

Cheatsheet TDDE01

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Miscellaneous

Vocabulary

Generalization error: error on test data.

Info

Test data is after validation, validation data is during testing of models.

Naïve Bayes: doesn't combine information to classify, tries to classify with individual properties. Doesn't work well with linear separations.

Gets biggest value:

```
which_max(data)
```

How to read R scripts:

```
{r, code = readLines("lab1/ass2.R"), eval=FALSE}
```

Read data and split into random sets

```
video = read.csv("video.csv")
data = subset(video, select=-utime)
data_size = dim(data)[1]
set.seed(12345)
i1 = sample(1:data_size, floor(data_size*0.5))
i2 = setdiff(1:data_size, i1)
train = data[i1,]
test = data[i2,]
```

Plotting

```
library("ggplot2")
library("gridExtra")
plot.projection = ggplot() +
  geom_point(data=spectra, mapping=aes(x=PC1, y=PC2, color=class))
grid.arrange(plot.projection)

plot(data, type='l', col="red", ylim=c(100, 500), ylab="Error")
plot(data2, type='l', col="blue")
```

PCA and select principal components

```
library("stats")
pca.fit = prcomp(data, scale.=T)
# screeplot(pca.fit) to get all eigen values
# Get eigen values (standard deviation ^ 2)
lambda = pca.fit$sdev^2
sprintf("%2.3f", lambda/sum(lambda))
```

```
PC1 = pca.fit$x[,1]
PC2 = pca.fit$x[,2]
```

Use *princomp* for loadings to get eigenvectors.

```
library("stats")
pca.fit = princomp(data)
loadings(pca.fit)
```

Confusion matrix

```
t <- table(prediction, true_values)
(t[1,2]+t[2,1])/sum(t)
```

Labs

Lab 1

Assignment 1

```
# Search for function: RSiteSearch("expression")
library("knn")
# 1.1

# Set working directory
setwd("~/courses/tdde01/lab1/")

# Read data
data = read.csv("spambase.csv")

n=dim(data)[1]
set.seed(12345)
id=sample(1:n, floor(n*0.5))
train=data[id,]
test=data[-id,]

# 1.2
# Create a General Linear Model
model = glm(formula = Spam~., data = train, family = 'binomial')

# Make prediction on test
predict_test = predict(model, test, 'response')
# Make prediction of train
predict_train = predict(model, train, 'response')
# Show result, match actual answers to predicted ones
table_test_0.5 = table(test$Spam, predict_test > 0.5)
table_train_0.5 = table(train$Spam, predict_train > 0.5)
cat("\nPrediction with GML model, test data. 0.5")
print(table_test_0.5)
cat("Missclassification rate: ")
cat((sum(table_test_0.5[2]) + sum(table_test_0.5[3]))/sum(table_test_0.5[1:4]))
cat("\n\n");
```

```

cat("Prediction with GML model, train data. 0.5")
print(table_train_0.5)

cat("Missclassification rate:")
cat((sum(table_train_0.5[2]) + sum(table_train_0.5[3]))/sum(table_train_0.5[1:4]))
cat("\n\n");
# 1.3
table_test_0.9 = table(test$Spam, predict_test > 0.9)
table_train_0.9 = table(train$Spam, predict_train > 0.9)
cat("Prediction with GML model, test data. 0.9")
print(table_test_0.9)
cat("Missclassification rate:")
cat((sum(table_test_0.9[2]) + sum(table_test_0.9[3]))/sum(table_test_0.9[1:4]))
cat("\n\n");

cat("Prediction with GML model, train data. 0.9")
print(table_train_0.9)
cat("Missclassification rate:")
cat((sum(table_train_0.9[2]) + sum(table_train_0.9[3]))/sum(table_train_0.9[1:4]))
cat("\n\n");

# 1.4
K = 30
# kknn is classifier
kknn_test = kknn(formula = Spam~., train = train, test = test, k = K)
kknn_train = kknn(formula = Spam~., train = train, test = train, k = K)
table_kknn_test = table(test$Spam, kknn_test$fitted.values > 0.5)
table_kknn_train = table(train$Spam, kknn_train$fitted.values > 0.5)
cat("KKNN result using test data test for K=30")
print(table_kknn_test)
cat("Missclassification rate:")
cat((sum(table_kknn_test[2]) + sum(table_kknn_test[3]))/sum(table_kknn_test[1:4]))
cat("\n\n");
cat("KKNN result using test data train for K=30")
print(table_kknn_train)
cat("Missclassification rate:")
cat((sum(table_kknn_train[2]) + sum(table_kknn_train[3]))/sum(table_kknn_train[1:4]))
cat("\n\n");

# 1.5
K = 1
# kknn is classifier
kknn_test = kknn(formula = Spam~., train = train, test = test, k = K)
kknn_train = kknn(formula = Spam~., train = train, test = train, k = K)
table_kknn_test = table(test$Spam, kknn_test$fitted.values > 0.5)
table_kknn_train = table(train$Spam, kknn_train$fitted.values > 0.5)
cat("KKNN result using test data test for K=1")
print(table_kknn_test)
cat("Missclassification rate:")
cat((sum(table_kknn_test[2]) + sum(table_kknn_test[3]))/sum(table_kknn_test[1:4]))
cat("\n\n");
cat("KKNN result using test data train for K=1")
print(table_kknn_train)

```

```

cat("Missclassification rate:")
cat((sum(table_kknn_train[2]) + sum(table_kknn_train[3]))/sum(table_kknn_train[1:4]))
cat("\n\n");

```

Assignment 2

```

# 2.1
# Set working directory
setwd("~/courses/tdde01/lab1/")
# Read data
data = read.csv("machines.csv")

n=dim(data)[1]
set.seed(12345)
id=sample(1:n, floor(n*0.5))
train=data[id,]
test=data[-id,]

# 2.2 Exponential distribution
# PxTheta
pxt = function(x, theta){
  # Prod returns product of all arguments
  return (log(prod(theta*exp(-theta*x))))
}
thetas = seq(from=0, to=2, by=0.005)
theta_fn = sapply(thetas, function(theta) pxt(data$Length, theta))
#par(mar=c(1,1,1,1))
plot(thetas, theta_fn, xlabel="X", ylabel="Y", type="p")
theta_max = thetas[which.max(theta_fn)]
cat("Max theta value: ")
cat(theta_max)
cat("\n\n")

# 2.3
short_data = data$Length[1:6]
short_theta_fn = sapply(thetas, function(theta) pxt(short_data, theta))
par(mar=c(4,4,2,1))
plot(thetas, theta_fn, xlab="Theta", ylab="", type="l", ylim=c(-100, 0))
lines(thetas, short_theta_fn, col="blue")
short_theta_max = thetas[which.max(short_theta_fn)]
cat("Max theta value of short dataset: ")
cat(short_theta_max)
cat("\n\n")

# 2.4
pt = function(theta){
  return (10*exp(-10*theta))
}
pxt = function(x, theta) {
  return (prod(theta*exp(-theta*x)))
}
l = function(x, theta){

```

```

        return (log(pt(x, theta)*pt(theta)))
    }
theta_fn = sapply(thetas, function(theta) l(data$Length, theta))
l_max = thetas[which.max(theta_fn)]
lines(thetas, theta_fn, col="red")
cat("Max theta value: ")
cat(l_max)
cat("\n\n")

# 2.5
new_data = rexp(50, theta_max)
hist(new_data, main="Random values, exponential distribution", xlab="")
hist(data$Length, main="Original data", xlab="")

```

Assignment 4

```

# Assignment 4
# Set working directory
setwd("~/courses/tdde01/lab1")

# Read data
data = read.csv("tecator.csv")

# 4.1 No?
plot(data$Protein, data$Moisture, xlab="Protein", ylab="Moisture", type = "p")

# 4.2 TODO:

# 4.3
n=dim(data)[1]
set.seed(12345)
id=sample(1:n, floor(n*0.5))
train=data[id,]
eval=data[-id,]

mse_eval_list = c()
mse_train_list = c()
for (x in c(1, 2, 3, 4, 5, 6)){
  model=lm(formula = Moisture ~ poly(Protein, x, raw = TRUE), data = train)
  # Eval data
  mse = mean((eval$Moisture - predict(model, eval))^2)
  mse_eval_list=c(mse_eval_list, mse)

  # Train data2
  mse = mean((train$Moisture - predict(model, train))^2)
  mse_train_list=c(mse_train_list, mse)
}

counts <- table(mse_eval_list, mse_train_list)
barplot(c(mse_eval_list, mse_train_list),
        main="Prediction on evaluation and training data",
        ylab="MSE",

```

```

    xlab="Blue: eval, Red: train",
    col=c("blue","blue","blue","blue","blue","red", "red", "red", "red", "red", "red"),
    ylim=c(32, 35))
stop()

# 4.4
channels = data[,2:102]
model = lm(formula = Fat~. , data = channels)
step_alg = stepAIC(model, direction="both", trace = FALSE)
cat("Length: ", length(coef(step_alg)) -1, "\nCoefficients: ", coef(step_alg))

# 4.5
covariates=channels[,1:100]
response=channels[, 101]
model0=glmnet(as.matrix(covariates),
              response,
              alpha=0,
              family="gaussian")
plot(model0, xvar="lambda", label=TRUE)
# The coefficients shrink when lambda increases

# 4.6
# LASSO, alpha = 1
model1=glmnet(as.matrix(covariates),
              response,
              alpha=1,
              family="gaussian")
plot(model1, xvar="lambda", label=TRUE)

# 4.7
model=cv.glmnet(as.matrix(covariates),
                 response,
                 lambda = seq(0, 5, 0.005),
                 alpha=1,
                 family="gaussian")
cat("\n\nMin lambda: ", model$lambda.min)
plot(model)
cat("\nNumber of coefficients of lambda min: ")
coeffs = coef(model, s=model$lambda.min)
coeffs
cat(sum (coeffs[2:101,] != 0))

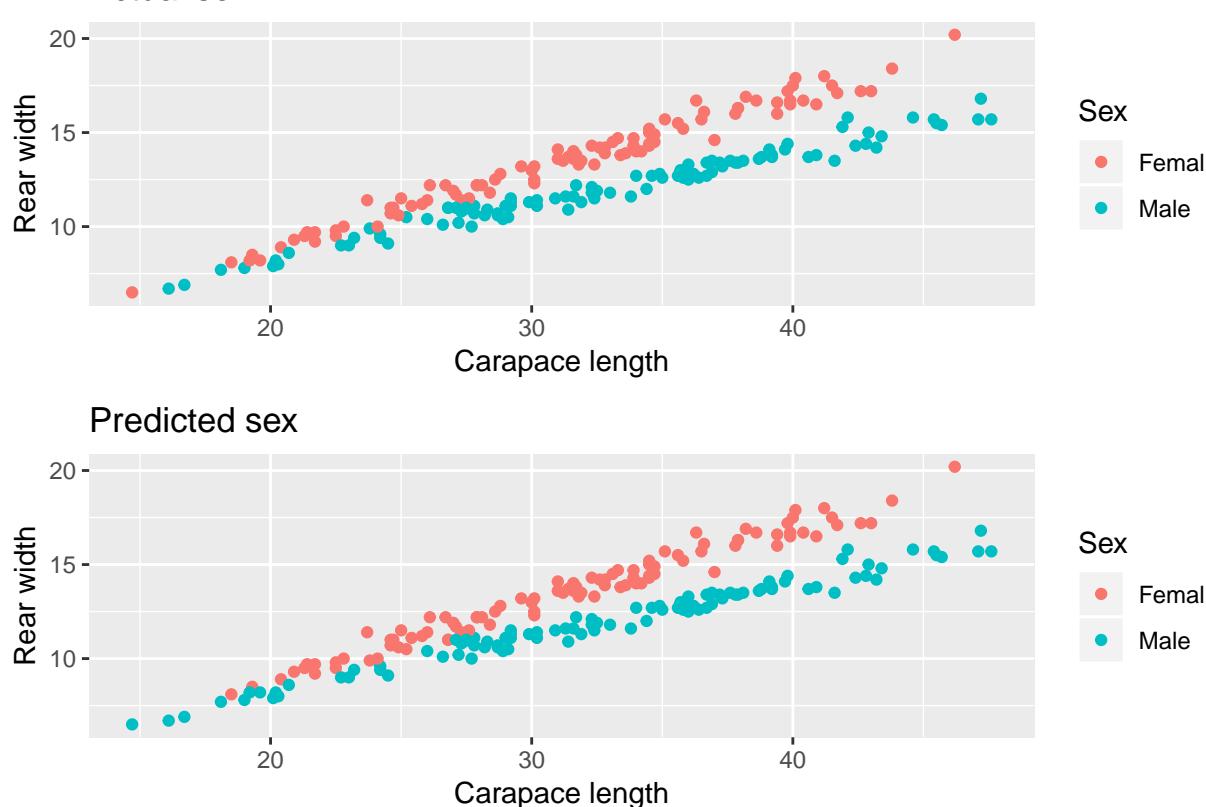
# 4.8 Compare 4 and 7

```

Lab 2

Assignment 1

Step 1 & 2



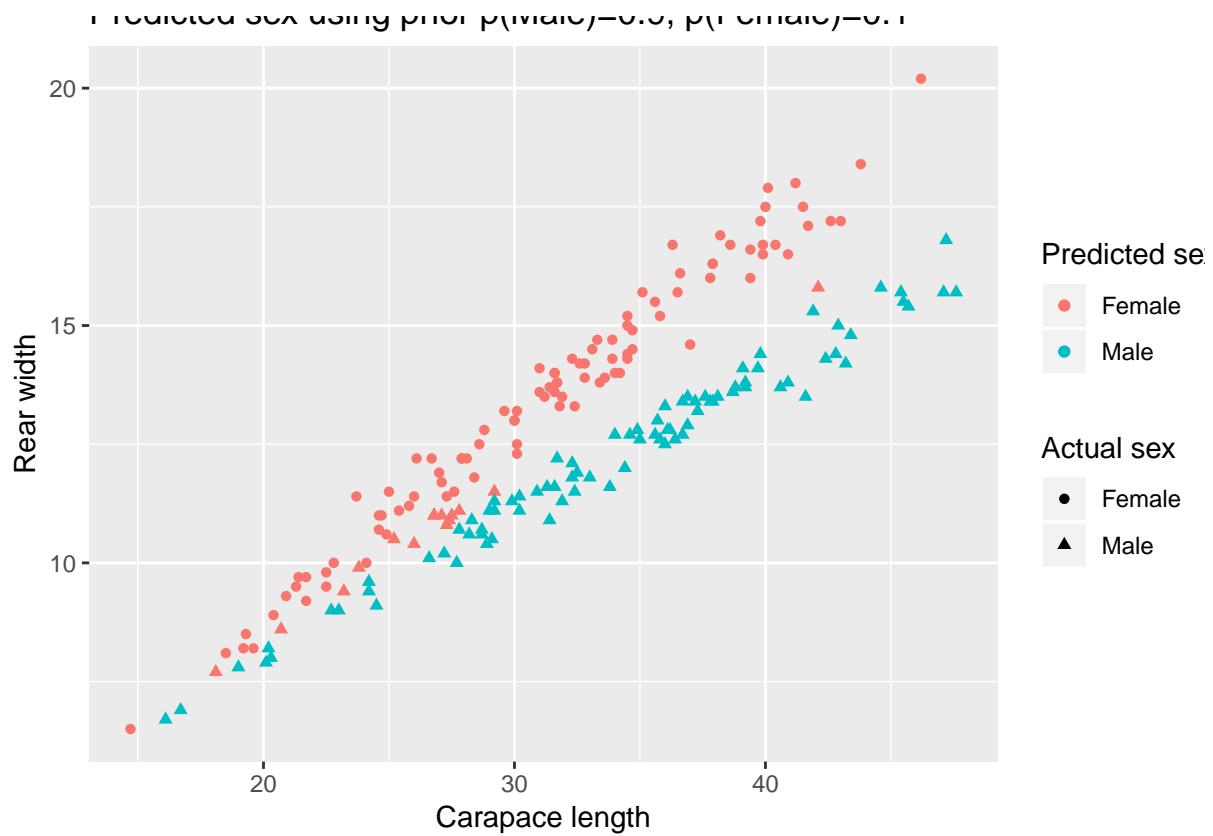
```
## Misclassification rate for lda:  0.035
```

Since the sexes seem to follow two separate lines, they are separable. Therefore it's appropriate to classify this data with a linear discriminant analysis. The only problem is where these two lines intersect and the sexes are impossible to differ. Some data may also be crossing this line and get a false classification.

The misclassification rate is really good, which strengthens the argument that the classification method is appropriate.

Step 3

This time, the same prediction is made, but with the priors $p(\text{Male}) = 0.9$ and $p(\text{Female}) = 0.1$. See plot below.



```
## Misclassification rate for lda with p(Male=0.9), p(Female)=0.1: 0.075
```

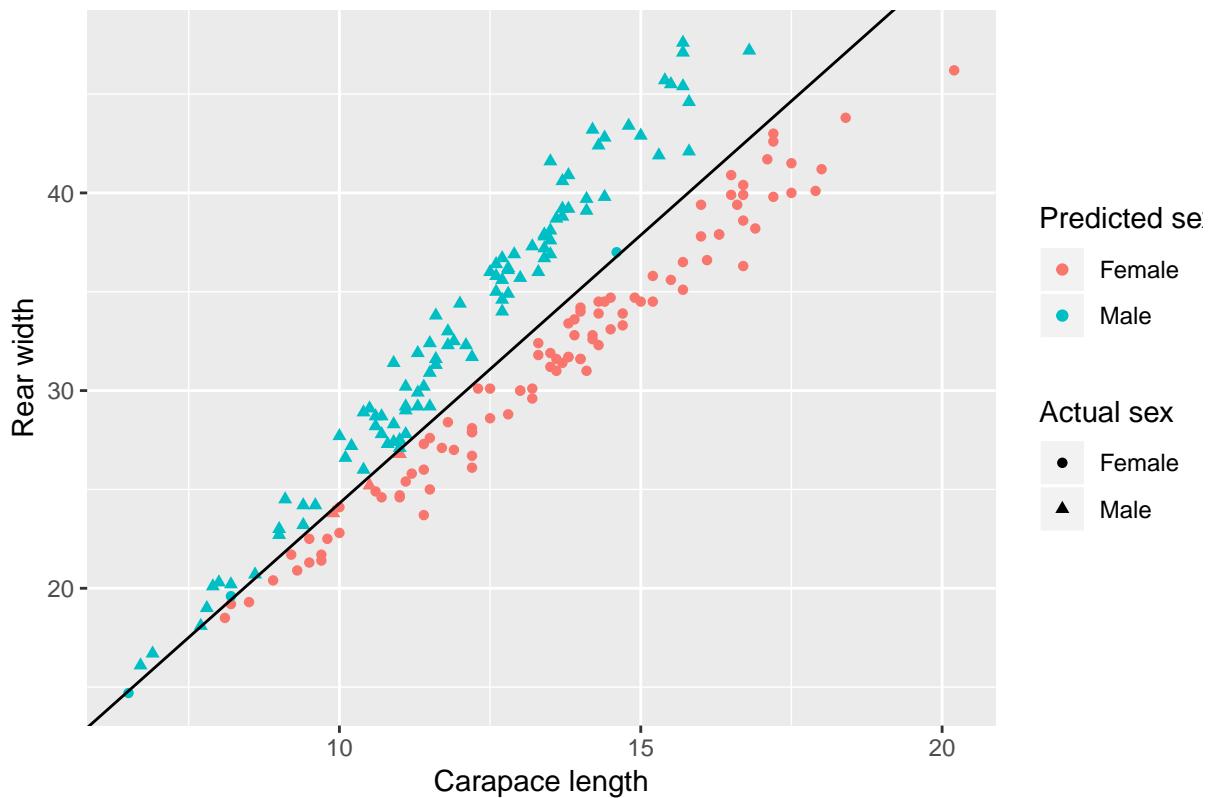
This time, the misclassification is greater. That is because the priors are not according to the actual distribution of sexes.

Step 4

Here the equation of the decision boundary is plotted together with classification using GLM.

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

Actual and predicted sex (GLM), and decision boundary



```
## Misclassification rate for GLM: 0.035
```

The misclassification rate is the same as in step 2.

Assignment 2

Step 1

Firstly, the data was separated into training, validation and test data.

