This is a one-document reference of the use of R commands.

General procedures

Pre-flight checklist

Make sure you can import these libraries in R notebook.

```r
library(ggplot2)
library(psych)
library(ggfortify)
library(leaps)
library(caTools)
library(mlogit)
library(zoo)
library(glmnet)
library(rpart)
library(rpart.plot)
library(tm)
library(randomForest)
library(SnowballC)
library(wordcloud)
library(e1071) # Naive Bayes
library(jpeg)
library(survival)
library(flexclust) # for finals
library(caret)

rm(list=ls())
```

If you cannot, please panic.

Common errors

Please remember the `.` when you are training against the rest of the data. `responsive~.,`

GLM requires you to put `family='binomial'`

Do not train on the test data FFS. Please copy correctly FFS.

Adjusted R-squared is not R-squared FFS, please ask the examiners.

Helper functions

To understand a function, use `?` to read the offline documentation. To understand an object, use `attributes(x)` to see the attributes.

For MacOS Refer to the the 'Run' option on the top right of this window to see the shortcut related to running and restarting the cell.

- Run line `Cmd + Enter`
- Run chunk `Shift + Cmd + Enter`
- Run all `Opt + Cmd + R`
- New R Cell `Cmd + Opt + I`
- Comment `Cmd + /` (custom)

Header to specify html-knitting output and remove environment variables

```
---
output:
  html_document: default
---

rm(list=ls())
```

Introduction to statistics

R-squared - higher better Adjusted R-squared - higher better **AIC - lower better** Likelihood - higher better Loglikehilood - higher better Negative loglikelihood (logloss?) - lower better KL divergence - zero the same, higher more different

Basics of R

A dataframe is not a matrix. A dataframe may have named or unnamed columns. A vector is not a column. Can a vector have named values? Can a matrix have named values?

Common functions

```
names()
apply()
# (X, MARGIN, FUN), MARGIN = row or columns
tapply()
# data(iris); tapply(iris$Sepal.Width, iris$Species, median)
unname()
unique()
paste0()
which()
subset()
coef() # extract coefficient from linear models
```

Numerical functions

```
sum(arr)
prod(arr)
exp(arr)
var(arr)
sd(arr)
summary(arr)
which.max(arr)
pmax(arr,arz)  # take maximum element-wise
arr > 3  # you can implement element-wise logical check
```

```
# colMeans() # calculate the mean of each column?
cor(matrix[,COL_S:COL_E])

is.na() # counts number of NA
mean() # R has this function, ignores NA values
```

Type casting

```r
z <- c(0:9)
class(z)  # prints class
as.numeric(z)  # casts into float?

z1 <- c("a","b","d")
w <- as.character(z1)
as.integer(w)  # returns array of NA

as.factor(w)  # required for classification models
```

Matrices

The matrix operations may require some explanation.

- definition `x<-matrix(c(3,-1,2,-1),nrow=2, ncol=2)`
- e-wise multiplication `x*x`, `x*2`
- matrix multiplication `x%*%x`
- transpose `t(x)`
- read element `r[2,2]`, `r[3]`, starts counting from one
- inverse of a matrix (?) `solve(x)`
- solving system of linear equations `a%*%solve(a)`
- get eigenvectors `eigen(a)$vectors`

Dataframes

You are unlikely to do this, you are likely to load csv files.

```
CELG <- data.frame(names=c("barack","serena"),
                   ages=c(58,38),
                   children=c(2,1))
# append to dataframe
CELG$spouse <- c("michelle","alexis")

# use negative signs to exclude columns or rows
test_2 <- df_2[-trainid_2,]
```

Statisitical testing

```
t.test(oscars$Nom[oscars$PP==1 & oscars$Ch==1],
       oscars$Nom[oscars$PP==1 & oscars$Ch==0],
       alternative = clib("greater"))
```

Miscellaneous

```
# date configuration
base::as.Date(32768, origin = "1900-01-01")

# to remove intercept, fit to -1
MPP2 <- mlogit(Ch~Nom+Dir+GG+PGA-1, data=D1)
```

Preprocessing

You need to preprocess the data.

Data reading

```
poll <- read.csv("AnonymityPoll.csv", stringsAsFactors=FALSE)
# consider stringsAsFactors
summary(poll)  # 7-figure summary of every column
str(poll)  # see some data

table(poll$Smartphone)  # freqency in a column
summary(poll$Smartphone)  # 7-figure summary of a column

# freqency matrix of two columns
table(poll$Internet.Use, poll$Smartphone)

# find the mean of the first value depending on second
tapply(limited$Info.On.Internet,
       limited$Smartphone,
       mean)

# count number of NA in a column
sum(is.na(poll$Internet.Use))
```

Data manipulation

```
# remove rows with any (?) NA variables
hitters = na.omit(hitters)

# obtain a subset
limited <- subset(poll, poll$Internet.Use == 1)

# obtain a subset without a column
eg1 <- subset(eg,select=-c(Country))

# obtain a subset with 'or' logic operator
limited <- subset(poll, poll$Internet.Use == 1|
                        poll$Smartphone == 1)

# row subset
# column subset
```

Combining dataframes

To combine dataframes one after another row, and fill empty cells.

```
library(plyr)
combined <- rbind.fill(train, test)
```

To combine dataframes beside one another and fill empty cells.

```
library(dplyr)
combined_features <- within(combined, rm(tweet, Id))
```

Train-test split

Please do it correctly and not lose two subgrades.

```
set.seed(144)
library(caTools)

# train-test split, stratified
split <- sample.split(framing1$TENCHD,SplitRatio=0.65)
training <- subset(framing1,split==TRUE)
test <- subset(framing1,split==FALSE)

SongsTrain <- subset(songs, songs$year<=2008)
SongsTest <- subset(songs, songs$year==2009 | songs$year==2010)
```

Cross validation

Week 5b

Simpler models often tend to work better for out-of-sample predictions and so we will penalize models for excessive model complexity.

With the increase in computational power, we can partition the data set into training, validation and test sets and conduct model assessment and selection.

- The training set is used to estimate the model parameters.
- The validation set is used to do model selection.
- The test set is the evaluation set on which we will simply evaluate or check how the model performs.

