B)** P(A | B) = P(A and B) / P(B) P(work | evening) = 1 / 25 = 4% P(work | afternoon) = 20 / 25 = 80%

Event A and B are **dependent** P(A) over event B hence $P(A) \neq P(A|B)$

```
we want to know:
P(work \mid afternoon), P(home \mid afternoon), ...
P(work \mid afternoon) = \frac{P(work \text{ and afternoon})}{P(afternoon)}
= \frac{P(work \text{ and afternoon})}{P(afternoon)} \cdot \frac{P(work)}{P(work)} = \frac{P(work \text{ and afternoon})}{P(work)} \cdot \frac{P(work)}{P(afternoon)}
= P(afternoon \mid work) \cdot \frac{P(work)}{P(afternoon)}
```

$$P(\text{outcome} = \text{True} \mid a = A) = \frac{P(\text{outcome} = \text{True}) \times P(a = A \mid \text{outcome} = \text{True})}{P(a = A)}$$

$$P(\text{outcome} = \text{True} \mid a = A) = \frac{P(\text{outcome} = \text{True}) \times P(a = A \mid \text{outcome} = \text{True})}{P(a = A)}$$

$$P(\text{outcome} = \text{True} \mid a = A) = \frac{P(\text{outcome} = \text{True}) \times P(a = A \mid \text{outcome} = \text{True})}{P(a = A)}$$

$$P(\text{outcome} = \text{True} \mid a = A) = \frac{P(\text{outcome} = \text{True}) \times P(a = A \mid \text{outcome} = \text{True})}{P(a = A)}$$

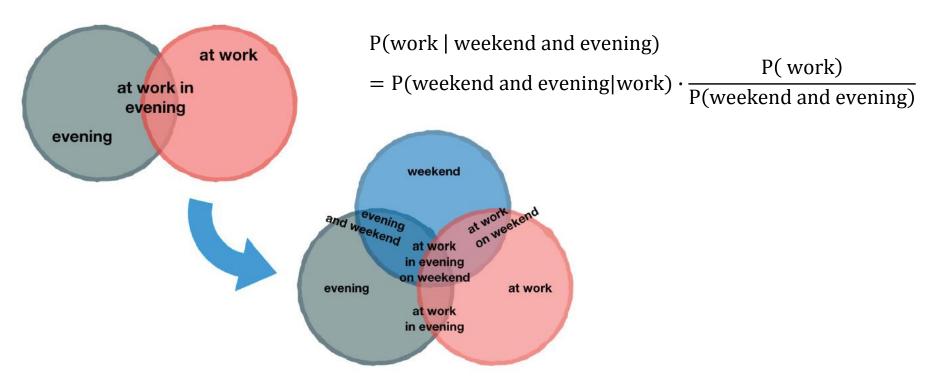
$$P(\text{outcome} = \text{True} \mid a = A) = \frac{P(\text{outcome} = \text{True}) \times P(a = A \mid \text{outcome} = \text{True})}{P(a = A)}$$

 $P(work \mid afternoon) = P(afternoon \mid work) \cdot \frac{P(work)}{P(afternoon)}$

frequency	morning	after noon	evening	total
work	14	14	2	30
home	5	5	25	35
church	5	8	2	15
downtown	2	6	12	20
total	26	33	41	100

likelihood	morning	after noon	evening	total
work	14/30	14/30	2/30	30
home	5/35	5/35	25/35	35
church	5/15	8/15	2/15	15
downtown	2/20	6/20	12/20	20
total	26/100	33/100	41/100	100

The challenge of multiple predictors



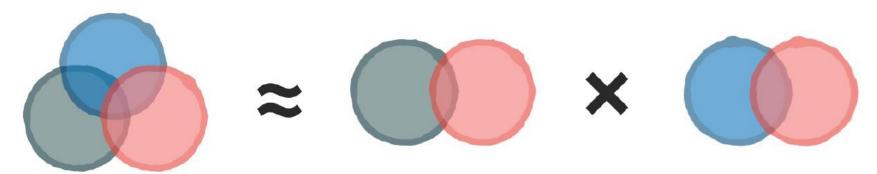
P(work | weekend and evening), P(work | weekend and morning), P(work | weekend and afternoon), P(work | weekday and evening), P(work | weekday and morning),

More input variables we have, more combination we need to consider...