Step 2

```
## Misclassification on deviance with test: 0.268
```

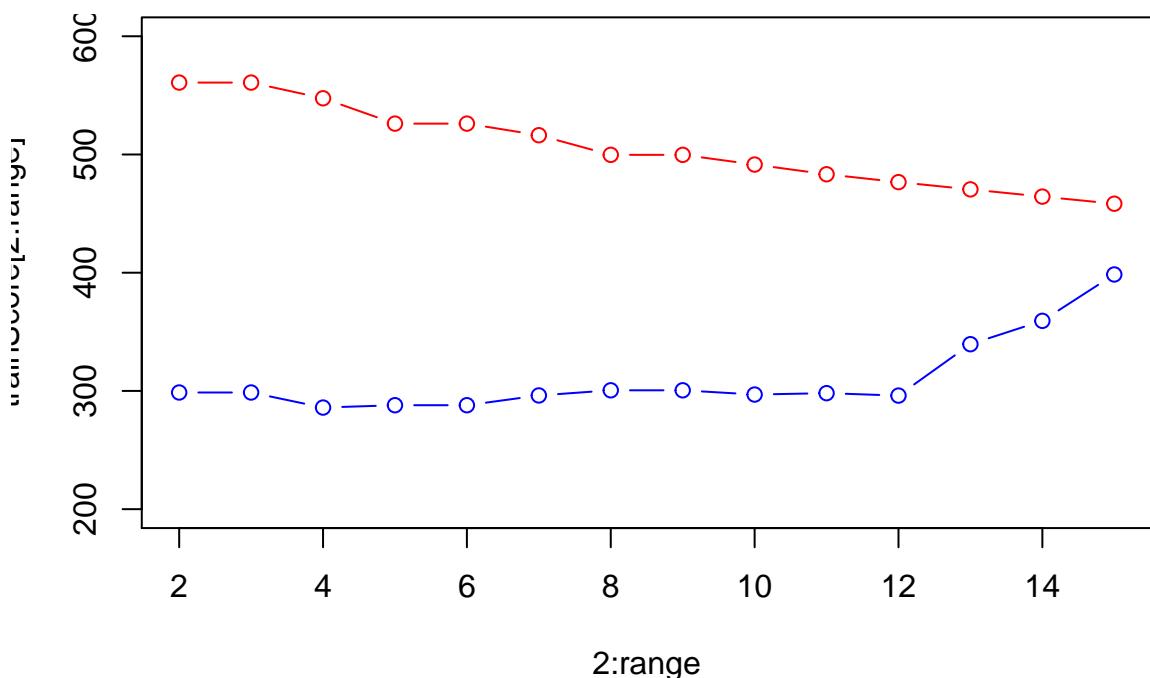
```
## Misclassification on deviance with train: 0.212
```

```
## Misclassification on gini with test: 0.368
```

```
## Misclassification on gini with train: 0.24
```

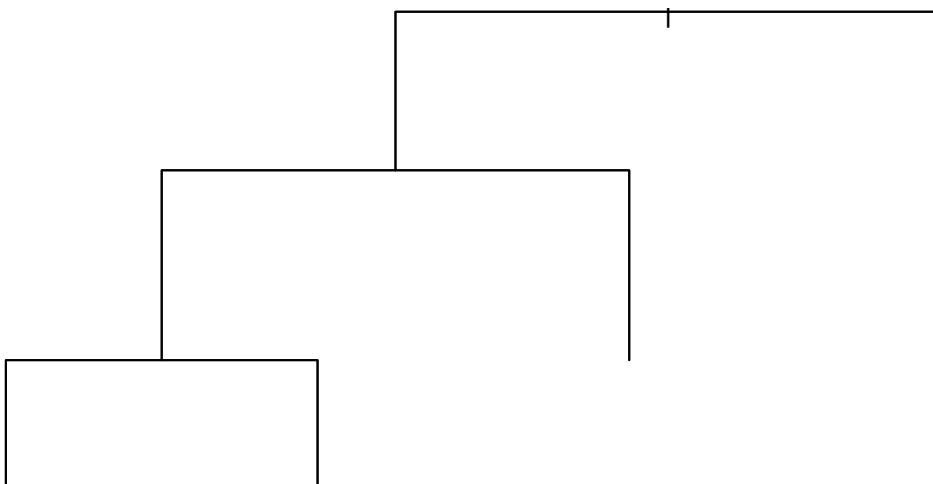
Here, misclassification rate is lower when using deviance as measure of impurity.

Step 3



```
## Misclassification on optimal tree: 0.256
```

```
## Tree depth is 3 as can be seen in the plot.
```



```
## Used variables in optimal tree:
```

```
## 'savings' 'duration' 'history'
```

Step 4

```
## Confusion table of naïve bayes (test):
```

```
##          Actual
```

```
## Predicted bad good
```

```
##      bad    46   49
```

```
##      good   30  125
```

```
## Misclassification with naive bayes (test): 0.316
```

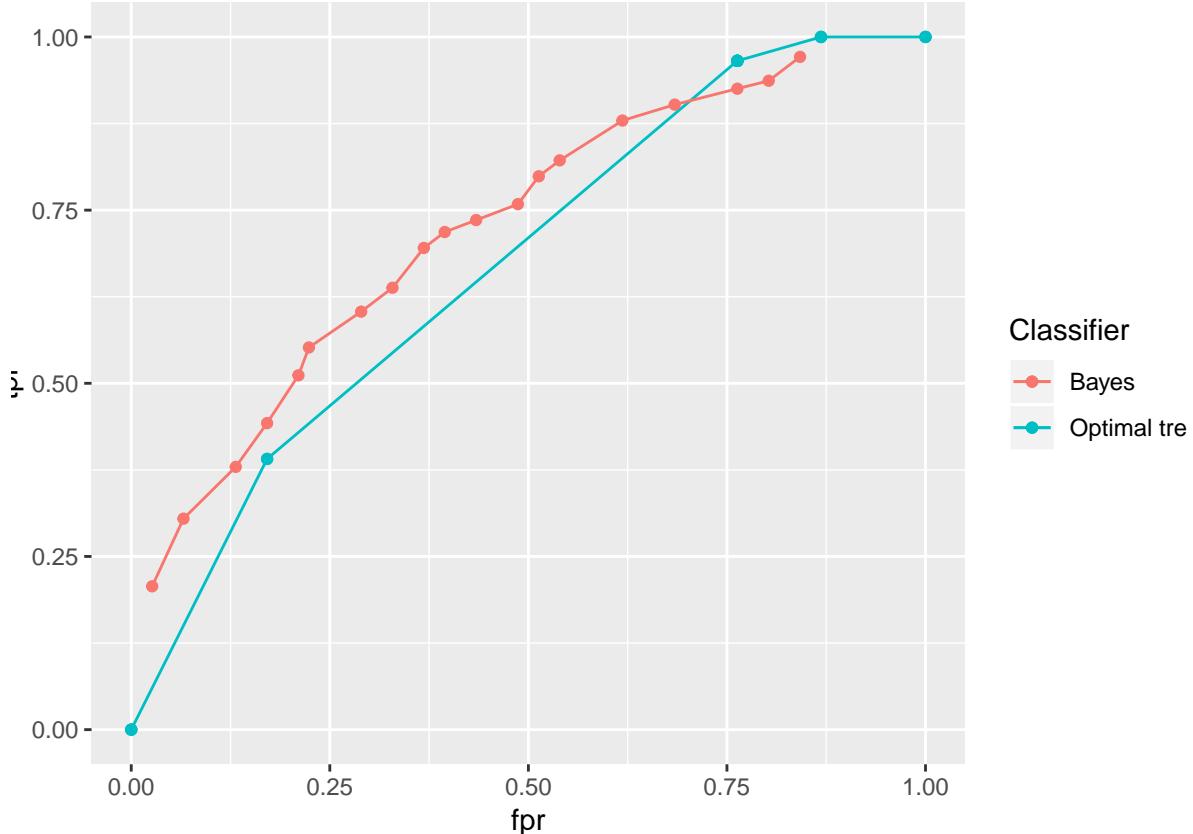
```

## Confusion table of naïve bayes (train):
##          Actual
## Predicted bad good
##      bad    95   98
##      good   52  255
## Misclassification with naive bayes (train):  0.3

```

Naïve Bayes has much better result than in step 3.

Step 5



Naïve Bayes has better ratio between TPR and FPR. The only exception is around $\pi = 0.75$, as can be seen in the graph.

Step 6

Using loss matrix with naïve bayes.

```

## Confusion table of naïve bayes (using test data):
##          Actual
## Predicted bad good
##      bad    71   122
##      good   5    52
## Misclassification with naive bayes (using test data):  0.508
## Confusion table of naïve bayes (using train data):

```

```

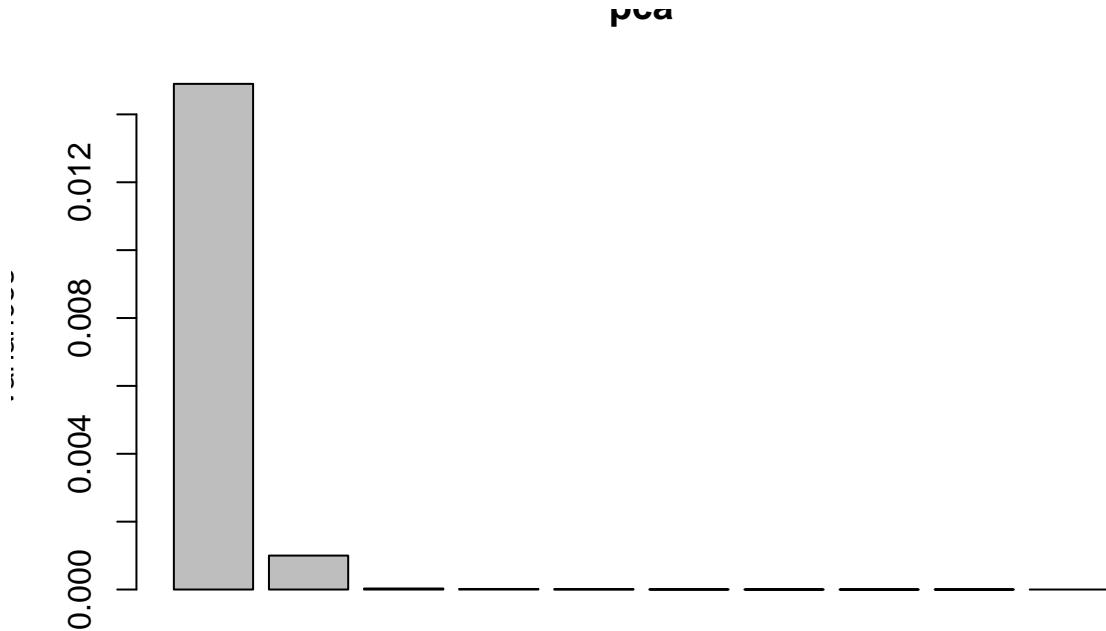
##           Actual
## Predicted bad good
##      bad 137 263
##      good 10   90
## Misclassification with naïve bayes (using train data): 0.546

```

The misclassification is much greater. But the confusion matrix is more favorable from an economic point of view for a company since less are predicted good that are actually bad.

Assignment 4

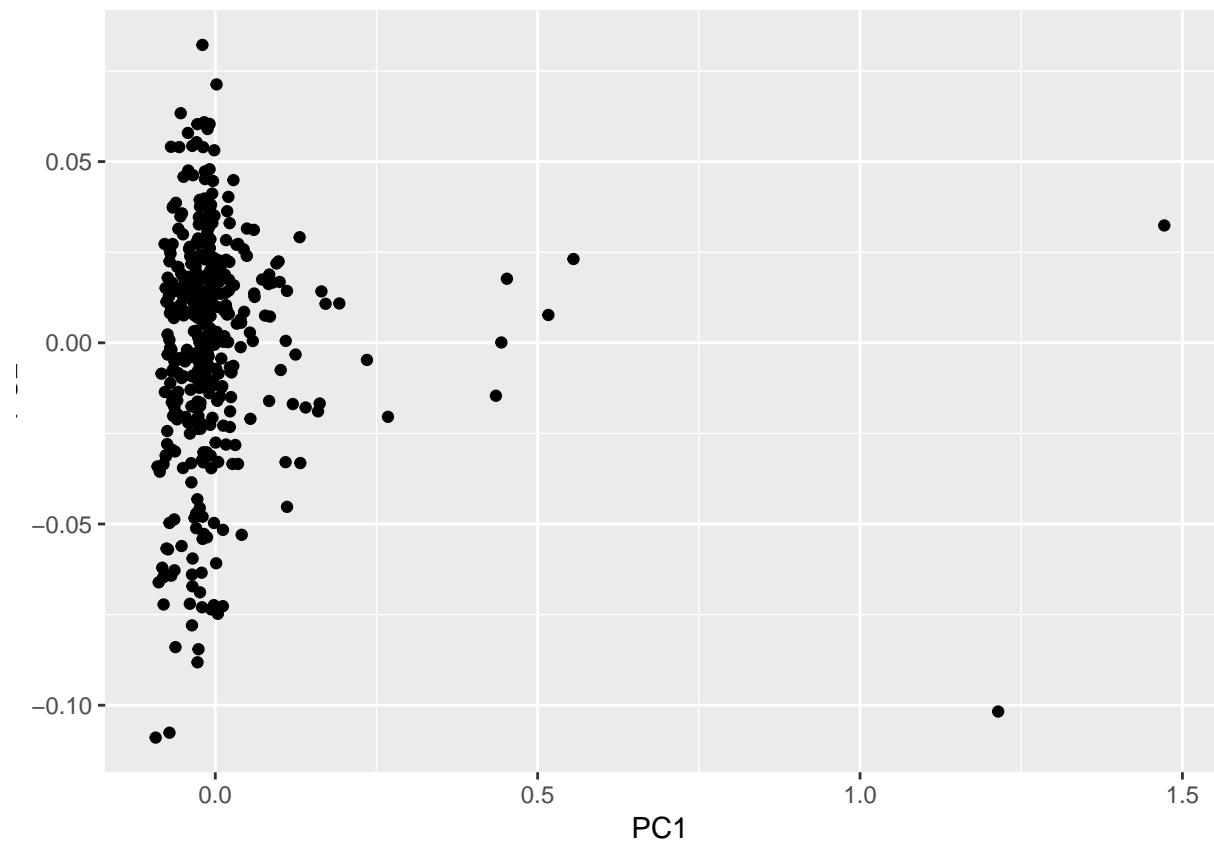
Step 1



```

## 99% of the variance can be explained by first two PC.

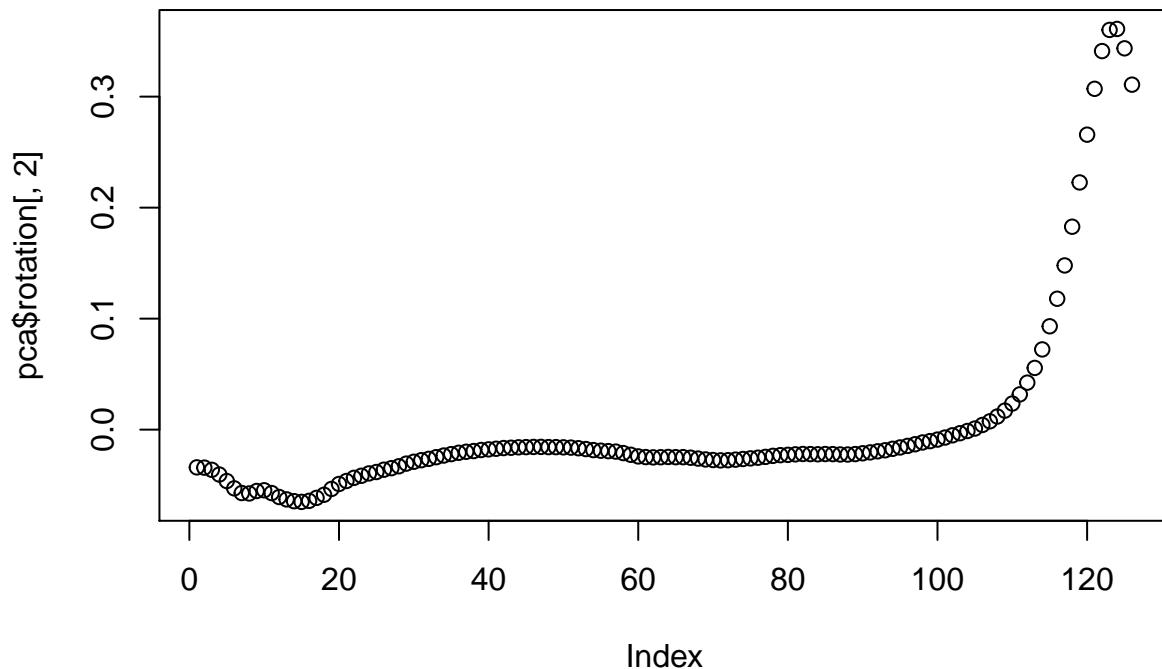
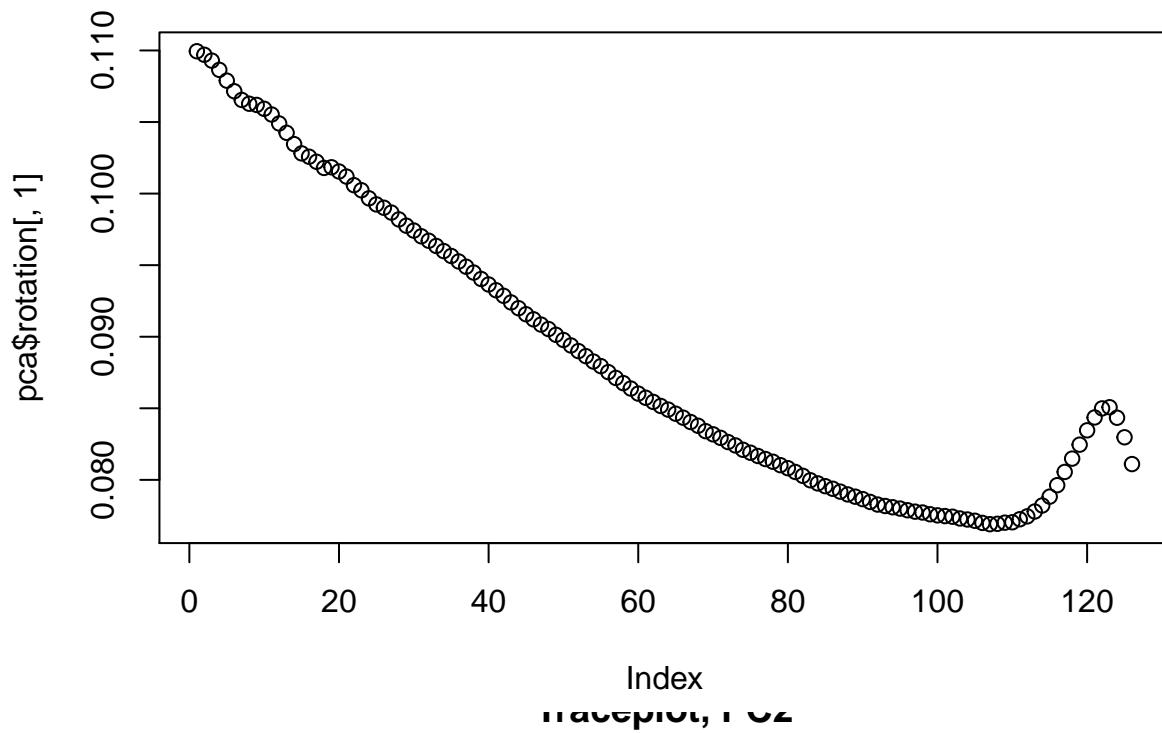
```



Some diesel fuels depend a lot on PC1, compared to other fuels, I would say that these are unusual.

Step 2

maeplot, 1 vs 1



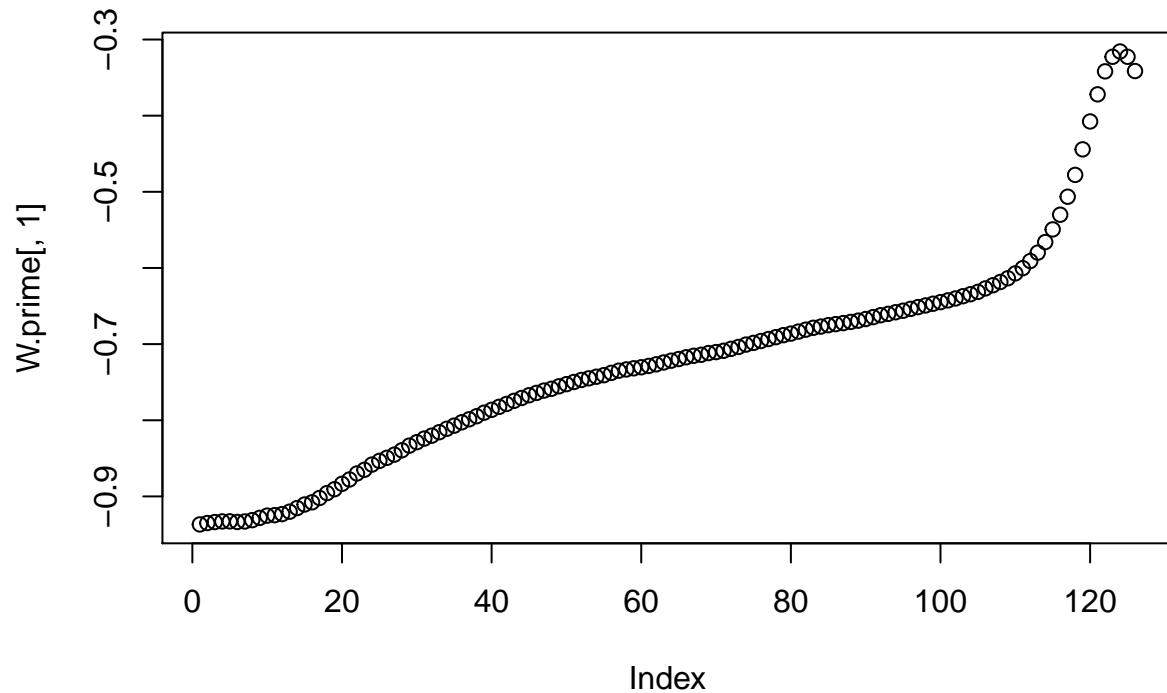
PC2 is explained by mainly a few original features. This can be seen in the graph since it's almost zero until Index is around 100-130.