Types of validation

- Simple validation set approach

- Leave out one cross validation (LOOCV)
- k-fold cross validation

Defining the folds.

```r
train <- train[sample(nrow(train)),]
# shuffle training set

val_idxx <- list()
trn_idxx <- list()

for (i in 1:NUM_FOLDS) {
    val_idx = c(((i-1)*22500/NUM_FOLDS+1):(i*22500/NUM_FOLDS))
    val_idxx[[i]] <- val_idx

    trn_idx <- c(0:((i-1)*22500/NUM_FOLDS),(i*22500/NUM_FOLDS+1):(22500+1))
    trn_idx <- trn_idx[-length(trn_idx)][-1]

    trn_idxx[[i]] <- trn_idx
}
```

Accessing the folds

```r
for (i in 1:NUM_FOLDS) {
    trn_idx <- trn_idxx[[i]]
    val_idx <- val_idxx[[i]]
    # and so on ...
}
```

Data visualization

Most likely not tested in exams.

```
# plot a histogram
hist(limited$Age)

# scatter plot
plot(limited$Age, limited$Info.On.Internet)

# scatter plot with jitter
plot(jitter(limited$Age),
     jitter(limited$Info.On.Internet))

# star plot
stars(swiss, key.loc = c(18,2))
```

Assorted plots

```
library(ggplot2)

# plot histogram
ggplot(data = Parole, aes(x = Age)) +
  geom_histogram()

# plot histogram with specified bin width and start point
# closed refer to whether the interval is closed
ggplot(data = Parole, aes(x = Age)) +
  geom_histogram(binwidth=5,
                 closed=c("left"),
                 center=17.5)

# bar plot
bar <- ggplot(WHO) +
  geom_bar(mapping = aes(x = Region, fill = Region),
           show.legend = FALSE, width = 1) +
  theme(aspect.ratio = 1) +
  labs(x = NULL, y = NULL)
bar  # to show plot

# plot with flipped coordinates, and polar plot
bar + coord_flip()
bar + coord_polar()
```

Scatter plots

```r
# many scatter plot
a <- ggplot(WHO, aes(x=GNI, y=FertilityRate))
a + geom_point(na.rm=T) + facet_wrap(.~Region)

# loess interpolation with confidence
a + geom_point(na.rm=T) + geom_smooth(na.rm=T)

# loess interpolation, continent represented with color
acol <- ggplot(WHO,
               aes(x=GNI, y=FertilityRate, color=Region))
acol + geom_point(na.rm=T)
acol + geom_point(na.rm=T) + geom_smooth(na.rm=T)

# scatter plot with attributed represented with size
ggplot(mtcars,aes(x=wt,
                  y=mpg,
                  color=cyl,
                  cex=disp))

# plot scatterplot matrix
ggplot(wine, aes(VINT,LPRICE)) +
  pairs.panels(wine, ellipses=F, breaks=10,
               hist.col="blue")

# scatterplot with hvlines demarcating means
br<-mean(winetrain$LPRICE)
ggplot(winetrain,
       aes(DEGREES,
           HRAIN,
           color=cut(LPRICE,c(-Inf,-1.42,Inf)))) +
  geom_point(na.rm=T) +
  scale_color_discrete(name = "LPRICE",
                       labels = c("< mean(LPRICE)",
                                  "> mean(LPRICE)")) +
  geom_vline(xintercept=mean(winetrain$DEGREES),
             color="blue",lwd=1) +
  geom_hline(yintercept=mean(winetrain$HRAIN),
             color="blue",lwd=1)

# scatterplot with jitter
ggplot(orings[orings$Field>=0,],aes(Temp,Field)) +
  geom_point(na.rm=T) +
  geom_jitter(na.rm=T,width=1,height=0.1)
```

Result analysis

After the prediction is made, we want to evaulate numbers for example.

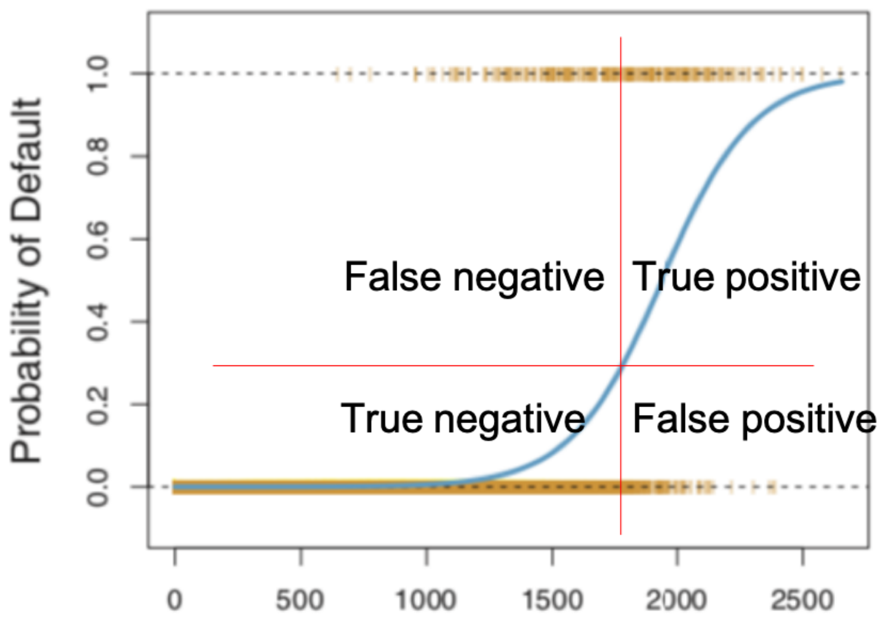
Deciding with probabilities

```
# if you have result from K-fold
pred_test_class <- c()

for (i in 1:nrow(pred_test_matrix)){
    class_with_max_prob <- names(pred_test_matrix[i,][pred_test_matrix[i,] ==
max(pred_test_matrix[i,])])[[1]]
    pred_test_class <- append(pred_test_class, class_with_max_prob)
    if (length(pred_test_class) != i){print(i)}
}
```