Computationally expensive!!

Naivety Assumption

Naïve Bayes assumes that all input variables are conditionally independent Which simplifies the problem



$$P(ev_1 \& \cdots ev_N | y = T) \approx P(ev_1 | y = T) \times P(ev_2 | y = T) \times \cdots P(ev_N | y = T)$$

$$P(ev_1 \& \cdots ev_N | y = F) \approx P(ev_1 | y = F) \times P(ev_2 | y = F) \times \cdots P(ev_N | y = F)$$

$$P(y = T | ev_1 \& \cdots ev_N) \approx \frac{P(y = T) \times (P(ev_1 | y = T) \times \cdots P(ev_N | y = T))}{P(ev_1 \& \cdots ev_N)}$$

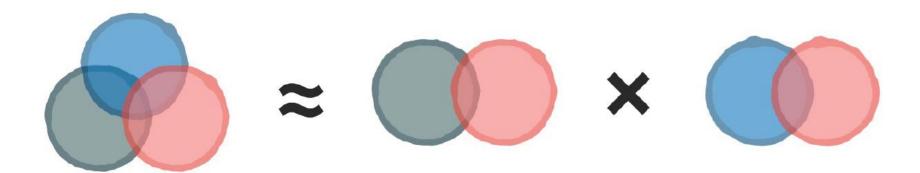
$$P(y==F \mid ev_1 \& \cdots ev_N) \approx \frac{P(y==F) \times (P(ev_1 \mid y==F) \times \cdots P(ev_N \mid y==F))}{P(ev_1 \& \cdots ev_N)}$$

Naivety Assumption

The independence assumption is rarely true in practice

However it performs admirably on many real-world tasks

Naïve Bayes is good approximation of complex probability model



sample dataset for trial

```
load(url('https://github.com/hbchoi/SampleData/raw/master/nb data.RData'))
head(locations)
##
    month day
               weekday daytype hour hourtype location
           4 wednesday weekday
## 1
                                0
                                    night
                                             home
       1 4 wednesday weekday
                                    night
                                             home
## 2
## 3
        1 4 wednesday weekday 2
                                    night
                                             home
           4 wednesday weekday 3
                                    night
                                             home
## 4
str(locations)
## 'data.frame':
                2184 obs. of 7 variables:
   $ month : int 1 1 1 1 1 1 1 1 1 ...
##
##
   $ day : int 4 4 4 4 4 4 4 4 4 ...
   $ daytype : Factor w/ 2 levels "weekday", "weekend": 1 1 1 1 1 1 1 1 1 1 ...
##
##
   $ hour
            : int 0123456789...
   $ hourtype: Factor w/ 4 levels "afternoon", "evening", ...: 4 4 4 4 4 4 3 3 3 3 ...
##
   $ location: Factor w/ 7 levels "appointment",..: 3 3 3 3 3 3 3 3 4 ...
##
head(where9am)
    daytype location
##
## 1 weekday
             office
             office
## 2 weekday
## 3 weekday
             office
## 4 weekend
               home
## 5 weekend
               home
## 6 weekday
             campus
```

simple Naïve Bayes model

```
library(naivebayes)
locmodel <- naive bayes(location ~ daytype, data = where9am)</pre>
locmodel
## ========= Naive Bayes ===========
## Call:
## naive bayes.formula(formula = location ~ daytype, data = where9am)
##
## A priori probabilities:
##
                                          office
## appointment
                                 home
                   campus
   0.01098901 0.10989011 0.45054945 0.42857143
##
##
## Tables:
##
          appointment
                                              office
## daytype
                           campus
                                      home
    weekday 1.0000000 1.0000000 0.3658537 1.0000000
##
    weekend 0.0000000 0.0000000 0.6341463 0.0000000
##
```