Step 3

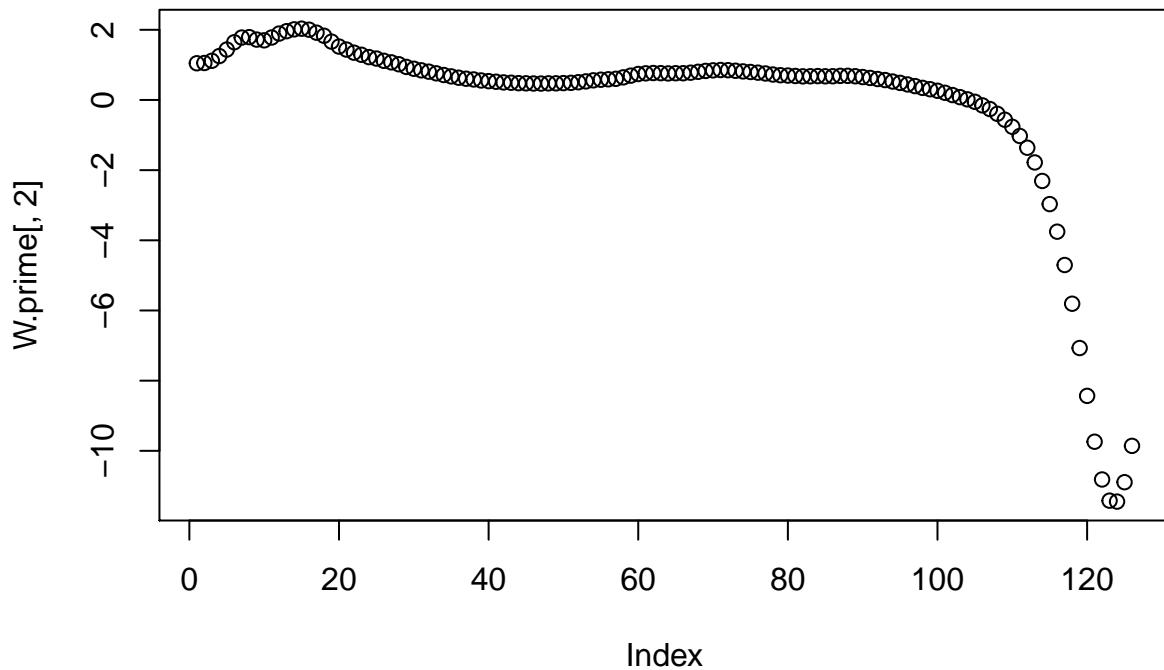
a

```
## Centering  
## Whitening  
## Symmetric FastICA using logcosh approx. to neg-entropy function  
## Iteration 1 tol = 0.01930239  
## Iteration 2 tol = 0.01303959  
## Iteration 3 tol = 0.002393582  
## Iteration 4 tol = 0.0006708454  
## Iteration 5 tol = 0.0001661602  
## Iteration 6 tol = 3.521604e-05
```

traceplot, 1 ~ 1

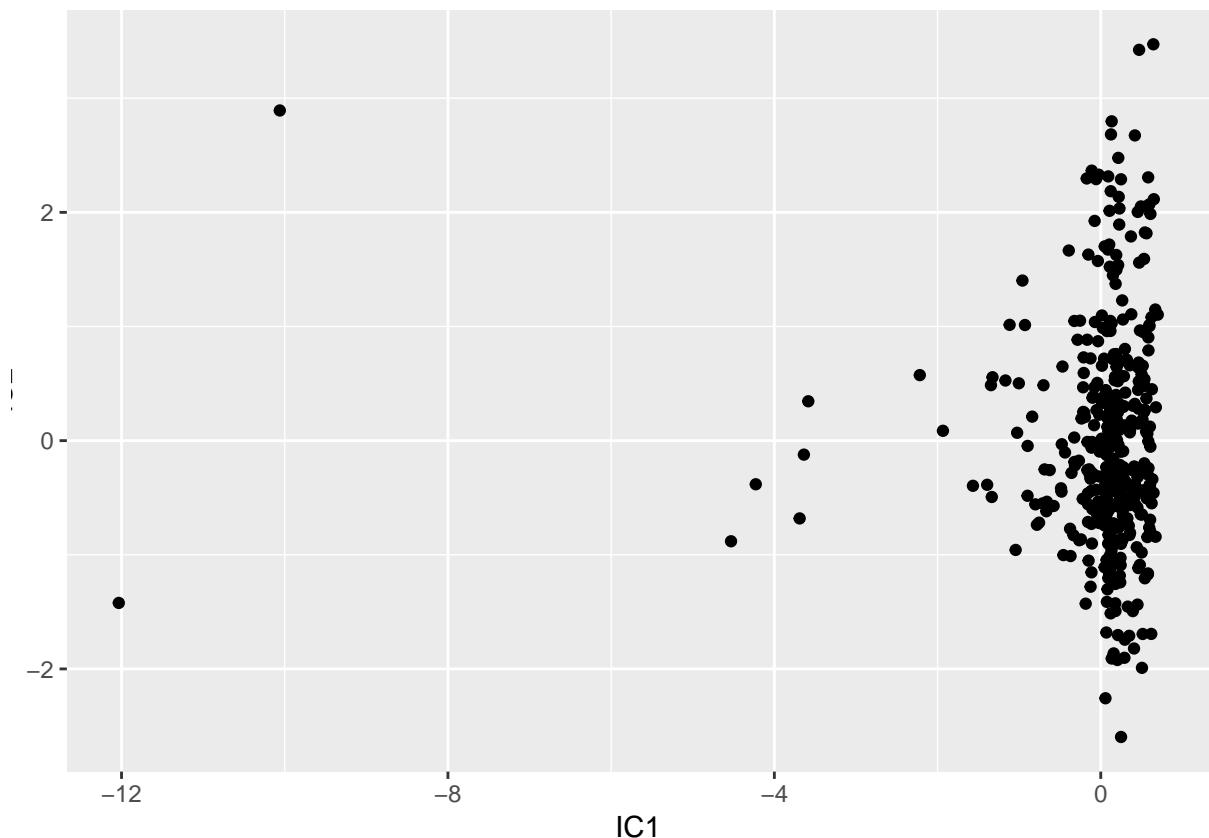


matplot, 1 vs 2



W' is an estimation of an un-mixing matrix.

b



This plot is very similar to the one in step 1, but it is flipped and scaled.

Appendix

Assignment 1

```
# Add libraries
library("gridExtra")
library("ggplot2")
library("MASS")

# Set working directory
setwd("~/courses/tdde01/lab2")

# Read data
crabs = read.csv("australian-crabs.csv")

crabs.plot = ggplot(data = crabs,
                     mapping = aes(x=CL,
                                   y=RW,
                                   color=sex)) +
  geom_point() +
  ggtitle("Actual sex") +
  scale_x_continuous(name = "Carapace length") +
```

```

scale_y_continuous(name = "Rear width") +
scale_color_discrete(name = "Sex")

lda.model = lda(formula = sex~CL+RW, data = crabs)
lda.predict = predict(lda.model, crabs)
crabs.predict = ggplot(data = crabs,
                        mapping = aes(x=CL,
                                      y=RW,
                                      color=lda.predict$class)) +
geom_point() +
ggtitle("Predicted sex") +
scale_x_continuous(name = "Carapace length") +
scale_y_continuous(name = "Rear width") +
scale_color_discrete(name = "Sex")

grid.arrange(crabs.plot, crabs.predict)

# Calculate misclassification
crabs.misclass = mean(crabs$sex != lda.predict$class)
cat("Misclassification rate for lda: ", crabs.misclass)

# Step 3
prior.male = 0.9
prior.female = 0.1
crabs.predict.prior = predict(lda.model,
                               crabs,
                               prior=c(Male=prior.male,
                                       Female=prior.female))
crabs.plot.prior = ggplot(data=crabs,
                           mapping=aes(x=CL,
                                         y=RW,
                                         shape=sex,
                                         color=crabs.predict.prior$class)) +
geom_point() +
ggtitle("Predicted sex using prior p(Male)=0.9, p(Female)=0.1") +
scale_x_continuous(name = "Carapace length") +
scale_y_continuous(name = "Rear width") +
scale_color_discrete(name = "Predicted sex") +
scale_shape_discrete(name = "Actual sex")
# Plot
grid.arrange(crabs.plot.prior)
# Calculate misclassification
crabs.prior.misclass = mean(crabs$sex != crabs.predict.prior$class)
cat("Misclassification rate for lda with p(Male=0.9), p(Female)=0.1: ",
    crabs.prior.misclass)

# Step 4
glm.model = glm(formula = sex~RW+CL,
                data = crabs,
                family = 'binomial')
glm.predict = predict(object = glm.model,
                      newdata = crabs,

```

```

        type = 'response')
glm.predicted.sex = ifelse(glm.predict > 0.5, "Male", "Female")

# Calculate line from model
intercept = coef(glm.model)[1]
rw = coef(glm.model)[2]
cl = coef(glm.model)[3]
border = 0.5
k = -rw/cl
m = -(intercept)/cl
# Print plot and line
glm.plot = ggplot(data = crabs,
                    mapping = aes(x=RW,
                                   y=CL,
                                   color=glm.predicted.sex,
                                   shape=crabs$sex)) +
  geom_point() +
  ggtitle("Actual and predicted sex (GLM), and decision boundary") +
  scale_x_continuous(name = "Carapace length") +
  scale_y_continuous(name = "Rear width") +
  scale_color_discrete(name = "Predicted sex") +
  scale_shape_discrete(name = "Actual sex") +
  geom_abline(intercept = m, slope = k)
grid.arrange(glm.plot)

# Print misclassification
glm.misclass = mean(crabs$sex != glm.predicted.sex)
cat("Misclassification rate for GLM: ",
    glm.misclass)

```

Assignment 2

```

# Step 1
# Add libraries
library("gridExtra")
library("ggplot2")
library("tree")
library("MASS")
library("e1071")

# Set working directory
setwd("~/courses/tdde01/lab2")

# Read data
scores = read.csv2("creditscoring.csv")
# Read as strings
scores$good_bad = as.factor(scores$good_bad)

# Split data into train/val/test
n=dim(scores)[1]
set.seed(12345)
id=sample(1:n, floor(n*0.5))
train=scores[id,]

```

```

id1=setdiff(1:n, id)
set.seed(12345)
id2=sample(id1, floor(n*0.25))
val=scores[id2,]
id3=setdiff(id1,id2)
test=scores[id3,]

# Step 2
# Create tree
tree.deviance = tree(formula = good_bad~.,
                      data = train,
                      split="deviance")
tree.gini = tree(formula = good_bad~.,
                  data = train,
                  split="gini")

# Make predictions
predict.deviance.test = predict(tree.deviance, test, type = "class")
predict.deviance.train = predict(tree.deviance, train, type = "class")
predict.gini.test = predict(tree.gini, test, type = "class")
predict.gini.train = predict(tree.gini, train, type = "class")

# Calculate misclassification rates
misclass = function(predicted, true) {
  return(mean(predicted != true))
}

deviance.test.misclass = misclass(predict.deviance.test, test$good_bad)
deviance.train.misclass = misclass(predict.deviance.train, train$good_bad)
gini.test.misclass = misclass(predict.gini.test, test$good_bad)
gini.train.misclass = misclass(predict.gini.train, train$good_bad)

# Print misclassification rates
cat("Misclassification on deviance with test: ",
    deviance.test.misclass)
cat("\nMisclassification on deviance with train: ",
    deviance.train.misclass)
cat("\nMisclassification on gini with test: ",
    gini.test.misclass)
cat("\nMisclassification on gini with train: ",
    gini.train.misclass, "\n")

# Step 3
# Lists of scores
range = 15
pruned=rep(0, range)
trainScore=rep(0, range)
testScore=rep(0, range)

test.tree = tree(formula=good_bad~., data=train)
for(i in 2:range) {
  # Prune the tree
  prunedTree=prune.tree(test.tree, best=i)
}

```

```

# Make trediction on validation data
pred=predict(prunedTree, newdata=val, type="tree")
# Append scores
trainScore[i]=deviance(prunedTree)
testScore[i]=deviance(pred)
}

# Plot the scores
plot(2:range, trainScore[2:range], type="b", col="red", ylim=c(200, 600))
points(2:range, testScore[2:range], type="b", col="blue")

optLeaves = 4

# Info on optimal tree
optTree = prune.tree(tree.deviance, best=optLeaves)
summary(optTree)
optTree.predict = predict(optTree, newdata=test)
optTree.predict.string = ifelse(optTree.predict[2] > 0.5, "good", "bad")
optTree.misclass = misclass(optTree.predict.string, test$good_bad)
cat("\nMisclassification on optimal tree: ",
   optTree.misclass)

cat("\nTree depth is 5 as can be seen in the plot. \n")
plot(optTree)
cat("\n\nUsed variables in optimal tree: \n'savings' 'duration' 'history' 'age' 'purpose'\n\n")

# Step 4
# Create model and classify
model.bayes = naiveBayes(formula = good_bad~., data=train)
predict.bayes.test = predict(model.bayes, newdata=test, type="class")
predict.bayes.train = predict(model.bayes, newdata=train, type="class")

# Print info on classification with prediction on test
table.bayes = table(predict.bayes.test, test$good_bad)
cat("Confusion table of naive bayes:")
print(table.bayes)

misclass.bayes = mean(predict.bayes.test != test$good_bad)
cat("Misclassification with naive bayes: ", misclass.bayes, "\n\n")

# Print info on classification with prediction on test
table.bayes = table(predict.bayes.train, train$good_bad)
cat("Confusion table of naive bayes:")
print(table.bayes)

misclass.bayes = mean(predict.bayes.train != train$good_bad)
cat("Misclassification with naive bayes: ", misclass.bayes, "\n\n")

# Step 5
# Calculate TPR and FPR of optimal tree and bayes
getROC = function(pred, pi) {
  tpr = c()
  fpr = c()

```

```

for (p in pi) {
  # Change probabilities to strings
  tmp = ifelse(pred[, 'good'] > p, "good", "bad")
  # Get confusion matrix
  cm = table(predicted=tmp, actual=test$good_bad)
  if('good' %in% rownames(cm)) {
    # Calculate TPR, first dim of cm is predicted
    t = cm['good', 'good'] / sum(cm[, 'good'])
    # Calculate FPR
    f = cm['good', 'bad'] / sum(cm[, 'bad'])
    # Append to list of values
    tpr = c(tpr, ifelse(is.finite(t), t, 0))
    fpr = c(fpr, ifelse(is.finite(f), f, 0))
  } else {
    tpr = c(tpr, 0)
    fpr = c(fpr, 0)
  }
}
df = data.frame(tpr, fpr)
return(df)
}

pi = seq(0.05, 0.95, 0.05)
pred.optTree = predict(optTree, newdata=test)
pred.bayes = predict(model.bayes, newdata=test, type='raw')
opt.roc = getROC(pred.optTree, pi)
bayes.roc = getROC(pred.bayes, pi)

#Plot
roc.plot = ggplot(mapping=aes(col=Classifier)) +
  geom_point(data=opt.roc, aes(x=fpr, y=tpr, col="Optimal tree")) +
  geom_line(data=opt.roc, aes(x=fpr, y=tpr, col="Optimal tree")) +
  geom_point(data=bayes.roc, aes(x=fpr, y=tpr, col="Bayes")) +
  geom_line(data=bayes.roc, aes(x=fpr, y=tpr, col="Bayes"))

grid.arrange(roc.plot)

# Step 6
# Create model and classify
model.bayes = naiveBayes(formula = good_bad~., data=train)
predict.bayes.test = predict(model.bayes, newdata=test, type="raw")
predict.bayes.train = predict(model.bayes, newdata=train, type="raw")

# Print info on classification with prediction on test
loss = 10/1
predict.bayes.test.loss = ifelse(predict.bayes.test[, 'good'] /
                                 predict.bayes.test[, 'bad'] > loss,
                                 'good',
                                 'bad')

table.bayes = table(Predict=predict.bayes.test.loss, Actual=test$good_bad)
cat("Confusion table of naive bayes (using test data):")
print(table.bayes)

```

```

misclass.bayes = mean(predict.bayes.test.loss != test$good_bad)
cat("Misclassification with naïve bayes (using test data): ", misclass.bayes, "\n")

# Print info on classification with prediction on train
predict.bayes.train.loss = ifelse(predict.bayes.train[, 'good'] /
                                  predict.bayes.train[, 'bad'] > loss,
                                  'good',
                                  'bad')
table.bayes = table(Predict=predict.bayes.train.loss, Actual=train$good_bad)
cat("Confusion table of naïve bayes (using train data): ")
print(table.bayes)

misclass.bayes = mean(predict.bayes.train.loss != train$good_bad)
cat("Misclassification with naïve bayes (using train data): ", misclass.bayes, "\n")

```

Assignment 4

```

# Step 1
# Add libraries
library("gridExtra")
library("ggplot2")
library("MASS")
library("stats")
library("fastICA")

# Set working directory
setwd("~/courses/tdde01/lab2")

# Read data
spectra = data.frame(read.csv2("NIRSpectra.csv"))
spectra = subset(spectra, select=-Viscosity)

# Calculate principal components
pca = prcomp(spectra)

# Get eigen values
lambda = pca$sdev^2
# Plot variance of each component
screeplot(pca)

# Print proportion of variation
sprintf("%2.3f", lambda/sum(lambda)*100)
cat("99% of the variance can be explained by first two PC.\n\n")

# Extract principal components
PC1 = pca$x[,1]
PC2 = pca$x[,2]

# Plot the data projected onto PC 1 and 2
plot.projection = ggplot() +
  geom_point(data=spectra, mapping=aes(x=PC1, y=PC2))
grid.arrange(plot.projection)

```

```

# Step 2
plot(pca$rotation[,1], main="Traceplot, PC1")
plot(pca$rotation[,2], main="Traceplot, PC2")

# Step 3a
set.seed(12345)
res = fastICA(X=spectra,
               n.comp=2,
               alg.typ= "parallel",
               fun = "logcosh",
               alpha = 1,
               method = "R",
               row.norm = FALSE,
               maxit= 200,
               tol = 0.0001,
               verbose = TRUE)

W.prime = res$K %*% res$W
# Traceplots of fastICA
plot(W.prime[,1], main="Traceplot, PC1")
plot(W.prime[,2], main="Traceplot, PC2")

# Step 3b
# Extract ICs
IC1 = res$S[,1]
IC2 = res$S[,2]

# Plot the data projected onto PC 1 and 2
plot.projection = ggplot() +
  geom_point(data=spectra, mapping=aes(x=IC1, y=IC2))
grid.arrange(plot.projection)

```

Lab 3

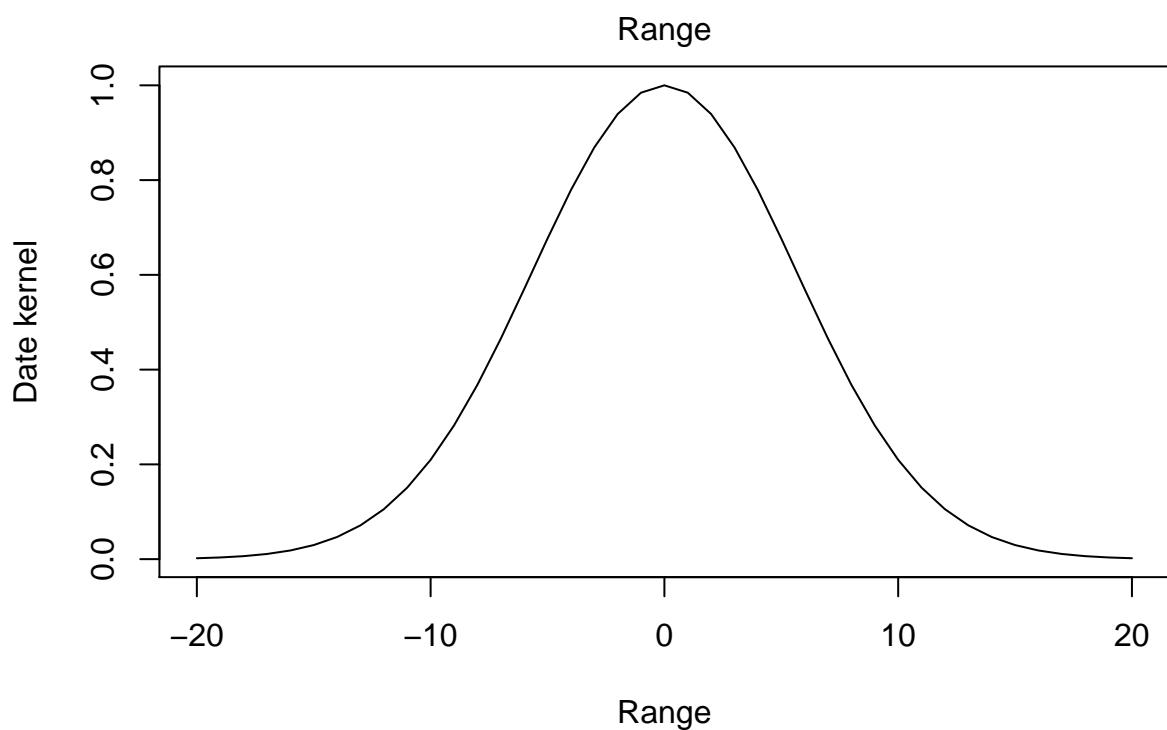
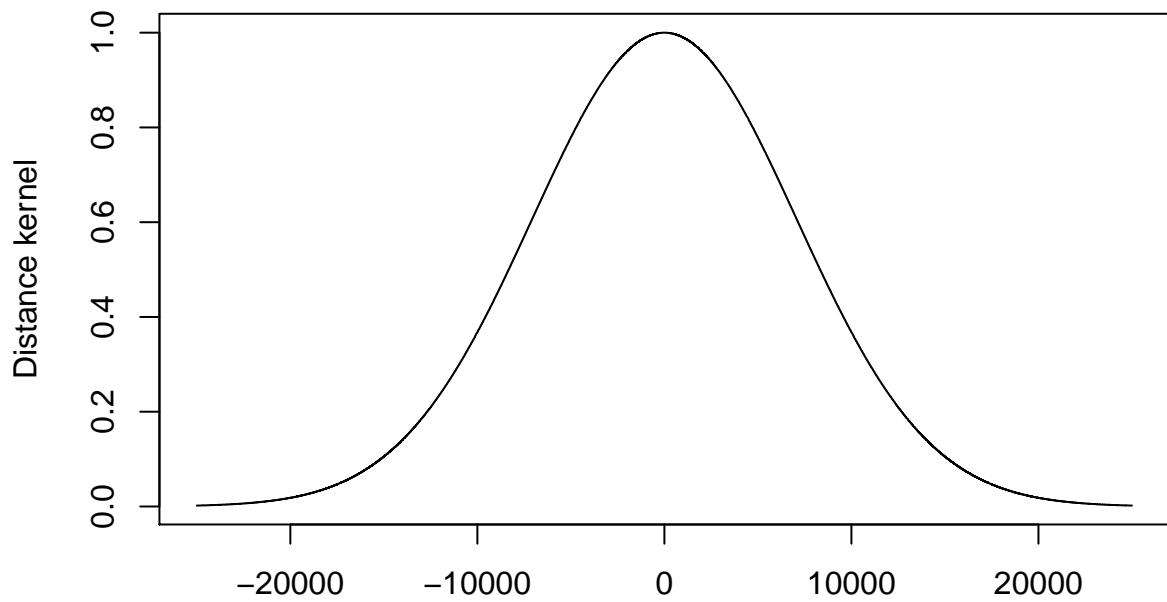
Assignment 1

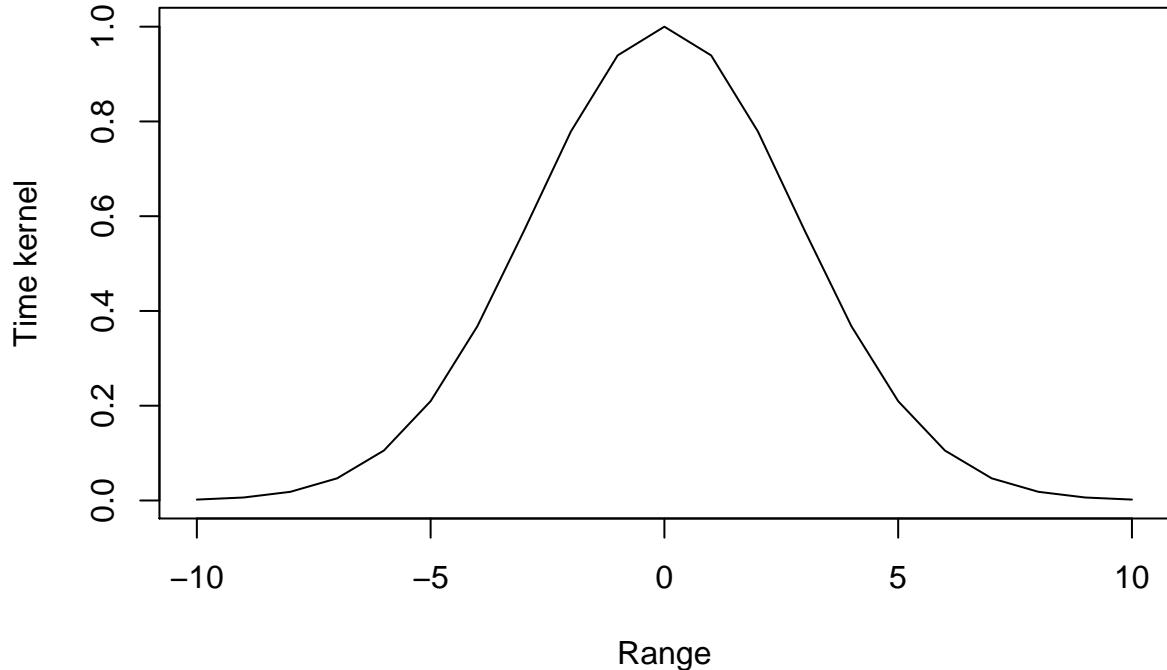
Part 1

The chosen width for each kernel is:

- h_distance: 10000 m
- h_date: 8 days
- h_time: 4 hours

The plots below show that the kernels gives more weight to closer points.