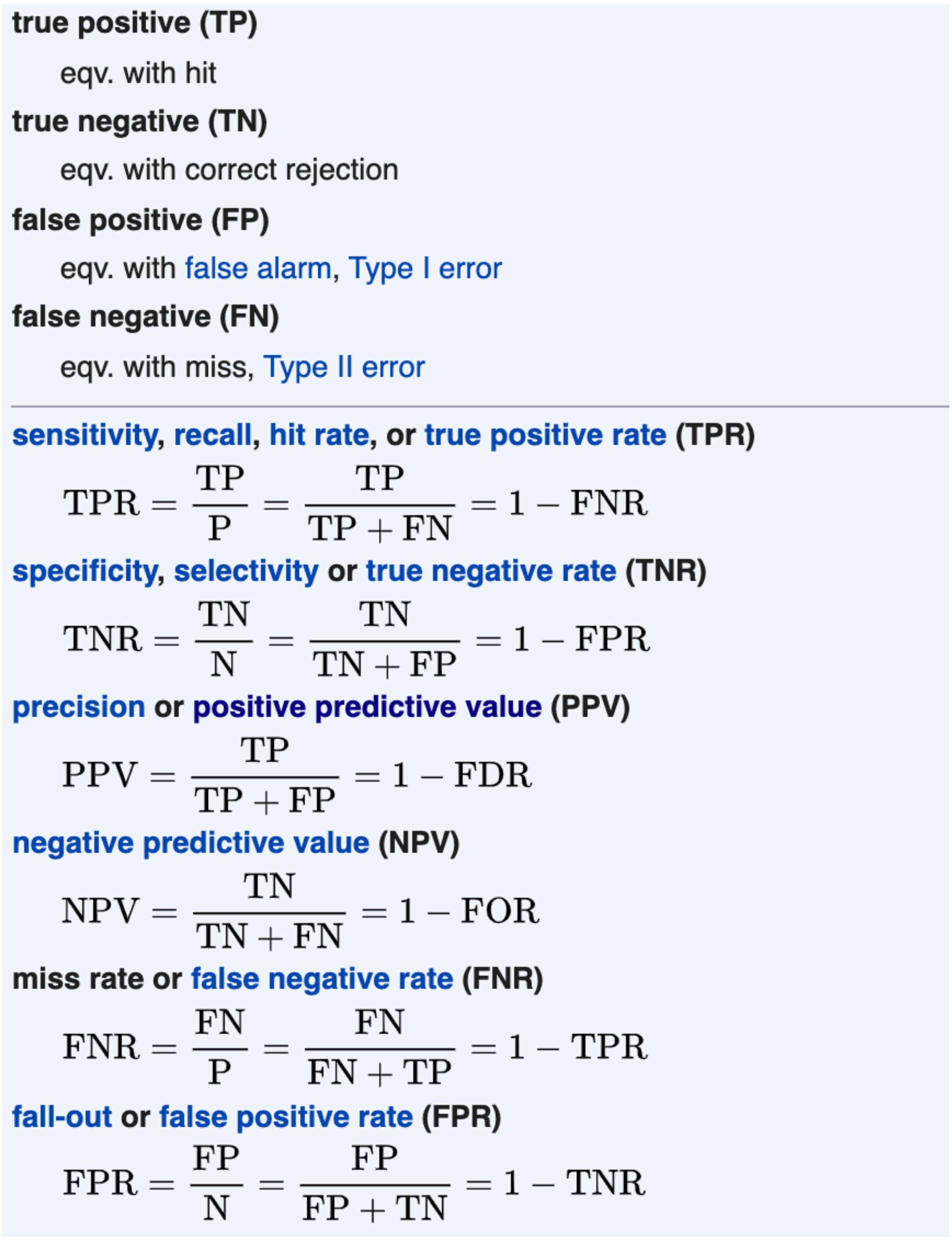
Confusion matrices

Names	Predict = 0	Predict = 1
Actual = 1	False Negative (FN)	True Positive (TP)
Actual = 0	True Negative (TN)	False Positive (FP)



Name	**Alt Name**	**Formula**
False Positive Rate	Type I error	$\frac{FP}{FP+TN}$
True Negative Rate	Specificity	$\frac{TN}{FP+TN} = \frac{TN}{N}$
True Positive Rate	Sensitivity, Recall	$\frac{TP}{TP+FN} = \frac{TP}{P}$
False Negative Rate	Type II error	$\frac{FN}{TP+FN}$
Precision		$\frac{TP}{TP+FP}$
Compiled measures		
Overall Accuracy		$\frac{TP+TN}{FP+FN+TP+TN}$
ROC Curve	Plot TPR against FPR	

Wikipedia reference



true positive (TP)

eqv. with hit

true negative (TN)

eqv. with correct rejection

false positive (FP)

eqv. with false alarm, Type I error

false negative (FN)

eqv. with miss, Type II error

---

sensitivity, recall, hit rate, or true positive rate (TPR)

$$\mathrm{TPR} = \frac{\mathrm{TP}}{\mathrm{P}} = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FN}} = 1 - \mathrm{FNR}$$

specificity, selectivity or true negative rate (TNR)

$$\mathrm{TNR} = \frac{\mathrm{TN}}{\mathrm{N}} = \frac{\mathrm{TN}}{\mathrm{TN} + \mathrm{FP}} = 1 - \mathrm{FPR}$$

precision or positive predictive value (PPV)

$$\mathrm{PPV} = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FP}} = 1 - \mathrm{FDR}$$

negative predictive value (NPV)

$$\mathrm{NPV} = \frac{\mathrm{TN}}{\mathrm{TN} + \mathrm{FN}} = 1 - \mathrm{FOR}$$

miss rate or false negative rate (FNR)

$$\mathrm{FNR} = \frac{\mathrm{FN}}{\mathrm{P}} = \frac{\mathrm{FN}}{\mathrm{FN} + \mathrm{TP}} = 1 - \mathrm{TPR}$$

fall-out or false positive rate (FPR)

$$\mathrm{FPR} = \frac{\mathrm{FP}}{\mathrm{N}} = \frac{\mathrm{FP}}{\mathrm{FP} + \mathrm{TN}} = 1 - \mathrm{TNR}$$

Evaluation Metrics

```
library(caret)
caret::confusionMatrix(as.factor(predictLog_train > 0.5),
                       as.factor(train$spam==1))



# please ensure correct order
CM = table(predictforest,test$rev)
CM
# predictforest  0  1
#              0 47 21
#              1 35 81
Accuracy = (CM[1,1]+CM[2,2])/sum(CM)
Accuracy # 0.6956522 vs 0.7119565
BaseAccuracy =  (sum(CM[1:2,1]))/sum(CM)
BaseAccuracy # or flip it
Sensitivity = (CM[1,1])/sum(CM[1:2,1])
Sensitivity
Specificity = (CM[2,2])/sum(CM[1:2,2])
Specificity
```