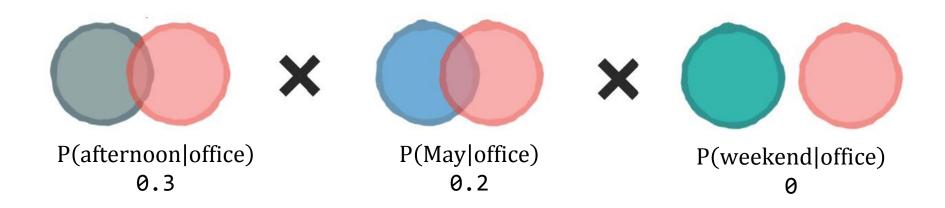
make prediction

```
test simple
##
   daytype
## 1 weekday
## 2 weekend
predict(locmodel, newdata = test simple)
## [1] office home
## Levels: appointment campus home office
predict(locmodel, newdata = test simple, type = 'prob')
## appointment campus home office
## [1,] 0.01538462 0.1538462 0.2307692
                                     0.6
## [2,] 0.00000000 0.0000000 1.0000000 0.0
```

A more sophisticated location model

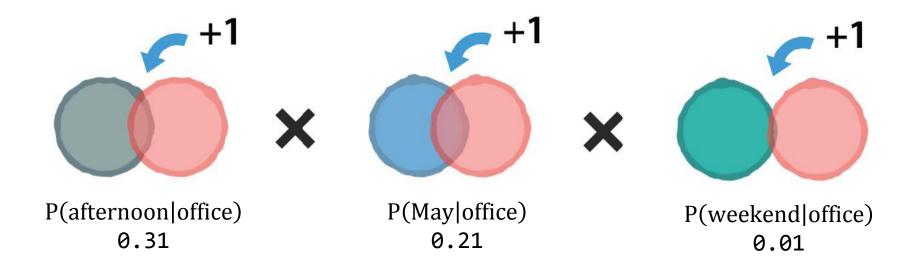
```
dim(locations_train)
## [1] 2088    7
dim(locations_test)
## [1] 96    7
locmodel <- naive_bayes(location ~ daytype + hourtype, data = locations_train)
pred <- predict(locmodel, locations_test)
## accuracy of our model
mean(locations_test$location == pred)
## [1] 0.8854167</pre>
```