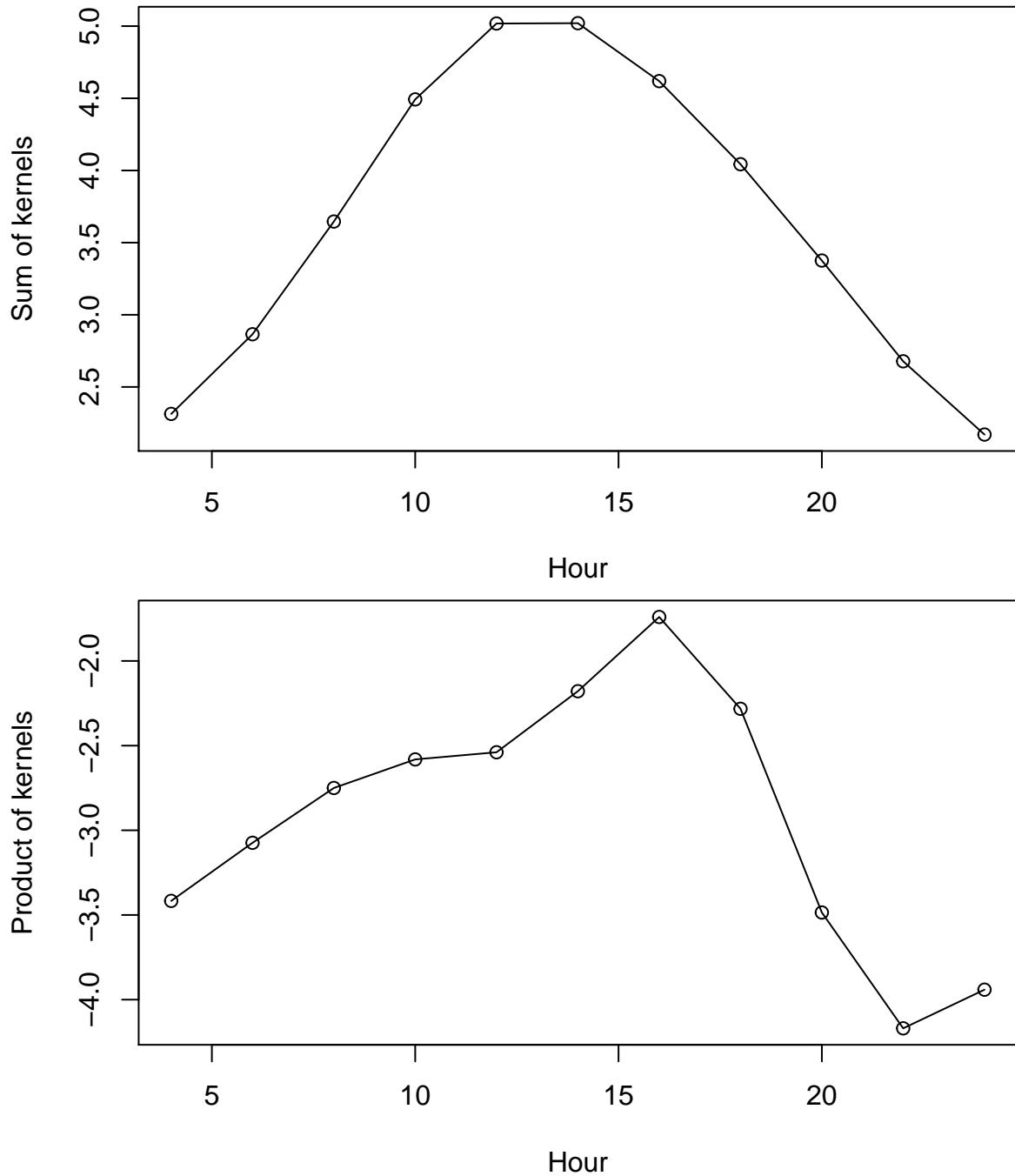
The values of widths were tested by changing them and evaluating predictions of temperature so that a plot of one day's temperature would look realistic. Each width defines where the amplification is e^{-1} , which gives some indication on where points starts to being cut away. The widths can be explained as:

- Measurements within a distance of 10000 m are weighted greatest.
- The closest 8 days affect the temperature the most.
- A measurement within 4 h contributes to the prediction the most.

Of course, all of these kernels give the greatest amplification at zero distance. Since this model for predicting temperature is far from perfect, it's hard to tell what widths that are realistic. For instance, the model does not take into account what year a measurement was made, only the day of a year. With that in mind, the chosen widths can be assumed somewhat adequate for this case.

Part 2

The plots below show a temperature prediction on Christmas Eve. The first one summarizing each kernel, the other multiplying them.



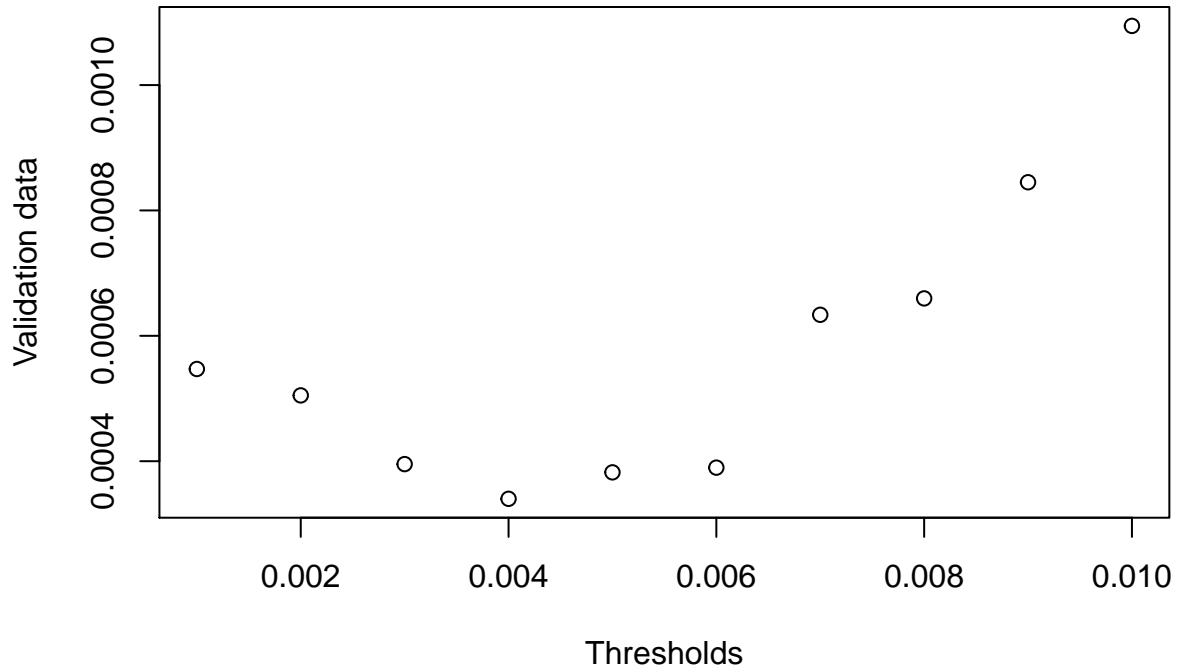
As can be seen, the product of the kernels give preferred results (since it's Christmas and I want snow). It is also more probable that it is minus degrees at the end of December.

A summation would not give a good result since then only one kernel need to have a good result to be counted in. Lets say a day is half a year away from target day, but at the exact same hour. That day should almost not count at all, but it still does with the summation method. That way, the product gives a better result.

Assignment 3

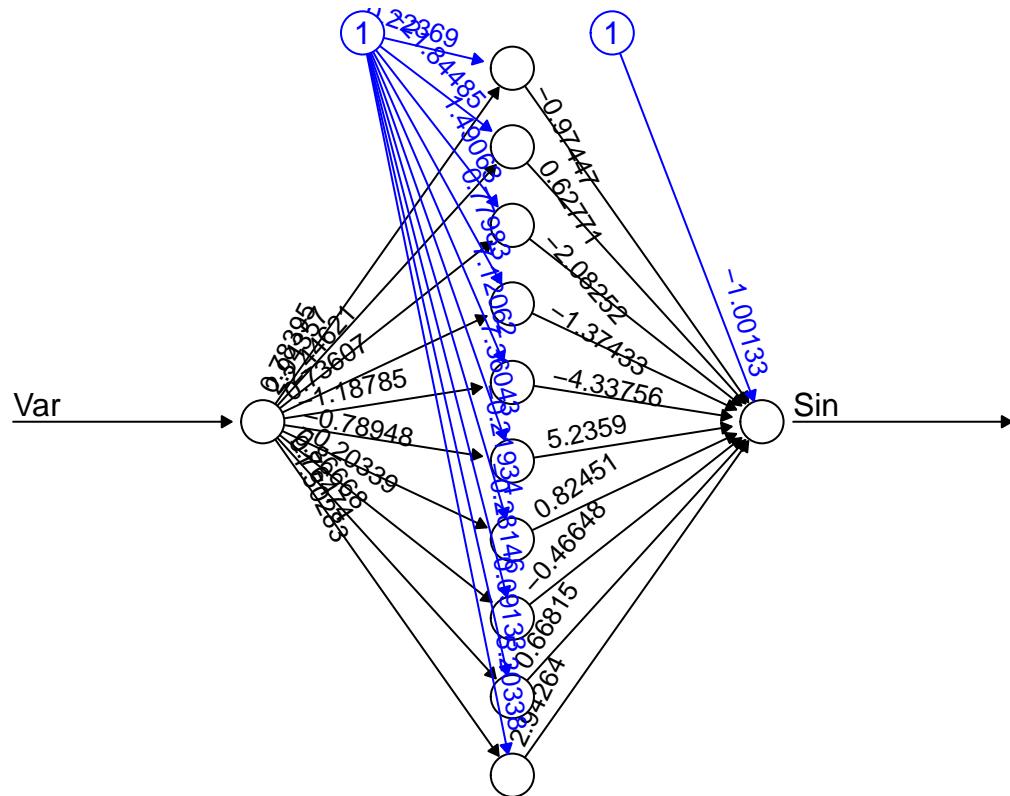
Validation

The threshold was chosen to the one that ended up resulting in the lowest mean square error when predicting the validation data. The MSE for thresholds in the interval $[1/1000, 10/1000]$ are plotted below.



As seen here, the best threshold in this case is $4/1000$.

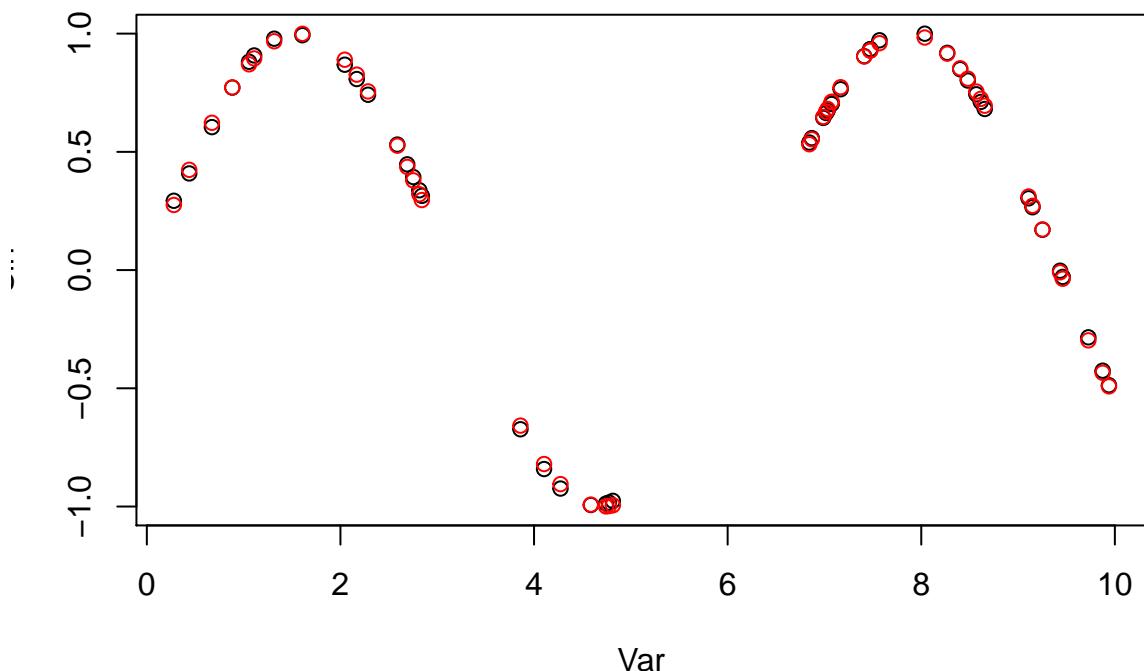
The final neural network



Prediction of Sin

Black dots are prediction, red ones are correct values.

```
## Data Error: 0;
```



Appendix

Assignment 1

```
library("geosphere")

setwd("~/courses/tdde01/lab3/")

stations = read.csv("stations.csv", fileEncoding = "Latin1")
temps = read.csv("temps50k.csv")
st = merge(stations, temps, by="station_number")

gauss_kernel = function(u) {
  return (exp(-(u^2)))
}

h_distance = 10000
h_date = 8
h_time = 4

# Station is station number, interest is vector(long, lat)
kernel_distance = function(station, interest) {
  distance = distHaversine(station, interest)
  res = gauss_kernel(distance/h_distance)
  return (res)
}

# Calculates gaussian kernel provided with difference in days from day to interest
kernel_date = function(dates, interest) {
  dates = as.Date(dates)
  interest = as.Date(interest)
  distance = as.numeric(difftime(dates, interest, units=c("days")))
  leap_years = floor(floor(distance/365)/4)
  distance = (distance - leap_years) %% 365
  distance = sapply(distance, function(d) min(d, abs(365 - d)))
  res = gauss_kernel(distance/h_date)
  return (res)
}

# Calculates gaussian kernel provided with difference of hour and target hour
kernel_time = function(hour, interest) {
  h1 = as.numeric(substr(hour, 1, 2))
  h2 = as.numeric(substr(interest, 1, 2))
  distance = abs((h2-h1) + 12) %% 24 - 12
  return (gauss_kernel(distance/h_time))
}

# Plot kernels
width = 2.5
range = -(h_distance*width):(h_distance*width)
plot(x=range, y=gauss_kernel(range/h_distance), type="l", ylab = "Distance kernel", xlab="Range")

range = -(h_date*width):(h_date*width)
plot(x=range, y=gauss_kernel(range/h_date), type="l", ylab = "Date kernel", xlab="Range")
```

```

range = -(h_time*width):(h_time*width)
plot(x=range, y=gauss_kernel(range/h_time), type="l", ylab = "Time kernel", xlab="Range")

# Summation of kernels. Passing product returns kernels multiplied
kernel_sum = function(long, lat, date, time, product=FALSE) {
  longlat = data.frame(st$longitude, st$latitude)
  distances = kernel_distance(longlat, c(long, lat))

  datediffs = kernel_date(st$date, date)

  timediffs = kernel_time(st$time, time)

  sum = sum((distances + datediffs + timediffs) * st$air_temperature)
  sum = sum / sum(distances + datediffs + timediffs)

  prod = sum((distances * datediffs * timediffs) * st$air_temperature)
  prod = prod / sum(distances * datediffs * timediffs)

  if (product) {
    return(prod)
  }
  else {
    return(sum)
  }
}

latitude = 58.4274 # The point to predict
longitude = 14.826
date = "2018-12-24" # The date to predict
times = c("04:00:00", "06:00:00", "08:00:00", "10:00:00", "12:00:00",
         "14:00:00", "16:00:00", "18:00:00", "20:00:00", "22:00:00",
         "00:00:00")
# Remove posterior dates
st = st[as.Date(st$date) < as.Date(date),]

temp = lapply(times, function(t) kernel_sum(longitude, latitude, date, t, FALSE))

plot(temp, x=seq(4, 24, 2), type="o", ylab="Sum of kernels", xlab="Hour")

temp = lapply(times, function(t) kernel_sum(longitude, latitude, date, t, TRUE))

plot(temp, x=seq(4, 24, 2), type="o", ylab="Product of kernels", xlab="Hour")

```

Assignment 3

```

library("neuralnet")
set.seed(1234567890)

# Random data from 0-10, uniformly distributed
Var = runif(50, 0, 10)
trva = data.frame(Var, Sin=sin(Var))
tr = trva[1:25,] # Training

```

```

va = trva[26:50,] # Validation

# Random initialization of the weights in the interval [-1, 1]
winit = runif(31, -1, 1)

# Loop over thresholds
validations = c()
for (i in 1:10) {
  nn = neuralnet(formula = Sin ~ Var, data = tr, hidden = 10, startweights = winit, threshold = i/1000
  comp = compute(nn, va$Var)

  mse = sum((comp$net.result - va$Sin)^2) / nrow(va)
  validations = c(validations, mse)
}
plot(x=seq(1/1000, 10/1000, 1/1000), y=validations, xlab="Thresholds", ylab="Validation data")
best_threshold = which.min(validations)/1000

# Optimal nn
nn = neuralnet(formula = Sin ~ Var, data = trva, hidden = 10, startweights = winit, threshold = best_threshold)

plot(nn, ylab="Neural network", rep="best")

# Plot of the predictions (black dots) and the data (red dots)
plot(prediction(nn)$rep1, ylim = c(-1, 1))
points(trva, col = "red")

```

Other

```

library("ggplot2")
library("gridExtra")
library("e1071")
library("MASS")

crabs = read.csv("australian-crabs.csv")

plot = ggplot() + geom_point(data=crabs, mapping=aes(x=CW, y=BD, color=species))
grid.arrange(plot)

# naive bayes
model = naiveBayes(formula=as.factor(species)~CW+BD, data=crabs)
pred = predict(model, crabs)

t = table(True=pred, Predicted=crabs$species)

# Only one property is not sufficient to classify, both has to be combined to get a good result.

model = glm(formula=as.factor(species)~CW+BD, data = crabs, family = "binomial")
pred = predict(model, crabs, type='response')
pred_spec = ifelse(pred > 0.5, "Blue", "Orange")

# Calculate line from model
intercept = coef(model)[1]

```

```

rw = coef(model)[2]
cl = coef(model)[3]
border = 0.5
k = -rw/cl
m = -(intercept)/cl
# Print plot and line
glm.plot = ggplot(data = crabs,
                    mapping = aes(x=CW,
                                   y=BD,
                                   color=pred_spec,
                                   shape=species)) +
  geom_point() +
  ggtitle("Actual and predicted species (GLM), and decision boundary") +
  scale_x_continuous(name = "Carapace length") +
  scale_y_continuous(name = "Rear width") +
  scale_color_discrete(name = "Predicted spec.") +
  scale_shape_discrete(name = "Actual spec.") +
  geom_abline(intercept = m, slope = k)
grid.arrange(glm.plot)

### PCA

model = prcomp(subset(crabs, select=c(CW, BD)), scale. = T)
screeplot(model) #to get all eigen values
# Get eigen values (standard deviation ^ 2)
lambda = model$sdev^2
sprintf("%2.3f", lambda/sum(lambda))
PC1 = model$x[,1]
PC2 = model$x[,2]

# Present eigenvector
model = princomp(subset(crabs, select=c(CW, BD)))
l = loadings(model)
print(loadings(model))

### 1.6
crabs$PC1 = PC1
crabs$PC2 = PC2
model = naiveBayes(formula=as.factor(species)~PC1+PC2, data=crabs)
pred = predict(model, crabs)

t = table(True=pred, Predicted=crabs$species)
print(t)

# The data is now rotated so that both components are separatable

setwd("/home/hitsnapper/courses/tdde01/exams/2017-04-18")
bank = read.csv2("bank.csv")

model = glm(formula=Visitors~Time, data=bank, family=poisson)

library("pls")
library("ggplot2")
library("gridExtra")