Recevier Operating Curve

Probably you should write an analysis procedure given predicted probs and actual binary.

```
library(ROCR)
# even shorter function names are advisable
# but we can be explicit in this document
accuracy <- function(predict_object, data, threshold=0.5) {
  return(sum(diag(table(predict_object >= threshold, data))) /
           sum(table(predict_object >= threshold, data)))
}
auc <- function(predict_object, data) {
  prediction_obj <- prediction(predict_object, data)
  perf_obj <- performance(prediction_obj, measure = "auc")
  return(perf_obj@y.values[[1]])
}




library(ROCR)
# ROCR method to obtain predicted probs and actual labels
ROCRpred <- prediction(Pred[1:138],orings$Field[1:138])
# ROCR method to plot ROC curve
ROCRperf <- performance(ROCRpred,x.measure="fpr",measure="tpr")
```

```r
plot(ROCRperf)  # simple plot
plot(ROCRperf,
     colorize=T,
     print.cutoffs.at=c(0,0.1,0.2,0.3,0.5,1),
     text.adj=c(-0.2,1.7))

# Calculate area under curve (AUC)
as.numeric(performance(ROCRpred,measure="auc")@y.values)
```

Predictive Models I

You will train a predictive model on training data, use the model to generate predictions on the test data (and check for accuracy if possible).

These model should have already been tested in the midterms and will not be tested in the finals.

All methods should have a prediction function. For classification models you need to specify whether you want the class (binary) or response (probability).

```
pred_1_p <- predict(tree_1_o_2, newdata = test_1, type = "class")
```

Linear regression

Week 2

Method	Linear Regression
Target	Number
Model	$y_i = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \epsilon_i$
Loss	Mean square error
Quality of fit	R-square Adjusted R-square AIC
Examples	Wine prices and quality Baseball batting average
Comments	Choose only the statistically significant variables This cannot predict binary objectives./

```
# fitting linear model
model1  <- lm(LPRICE~VINT+HRAIN,
              data=winetrain)
summary(model1)
confint(model7, level=0.99)  # see confidence interval

# predicting values with model
pred <- predict(model1,
                newdata=winetest,
                type="response")  # not sure if correct

coef(model1)
```

Logistic Regression

Week 3

Method	Logistic Regression
Target	Binary
Model	$P(y_i = 1) = \frac{1}{1 + e^{-(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \epsilon_i)}}$
Loss	$LL(\beta)$ $= \sum_{i=1}^{n} \sum_{k=1}^{2} y_{ik} \log(P(y_{ik} = 1))$ $= \sum_{i=1}^{n} \sum_{k=1}^{2} y_{ik} \log\left(\frac{e^{\beta' x_{ik}}}{\sum_{l=1}^{k} e^{\beta' x_{il}}}\right)$
Explanation	$x \log(x')$, sum over $x = 1$ and $x = 0$ (elaborate)
Quality of fit	$AIC = -2LL(\hat{\beta}) + 2(p+1)$ Confusion matrix AUC-ROC
Examples	Space shuttle failures Risk of heart disease
Comment	

```r
# fitting logisitic model (family = binomial)
model3 <- glm(Field~Temp+Pres,
              data=orings,
              family=binomial)
summary(model3)

# predicting probabilities with model
Pred <- predict(model4,
                newdata=orings,
                type="response")

coef(model4)
```

Predictive Models II

Models that will be tested in finals.

CART

Week 8

Method	Classification and Regression Trees
Target	Customisable
Model	?
Loss	Does not attempt to find global minimum
Quality of fit	?
Prediction	Supreme Court decision
Comments	

```
library(rpart)
library(rpart.plot)


# fitting with CART
cart1 <- rpart(rev~petit+respon+circuit+lctdir+issue+unconst,
               data=train,
               method="class")
# plot the tree
prp(cart1, type=4, extra=2)
```

Pruning the tree

```
# Display the cp table for model cart1
printcp(cart1)
# We can also plot the relation between cp and error
plotcp(cart1)
# printcp() gives the minimal cp for which the pruning happens.
# plotcp() plots against the geometric mean

# print number of splits
unname(tail(tree_1_e$cptable[,2], 1))

# pruning the tree based on complexity parameter
cart2 <- prune(cart1,cp=0.01)
```

```r
fancyRpartPlot(cart2)
predictcart2 <- predict(cart2,newdata=test,type="class")
table(test$rev,predictcart2)
```

```r
# predicting with CART
predictcart1_prob <- predict(cart1, newdata = test)
# AUC procedure
#pred_cart1 <- prediction(predictcart1[,2], test$rev)
#perf_cart1 <- performance(pred_cart1,
#                           x.measure="fpr",measure="tpr")
#plot(perf_cart1)
#as.numeric(performance(pred_cart1,measure="auc")@y.values)

# to understand the options of rpart
?rpart.control
```

As the optimisation for global minimum is not computationally feasible, we use a heuristic approach instead.

$$\min_{\{R\}} \sum_{m=1}^{M} \sum_{i \in R_m} (y_i - \hat{y}_{R_M})^2$$

Start with all observations in one region.

Choose predictor and cut-point such that

$$\min_{\{p\}} \min_{S} \left[\sum_{i: x_{is} \leq S} (y_i - \hat{y}_{R_1})^2 + \sum_{i: x_{is} > S} (y_i - \hat{y}_{R_1})^2 \right]$$

or other metric of performance such as entropy.

Solve a sequence of locally optimal problems with exhaustive search. The cut point is one of the the data points, along one of the dimensions.

Repeat each branch iteratively. Exit the branch when one exit condition is met.

- For example, each prescribed bucket of leaves reached the prescribed minimum size.

> Note that all observations belong to a single sub-region beyond which greedy splits are made at each step without looking necessarily at the best split that might lead to a better tree in future steps (greedy strategy) - in other words, local optimum at each step may not provide the global optimum.

Bias variance trade-off

There is a trade-off between the model interpretability and performance on the training set.

To control the bias-variance trade-off (or, simply, the model complexity), CARTs use prepruning and pruning.

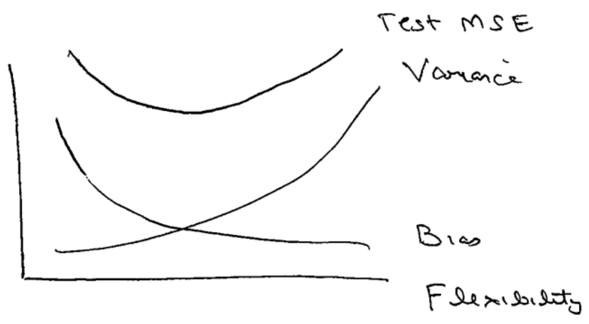


Figure 0.7: Bias-variance trade-off.