An "infrequent" problem



Joint Event that never happened before, nullify effect of all other events

The Laplace correction



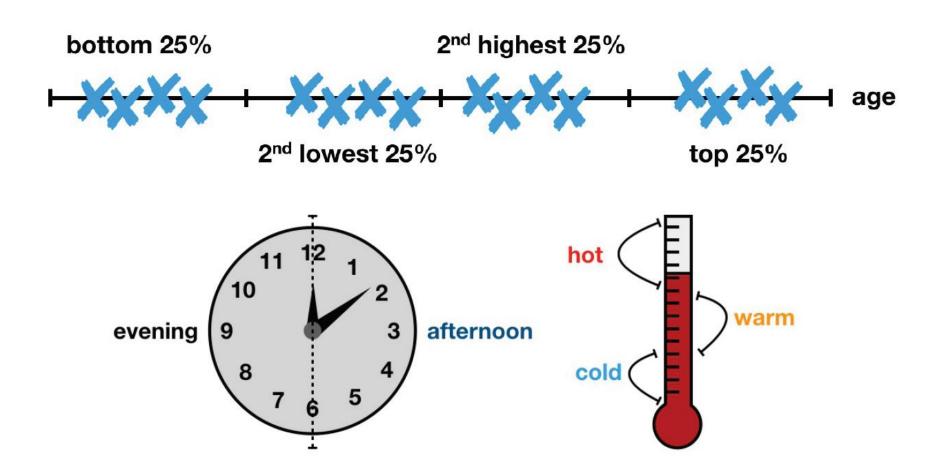
```
locmodel <- naive bayes(location ~ daytype + hourtype, data = locations train)</pre>
pred <- predict(locmodel, locations test, type = 'prob')</pre>
head(pred, n = 4)
##
       appointment campus
                              home office
                                            restaurant
                                                             store theater
## [1,]
                 0
                        0 0.9978926
                                        0 0.0007773246 0.001330089
## [2,]
                        0 0.9978926
                                        0 0.0007773246 0.001330089
                        0 0.9978926
                 0
                                        0 0.0007773246 0.001330089
## [3,]
                        0 0.9978926
                                        0 0.0007773246 0.001330089
## [4,]
locmodel
##
## daytype
            appointment
                          campus
                                      home
                                              office restaurant
                                                                    store
    weekday 0.5000000 1.0000000 0.6396517 1.0000000 0.8051948 0.6666667
##
##
    weekend
              0.5000000 0.0000000 0.3603483 0.0000000 0.1948052 0.3333333
##
## daytype
              theater
##
    weekday 0.0000000
    weekend 1,0000000
##
##
##
              appointment
## hourtype
                                                   office restaurant
                             campus
                                          home
    afternoon 0.50000000 0.54166667 0.11587408 0.66666667 0.51948052
##
               0.25000000 0.01388889 0.18687207 0.03307888 0.16883117
##
    evening
##
    morning
               0.25000000 0.44444444 0.23241795 0.30025445 0.29870130
    night
##
               0.0000000 0.00000000 0.46483590 0.00000000 0.01298701
##
## hourtype
                   store
                           theater
    afternoon 0.10256410 0.00000000
##
##
    evening
              0.87179487 1.00000000
##
    morning
              0.00000000 0.00000000
##
    night
              0.02564103 0.00000000
```

```
pred <- predict(locmodel lap, locations test, type = 'prob')</pre>
head(pred, n = 4)
         appointment
                         campus
                                     home
                                                office restaurant
##
## [1,] 0.0007114617 4.61692e-05 0.9947752 9.829844e-06 0.001397514
## [2,] 0.0007114617 4.61692e-05 0.9947752 9.829844e-06 0.001397514
## [3,] 0.0007114617 4.61692e-05 0.9947752 9.829844e-06 0.001397514
## [4.] 0.0007114617 4.61692e-05 0.9947752 9.829844e-06 0.001397514
##
             store
                      theater
## [1,] 0.00206529 0.000994573
## [2,] 0.00206529 0.000994573
## [3,] 0.00206529 0.000994573
## [4,] 0.00206529 0.000994573
locmodel lap
##
## daytype appointment
                            campus
                                         home
                                                   office restaurant
    weekday 0.33333333 0.92405063 0.63733333 0.98500000 0.75000000
##
##
    weekend 0.33333333 0.01265823 0.35933333 0.00250000 0.19047619
##
## daytype
                  store
                          theater
    weekday 0.58695652 0.07692308
##
##
    weekend 0.30434783 0.53846154
##
              appointment
## hourtype
                               campus
                                           home
                                                     office restaurant
##
    afternoon 0.33333333 0.50632911 0.11600000 0.65750000 0.48809524
    evening 0.20000000 0.02531646 0.18666667 0.03500000 0.16666667
##
    morning 0.20000000 0.41772152 0.23200000 0.29750000 0.28571429
##
    night
               0.06666667 0.01265823 0.46333333 0.00250000 0.02380952
##
##
## hourtype
                             theater
                    store
##
    afternoon 0.10869565 0.07692308
##
    evening 0.76086957 0.53846154
##
    morning 0.02173913 0.07692308
    night
##
              0.04347826 0.07692308
```

locmodel lap <- naive_bayes(location ~ daytype + hourtype, data = locations train, laplace = 1)</pre>

laplace corrected model

Binning numeric data for Naive Bayes



Weaknesses Strengths Simple, fast, and very effective Relies on an often-faulty assumption of equally important Does well with noisy and missing data and independent features Requires relatively few examples for Not ideal for datasets with large training, but also works well with very numbers of numeric features large numbers of examples Estimated probabilities are less Easy to obtain the estimated reliable than the predicted classes probability for a prediction