```

```

library("MASS")
library("tree")

### FUNCTIONS
PC_needed = function(eigenv, border) {
  pc.sum = 0
  count = 0
  for (pc in eigenv/sum(eigenv)) {
    if (pc.sum < border) {
      count = count + 1
      pc.sum = pc.sum + pc
    }
  }
  return (count)
}

video = data.frame(read.csv("video.csv"))

data = subset(video, select=c(-utime, -codec))
data_size = dim(data)[1]
set.seed(12345)
i1 = sample(1:data_size, floor(data_size*0.5))
i2 = setdiff(1:data_size, i1)
train = data[i1,]
test = data[i2,]

### Without scaling
pca = prcomp(data, scale. = FALSE)

# get eigen values
lambda = pca$sdev^2
screeplot(pca)
message(sprintf("%1.3f", lambda/sum(lambda)))
message(sprintf("PC needed with no scaling: %i", PC_needed(lambda, 0.95)))

### With scaling
pca = prcomp(data, scale. = TRUE)
screeplot(pca)
# get eigen values
lambda = pca$sdev^2
message(sprintf("%1.3f", lambda/sum(lambda)))
message(sprintf("PC needed with scaling: %i", PC_needed(lambda, 0.95)))

# With scaling, each data column is normalized to prevent some vectors
# to contribute to the eigenvalues unproportionally much

## 1.2
data = subset(video, select=c(-codec))
data_size = dim(data)[1]
set.seed(12345)
i1 = sample(1:data_size, floor(data_size*0.5))
i2 = setdiff(1:data_size, i1)
train = data[i1,]

```

```

test = data[i2,]

trainE = numeric(17)
testE = numeric(17)
pcrN = pcr(utime~., 17, data=train, scale=T)
for (comp in 1:17) {
  trP = predict(pcrN, ncomp=comp)
  teP = predict(pcrN, ncomp=comp, newdata=test)
  trainE[comp] = mean((trP-train$utime)^2)
  testE[comp] = mean((teP-test$utime)^2)
}

plot(trainE, type='l', col="red", ylab="Error")
lines(testE, type='l', col="blue")

# The more components used, the more complex and biased the model will be to the
# training data. This will increase the risk of the model only giving correct results on
# training data and not test data. To allow other data predictions, there must be
# variance, and that is the bias-variance tradeoff. As seen in the graph, train and
# test prediction correctness increase greatly to component 8, and afterwards there is
# no big difference in prediction error. Increasing number of components used increases
# the risk that the model is too biased.

pcrF = pcr(utime~., 8, data=train, validation="none", scale=T)
message(sprintf("%f", mean(residuals(pcrF)^2)))
message(Yloadings(pcrF))

### 1.4
dat = subset(video, select=c(duration, frames))
dat$class = ifelse(video$codec == "mpeg4", "mpeg", "other")
plot.projection = ggplot() + geom_point(data=dat, mapping=aes(x=duration, y=frames, color=class))
grid.arrange(plot.projection)
#class = ifelse(video$codec=="mpeg4", "mpeg", "other")
#durs = video$duration

# Almost, just a few won't fit to a linear regression

### 1.5
lda.fit = lda(class~., dat)
lda.pred = predict(lda.fit)
dat.tmp = dat
dat.tmp$pred = lda.pred$class

missclass = mean(dat$class != dat.tmp$pred)

plot = ggplot() +
  geom_point(dat.tmp, mapping = aes(x=duration, y=frames, color=pred, shape=class))

grid.arrange(plot)

# The data cannot be separated by a linear equation.

### 1.6

```

```

tree.fit = tree(formula=as.factor(class)~frames+duration, data=dat)
tree.prune = cv.tree(tree.fit)
pred = predict(tree.fit, type="class")
misclass = mean((pred!=dat$class))
plot(tree.fit)

# Not parallel to any coordinate axes. The tree must therefore separate decisions into stair-like
# branches.

library("kernlab")

spam = read.csv2("spambase.csv")
set.seed(12345)
len = dim(spam)[1]
index=sample(1:len)
tr = spam[index[1:3000], ]
va = spam[index[3001:3900], ]
te = spam[index[3901:len], ]

C = c(0.5, 1, 5)
for (c in 1:3) {
  ksvm.fit = ksvm(as.factor(Spam)~., data = tr, kpar = list(sigma=0.05), C=C[c], kernel="rbfdot")
  pred = predict(ksvm.fit, va[-58])
  t = table(pred, as.factor(va$Spam))
  message(sprintf("%i, error: %s \n", c, (t[1,2]+t[2,1])/sum(t)))
}

ksvm.fit = ksvm(as.factor(Spam)~., data = tr, kpar = list(sigma=0.05), C=1, kernel="rbfdot")
pred = predict(ksvm.fit, te[-58])
t = table(pred, as.factor(te$Spam))
message(sprintf("C=1, error: %s \n", (t[1,2]+t[2,1])/sum(t)))

library("neuralnet")

set.seed(12345)

Points = runif(50, 0, 10)
data = data.frame(Points, Sin=sin(Points))

#indexes = sample(1:50)
indexes=1:50
tr = data[indexes[1:25],]
va = data[indexes[26:50],]

its=10
vals = numeric(its)
w = runif(31, -1, 1)
for (i in (1:its)) {
  model = neuralnet(Sin~Points, data=tr, hidden=c(10), startweights = w, threshold = i/1000)
  comp = compute(model, va$Points)
  mse = sum((comp$net.result - va$Sin)^2) / nrow(va)
  vals[i] = mse
}
plot(x=(1:its)/1000, y=vals)

```

```

message(sprintf("First model: %f", vals[1]))

# Next model
w = runif(22, -1, 1)
for (i in (1:its)) {
  model = neuralnet(Sin~Points, data=tr, hidden=c(3, 3), startweights = w, threshold = i/1000)
  comp = compute(model, va$Points)
  mse = sum((comp$net.result - va$Sin)^2) / nrow(va)
  vals[i] = mse
}
plot(x=(1:its)/1000, y=vals)
message(sprintf("Second model: %f", vals[9]))

w = runif(31, -1, 1)
model = neuralnet(Sin~Points, data=tr, hidden=c(10), startweights = w, threshold = 1/1000)
Points = runif(50, 0, 10)
te = data.frame(Points, Sin=sin(Points))
comp = compute(model, te$Points)
mse = sum((comp$net.result - te$Sin)^2) / nrow(te)
message(sprintf("Final model generalization error: %f", mse))

```

Types of data sets

- **Training data** (training set D): used for fitting the model

– Supervised learning: w_i in $P(y|x, w_1, \dots, w_k)$ estimated using D

x	y
1.1	M
2.3	F

- **Test data** (test set T): used for predictions

– Supervised learning: estimate $p(Y)$ or \hat{Y} for new x

x	y
1.3	?
2.9	?

732A99/TDDE01

Logistic regression

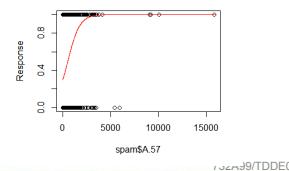
- Data $Y_i \in \{\text{Spam}, \text{Not Spam}\}, X_i = \# \text{of a word}$

$$\text{Model: } p(Y = \text{Spam}|w, x) = \frac{1}{1+e^{-w_0-w_1x}}$$

- Fitting: maximum likelihood

- Prediction : $p(\text{spam}) = p(Y = \text{spam}|x)$

We can also make point predictions
- how?



732A99/TDDE01

K-nearest neighbor density estimation

- Data: Fish length X_1, \dots, X_N

$$\text{Model } p(x|K) = \frac{K}{N \cdot \Delta}$$

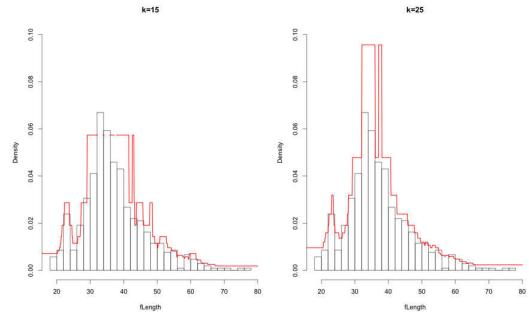
– K: #neighbors in training data

– Δ : length of the interval containing K neighbors

- Learning: Fix some K or find an appropriate K
- Prediction: predict $p(x|K)$

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K-nearest neighbor density estimation

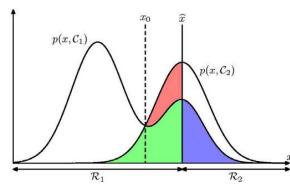


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K-nearest neighbor density estimation

- Why estimating a density can be interesting:

1. Estimate **class-conditional densities** $p(x|y = C_i)$
2. Predict



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K-nearest neighbor classification

- Given N observations (X_j, Y_j)

– $Y_j = C_i$, where C_1, \dots, C_m are possible class values

- Model assumptions

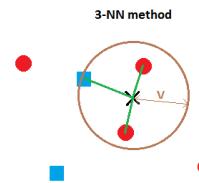
– Apply K-NN density estimation:

$$p(X = x|Y = C_i) = \frac{K_i}{N_i V}, p(C_i) = \frac{N_i}{N}$$

– V : volume of the sphere

– K_i : #obs from training data of $Y = C_i$ in the sphere

– N_i : #obs from training data of $Y = C_i$



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Bayesian classification

- Prediction $\hat{Y}(x) = C_l$

$$l = \arg \max_{i \in \{1, \dots, m\}} p(C_i | x)$$

Bayes theorem

$$p(C_i | x) = \frac{p(x | C_i)p(C_i)}{p(x)}$$

- We get

$$p(C_i | x) \propto \frac{K_i}{K}$$

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K-nearest neighbor classification

Algorithm

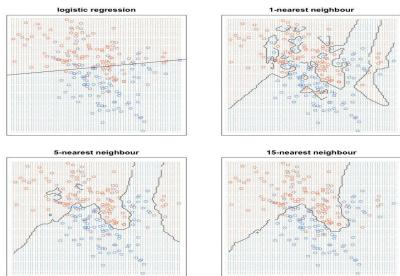
- Given training set D , number K , and test set T
- For each $x \in T$
 - For each $i = 1, \dots, M$
 - $p'(C_i | x) = \frac{K_i}{K}$
 - Compute $l = \arg \max_{i \in \{1, \dots, m\}} p'(C_i | x)$
 - Predict $\hat{Y}(x) = C_l$

Majority voting: prediction for x is defined by majority voting of K neighbors

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K-nearest neighbor example

Why classification results are so different for K-NN?

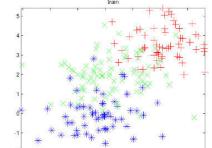


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Model types

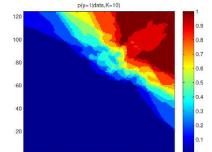
Parametric models

- Have certain number of parameters independently of the size of training data
- Assumption about the data distribution
- Ex: logistic regression



Nonparametric models

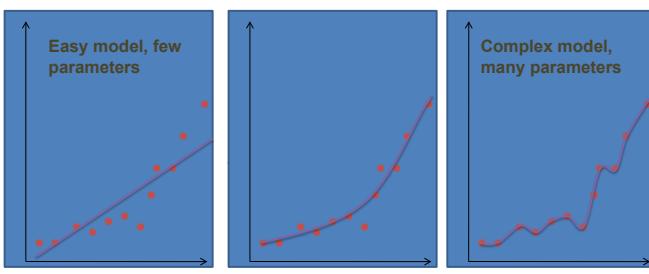
- Number of parameters (complexity) grows with training data
 - Example: K-NN classifier



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Overfitting

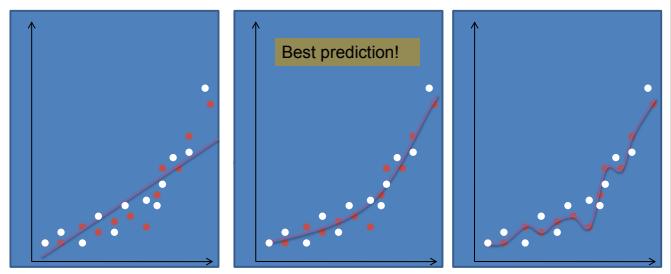
- Which model feels appropriate?



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Overfitting

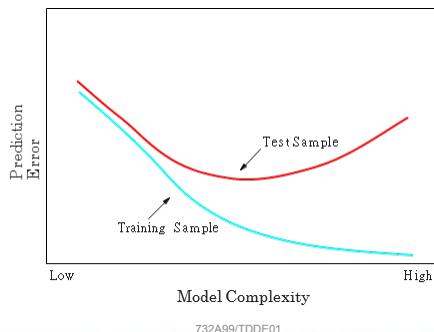
Now new data from the same process



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Overfitting

- Observed:



Model selection

- Given several models M_1, \dots, M_m
- Divide data set into **training** and **test** data

Training	Test
----------	------
- Fit models M_i to training data → get parameter values
- Use fitted models to predict test data and compare **test errors** $R(M_1), \dots, R(M_m)$
- Model with lowest prediction error is best

Comment:

- Approach works well for moderate/large data

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Typical error functions

- Regression, **MSE** :

$$R(Y, \hat{Y}) = \frac{1}{N} \sum_{i=1}^N (Y_i - \hat{Y}_i)^2$$

- Classification, **misclassification rate**

$$R(Y, \hat{Y}) = \frac{1}{N} \sum_{i=1}^N I(Y_i \neq \hat{Y}_i)$$

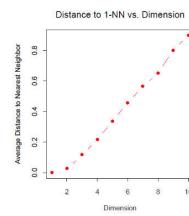
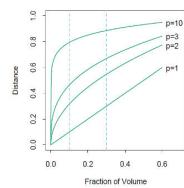
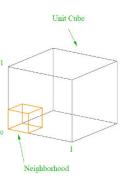
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Curse of dimensionality

- Given data D :
 - Features X_1, \dots, X_p
 - Targets Y_1, \dots, Y_r
- When p increases models using "proximity" measures work badly
- Curse of dimensionality:** A point has no "near neighbors" in high dimensions → using class labels of a neighbor can be misleading
 - Distance-based methods affected

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Curse of dimensionality



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Curse of dimensionality

- Hopeless? No!
- Real data normally has much lower effective dimension
 - Dimensionality reduction techniques
- Smoothness assumption**
 - small change in one of X s should lead to small change in Y → interpolation

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Basics of Statistics

Lecture 1b

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Probability

How likely it is that some event will happen?

Idea:

- Experiment
- Outcomes (sample points) O_1, O_2, \dots, O_n
- Sample space Ω
- Event A
- Probability function P: Events $\rightarrow [0,1]$

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Probability

Example: Tossing a coin two times



<http://clipart-library.com/images/2512237/clipart-vector-14227-040.jpg>

Example:

- $p(A)$ frequency of observing A
- $p(A, B)$ frequency of observing A and B
- $p(B|A)$ frequency of observing B given A

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Properties and definitions

- One can think of events as sets
 - Set operations are defined: $A \cup B, A \cap B, \bar{A} \setminus B$
- **P(A \cup B) = P(A) + P(B) if $A \cap B = \emptyset$**
- **Independence** $P(A, B) \equiv P(A \cap B) = P(A)P(B)$
- **Conditional probability** $P(A|B) = \frac{P(A,B)}{P(B)}$

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Bayes theorem

Example:

- We have constructed spam filter that
 - identifies spam mail as spam with probability 0.95
 - Identifies usual mail as spam with probability 0.005
- This kind of spam occurs once in 100,000 mails
- If we found that a letter is a spam, what is the probability that it is actually a spam?

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Bayes theorem

- We have some knowledge about event B
 - **Prior probability** $P(B)$ of B
- We get new information A
 - $P(A)$
 - $P(A|B)$ probability of A can occur given B has occurred
- New (updated) knowledge about B
 - Posterior probability $P(B|A)$

$$P(B|A) = \frac{P(A|B)P(B)}{P(A)}$$

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Random variables

- Instead of having events, we can have a variable X :
 - Events $\rightarrow \mathbb{R}$ **Continuous random variables**
 - Events $\rightarrow \mathbb{N}$ **Discrete random variables**

Examples:

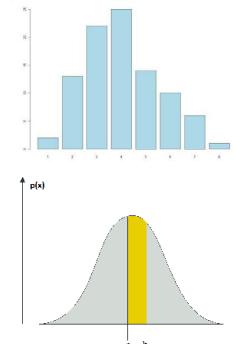
- $X = \{\text{amount of times the word "crisis" can be found in financial documents}\}$
 - $P(X=3)$
- $X = \{\text{Time to download a specific file to a specific computer}\}$
 - $P(X=0.36 \text{ min})$

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7

Distributions

- Discrete
 - Probability mass function $P(x)$ for all feasible x
- Continuous
 - Probability density function $p(x)$
 - $p(x \in [a, b]) = \int_a^b p(x)dx$
 - $p(x) \geq 0, \int_{-\infty}^{+\infty} p(x)dx = 1$
 - Cumulative distribution function $F(x) = \int_0^x p(t)dt$



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Expected value and variance

- Expected value = mean value
 - $E(X) = \sum_{i=1}^n X_i P(X_i)$
 - $E(X) = \int X p(X)dX$
- Variance how much values of random variable can deviate from mean value
 - $Var(X) = E(X - E(X))^2 = E(X^2) - E(X)^2$

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9

Probabilities

- Laws of probabilities
 - Sum rule (compute **marginal** probability)

$$p(X) = \sum_Y p(X, Y)$$

$$p(X) = \int p(X, Y)dY$$
 - Product rule

$$p(X, Y) = p(X|Y)p(Y)$$

Combination 1:

$$p(X) = \sum_Y p(X|Y)p(Y)$$

$$p(X) = \int p(X|Y)p(Y)dY$$

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10

Bayes theorem

For random variables:

Bayes Theorem

$$p(Y|X) = \frac{p(X|Y)p(Y)}{p(X)}$$

$$p(Y|X) \propto p(X|Y)p(Y)$$

$$p(Y|X) = \frac{p(X|Y)p(Y)}{\int p(X|Y)p(Y)dY}$$



Some conventional distributions

Bernoulli distribution

- Events: Success ($X=1$) and Failure ($X=0$)
- $P(X=1)=p, P(X=0)=1-p$
- $E(X) = p$
- $Var(X) = 1 - p$

Examples: Tossing coin, winning a lottery,..

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11

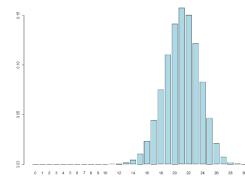
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12

Some conventional distributions

Binomial distribution

- Sequence of n Bernoulli events
 - $X=\{\text{Amount of successes among these events}\}, X=0,\dots,n$
- $$P(X = r) = \frac{n!}{(n-r)!r!} p^r (1-p)^{n-r}$$
- $EX = np$
 - $Var(X) = np(1-p)$



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13

Poisson distribution

- Customers of a bank n (in theory, endless population)
- Probability that a specific person will make a call to the bank between 13.00 and 14.00 a certain day is p
 - p can be very small if population is large (rare event)
 - Still, some people will make calls between 13.00 and 14.00 that day, and their amount may be quite big
 - A known quantity $\lambda=np$ is mean amount of persons that call between 13.00 and 14.00
 - $X=\{\text{amount of persons that have called between 13.00 and 14.00}\}$

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14

Poisson distribution

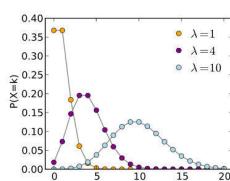
$$\bullet P(X = r) = \lim_{n \rightarrow \infty} \frac{n!}{(n-r)!r!} p^r (1-p)^{n-r}$$

• It can be shown that

$$P(X = r) = \frac{\lambda^r e^{-\lambda}}{r!}$$

$$\bullet E(X) = \lambda$$

$$\bullet Var(X) = \lambda$$



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Poisson distribution

• Further properties:

- Poisson distribution is a good approximation of the binomial distribution if $n > 20$ and $p < 0.05$
- Excellent approximation if $n \geq 100$ and $np \leq 10$

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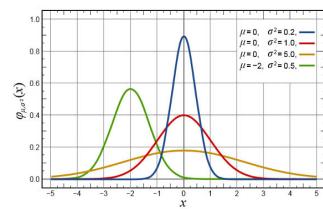
16

Normal distribution

- Appears in almost all applications
 - Difference between the times required to download two specific documents to a specific computer

$$f(x) = \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{(x-\mu)^2}{2\sigma^2}}, \sigma > 0$$

- $E(X) = \mu$
- $Var(X) = \sigma^2$

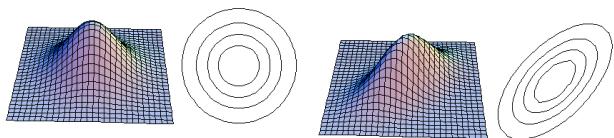


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17

Multivariate distributions

- Probability of two variables having certain values at the same time
 - P.D.F. $p(x,y)$
 - Correlation



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18

Basic ML ingredients

- Data D : observations
 - Features X_1, \dots, X_p
 - Targets Y_1, \dots, Y_r
- Model $P(x|w_1, \dots, w_k)$ or $P(y|x, w_1, \dots, w_k)$
 - Example: Linear regression $p(y|x, w) = N(w_0 + w_1 x, \sigma^2)$
- Learning procedure (data → get parameters \hat{w} or $p(w|D)$)
 - Maximum likelihood, Bayesian estimation
- Predict new data X^{new} by using the fitted model

Case	X_1	X_2	Y
1			
2			
...			