Breaking down the CART

When you print the model you get this guide

```
node), split, n, loss, yval, (yprob)
      * denotes terminal node
```

Following is the root node, with 434 points. If the leaf terminates here the absolute error is 195 points by predicting all 1s.

```
  1) root 434 195 1 (0.44930876 0.55069124)
```

After the first split (lctdir=liberal) there are 205 points that belongs to this split.

If the leaf terminates there, the absolute error is 82 points by predicting all 0s.

```
     2) lctdir=liberal 205  82 0 (0.60000000 0.40000000)
```

After the first split (lctdir=conser) there are 229 points that belongs to this split.

If the leaf terminates there, the absolute error is 72 points by predicting all 1s.

```
     3) lctdir=conser  229  72 1 (0.31441048 0.68558952)
```

Random Forests

Week 9

Method	**Random Forests**
Target	Customisable
Model	?
Loss	Customisable
Quality of fit	Customisable
Prediction	Social media
Comments	?

Intuition of ensemble training - each person have different knowledge, and different logical framework. Individual trees may not be accurate (and are faster to train), but make the ensembled prediction is more accurate. (Analogy - Who Wants to be a Millionaire)

Sample the training dataset with replacement (boosting or bagging)

- Build a classification or regression tree
- When splitting a node
- Randomly choose m parameters
- Find the best cut-point by exhasutive search
- Stop when the exit condition is met

Training a tree in a forest is faster than training a CART because only a subset of predictors are used.

Meta-parameters

The training does not optimise the meta-parameters.

- T^* number of tree in the ensemble `ntree` (recommended 100 to 1000)
- m = number of predictors chosen when creating a split `mtry` (recommended sqrt(p) for classification, p/r for regression)
- n_{min} minimum number of nodes in each leaf `nodesize` (recommended 2 to 20)

Downsides (compart to CART)

- slower (though parallelizable across cores)
- less interpretable

```
library(randomForest)

# set seed
#
# Build a forest of 200 trees, with leaves 5 observations in the terminal nodes

forest <-
randomForest(as.factor(rev)~petit+respon+circuit+unconst+lctdir+issue,
data=train, nodesize=5, ntree=200)
forest
# remember to convert the target variable into a factor

# The prediction is carried out through majority vote (across all trees)
predictforest <- predict(forest, newdata = test, type="class")
table(predictforest, test$rev)
```

Which of the variables is the most important in terms of the number of splits?

```
vu <- varUsed(rf_1, count = TRUE)
vusorted <- sort(vu, decreasing = FALSE, index.return = TRUE)
dotchart(vusorted$x, names(rf_1$forest$xlevel[vusorted$ix]))
```

Which of the following variables is the most important in terms of mean reduction in impurity?

```
varImpPlot(forest)
# forest$importance
```

Naive Bayes

Week 10

Method	**Naive Bayes'**
Target	Binary
Model	?
Loss	?
Quality of fit	?
Prediction	?
Comments	Based on a (naive) hypothesis of **conditional independence** of the features

Bayes Theorem

$$P(A|B) \cdot P(B) = P(B|A) \cdot P(A)$$

> We now make a (naive) hypothesis of **conditional independence** of the features, that is, x_i is conditionally independent of every other feature x_j (with $i \neq j$).

```
library(e1053)
# train the model
model3 <- naiveBayes(as.factor(responsive)~.,data=train)
summary(model3)

# ???
model3$apriori
# Y
# 0    1
# 500  96

# List tables for each predictor. For each numeric variable, it gives target
class, mean and standard deviation.
model3$tables[5]

# predict with model
predict3 <- predict(model3,newdata=test,type="class")
table(predict3,test$responsive)
```

Naive Bayes classifier

The Naive Bayes classifier is a simple classification rule based on Bayes' rule, which can be used with the bag of words model. Given a problem instance (say a document) to be classified, represented by a vector $\{x_1, \dots, x_p\}$ of terms (predictors), a Naive Bayes classifier assigns to this instance probabilities $P(C_k|x_1, \dots, x_p)$ for each of the K possible classes or outcomes C_k. Using Bayes' rule, let's rewrite this as:

$$P(C_k|x_1, \dots, x_p) = \frac{P(C_k) \cdot P(x_1, \dots, x_p|C_k)}{P(x_1, \dots, x_p)}.$$

The denominator $P(x_1, \dots, x_p)$ does not depend on C_k, so it can be treated as a constant Z (since the values of $x_1, \dots, x_p$ are given). Let's thus focus on the numerator $P(C_k) \cdot P(x_1, \dots, x_p|C_k)$, which is equal to the joint probability $P(C_k, x_1, \dots, x_p) = P(x_1, \dots, x_p, C_k)$. Using the chain rule, we can write:

$$\begin{aligned} P(x_1, \dots, x_p, C_k) &= P(x_1|x_2, \dots, x_p, C_k) \cdot P(x_2, \dots, x_p, C_k) \\ &= P(x_1|x_2, \dots, x_p, C_k) \cdot P(x_2|x_3, \dots, x_p, C_k) \cdot \dots \cdot P(x_{p-1}|x_p, C_k) \cdot P(x_p|C_k) \cdot P(C_k). \end{aligned}$$

We now make a (naive) hypothesis of conditional independence of the features, that is, x_i is conditionally independent of every other feature x_j (with $i \neq j$). With this hypothesis in place, we can write:

$$\begin{aligned} P(C_k|x_1, \dots, x_p) \propto P(C_k, x_1, \dots, x_p) &= P(x_1, \dots, x_p, C_k) \\ &= P(x_1|C_k) \cdot P(x_2|C_k) \cdot \dots \cdot P(x_{p-1}|C_k) \cdot P(x_p|C_k) \cdot P(C_k) \\ &= P(C_k) \prod_{i=1}^{p} P(x_i|C_k). \end{aligned}$$

Recalling that $P(x_1, \dots, x_p)$ is a constant Z, we can finally write:

$$P(C_k|x_1, \dots, x_p) = \frac{1}{Z} P(C_k) \prod_{i=1}^{p} P(x_i|C_k).$$

The prediction rule is to assign a class k such that:

$$\arg \max_{k=1,\dots,K} P(C_k) \prod_{i=1}^{p} P(x_i|C_k),$$

which is estimated from the training set and then applied to the test set.