References

- Practical Data Science with R, by Nina Zumel and John Mount
- R을 이용한 데이터 분석 실무, 서민구, 길벗
- [DBGUIDE 연재] ggplot2를 이용한 R 시각화
 - http://freesearch.pe.kr/archives/3134

Appendix - Example

- SMS (short message service) spam filtering
 - Spam spam

Congratulations ur awarded 500 of CD vouchers or 125gift guaranteed & Free entry 2 100 wkly draw txt MUSIC to 87066

December only! Had your mobile 11mths+? You are entitled to update to the latest colour camera mobile for Free! Call The Mobile Update Co FREE on 08002986906

Valentines Day Special! Win over £1000 in our quiz and take your partner on the trip of a lifetime! Send GO to 83600 now. 150p/msg rcvd.

Non-spam – ham

Better. Made up for Friday and stuffed myself like a pig yesterday. Now I feel bleh. But at least its not writhing pain kind of bleh.

If he started searching he will get job in few days. He have great potential and talent.

I got another job! The one at the hospital doing data analysis or something, starts on monday! Not sure when my thesis will got finished

Data Loading

- SMS (short message service) spam filtering
- > sms_raw<-read.csv("sms_spam.csv",stringsAsFactors = FALSE)

	type 🗘	text
1	ham	Hope you are having a good week. Just checking in
2	ham	Kgive back my thanks.
3	ham	Am also doing in cbe only. But have to pay.
4	spam	complimentary 4 STAR Ibiza Holiday or 짙10,000 cash n
5	spam	okmail: Dear Dave this is your final notice to collect yo
6	ham	Aiya we discuss later lar Pick u up at 4 is it?
7	ham	Are you this much buzy
8	ham	Please ask mummy to call father
9	spam	Marvel Mobile Play the official Ultimate Spider-man gam
10	ham	fyi I'm at usf now, swing by the room whenever
11	ham	Sure thing big man. i have hockey elections at 6, shoul

```
> sms_raw$type<-factor(sms_raw$type)
> str(sms_raw$type)
Factor w/ 2 levels "ham","spam": 1 1 1 2 2 1 1 1 2 1 ...
> table(sms_raw$type)
ham spam
4811 747
```

- text -> bag of words
 - text mining package "tm"

```
> install.packages("tm")
Installing package into 'C:/Users/Hyebong Choi/Documents/R/win-library/3.2'
(as 'lib' is unspecified)
also installing the dependencies 'NLP', 'slam'
trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.2/NLP_0.1-9.zip'
Content type 'application/zip' length 278734 bytes (272 KB)
downloaded 272 KB
trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.2/slam_0.1-34.zip'
Content type 'application/zip' length 111493 bytes (108 KB)
downloaded 108 KB
trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.2/tm_0.6-2.zip'
Content type 'application/zip' length 710657 bytes (694 KB)
downloaded 694 KB
package 'NLP' successfully unpacked and MD5 sums checked
package 'slam' successfully unpacked and MD5 sums checked
package 'tm' successfully unpacked and MD5 sums checked
The downloaded binary packages are in
       C:\Users\Hyebong Choi\AppData\Local\Temp\RtmpUHLcnN\downloaded_packages
> library(tm)
필요한 패키지를 로딩중입니다: NLP
```

- text -> bag of words
 - text mining package "tm"
 - > sms_corpus <- Corpus(VectorSource(sms_raw\$text))</pre>

This command uses two functions. First, the Corpus () function creates an R object to store text documents. This function takes a parameter specifying the format of the text documents to be loaded. Since we have already read the SMS messages and stored them in an R vector, we specify VectorSource(), which tells Corpus() to use the messages in the vector sms_train\$text. The Corpus() function stores the result in an object named sms_corpus.