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19

Probabilistic models

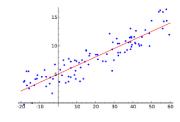
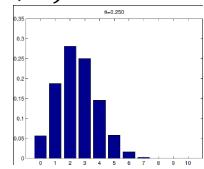
- A distribution $p(x|w)$ or $p(y|x, w)$

- Example:

– $x \sim Bin(n, \theta)$

$$p(x=k|n, \theta) = \binom{n}{k} \theta^k (1-\theta)^{n-k}$$

– $y \sim N(\alpha_0 + \alpha_1 x, \sigma^2)$



Learn basic distributions and their properties → PRML, chapter 2!

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20

Fitting a model

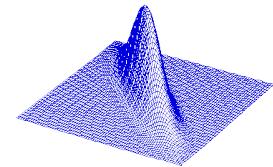
- Given dataset D and model $p(x|w)$ or $p(y|x, w)$
 - Frequentist approach: which combination of parameter values fits my data best?
 - Bayesian approach: parameters are random variables, all feasible values are acceptable
 - Different parameter values have different probabilities

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21

Fitting a model

- Frequentist principle: **Maximum likelihood** principle
 - Compute likelihood $p(D|w)$
 - $$p(D|w) = \prod_{i=1}^n p(X_i|w)$$
 - $$p(D|w) = \prod_{i=1}^n p(Y_i|X_i, w)$$
 - Maximize the likelihood and find the optimal w^*



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22

Fitting a model

Remarks:

- Likelihood shows how much the chosen parameter value is proper for a specific model and the given data
- Normally **log-likelihood** is used in computations instead
- Other alternatives to ML exist...

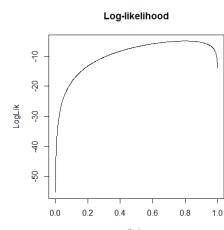
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23

Fitting a model

Example: tossing a coin.

$$D = \{0, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1\}, \\ p(x=1|\theta) = \theta, p(x=0|\theta) = 1 - \theta$$



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24

Bayesian probabilities

- Probability reflects your knowledge (uncertainty) about a phenomenon → **subjective probabilities**
 - **Prior probability** $p(w)$, can be uninformative $p(w) \propto 1$
 - Formulate a model, compute **likelihood** $p(D|w)$
 - **Posterior probability** $p(w|D)$, after observing data
 - $p(w|D) \propto p(D|w)p(w)$
- Model parameters are considered as random variables
 - In real life, do not need to be random, but we model as random

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25

Fitting a model

- Bayesian principle
 - Compute $p(w|D)$ and then decide yourself what to do with this (for ex. MAP, mean, median)
- Use bayes theorem
$$p(w|D) = \frac{p(D|w)p(w)}{p(D)} \propto p(D|w)p(w)$$
- $p(D)$ is **marginal likelihood**
 - $p(D) = \int p(D|w)p(w)dw$ or
 - $p(D) = \sum_i p(D|w_i)p(w_i)$

Example: tossing a coin. Find $p(\theta|D)$, estimate posterior mean θ^*

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26

Fitting a model

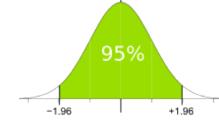
- How to chose the prior?
 - Expert knowledge about the phenomenon
 - Forcing a model to have a certain structure
 - Example: decision trees: prior prefers smaller trees
http://en.wikipedia.org/wiki/Conjugate_prior
 - Conjugacy
 - Distribution of the posterior is the same type as the distribution of the likelihood or prior
- Prior is the most controversial about Bayesian methods, but
 - When $N \rightarrow \infty$, data overwhelms the prior

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27

Measuring uncertainty

- **Confidence interval** (frequentist)
 1. Model $p(x|w)$ is known
 2. \hat{w} is a function of x by ML
 3. Derive distribution of \hat{w}
 4. Compute quantiles
- **Credible interval** (Bayes)
- **Prediction interval** (models)
- **Example:** Prediction interval for $Y \sim N(2x + 4, 1)$ at $x = 5$



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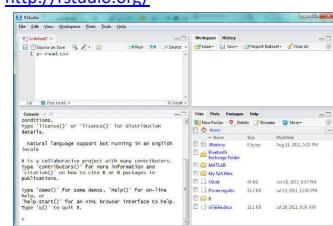
28

Introduction to R

Lecture 1c

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- R is a **programming language** of a higher-level
- Constantly increasing amount of packages (new research)
- Free of charge
- Website: <http://www.r-project.org/>
- Code Editor: <http://rstudio.org/>



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Overview

- Linear regression
- Ridge Regression
- Lasso
- Variable selection

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Simple linear regression

Model:

$$y \sim N(w_0 + w_1 x, \sigma^2)$$

or

$$y = w_0 + w_1 x + \epsilon, \quad \epsilon \sim N(0, \sigma^2)$$

or

$$p(y|x, w) = N(w_0 + w_1 x, \sigma^2)$$

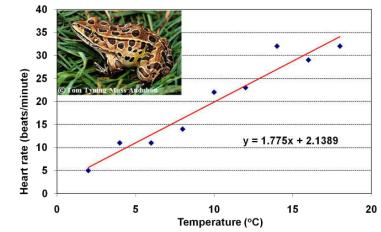
Terminology:

w_0 : intercept (or bias)

w_1 : regression coefficient

Response

The target responds directly and linearly to changes in the feature



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3

Ordinary least squares regression (OLS)

Model:

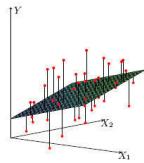
$$y \sim N(\mathbf{w}^T \mathbf{x}, \sigma^2)$$

where

$$\mathbf{w} = \{w_0, \dots, w_d\}$$

$$\mathbf{x} = \{1, x_1, \dots, x_d\}$$

Why is "1" here?



The response variable responds directly and linearly to changes in each of the inputs

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Ordinary least squares regression

Given data set D

Case	X_1	X_2			X_p	Y
1	x_{11}	x_{21}			x_{p1}	y_1
2	x_{12}	x_{22}			x_{p2}	y_2
3	x_{13}	x_{23}			x_{p3}	y_3
N	x_{1N}	x_{2N}			x_{pN}	y_N

Estimation: maximizing the likelihood

$$\hat{\mathbf{w}} = \max_{\mathbf{w}} p(D|\mathbf{w})$$

Is equivalent to minimizing

$$RSS(\mathbf{w}) = \sum_{t=1}^n (y_t - \mathbf{w}^T \mathbf{X}_t)^2$$

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5

Matrix formulation of OLS regression

Optimality condition:

where $\mathbf{X}^T (\mathbf{y} - \mathbf{X}\mathbf{w}) = 0$

$$\mathbf{X} = \begin{pmatrix} 1 & x_{11} & x_{21} & & x_{p1} \\ 1 & x_{12} & x_{22} & & x_{p2} \\ & & & \ddots & \\ 1 & x_{1N} & x_{2N} & & x_{pN} \end{pmatrix} \quad \text{and} \quad \mathbf{y} = \begin{pmatrix} y_1 \\ y_2 \\ \vdots \\ y_N \end{pmatrix}$$

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Parameter estimates and predictions

- Least squares estimates of the parameters

$$\hat{\mathbf{w}} = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{y}$$

- Predicted values

$$\hat{\mathbf{y}} = \mathbf{X}\hat{\mathbf{w}} = \mathbf{X}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{y} = \mathbf{P}\mathbf{y}$$



Why is it called so?

- Linear regression belongs to the class of **linear smoothers**

6

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7

Degrees of freedom

Definition:

$$df(\hat{y}) = \frac{1}{\sigma^2} \sum_{i=1}^N \text{Cov}(\hat{y}_i, y_i)$$

- Larger covariance → stronger connection → model can approximate data better → model more flexible (complex)
 - For linear smoothers $\hat{Y} = S(X)Y$
- $$df = \text{trace}(S)$$
- For linear regression, degrees of freedom is
- $$df = \text{trace}(P) = p$$

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8

Different types of features

- Interval variables
- Numerically coded ordinal variables
 - (small=1, medium=2, large=3)
- Dummy coded qualitative variables

Example of dummy coding:

$$x_1 = \begin{cases} 1, & \text{if Jan} \\ 0, & \text{otherwise} \end{cases}$$

Basis function expansion:

$$\text{If } y = w_0 + w_1 x_1 + w_2 x_1^2 + w_3 e^{-x_2} + \epsilon,$$

Model becomes linear if to recompute:

$$\begin{aligned}\phi_1(x_1) &= x_1 \\ \phi_2(x_1) &= x_1^2 \\ \phi_3(x_1) &= e^{-x_2}\end{aligned}$$

$$x_2 = \begin{cases} 1, & \text{if Feb} \\ 0, & \text{otherwise} \end{cases}$$

$$x_{11} = \begin{cases} 1, & \text{if Nov} \\ 0, & \text{otherwise} \end{cases}$$

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9

Basis function expansion

- In general $\phi_1(\dots)$ may be a function of several x components
- Having data given by X , compute new data
- $\Phi = \begin{pmatrix} 1 & \phi_1(x_{11}, \dots, x_{1p}) & \dots & \phi_p(x_{11}, \dots, x_{1p}) \\ \dots & \dots & \dots & \dots \\ 1 & \phi_1(x_{n1}, \dots, x_{np}) & \dots & \phi_p(x_{n1}, \dots, x_{np}) \end{pmatrix}$
- If doing a basis function in a model, replace X by Φ everywhere where X is used:

$$\hat{y} = \Phi(\Phi^T \Phi)^{-1} \Phi^T y$$

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10

Linear regression in R

- fit=lm(formula, data, subset, weights,...)**
 - data** is the data frame containing the predictors and response values
 - formula** is expression for the model
 - subset** which observations to use (training data)?
 - weights** should weights be used?

fit is object of class **lm** containing various regression results.

- Useful functions (many are generic, used in many other models)
 - Get details about the particular function by "", for ex. `predict.lm`

```
summary(fit)
predict(fit, newdata, se.fit, interval)
coefficients(fit) # model coefficients
confint(fit, level=0.95) # CIs for model parameters
fitted(fit) # predicted values
residuals(fit) # residuals
```

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11

An example of ordinary least squares regression

```
mydata=read.csv2("Bilexempel.csv")
fit1=lm(Price~Year, data=mydata)
summary(fit1)
fit2=lm(Price~Year+Mileage+Equipment,
       data=mydata)
summary(fit2)

Response variable:
Requested price of used Porsche cars
(1000 SEK)

Inputs:
X1 = Manufacturing year
X2 = Milage (km)
X3 = Equipment (0 or 1)

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 78161027 8448038 -9.252 6.00e-13 ***
Year        1.062e+04 3.154e+03 3.366 0.00139 **
Mileage     -2.077e+00 2.022e-01 -10.269 2.14e-14 ***
Equipment   5.790e+04 1.041e+04 5.563 8.08e-07 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 57270 on 57 degrees of freedom
Multiple R-squared: 0.8997, Adjusted R-squared: 0.8942
F-statistic: 164.5 on 3 and 57 DF, p-value: 2.2e-16
```

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12

An example of ordinary least squares regression

```
> summary(fit2)
Call:
lm(formula = Price ~ Year + Mileage + Equipment, data = mydata)
Residuals:
    Min      1Q      Median      3Q      Max 
-66223 -10525    -739    14128   65332 
Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 78161027 8448038 -9.252 6.00e-13 ***
Year        1.062e+04 3.154e+03 3.366 0.00139 **  
Mileage     -2.077e+00 2.022e-01 -10.269 2.14e-14 ***
Equipment   5.790e+04 1.041e+04 5.563 8.08e-07 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 59270 on 55 degrees of freedom
Multiple R-squared: 0.8997, Adjusted R-squared: 0.8942
F-statistic: 164.5 on 3 and 55 DF, p-value: 2.2e-16
```

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13

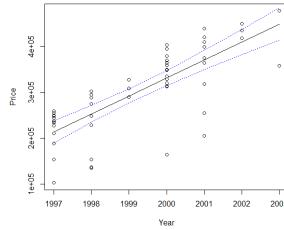
An example of ordinary least squares regression

- Prediction

```
fitted <- predict(fit1, interval =
"confidence")

# plot the data and the fitted line
attach(mydata)
plot(Year, Price)
lines(Year, fitted[, "fit"])

# plot the confidence bands
lines(Year, fitted[, "lwr"], lty = "dotted",
col="blue")
lines(Year, fitted[, "upr"], lty = "dotted",
col="blue")
detach(mydata)
```



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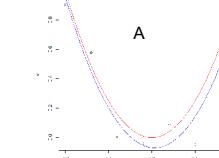
14

Ridge regression

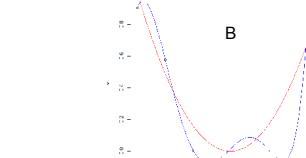
- Problem: linear regression can overfit:

- Take $Y := Y, X_1 = X, X_2 = X^2, \dots, X_p = X^p \rightarrow$ polynomial model, fit by linear regression

- High degree of polynomial leads to overfitting.



A



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15

Ridge regression

- Idea: Keep all predictors but shrink coefficients to make model less complex

$$\text{minimize } -\log \text{likelihood} + \lambda_0 \|w\|_2^2$$

→ L_2 regularization

- Given that model is Gaussian, we get Ridge regression:

$$\hat{w}^{\text{ridge}} = \underset{w}{\operatorname{argmin}} \left\{ \sum_{i=1}^N (y_i - w_0 - w_1 x_{1j} - \dots - w_p x_{pj})^2 + \lambda \sum_{j=1}^p w_j^2 \right\}$$

- $\lambda > 0$ is penalty factor

Equivalent form

$$\begin{aligned} \hat{w}^{\text{ridge}} &= \underset{w}{\operatorname{argmin}} \sum_{i=1}^N (y_i - w_0 - w_1 x_{1j} - \dots - w_p x_{pj})^2 \\ &\text{subject to } \sum_{j=1}^p w_j^2 \leq s \end{aligned}$$

Solution

$$\hat{w}^{\text{ridge}} = (X^T X + \lambda I)^{-1} X^T y$$

$$\hat{y} = X \hat{w} = X (X^T X + \lambda I)^{-1} X^T y = P y$$

Hat matrix

How do we compute degrees of freedom here?

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17

Ridge regression

Properties

- Extreme cases:
 - $\lambda = 0$ usual linear regression (no shrinkage)
 - $\lambda = +\infty$ fitting a constant ($w = 0$ except of w_0)
- When input variables are orthogonal (not realistic), $X^T X = I \rightarrow \hat{w}^{\text{ridge}} = \frac{1}{1+\lambda} w^{\text{linreg}}$ → coefficients are equally shrunk
- Ridge regression is particularly useful if the explanatory variables are strongly correlated to each other.
 - Correlated variables often correspond large $w \rightarrow$ shrunk
- Degrees of freedom decrease when λ increases
 - $\lambda = 0 \rightarrow d.f. = p$

Properties

- Shrinking enables estimation of regression coefficients even if the number of parameters exceeds the number of cases! ($X^T X + \lambda I$ is always nonsingular)
 - Compare with linear regression
- How to estimate λ ?
 - cross-validation

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18

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19

Ridge regression

- Bayesian view

- Ridge regression is just a special form of Bayesian Linear Regression with constant σ^2 :

$$y \sim N(y | \mathbf{w}_0 + \mathbf{X}\mathbf{w}, \sigma^2 I)$$

$$\mathbf{w} \sim N\left(\mathbf{0}, \frac{\sigma^2}{\lambda} I\right)$$

Theorem MAP estimate to the Bayesian Ridge is equal to solution in frequentist Ridge

$$\hat{\mathbf{w}}^{ridge} = (\mathbf{X}^T \mathbf{X} + \lambda I)^{-1} \mathbf{X}^T \mathbf{y}$$

- In Bayesian version, we can also make inference about λ

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Example Computer Hardware Data Set: performance measured for various processors and also

- Cycle time
- Memory
- Channels
- ...

Build model predicting performance



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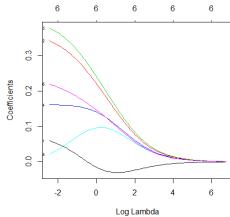
21

Ridge regression

- R code: use package **glmnet** with alpha=0 (Ridge regression)
- Seeing how Ridge converges

```
data=read.csv("machine.csv", header=F)
covariates=scale(data[,3:8])
response=scale(data[, 9])

model0=glmnet(as.matrix(covariates),
              response, alpha=0,family="gaussian")
plot(model0, xvar="lambda", label=TRUE)
```



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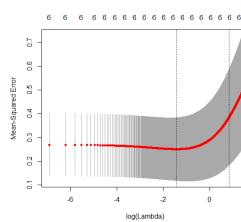
22

Ridge regression

- Choosing the best model by cross-validation:

```
model=cv.glmnet(as.matrix(covariates),
                 response, alpha=0,family="gaussian")
model$lambda.min
plot(model)
coef(model, s="lambda.min")
```

```
> coef(model, s="lambda.min")
7 x 1 sparse Matrix of class "dgCMatrix"
(Intercept) -4.530442e-17
v3 3.420739e-02
v4 3.085696e-01
v5 3.403839e-01
v6 1.593470e-01
v7 5.489116e-02
v8 1.970982e-01
```



```
> model$lambda.min
[1] 0.046
```

23

Ridge regression

- How good is this model in prediction?

```
ind=sample(209, floor(209*0.5))
data1=scale(data[,3:9])
train=data1[ind,]
test=data1[-ind,]

covariates=train[,1:6]
response=train[, 7]
model=cv.glmnet(as.matrix(covariates), response, alpha=1,family="gaussian",
                 lambda=seq(0,1,0.001))
y=test[,7]
ynew=predict(model, newx=as.matrix(test[, 1:6]), type="response")

#Coefficient of determination
sum((ynew-mean(y))^2)/sum((y-mean(y))^2)
```

Note that data are so small so numbers change much for other train/test

```
sum((ynew-y)^2)

> sum((ynew-mean(y))^2)/sum((y-mean(y))^2)
[1] 0.5438148
> sum((ynew-y)^2)
[1] 18.04988
> 1
```

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LASSO

- Idea: Similar idea to Ridge

- Minimize minus loglikelihood plus linear penalty factor $\rightarrow \mathbf{I}_1$ regularization

- Given that model is Gaussian, we get LASSO (least absolute shrinkage and selection operator):

$$\hat{\mathbf{w}}^{lasso} = \operatorname{argmin}_{\mathbf{w}} \left\{ \sum_{i=1}^N (y_i - w_0 - w_1 x_{1i} - \dots - w_p x_{pi})^2 + \lambda \sum_{j=1}^p |w_j| \right\}$$

- $\lambda > 0$ is penalty factor



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LASSO

- Equivalently

$$\hat{w}^{\text{LASSO}} = \underset{\mathbf{w}}{\operatorname{argmin}} \sum_{i=1}^N (\mathbf{y}_i - \mathbf{w}_0 - \mathbf{w}_1 \mathbf{x}_{1i} - \dots - \mathbf{w}_p \mathbf{x}_{pi})^2$$

subject to $\sum_{j=1}^p |w_j| \leq s$

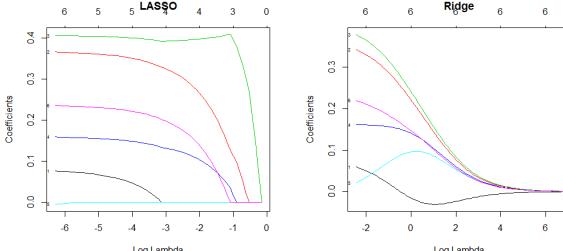
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LASSO vs Ridge

- LASSO yields sparse solutions!

Example Computer hardware data



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LASSO vs Ridge

- Only 5 variables selected by LASSO

```
> coef(model1, s="lambda.min")
7 x 1 sparse Matrix of class "dgCMatrix"
 1
(Intercept) -5.091825e-17
V3           6.350488e-02
V4           3.578607e-01
V5           4.033670e-01
V6           1.541329e-01
V7           2.287134e-01
V8           16.63756
```

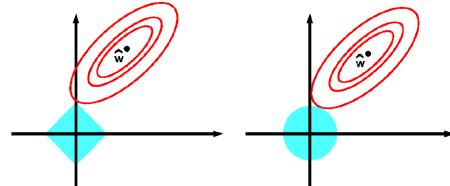
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28

LASSO vs Ridge

- Why Lasso leads to sparse solutions?