To estimate the $P(x_i|C_k)$, one can, for example, use a Gaussian distribution. Denoting with μ_{ki} and σ^2_{ki} the mean and variance of x_i in class k (i.e., x_{ki}), we get:

$$P(x_i|C_k) = \frac{1}{\sqrt{2\pi\sigma^2_{ki}}} \, e^{-\frac{(x_{ki} - \mu_{ki})^2}{2\sigma^2_{ki}}}.$$

Collaborative Flitering

Week 10

Method	**Collaborative Flitering**
Target	Rating (regression)
Model	?
Loss	RSME $= \sqrt{\sum_{i=1}^{u}(r_{ui} - p_{ui})^2/u}$
Quality of fit	?
Prediction	Recommendation Systems
Comments	Objective of recommendation systems - accuracy, variety, updatable, computationally efficient

Essentially, take the average of the nearest 250 users, promixity is calculated by correleation.

Limitations

- Inconsistent number of ratings given to each items
- "Cold start" - struggles with new users

Instead of clustering by genres, we can predict a user's rating on a movie, with all the past ratings done by all the users.

We can calculate the similarity across different users (we only calculate for the obects that has been rated by both users).

Baseline predictions for a movie by a user

- take the average of the prediction on the movie
- take the average of the prediction by the user

Predictive models

- Identify the cluster that the test user was classified into
    - Take the average rating by the cluster on the movie
    - Take a weighted average taking into account of the relative importance of each user in the subcluster (not all people in the cluster has rated the novie.)
    - Take into account bias of the user on movie - replace the average rating the user has been given with the average rating the subcluster gives.

Dataset processing

To decrease storage and transfer size, we are usually given list of ratings. Each rating consists of the rater (user) and the rated (movie), and the score.

```
length(unique(ratings$userId))  # 706
length(unique(ratings$movieId)) # 8552
sort(unique(ratings$rating))    # 0.5 1.0 ... 5.0
```

We need to transform this into a spare matrix for our input. We first create an empty matrix and them populate it.

```
Data <- matrix(nrow=length(unique(ratings$userId)),
ncol=length(unique(ratings$movieId)))

for(i in 1:nrow(ratings)){
  Data[as.character(ratings$userId[i]),
       as.character(ratings$movieId[i])] <- ratings$rating[i]}
```

Train test split in a matrix

Type	Movies	
Users	Training data	Data to make baseline prediction
	Data to make baseline prediction	Test set

```r
# We want to create a matrix with
# spl1 + spl1c rows and spl2 + spl2c columns

set.seed(1)
spl1 <- sample(1:nrow(Data), 0.98*nrow(Data))
# spl1 has 98% of the rows
spl1c <- setdiff(1:nrow(Data),spl1)
# spl1c has the remaining ones

set.seed(2)
spl2 <- sample(1:ncol(Data), 0.8*ncol(Data))
# spl2 has 80% of the columns
spl2c <- setdiff(1:ncol(Data),spl2)
# spl2c has the rest

# spl(s) are indices
length(spl1)  # 691
length(spl1c) # 15
length(spl2)  # 6841
length(spl2c) # 1711
```

We initialise the matrices to fill in our predictions. It should have the same dimension with our test set.

```r
test_set <- Data[spl1c, spl2c]
Base1    <- matrix(nrow=length(spl1c), ncol=length(spl2c))
Base2    <- matrix(nrow=length(spl1c), ncol=length(spl2c))
UserPred <- matrix(nrow=length(spl1c), ncol=length(spl2c))
```

Baseline predictions

The predicted rating by each user on a movie is the average of all predictions on the movie. A movie will have the same prediction, by any user.

```
for(i in 1:length(spl1c))
{Base1[i,] <- colMeans(Data[spl1,spl2c], na.rm=TRUE)}
Base1[,1:10]
# All rows (users) contain the same information
```

The predicted rating by a user on each movie is the average of all predictions by the user. A user will provide the same rating for all movies.

```
for(j in 1:length(spl2c))
{Base2[,j] <- rowMeans(Data[spl1c,spl2], na.rm=TRUE)}
Base2[,1:10]
# All columns (movies) contain the same information
```

Correlation model

Essentially, we are taking the average prediction of the nearest N users. We first initialse a matrix to contain the correleation between each pair of users.

```
# Initialize matrices
Cor <- matrix(nrow=length(spl1),ncol=1)
# keeps track of the correlation between users
Order <- matrix(nrow=length(spl1c), ncol=length(spl1))
# sort users in term of decreasing correlations
```

For each user, we calculate the correlation with all other users. Then each user will have a list of all (or most due to NAs) other user, ordered with decreasing correlation.

```
# The NAs account for users who have no common ratings of movies with the user.
for(i in 1:length(spl1c)){
  for(j in 1:length(spl1)){
      Cor[j] <- cor(Data[spl1c[i],spl2],
                    Data[spl1[j],spl2],
                    use = "pairwise.complete.obs")
      }
  V <- order(Cor, decreasing=TRUE, na.last=NA)
  Order[i,] <- c(V, rep(NA, times=length(spl1)-length(V)))
}
```

The prediction of the user on a movie will be average of the nearest N users. N is a hyperparameter chosen by us.

```
# Now, we compute user predictions by looking at the 250 nearest neighbours and
averaging equally over all these user ratings in the items in spl2c
for(i in 1:length(spl1c))
{UserPred[i,] <- colMeans(Data[spl1[Order[i,1:250]],spl2c], na.rm=TRUE)}
UserPred[,1:10]
```

Compare the model performance

We take the average of the squared difference with the test set.

```
RMSEBase1    <- sqrt(mean((Base1 - test_set)^2, na.rm=TRUE))
RMSEBase2    <- sqrt(mean((Base2 - test_set)^2, na.rm=TRUE))
RMSEUserPred <- sqrt(mean((UserPred - test_set)^2, na.rm=TRUE))


# Last step: we vary the neighborhood set for the third model to see whether it
positively affects the results
RMSE <- rep(NA, times=490)
for(k in 10:499)
{for(i in 1:length(spl1c))
  {UserPred[i,] <- colMeans(Data[spl1[Order[i,1:k]],spl2c], na.rm=TRUE)}
  RMSE[k-10] <- sqrt(mean((UserPred - test_set)^2, na.rm=TRUE))}
plot(10:499,RMSE)
```

Each user is represented through a vector of items (e.g. movie) and the associated rating given to each itme.