The Corpus () function is extremely flexible and can read documents from many different sources such as PDFs and Microsoft Word documents. To learn more, examine the Data Import section in the tm package vignette using the command: print (vignette ("tm"))

```
> print(sms_corpus)
<<VCorpus>>
Metadata: corpus specific: 0, document level (indexed): 0
Content: documents: 5558
> inspect(sms_corpus[1:2])
<<VCorpus>>
Metadata: corpus specific: 0, document level (indexed): 0
Content: documents: 2
[[1]]
<<PlainTextDocument>>
Metadata: 7
Content: chars: 49
ΓΓ211
<<PlainTextDocument>>
Metadata: 7
Content: chars: 23
> sms_corpus[[1]]
<<PlainTextDocument>>
Metadata: 7
Content: chars: 49
> sms_corpus[[1]]$content
[1] "Hope you are having a good week. Just checking in"
> sms_corpus[[1]]$meta
           : character(0)
  author
  datetimestamp: 2016-05-25 16:00:51
  description : character(0)
  heading : character(0)
  id
              : 1
  language
             : en
              : character(0)
  origin
```

```
hello!, HELLO..., and Hello count as all "hello"
```

- remove numbers, punctuation, white space, and stop words.
- to make all lower-cased

```
> corpus_clean<-tm_map(sms_corpus,content_transformer(tolower))
> corpus_clean<-tm_map(corpus_clean,content_transformer(removeNumbers))
> corpus_clean<-tm_map(corpus_clean,content_transformer(removeWords),stopwords())
> corpus_clean<-tm_map(corpus_clean,content_transformer(removePunctuation))
> corpus_clean<-tm_map(corpus_clean,content_transformer(stripWhitespace))

> sms_corpus[[1]]$content
[1] "Hope you are having a good week. Just checking in"
> corpus_clean[[1]]$content
[1] "hope good week just checking "
> sms_corpus[[1234]]$content
[1] "Can u all decide faster cos my sis going home liao.."
> corpus_clean[[1234]]$content
[1] "can u decide faster cos sis going home liao"
```

to document and term matrix (tokenizing)

Α	В	С	D	Е	F	G
	balloon	balls	bam	bambling	band	bandages
1	0	0	0	0	0	0
2	0	0	0	0	0	0
3	0	0	0	0	0	0
4	0	0	0	0	0	0
5	0	0	0	0	0	0

> sms_dtm <- DocumentTermMatrix(corpus_clean)</pre>

```
> inspect(sms_dtm[1:10, 1000:1010])
                                                      > dim(sms_dtm)
<<DocumentTermMatrix (documents: 10, terms: 11)>>
                                                       [11] 5558 7989
Non-/sparse entries: 0/110
                   : 100%
Sparsity
Maximal term length: 10
                  : term frequency (tf)
Weighting
    Terms
Docs caps captain captaining car card cardiff cardin cards care careabout cared
       0
                              0
                                                             0
                0
                                                                             0
```

Spliting Training and Test set

```
> sms raw train <- sms raw[1:4169, ]</pre>
> sms raw test <- sms raw[4170:5559, ]</pre>
Then the document-term matrix:
> sms dtm train <- sms dtm[1:4169, ]</pre>
> sms dtm test <- sms dtm[4170:5559, ]</pre>
And finally, the corpus:
> sms corpus train <- corpus clean[1:4169]</pre>
> sms corpus test <- corpus clean[4170:5559]</pre>
> prop.table(table(sms raw train$type))
       ham
                 spam
0.8647158 0.1352842
> prop.table(table(sms raw test$type))
       ham
                 spam
0.8683453 0.1316547
```

Visualization - word cloud

> install.packages("wordcloud") The downloaded binary packages are in C:\Users\Hyebong Choi\AppData\Local\Temp\RtmpUHLcnN\downloaded_packages > library(wordcloud) 필요한 패키지를 로딩중입니다: RColorBrewer Warning message: 패키지 'wordcloud'는 R 버전 3.2.5에서 작성되었습니다 > wordcloud(sms_corpus_train,min.freq = 40,random.order = FALSE) coming late something around contact morning wait ≧ prize keep happydear already someone week mobile stop give went send txt still alwayspick say of School In the great also follows thing set today last things message tomorrow customer anything first