- Feasible area for Ridge is a circle (2D)
- Feasible area for LASSO is a polygon (2D)



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LASSO properties

- Lasso is widely used when $p \gg n$
 - Linear regression breaks down when $p > n$
 - Application: DNA sequence analysis, Text Prediction
- When inputs are orthonormal,

$$\hat{w}_i^{\text{Lasso}} = \text{sign}(w_i^{\text{linreg}}) \left(|w_i^{\text{linreg}}| - \frac{\lambda}{2} \right)_+$$

- No explicit formula for \hat{w}^{Lasso}
 - Optimization algorithms used

Coding in R: use
glmnet() with
alpha=1

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30

Variable selection

- .. Or “Feature selection”

Often, we do not need all features available in the data to be in the model

Reasons:

- Model can become overfitted (recall polynomial regression)
- Large number of predictors → model is difficult to use and interpret

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31

Variable selection

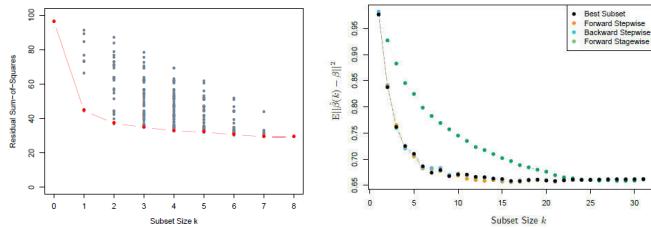
Alternative 1: Variable subset selection

- Best subset selection:
 - Consider different subsets of the full set of features, fit models and evaluate their quality
 - Problem: computationally difficult for p around 30 or more
 - How to choose the best model size? Some measure of predictive performance normally used (ex. AIC).
- Forward and Backward stepwise selection
 - Starts with 0 features (or full set) and then adds a feature (removes feature) that most improves the measure selected.
 - Can handle large p quickly
 - Does not examine all possible subsets (not the “best”)

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RSS and MSE depend on k



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33

Variable selection in R

- Use stepAIC() in MASS

```
> library(MASS)
> fit <- lm(V9~.,data=data.frame(data1))
> step <- stepAIC(fit, direction="both")
> step$anova
> summary(step)

Call:
lm(formula = V9 ~ V3 + V4 + V5 + V6 + V8, data = data.frame(data1))

Residuals:
    Min      1Q  Median      3Q     Max 
-1.20232 -0.15512  0.03579  0.16567  2.42280 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -5.783e-17  2.574e-02   0.000  1.0000    
V3          7.948e-02  2.876e-02   2.813  0.0054 **  
V4          3.934e-01  4.664e-02   8.691 1.18e-15 ***  
V5          4.055e-01  4.664e-02   8.691 1.18e-15 ***  
V6          1.591e-01  3.394e-02   4.687 3.07e-06 ***  
V8          2.360e-01  3.396e-02   7.032 3.06e-11 ***  
                                          
Step:  AIC=-407.25
V9 ~ V3 + V4 + V5 + V6 + V8

> step <- stepAIC(fit, direction="both")
> step$anova
> summary(step)

Call:
lm(formula = V9 ~ V3 + V4 + V5 + V6 + V8, data = data.frame(data1))

Residuals:
    Min      1Q  Median      3Q     Max 
-1.20232 -0.15512  0.03579  0.16567  2.42280 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -5.783e-17  2.574e-02   0.000  1.0000    
V3          7.948e-02  2.876e-02   2.813  0.0054 **  
V4          3.934e-01  4.664e-02   8.691 1.18e-15 ***  
V5          4.055e-01  4.664e-02   8.691 1.18e-15 ***  
V6          1.591e-01  3.394e-02   4.687 3.07e-06 ***  
V8          2.360e-01  3.396e-02   7.032 3.06e-11 ***  

```

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34

Model selection

Lecture 1e

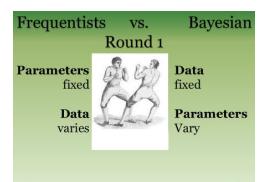
Overview

- Model fitting
- Model selection

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Frequentist vs Bayesian

- Probabilistic Model $p(y, x, w)$
 - **Frequentists:** w is a parameter that should be estimated by model fitting
 - **Bayesians:** w is a random variable that has a prior distribution $p(w)$
 - How to set $p(w)$??



Example: Linear regression, what are parameters here?

$$y \sim w_0 + \mathbf{w}x + e, e \sim N(0, \sigma^2)$$

$$y \sim N(w_0 + \mathbf{w}x, \sigma^2)$$

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3

An estimator

- $\hat{w} = \delta(D)$ (some function of your data) – an **estimator**
- Optimal parameter values? → there can be many ways to compute them (MLE, shrinkage...)
 - Compare Bayesian: given estimators w^1 and w^2 , we **can** compare them! $p(w^1|D) > p(w^2|D)$
 - There is no easy way to compare estimators in frequentist tradition

Example: Linear regression

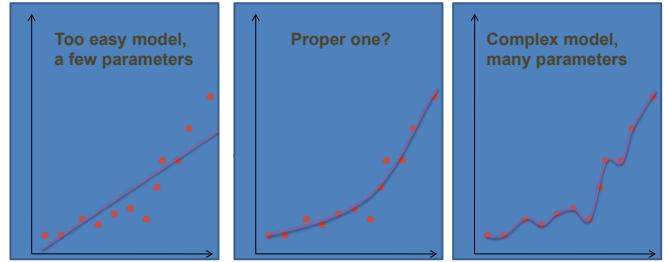
- Estimator 1: $w = (X^T X)^{-1} X^T Y$ (maximum likelihood)
- Estimator 2: $w = (0, \dots, 0, 1)$
- Which one is better?
 - A comparison strategy is needed!

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Overfitting

- Complex model can overfit your data



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5

Overfitting: solutions

- Observed:** Maximum likelihood can lead to overfitting.
- Solutions**
 - Selecting proper parameter values
 - Regularized risk minimization
 - Selecting proper model type, for ex. number of parameters
 - Houldout method
 - Cross-validation

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6

Model selection

- Given a model, choose the optimal parameter values
 - Decision theory
- Define loss $L(Y, \hat{Y})$
 - How much we loose in guessing true Y incorrectly
- If we know the true distribution $p(y, x|w)$ then we choose \hat{y}

$$\min_f EL(y, \hat{y}) = \min_{\hat{y}} \int L(y, \hat{y}) p(y, x|w) dx dy$$

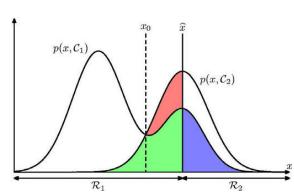
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7

Model selection

Example: Spam classification

- Loss for incorrect classifying mails and spams
 - $L_{12} = 100, L_{21} = 1$



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Loss functions

- How to define loss function?
 - No unique choice, often defined by application
 - Normal practice:** Choose the loss related to minus loglikelihood

Example: Predicting the amount of the product at the storage:

$$L(Y, \hat{Y}) = \begin{cases} 10 + \frac{\hat{Y}}{Y}, \hat{Y} \geq Y \\ 1000, \hat{Y} < Y \end{cases}$$

Example: Compute loss function related to

- Normal distribution

Guess why such loss function was chosen

8

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9

Loss functions

- Classification problems

– Common loss function $L(Y, \hat{Y}) = \begin{cases} 0, Y = \hat{Y} \\ 1, Y \neq \hat{Y} \end{cases}$

– When minimizing the loss, equivalent to misclassification rate

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10

Model selection

- Problem:** true model and true w are unknown → can not compute expected loss!
- How to find an optimal model?
 - Consider what expected loss (**risk**) depends on $R(Y, \hat{Y}) = E[L(Y, \hat{Y}(X, D))]$
- Random factors:
 - D – **training set**
 - Y, X – data to be predicted (**validation set**)

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11

Holdout method

- Simplify the risk estimation:

– Fix D as a particular training set T
– Fix Y, X as a particular validation set V

- Risk becomes (**empirical risk**)

$$\hat{R}(y, \hat{Y}) = \frac{1}{|V|} \sum_{(X, Y) \in V} L(Y, \hat{Y}(X, T))$$

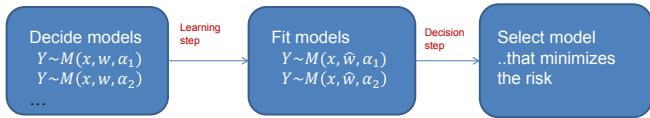
– Estimator is fit by Maximum Likelihood using training set
– Risk estimated by using validation set
– Model with minimum empirical risk is selected

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General model selection strategy

- Given data $D = \{X_i, Y_i, i = 1 \dots n\}$



- When fitting data, Maximum Likelihood is usually used

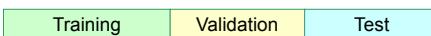
- α_i can be different things:
 - Type of distribution
 - Number of variables in the model
 - Regularization parameter value
 - ...

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13

Holdout method

Divide into training, validation and test sets



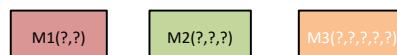
- Choose proportions in some way

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14

Holdout method

- Given: training, validation, test sets and models to select between

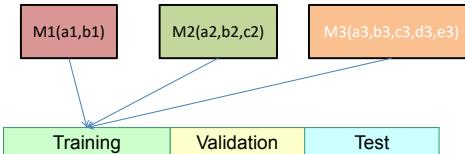


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15

Holdout method

- Training set is used for fitting models to the dataset by using maximum likelihood

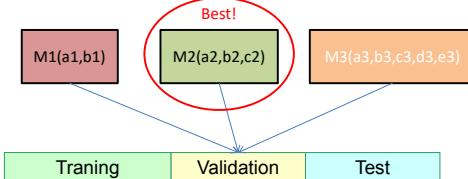


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16

Holdout method

- Validation set is used to choose the best model (lowest risk)

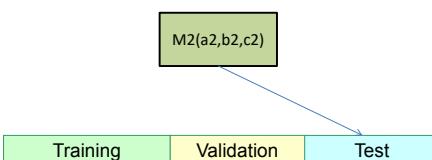


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17

Holdout method

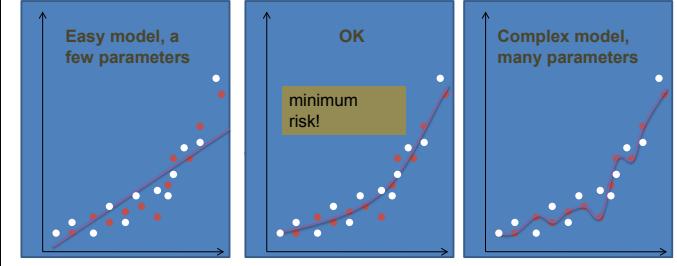
- Test set is used to test a performance on a new data



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Holdout method



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19

Holdout in R

- How to partition into train/test?
- Use `set.seed(12345)` in the labs to get identical results

```
n<-dim(data)[1]
set.seed(12345)
id<-sample(1:n, floor(n*0.7))
train<-data[id,]
test<-data[-id,]
```

- How to partition into train/valid/test?

```
n<-dim(data)[1]
set.seed(12345)
id<-sample(1:n, floor(n*0.4))
train<-data[id,]

id1<-setdiff(1:n, id)
set.seed(12345)
id2<-sample(id1, floor(n*0.3))
valid<-data[id2,]

id3<-setdiff(id1,id2)
test<-data[id3,]
```

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20

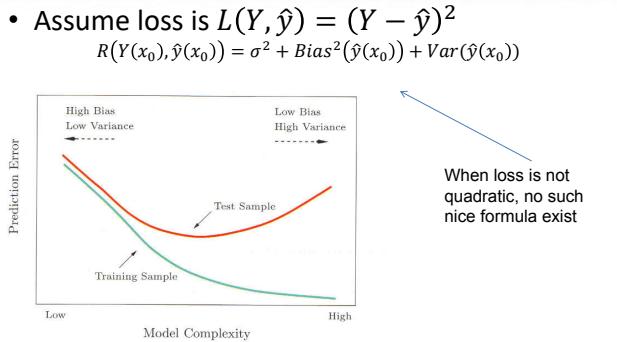
Bias-variance tradeoff

- Bias of an estimator** $Bias(\hat{y}(x_0)) = E[\hat{y}(x_0)] - f(x_0)$, $f(x_0)$ is expected response
 - If $Bias(\hat{y}(x_0)) = 0$, the estimator is **unbiased**
 - ML estimators are asymptotically unbiased if the model is enough complex
 - However, unbiasedness does not mean a good choice!

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Bias-variance tradeoff



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22

Cross-validation

- Compared to holdout method:
 - Why do we use only some portion of data for training- can we use more (increase accuracy)?

Cross-validation (Estimates Err)

K-fold cross-validation (rough scheme, show picture):

- Permute the observations randomly
- Divide data-set in K roughly equally-sized subsets
- Remove subset #i and fit the model using remaining data.
- Predict the function values for subset #i using the fitted model.
- Repeat steps 3-4 for different i
- CV= squared difference between observed values and predicted values (another function is possible)

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Cross-validation

Cross-validation



Note: if $K=N$ then method is **leave-one-out** cross-validation.

$$\kappa : \{1, \dots, N\} \mapsto \{1, \dots, K\}$$

K-fold cross-validation: $CV =$

$$\frac{1}{N} \sum_{i=1}^N L(Y_i, \hat{y}^{-k(i)}(x_i))$$

What to do if N is not a multiple of K?

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Cross-validation vs Holdout

- Holdout is easy to do (a few model fits to each data)
- Cross validation is computationally demanding (many model fits)
- Holdout is applicable for large data
 - Otherwise, model selection performs poorly
- Cross validation is more suitable for smaller data

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25

Analytical methods

- Analytical expressions to select models
 - **AIC** (Akaike's information criterion)

Idea: Instead of $R(Y, \hat{y}) = E[L(Y, \hat{y}(X, D))]$ consider **in-sample** risk (only Y in D is random):

$$R_{in}(Y, \hat{y}) = \frac{1}{N} \sum_{i=1}^N E_{Y_i} [L(Y_i, \hat{y}(X, D)) | D, X \in D]$$

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26

Analytical methods

- One can show that

$$R_{in}(Y, \hat{y}) \approx R_{train} + \frac{2}{N} \sum_t cov(\hat{y}_t, Y_t)$$

where $R_{train} = \sum_{X_t, Y_t \in T} L(Y_t, \hat{y}_t)$

- Recall, **degrees of freedom** $df(model) = \frac{1}{\sigma^2} \sum_i cov(\hat{y}_i, Y_i)$
 - When model is linear, df is the number of parameters.

- If loss is defined by minus two loglikelihood,
 $AIC \equiv -2loglik(D) + 2df(model)$

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27

Model selection

Example Computer Hardware Data Set : performance measured for various processors and also

- Cycle time
- Memory
- Channels
- ...

Build model predicting performance



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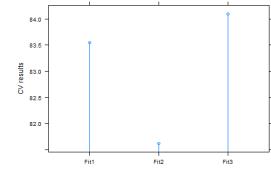
28

Cross-validation

- Try models with different predictor sets

```
data=read.csv("machine.csv", header=F)
library(cvTools)

fit1=lm(V9~V3+V4+V5+V6+V7+V8, data=data)
fit2=lm(V9~V3+V4+V5+V6+V7, data=data)
fit3=lm(V9~V3+V4+V5+V6, data=data)
f1=cvFit(fit1, y=data$V9, data=data,K=10,
foldType="consecutive")
f2=cvFit(fit2, y=data$V9, data=data,K=10,
foldType="consecutive")
f3=cvFit(fit3, y=data$V9, data=data,K=10,
foldType="consecutive")
res=cvSelect(f1,f2,f3)
plot(res)
```



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29

Linear classification methods

Lecture 2a

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Overview

- Elements of decision theory
- Logistic regression
- Discriminant Analysis models

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Classification

- Given data $D = ((X_i, Y_i), i = 1 \dots N)$
 - $Y_i = Y(X_i) = C_j \in \mathcal{C}$
 - Class set $\mathcal{C} = (C_1, \dots, C_K)$

Classification problem:

- Decide $\hat{Y}(x)$ that maps **any** x into some class C_k
 - Decision boundary

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Classifiers

- Deterministic:** decide a rule that directly maps X into \hat{Y}
- Probabilistic:** define a model for $P(Y = C_i | X), i = 1 \dots K$

Disadvantages of deterministic classifiers:

- Sometimes simple mapping is not enough (risk of cancer)
- Difficult to embed loss → rerun of optimizer is often needed
- Combining several classifiers into one is more problematic
 - Algorithm A classifies as spam, Algorithm B classifies as not spam → ???
 - $P(\text{Spam} | A) = 0.99, P(\text{Spam} | B) = 0.45 \rightarrow$ better decision can be made

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Bayesian decision theory

- Machine learning models estimate $p(y|x)$ or $p(y|x, \hat{w})$
- Transform probability into action → which value to predict? → decision step
 - $- p(Y = \text{Spam}|x) = 0.83 \rightarrow$ do we move the mail to Junk?
 - What is more dangerous: deleting 1 non-spam mail or letting 1 spam mail enter Inbox?
- **Loss function** or **Loss matrix**

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Loss matrix

- Costs of classifying $Y = C_k$ to C_j :
 - Rows: true, columns: predicted
$$L = \|L_{ij}\|, i = 1, \dots, n, j = 1, \dots, n$$
- Example 1:** 0/1-loss

$$L = \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix}$$
- Example 2:** Spam

$$L = \begin{pmatrix} 0 & 100 \\ 1 & 0 \end{pmatrix}$$

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Loss and decision

- Expected loss minimization

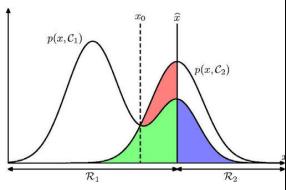
– R_j : classify to C_j

$$EL = \sum_k \sum_j \int_{R_j} L_{kj} p(x, C_k) dx$$

- Choose such R_j that EL is minimized

- Two classes

$$EL = \int_{R_1} L_{21} p(x, C_2) dx + \int_{R_2} L_{12} p(x, C_1) dx$$



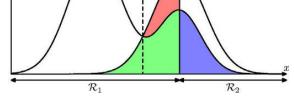
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7

- Loss minimization

$$\min_{\hat{f}} EL(y, \hat{f}) = \min_{\hat{f}} \int L(y, \hat{f}) p(y, x|w) dxdy$$

When loss is
 $\begin{cases} 1, & \text{wrongly classified} \\ 0, & \text{correctly classified} \end{cases}$



Classify Y as
 $\hat{Y} = \arg \max_c p(Y = c|X)$

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8

Loss and decision

- How to minimize EL with two classes?
- Rule:
 - $- L_{12} p(x, C_1) > L_{21} p(x, C_2) \rightarrow$ predict y as C_1
- 0/1 Loss: classify to the class which is more probable!

$$\frac{p(C_1|x)}{p(C_2|x)} > \frac{L_{21}}{L_{12}} \rightarrow \text{predict } y \text{ as } C_1$$

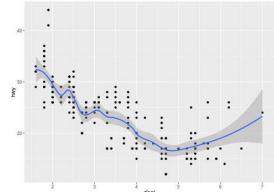
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9

- Continuous targets: squared loss

– Given a model $p(x, y)$, minimize

$$EL = \int L(y, \hat{Y}(x)) p(x, y) dxdy$$



- Using square loss, the optimal is posterior mean

$$\hat{Y}(x) = \int y p(y|x) dy$$

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10

ROC curves

- Binary classification
- The choice of the threshold $\hat{x} = \frac{L_{21}}{L_{12}}$ affects prediction → what if we don't know the loss? Which classifier is better?
- Confusion matrix

		PREDICTED		
		1	0	Total
T	1	TP	FN	N_+
	0	FP	TN	N_-

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11

ROC curves

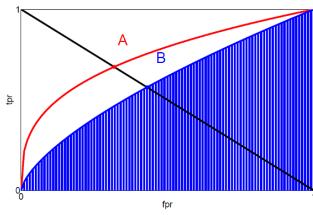
- True Positive Rates (TPR) = sensitivity = recall
 - Probability of detection of positives: $TPR = \frac{TP}{N_+}$
- False Positive Rates (FPR)
 - Probability of false alarm: system alarms (1) when nothing happens (true=0)
- Specificity
 $Specificity = 1 - FPR$
- Precision
 $Precision = \frac{TP}{TP + FP}$

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12

ROC curves

- ROC=Receiver operating characteristics
- Use various thresholds, measure TPR and FPR
- Same FPR, higher TPR → better classifier
- Best classifier = greatest Area Under Curve (AUC)



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13

Types of supervised models

- **Generative models:** model $p(X|Y, w)$ and $p(Y|w)$

– Example: k-NN classification

$$p(X = x|Y = C_i, K) = \frac{K_i}{N_i V}, p(C_i|K) = \frac{N_i}{N}$$

From Bayes Theorem,

$$p(Y = C_i|x, K) = \frac{K_i}{K}$$

- **Discriminative models:** model $p(Y|X, w)$, X constant

– Example: logistic regression

$$p(Y = 1|w, x) = \frac{1}{1 + e^{-w^T x}}$$

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14

Generative vs Discriminative

- Generative can be used to generate new data
- Generative normally easier to fit (check Logistic vs K-NN)
- Generative: each class estimated separately → do not need to retrain when a new class added
- Discriminative models: can replace X with $\phi(X)$ (preprocessing), method will still work
 - Not generative, distribution will change
- Generative: often make too strong assumptions about $p(X|Y, w)$ → bad performance

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15

Logistic regression

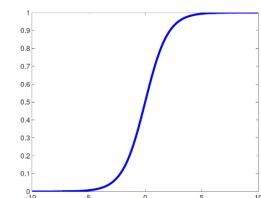
- Discriminative model
- Model for binary output
 - $C = \{C_1 = 1, C_2 = 0\}$
 $p(Y = C_1|X) = \text{sigm}(w^T x)$

What is $P(Y = C_2|X)$?

$$\text{sigm}(a) = \frac{1}{1 + e^{-a}}$$

- Alternatively
 $Y \sim \text{Bernoulli}(\text{sigm}(a)), a = w^T x$

$$\text{sigm}(a) = \frac{1}{1 + e^{-a}}$$



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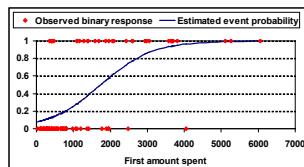
16

Logistic regression

- Logistic model- yet another form
 $\ln \frac{p(Y = 1|X = x)}{P(Y = 0|X = x)} = \ln \frac{p(Y = 1|X = x)}{1 - P(Y = 1|X = x)} = \text{logit}(p(Y = 1|X = x)) = w^T x$
- Here $\text{logit}(t) = \ln \left(\frac{t}{1-t} \right)$
- Note $p(Y|X)$ is connected to $w^T x$ via logit link

The log of the odds is linear in x

Example: Probability to buy more than once as function of First Amount Spend

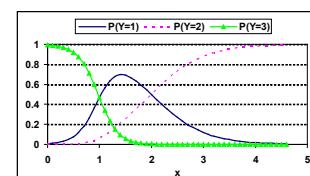


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17

Logistic regression

- When Y is categorical,
 $p(Y = C_i|x) = \frac{e^{w_i^T x}}{\sum_{j=1}^K e^{w_j^T x}} = \text{softmax}(w_i^T x)$
- Alternatively
 $Y \sim \text{Multinoulli}(\text{softmax}(w_1^T x), \dots, \text{softmax}(w_K^T x))$



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18

Logistic regression

Fitting logistic regression

- In binary case,
$$\log P(D|w) = \sum_{i=1}^N y_i \log(\text{sigm}(w^T x_i)) + (1 - y_i) \log(1 - \text{sigm}(w^T x_i))$$
 - Can not be maximized analytically, but unique maximizer exists
- To maximize loglikelihood, optimization used
 - Newton's method traditionally used (Iterative Reweighted Least Squares)
 - Steepest descent, Quasi-newton methods...