Inconsistent number of rating across items

Each items is represented by a vector of attributes.

Tobit model

Week 11

Method	Tobit model
Target	Number
Model	?
Loss	?
Quality of fit	?
Prediction	?
Comments	For left or right censored data

```r
library(survival)
# the Tobit model
model1 <- survreg(Surv(time_in_affairs,
                       time_in_affairs>0,type="left")~.,
                  data=train, dist="gaussian")
summary(model1)
predict1 <- predict(model1,newdata=test)
table(predict1<=0,test$time_in_affairs<=0)

# using linear model as baseline
model2 <- lm(time_in_affairs~., data=train)
summary(model2)
predict2 <- predict(model2,newdata=test)
table(predict2 <= 0, test$time_in_affairs==0)
```

This applies to censored target, does this apply to censored parameters as well?

Non-predictive models

These are models that do not produce a prediction. The output, however, can be used as a feature to the predictive models.

Supervised learning versus unsupervised learning Supervised learning. Given a set of **predictors** $\{x_1, \ldots, x_p\}$ and an output of $\{y\}$, we want to find a function $f(x_1, \ldots, x_p) = \hat{y}$ that minimise the error on some metric.

Unsupervised learning. Given a set of features, we want to find "**patterns**" within the data. Find a group of clusters that minimise the intra-cluster variance and maxisies the inter-cluter vairance.

K-means clustering

Week 10

Method	**K-means clustering**
Target	Clusters
Model	?
Loss	?
Quality of fit	?
Prediction	Recommendation Systems
Comments	?

Algorithmic Procedure

Initialisation - Given a number of clusters k, randomly generate k different means/centroids.

Assign each observation to the cluster whose mean/centroid has the closest Eculidean distance.

Update calculate the new means/centroid, and repeat assignment.

Stop when the assignment does not change.

Downsides

- May end up with different results
- May not converge or take a very long time to converge.

```r
# execute k-means clustering
# n-start is the number of different starting points
# choose the best clustering from each of the n-start
clusterMovies2 <- kmeans(Data[,1:19], centers=10, nstart=20)

# the loss within each cluster
clusterMovies3$withinss

# the total loss for all the clusters
clusterMovies2$tot.withinss # 7324.78

# Plot loss against k
fit <- c()
for(k in 1:15){
  clusterMovies4 <- kmeans(Data[,1:19], centers=k, nstart=20);
  fit[k] <- clusterMovies4$tot.withinss}
plot(1:15,fit)

# calculate the average of each feature in the cluster
Cat2 <- matrix(0,nrow=19,ncol=10)
for(i in 1:19){
  Cat2[i,] <- tapply(Data[,i], clusterMovies2$cluster, mean)}
rownames(Cat2) <- colnames(Data)[1:19]
Cat2

# list the elements in the cluster
subset(Data$title, clusterMovies2$cluster==6)
```

Hierarchical clustering

Week 10

Method	**Hierarchical clustering**
Target	Dendrogram, Clusters
Model	?
Loss	?
Quality of fit	?
Prediction	Recommendation Systems
Comments	?

Algorithmic Procedure

Compute the **Euclidean distance** between each pair. The closest pair forms a cluster and we take the midpoint. The output is a **dendrogram** (which is a binary tree).

In the visualisation, the distance of the **vertical edge** represents the distance between adjacent leaves. The horizontal placement and distance do not have a meaning. Unlike K-means clustering, there is no need for any hyperparamter tuning to build a dendrogram.

To create a cluster, we need to select a cutoff distance. Each tree cut by the cutoff is one cluster each. A cluster may only have one leaf, we can this an atomic cluster.

One reason not to use hierarchical clustering - We might have too many observations in the dataset for hierarchical clustering to handle.

You need to do **preprocessing** to convert the list of genre for each movie into to a binary list.

```r
# compute the distance between every pair
distances <- dist(Data[,1:19], method="euclidean")
dim(Data)
length(distances)

# execute hierarchical clustering
# Ward's distance method is used to find compact clusters.
clusterMovies1 <- hclust(distances, method="ward.D2")

# plot dendrogram
plot(clusterMovies1)

# create 10 clusters (by what criteria? binary search for cutoff?)
clusterGroups1 <- cutree(clusterMovies1, k=10)

# calculate the average of each feature in the cluster
Cat1 <- matrix(0,nrow=19,ncol=10)
for(i in 1:19){
  Cat1[i,] <- tapply(Data[,i], clusterGroups1, mean)}
rownames(Cat1) <- colnames(Data)[1:19]
Cat1

# list the elements in the cluster
subset(Data$title, clusterGroups1==6)
```

Text mining

Converts text into number for predictive models.

Read the dataset. Each entry of the dataset is a 'document'. A corpus is a set of documents

```r
library(tm)
library(SnowballC)
library(wordcloud)

twitter <- read.csv("wk9a-text.csv",stringsAsFactors=FALSE)
corpus <- Corpus(VectorSource(twitter$tweet))
```

Conduct text transformations to simplify the dataset.

```r
# list of text transfomrations
getTransformations()

# transformation into lower case
corpus <- tm_map(corpus, function(x) iconv(enc2utf8(x), sub = "byte"))
corpus <- tm_map(corpus, content_transformer(function(x) iconv(enc2utf8(x), sub
= "bytes")))
corpus <- tm_map(corpus,content_transformer(tolower))

# remove stop words
corpus <- tm_map(corpus,removeWords,
stopwords("english"))

# remove specific words because they confuse the objective
corpus <- tm_map(corpus,removeWords,
c("drive","driving","driver","self-driving","car","cars"))

# remove punctuation
corpus <- tm_map(corpus,removePunctuation)

# stemming words (get root word)
corpus <- tm_map(corpus,stemDocument)
```

Convert into a document term matrix. This is a freqlist of every document in the corpus.

```
# convert into freqlist of words this will be a sparse matrix
dtm <- DocumentTermMatrix(corpus)
dim(dtm) # dimensions before removal
dtm <- removeSparseTerms(dtm,0.995)
```

Transforming into a dataframe to train and test

```
# converting DTM into dataframe
twittersparse <- as.data.frame(as.matrix(dtm))

# make sure column names start with a character
colnames(twittersparse) <- make.names(colnames(twittersparse))

# assign labels to dataframe
twittersparse$Neg <- twitter$Neg
```

Visualise the dataset with a wordcloud.

```
# plot wordcloud
colnames(twittersparse) <- make.names(colnames(twittersparse))
colnames(twittersparse)
word_freqs = sort(colSums(twittersparse), decreasing=TRUE)
# Create dataframe with words and their frequencies
dm = data.frame(word=names(word_freqs), freq=unname(word_freqs))
# Plot wordcloud
wordcloud(dm$word, dm$freq, random.order=FALSE, max.words=100,
colors=brewer.pal(8, "Dark2"), min.freq=2)
```

Then carry out your model based on their mdoels.