Peoplesleep

Visualization - word cloud

```
> spam<-subset(sms_raw_train,type=="spam")
> ham<-subset(sms_raw_train,type=="ham")
> wordcloud(spam$text,min.freq=20,max.words = 40,scale=c(3,0.5))
> wordcloud(ham$text,max.words = 40,scale=c(3,0.5))
```

```
nokia Calle claim
youjust service text
150ppm won reply
willdraw send new urgent
prize customer tone awarded
get bline win txt camera
cashthis txt camera
guaranteed chat stop

NOW please bline win
contact mobile
```

```
spam
```

```
day time dont ham
```

Filtering frequent terms

Remove terms that appear less than 5 times

```
findFreqTerms(sms_dtm_train,5)
sms_dict<-findFreqTerms(sms_dtm_train,5)
sms_train<-DocumentTermMatrix(sms_corpus_train,list(dictionary=sms_dict))
sms_test<-DocumentTermMatrix(sms_corpus_test,list(dictionary=sms_dict))</pre>
```

term frequency -> term occurrence

Naive Bayes classification syntax

using the naiveBayes() function in the e1071 package

Building the classifier:

```
m <- naiveBayes(train, class, laplace = 0)</pre>
```

- train is a data frame or matrix containing training data
- class is a factor vector with the class for each row in the training data
- laplace is a number to control the Laplace estimator (by default, 0)

The function will return a naive Bayes model object that can be used to make predictions.

Making predictions:

```
p <- predict(m, test, type = "class")</pre>
```

- m is a model trained by the naiveBayes() function
- test is a data frame or matrix containing test data with the same features as the training data used to build the classifier
- type is either "class" or "raw" and specifies whether the predictions should be the most likely class value or the raw predicted probabilities

The function will return a vector of predicted class values or raw predicted probabilities depending upon the value of the **type** parameter.

Example:

```
sms_classifier <- naiveBayes(sms_train, sms_type)
sms_predictions <- predict(sms_classifier, sms_test)</pre>
```

```
> install.packages("e1071")
Installing package into 'C:/Users/Hyebong Choi/Documents/R/win-library/3.2'
(as 'lib' is unspecified)
trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.2/e1071_1.6-7.zip'
Content type 'application/zip' length 814476 bytes (795 KB)
downloaded 795 KB
package 'e1071' successfully unpacked and MD5 sums checked
The downloaded binary packages are in
       C:\Users\Hyebong Choi\AppData\Local\Temp\RtmpUHLcnN\downloaded_packages
> library(e1071)
Warning message:
패키지 'e1071'는 R 버전 3.2.5에서 작성되었습니다
> sms_classifier<-naiveBayes(sms_train,sms_raw_train$type)
> sms_test_pred<-predict(sms_classifier,sms_test)</pre>
```

This produces the following table:

Total Observations in Table: 1390

predicted	actual ham	spam	Row Total
ham	1203 0.997	32 0.175	1235
spam	4 0.003	151 0.825	155
Column Total	1207 0.868	183 0.132	1390

Improvement

```
> sms_classifier2 <- naiveBayes(sms_train, sms_raw_train$type, laplace = 1)
> sms_test_pred2 <- predict(sms_classifier2, sms_test)
> CrossTable(sms_test_pred2, sms_raw_test$type,
+ prop.chisq = FALSE, prop.t = FALSE, prop.r = FALSE,
+ dnn = c('predicted', 'actual'))
```

Total Observations in Table: 1390

actual ham	spam	Row Total
1204 0.998	31 0.169	1235
0.002	152 0.831	155
1207 0.868	183 0.132	1390
	ham 1204 0.998 3 0.002 1207	ham spam 1204 31 0.998 0.169 3 152 0.002 0.831