Singular Value Decomposition

Week 11

Method	Singular Value Decomposition
Target	?
Model	?
Loss	?
Quality of fit	?
Prediction	NA
Comments	For image compression

Review of linear algebra

```r
# define a matrix
A <- matrix(c(2, 2, 3, 1), nrow=2, ncol=2)

# Get eigenvectors and eigenvalues
A_eig <- eigen(A)
A_eig$values
A_eig$vectors # these vectors are normalised
```

Eigen decomposition

$$A = V \cdot S \cdot V^{-1}$$

V is a square matrix made up of columns of eigenvectors, and S is a square matrix with its main diagonal made up of eigenvalues is the corresponding order.

```r
# reconstruct the matrix
# (note the operator %*% for the matrix multiplication)
A_eig$vectors %*% diag(A_eig$values) %*% solve(A_eig$vectors)
```

If A is positive semi definite (eigenvalues of A is non-negative), $V^{-1} = V^T$

Singular Value Decomposition

$$\underset{m\times n}{X} = \underset{m\times n}{U} \cdot \underset{n\times n}{S} \cdot \underset{n\times n}{V^T}$$

It can be shown that

$$X \cdot X^T = U \cdot S^2 U^T$$

$$X^T \cdot X = V \cdot S^2 V^T$$

U contains the m eigenvectors of $X \cdot X^T$ (left singular vectors)

S contains the n square roots of $X \cdot X^T$ eigenvalues (singular **values**)

V contains the n eigenvectors of $X^T \cdot X$ (right singular vectors)

```
X <- matrix(c(2,1,5,7,0,0,6,0,0,10,
              8,0,7,8,0,6,1,4,5,0), nrow=5, ncol=4)

s <- svd(X) # apply SVD
s$u # U
s$d # S
s$v # V

# reconstruct the matrix
s$u %*% diag(s$d) %*% t(s$v)
```

When R implements SVD it transforms it into $m > n$. Check the function parameters of `svd()` for variations.

Approximating a matrix

$$\underset{m\times n}{\hat{X}} = \underset{m\times k}{U_k} \cdot \underset{k\times k}{S_k} \cdot \underset{k\times n}{V_k^T}$$

```
# reconstruct a matrix with limited elements
k <- 2  # less than or equal to n
s$u[,1:k] %*% diag(s$d[1:k]) %*% t(s$v[,1:k])
```

Calculate explained variance Frobenius norm of a matrix $||x||_F$

$$||X||_F = \sqrt{\sum_{i=1}^{m}\sum_{j=1}^{n} x_{i,j}^2}$$

$$\frac{||\hat{X}||_F}{||X||_F} = \frac{\sigma_1^2 + \ldots + \sigma_k^2}{\sigma_1^2 + \sigma_1^2 + \ldots + \sigma_n^2}$$

```
# calculate the explained variance
var <- cumsum(s$d^2)
plot(1:4,var/max(var))
```

Image compression with SVD

For grayscale images

```r
# read image
lky <- readJPEG("wk11-gray.jpg")

# grayscale images has same values for all channels
# apply SVD on the image
s <- svd(lky[,,1])

# compress and save the image
k = 10
lky10 <- s$u[,1:k] %*% diag(s$d[1:k]) %*% t(s$v[,1:k])

# write image to file
writeJPEG(lky10,"wk11-gray10.jpg")

# calculate the explained variance
var <- cumsum(s$d^2)
plot(1:4,var/max(var))
```

For colored images

```r
# read image
pansy <- readJPEG("wk11-color.jpg")

# apply SVD on the image
s1 <- svd(pansy[,,1])
s2 <- svd(pansy[,,2])
s3 <- svd(pansy[,,3])

# compress and save the image
k = 50
pansy50 <- array(dim=dim(pansy))
pansy50[,,1] <- s1$u[,1:k] %*% diag(s1$d[1:k]) %*% t(s1$v[,1:k])
pansy50[,,2] <- s2$u[,1:k] %*% diag(s2$d[1:k]) %*% t(s2$v[,1:k])
pansy50[,,3] <- s3$u[,1:k] %*% diag(s3$d[1:k]) %*% t(s3$v[,1:k])

# write image to file
writeJPEG(pansy50,"wk11-color50.jpg")
```

Kaplan-Meier estimator

Not a prediction model, estimate the chances of "occurance" over time just by the results.

An event will happen at a distribution with pdf $f(x)$ and corresponding cdf $F(x)$.

The hazard function is the instantaneous rate of probability the event happening

$$\lambda(t) = \frac{f(t)}{1 - F(t)} = \frac{f(t)}{S(t)}$$

Given the data, you can estimate $S(t) = 1 - F(t)$.

$$\hat{S}(t) = \prod_{t_i < t} \frac{n_i - d_i}{n_i}$$

n_i is the number of people who have survived until before t_i. If t_i are continuous values, d_i will always be one.

```r
km <- survfit(Surv(start,stop,event)~1,data=heart)
summary(km,censored=TRUE)
# summary of the model, with patients' survival probability

# plot the Kaplan-Meier curve along with 95% confidence interval
plot(km)
```

Cox proportional hazard model

This is a prediction model but I put it here. This estimate the chances of occurance over time, now taking into account of some parameters.

Week 11

Method	**Cox proportional hazard model**
Target	?
Model	$\lambda(t) = \lambda_0(t) \cdot e^{\beta_1 x_1 + \beta_2 x_2 + \ldots}$
Loss	?
Quality of fit	?
Prediction	This is a linear model, with censored values.
Comments	?

An event will happen at a distribution with pdf $f(x)$ and corresponding cdf $F(x)$.

$$\lambda(t) = \lambda_0 \cdot exp(\beta_1 x_1 + \ldots + \beta)$$

```
cox <- coxph(Surv(start,stop,event)~age+surgery+transplant,
             data=heart)
summary(cox)

# plot S(t)
plot(survfit(cox))
summary(survfit(cox))

predict(cox, data=heart)
```