Estimation:

For new x , estimate $p(y) = [p_1, \dots, p_C]$ and classify as $\arg \max_i p_i$

Decision boundaries of logistic regression are linear

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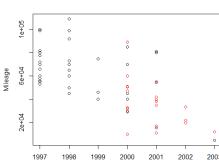
19

Logistic regression

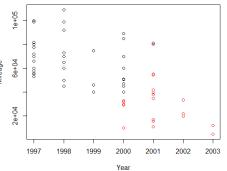
- In R, use `glm()` with `family="binomial"`
 - Predicted probabilities: `predict(fit,newdata, type="response")`

Example `Equipment=f(Year, mileage)`

Original data



Classified data



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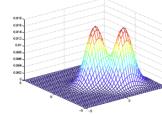
20

Quadratic discriminant analysis

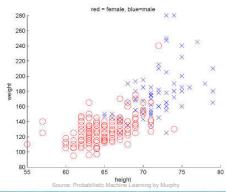
- Generative classifier
- Main assumptions:

x is now **random** as well as y

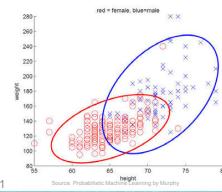
$$p(x|y = C_i, \theta) = N(x|\mu_i, \Sigma_i)$$



Unknown parameters $\theta = \{\mu_i, \Sigma_i\}$



Source: Probabilistic Machine Learning by Murphy

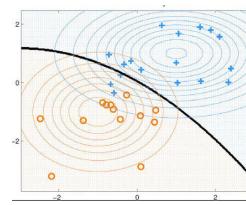


Source: Probabilistic Machine Learning by Murphy

Quadratic discriminant analysis

- If parameters are estimated, classify:

$$\hat{y}(x) = \arg \max_c p(y = c|x, \theta)$$



Source: Probabilistic Machine Learning by Murphy

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22

Linear discriminant analysis (LDA)

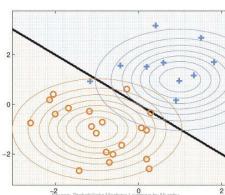
- Assumption $\Sigma_i = \Sigma, i = 1, \dots, K$
- Then $p(y = c_i|x) = \text{softmax}(w_i^T x + w_{0i}) \rightarrow$ exactly the same form as the logistic regression

$$\begin{aligned} w_{0i} &= -\frac{1}{2} \mu_i^T \Sigma^{-1} \mu_i + \log \pi_i \\ w_i &= \Sigma^{-1} \mu_i \end{aligned}$$

- Decision boundaries are linear

– **Discriminant function:**

$$\delta_k(x) = x^T \Sigma^{-1} \mu_k - \frac{1}{2} \mu_k^T \Sigma^{-1} \mu_k + \log \pi_k$$



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23

Linear discriminant analysis (LDA)

- Difference LDA vs logistic regression??

– Coefficients will be estimated differently! (models are different)

- How to estimate coefficients

– find MLE.

$$\begin{aligned} \hat{\mu}_c &= \frac{1}{N_c} \sum_{i:y_i=c} \mathbf{x}_i, \quad \hat{\Sigma}_c = \frac{1}{N_c} \sum_{i:y_i=c} (\mathbf{x}_i - \hat{\mu}_c)(\mathbf{x}_i - \hat{\mu}_c)^T \\ \hat{\Sigma} &= \frac{1}{N} \sum_{c=1}^k N_c \hat{\Sigma}_c \end{aligned}$$

– Sample mean and sample covariance are MLE!

– If class priors are parameters (**proportional priors**),

$$\hat{\pi}_c = \frac{N_c}{N}$$

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24

LDA and QDA: code

- Syntax in R, library **MASS**

```
lda(formula, data, ..., subset, na.action)
```

- Prior – class probabilities

- Subset – indices, if training data should be used

```
qda(formula, data, ..., subset, na.action)
```

```
predict(..)
```

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25

LDA: output

```
resLDA=lda(Equipment~Mileage+Year, data=mydata)
print(resLDA)
```

```
> print(resLDA)
Call:
lda(Equipment ~ Mileage + Year, data = mydata)

Prior probabilities of groups:
 0           1 
0.6440678 0.3559322 

Group means:
  Mileage   Year  
0 63539.21 1998.447 
1 36857.62 2000.762 

Coefficients of linear discriminants:
            LD1
Mileage -1.500069e-05
Year      5.745893e-01
```

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26

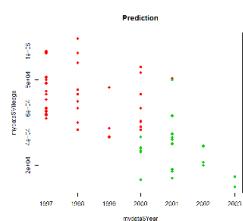
LDA: output

- Misclassified items

```
plot(mydata$Year, mydata$Mileage,
col=as.numeric(Pred$class)+1, pch=21,
bg=as.numeric(Pred$class)+1,
main="Prediction")
```

```
> table(Pred$class, mydata$Equipment)
```

	0	1
0	31	6
1	7	15

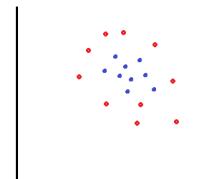


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LDA versus Logistic regression

- Generative classifiers are easier to fit, discriminative involve numeric optimization
- LDA and Logistic have same model form but are fit differently
- LDA has stronger assumptions than Logistic, some other generative classifiers lead also to logistic expression
- New class in the data?
 - Logistic: fit model again
 - LDA: estimate new parameters from the new data
- Logistic and LDA: complex data fits badly unless interactions are included



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LDA versus Logistic regression

- LDA (and other generative classifiers) handle missing data easier
- Standardization and generated inputs:
 - Not a problem for Logistic
 - May affect the performance of the LDA in a complex way
- Outliers affect $\Sigma \rightarrow$ LDA is not robust to gross outliers
- LDA is often a good classification method even if the assumption of normality and common covariance matrix are not satisfied.

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29

Naïve Bayes classifiers Decision trees

Lecture 2b

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Naive Bayes classifiers: motivation

- Consider n labeled text documents

$- Y = \{0,1\}$, $0 = "Science fiction"$, $1 = "Comedy"$

$- X = \{X_1, \dots, X_{100}\}$ does the document contain the keyword ($0=No, 1=Yes$)
 $\quad X_1$ corr. "space", X_2 corr. "fun", ...



- Want to classify a new document

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2

Naive Bayes classifiers: motivation

Idea: use Bayes classifier

$$p(Y = y|X) = \frac{P(X|Y = y)P(Y = y)}{\sum_j P(X|Y = y_j)P(Y = y_j)}$$

Chance of observing a given combination of words in science fiction

Proportion of science fiction documents

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Naive Bayes classifiers: motivation

Attempt 1:

- Model $P(X = (x_1, \dots, x_p)|Y = y_i)$ and $P(Y = y_i)$ as unknown parameters
- Use data to derive those with Maximum Likelihood
- Classify by use of the posterior distribution

How many parameters?

- How many different combinations of X ? 2^p
- Amount of $P(X = (x_1, \dots, x_p)|Y = y_i)$ is $2 * 2^p - 2$
 \quad Probabilities for each Y sum up to one

- If $p = 100, 10^{30}$ parameters need to be estimated → ouch!

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Naive Bayes classifiers

- Naive Bayes assumption: **conditional independence**

$$P(X = (x_1, \dots, x_p)|Y = y) = \prod_{i=1}^p P(X_i = x_i|Y = y)$$

- How many parameters now?

$$- P(X_i = x_i|Y = y), i = 1, \dots, p, x_i = \{0,1\}, y = \{0,1\} \quad 2 * p$$

- Is Naive Bayes assumption always valid?

$$- P(\text{Space, ship}|\text{SciFi}) = P(\text{Space}|\text{SciFi}) * P(\text{Ship}|\text{SciFi}) ?$$

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5

Naive Bayes classifiers - discrete inputs

- Given $D = \{(X_{m1}, \dots, X_{mp}, Y_m), m = 1, \dots, n\}$

- Assume $X_i \in \{x_1, \dots, x_j\}, i = 1, \dots, p, Y \in \{y_1, \dots, y_k\}$

- Denote $\theta_{ijk} = p(X_i = x_j|Y = y_k)$
 \quad How many parameters? $(J - 1)Kp$

- Denote $\pi_k = p(Y = y_k)$

- Maximum likelihood:** assume θ_{ijk} and π_k are constants

$$- \hat{\theta}_{ijk} = \frac{\#\{X_i = x_j \& Y = y_k\}}{\#\{Y = y_k\}}$$

$$- \hat{\pi}_k = \frac{\#\{Y = y_k\}}{n}$$

- Classification using 0-1 loss: $\hat{Y} = \arg \max_y p(Y = y|X)$

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Naive Bayes classifiers - discrete inputs

- Example** Loan decision

- Classify a person: Home Owner=No, Single=Yes

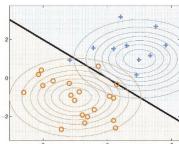
Tid	Home Owner	Marital Status	Annual Income	Defaulted Borrower
1	Yes	Single	125K	No
2	No	Married	100K	No
3	No	Single	70K	No
4	Yes	Married	120K	No
5	No	Divorced	95K	Yes
6	No	Married	60K	No
7	Yes	Divorced	220K	No
8	No	Single	85K	Yes
9	No	Married	75K	No
10	No	Single	90K	Yes

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Naive Bayes – continuous inputs

- X_i are continuous
- Assumption A:** $x_j|y = C$ are univariate Gaussian
 - $p(x_j|y = C_i, \theta) = N(x_j|\mu_{ij}, \sigma_{ij}^2)$
- Therefore $p(x|y = C_i, \theta) = N(x|\mu_i, \Sigma_i)$
 - $\Sigma_i = \text{diag}(\sigma_{i1}^2, \dots, \sigma_{ip}^2)$
- Naive bayes is a special case of LDA (given A)
 - MLE are means and variances (per class)

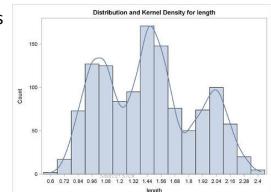


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8

Naive Bayes – continuous inputs

- Assumption B:** $p(x_j|y = C)$ are unknown functions of x_j that can be estimated from data
 - Nonparametric density estimation (kernel for ex.)
- Estimate $p(X_i = x_i|Y = y_k)$ using nonparametric methods
 - Estimate $p(Y = y_k)$ as class proportions
 - Use Bayes rule and 0-1 loss to classify



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9

Naive Bayes in R

- naiveBayes in package **e1071**

Example: Satisfaction of householders with their present housing circumstances

```
library(MASS)
library(e1071)
n=dim(housing)[1]
ind=rep(1:n, housing[,5])
housing1=housing[ind,-5]

fit=naiveBayes(Sat~, data=housing1)
table(Yfit,housing1$Sat)

Yfit      Low Medium High
  Low     294    162   144
  Medium   20     23    20
  High    253    261   504

Yfit=predict(fit, newdata=housing1)
table(Yfit,housing1$Sat)
```

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10

Decision trees

Idea

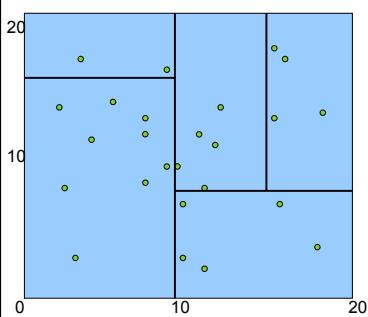
Split the domain of feature set into the set of hypercubes (rectangles, cubes) and define the target value to be constant within each hypercube

- Regression trees:
 - Target is a continuous variable
- Classification trees
 - Target is a class (qualitative) variable

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11

Classification tree toy example

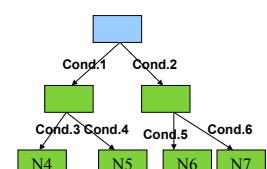


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12

Definitions

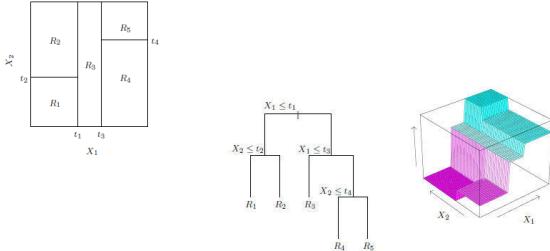
- Root node
- Nodes
- Leaves (terminal nodes)
- Parent node, child node
- Decision rules
- A value is assigned to the leaves



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13

Regression tree toy example



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14

A classification problem

Create a classification tree that would describe the following patterns

ID x1 x2 x3 x4 x5 x6 x7 y

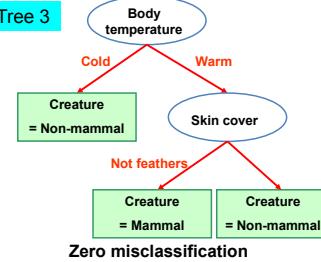
Name	Body temperature	Skin cover	Gives birth	Aquatic creature	Aerial creature	Has legs	Hibernates	Class label
human	warm-blooded	hair	yes	no	no	yes	no	mammal
python	cold-blooded	scales	no	no	no	no	yes	non-mammal
salmon	cold-blooded	scales	no	yes	no	no	no	non-mammal
whale	warm-blooded	hair	yes	yes	no	no	no	mammal
frog	cold-blooded	none	no	semi	no	yes	yes	non-mammal
komodo	cold-blooded	scales	no	no	no	yes	no	non-mammal
bat	warm-blooded	hair	yes	no	yes	yes	yes	mammal
pigeon	warm-blooded	feathers	no	no	yes	yes	no	non-mammal
cat	warm-blooded	fur	yes	no	no	yes	no	mammal
shark	cold-blooded	scales	yes	yes	no	no	no	non-mammal
turtle	cold-blooded	scales	no	semi	no	yes	no	non-mammal
penguin	warm-blooded	feathers	no	semi	no	yes	no	non-mammal
porcupine	warm-blooded	quills	yes	no	no	yes	yes	mammal
eel	cold-blooded	scales	no	yes	no	no	no	non-mammal
salamander	cold-blooded	none	no	semi	no	yes	yes	non-mammal

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15

Several solutions

Tree 1
Creature = Non-mammal
Large misclassification rate!



A lower misclassification rate

Green boxes represent pure nodes =nodes where observed values are the same

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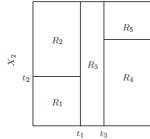
16

- A tree $T = \langle r_i, s_{r_i}, R_j, i = 1 \dots S, j = 1 \dots L \rangle$

- $- x_{r_i} \leq s_{r_i}$ splitting rules (conditions), S - their amount
- $- R_j$ -terminal nodes, L - their amount
- $-$ labels μ_j in each terminal node

Model:

- $Y|T$ for R_j comes from exponential family with mean μ_j
- Fitting by MLE:
 - Step 1: Finding optimal tree
 - Step 2: Finding optimal labels in terminal nodes



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17

Decision trees

Example:

- Normal model** leads to regression trees
 - Objective: MSE
- Multinoulli model** leads to classification trees
 - Objective: cross-entropy (deviance)

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18

Classification trees

- Target is categorical
- Classification probability $p_{mk} = p(Y = k | X \in R_m)$ is estimated for every class in a node
- How to estimate p_{mk} for class k and node R_m ?

Class proportions

$$\hat{p}_{mk} = \frac{1}{N_m} \sum_{x_i \in R_m} I(y_i = k)$$

- For any node (leave), a label can be assigned

$$k(m) = \arg \max_k \hat{p}_{mk}$$

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19

Classification trees

- Impurity measure $Q(R_m)$

- R_m is a tree node (region)
- Node can be split unless it is pure

Misclassification error: $\frac{1}{N_m} \sum_{i \in R_m} I(y_i \neq k(m)) = 1 - \hat{p}_{mk(m)}$

Gini index: $\sum_{k \neq k'} \hat{p}_{mk} \hat{p}_{mk'} = \sum_{k=1}^K \hat{p}_{mk} (1 - \hat{p}_{mk})$

Cross-entropy or deviance: $-\sum_{k=1}^K \hat{p}_{mk} \log \hat{p}_{mk}$.

- Note: In many sources, deviance is $Q(R_m) N(R_m)$

Example: Cross -entropy is MLE of $Y_j | T \sim \text{Multinomial}(p_{j1}, \dots, p_{jc})$

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20

Fitting regression trees: CART

Step 1: Finding optimal tree: grow the tree in order to minimize global objective

- Let C_0 be a hypercube containing all observations
- Let queue $C = \{C_0\}$
- Pick up some C_j from C and find a variable X_j and value s that split C_j into two hypercubes
 $R_1(j, s) = \{X | X_j \leq s\}$ and $R_2(j, s) = \{X | X_j > s\}$
and solve

$$\min_{j,s} [N_1 Q(R_1) + N_2 Q(R_2)]$$
- Remove C_j from C and add R_1 and R_2
- Repeat 3-4 as many times as needed (or until each cube has only 1 observation)

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21

CART: comments

- Greedy algorithm (optimal tree is not found)
- The largest tree will interpolate the data \rightarrow large trees = **overfitting** the data
- Too small trees = **underfitting** (important structure may not be captured)
- Optimal tree length?

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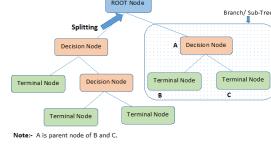
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Optimal trees

Postpruning

Weakest link pruning:

- Merge two leaves that have smallest $N(\text{parent}) * Q(\text{parent}) - N(\text{leave1})Q(\text{leave1}) - N(\text{leave2})Q(\text{leave2})$
- For the current tree T , compute
 $I(T) = \sum_{R_i \in \text{leaves}} N(R_i)Q(R_i) + \alpha|T|$
 $|T| = \# \text{leaves}$
- Repeat 1-2 until the tree with one leave is obtained
- Select the tree with smallest $I(T)$



How to find the optimal α ? Cross validation!

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Decision trees: comments

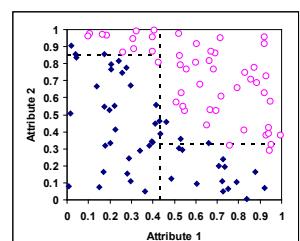
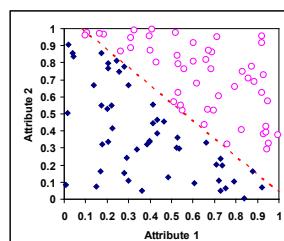
- Similar algorithms work for regression trees – replace $N \cdot Q(R)$ by $SSE(R)$
- Easy to interpret
- Easy to handle all types of features in one model
- Automatic variable selection**
- Relatively robust to outliers
- Handle large datasets
- Trees have high variance: a small change in response \rightarrow totally different tree
- Greedy algorithms \rightarrow fit may be not so good
- Lack of smoothness

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Decision trees: issues

- Large trees may be needed to model an easy system:



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25

Generalized Linear Models. Uncertainty estimation

Lecture 2c

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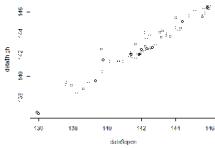
Moving beyond typical distributions

- We know how to model
 - Normally distributed targets \rightarrow linear regression
 - Bernoulli and Multinomial targets \rightarrow logistic regression
 - What if target distribution is more complex?

Example 1: Daily Stock prices NASDAQ

- Open
- High (within day)

Does it seem that the error is normal here?



Example 2: Number of calls to bank

- Y=Number of calls
- X=time

Endless amount of classes \rightarrow multinomial does not work... (Poisson)

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Exponential family

- More advanced error distributions are sometimes needed!
- Many distributions belong to **exponential** family:
 - Normal, Exponential, Gamma, Beta, Chi-squared..
 - Bernoulli, Multinoulli, Poisson...
$$p(\mathbf{x}|\boldsymbol{\eta}) = h(\mathbf{x})g(\boldsymbol{\eta})e^{(\boldsymbol{\eta}^T u(\mathbf{x}))}$$
- Easy to find MLE and MAP
- Non-exponential family distributions: uniform, Student t

Example: Bernoulli

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Generalized linear models

- Assume Y from the exponential family
- Model** is $Y \sim EF(\mu, \dots)$, $f(\mu) = \mathbf{w}^T \mathbf{x}$
 - Alt $\mu = f^{-1}(\mathbf{w}^T \mathbf{x})$
 - f^{-1} is activation function
 - f is link function (in principle, arbitrary)
- Arbitrary f will lead to (s – dispersion parameter)

$$p(y|\mathbf{w}, s) = h(y, s)g(\mathbf{w}, \mathbf{x})e^{\frac{b(\mathbf{w}, \mathbf{x})y}{s}}$$

- If f is a canonical link, then

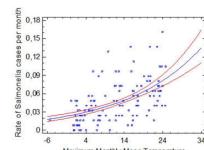
$$p(y|\mathbf{w}, s) = h(y, s)g(\mathbf{w}, \mathbf{x})e^{\frac{(\mathbf{w}^T \mathbf{x})y}{s}}$$

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Generalized linear models

- Canonical links are normally used
 - MLE computations simplify
 - MLE $\hat{\mathbf{w}} = F(X^T Y) \rightarrow$ computations do not depend on all data but rather a summary (sufficient statistics) \rightarrow computations speed up



Example: Poisson regression

$$f^{-1}(\mu) = e^\mu, Y \sim Poisson(e^{\mathbf{w}^T \mathbf{x}})$$

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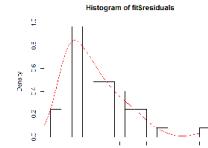
Generalized linear model: software

- Use **glm(formula, family, data)** in R

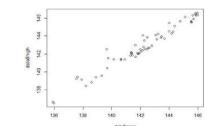
Example: Daily Stock prices NASDAQ

- Open
- High (within day)

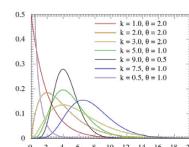
- Try to fit usual linear regression, study histogram of residuals



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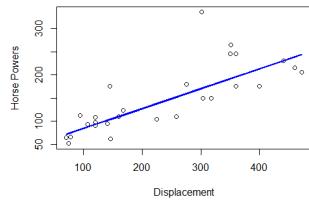
Gamma distribution: Wikipedia



6

Least absolute deviation regression

- Model $Y \sim \text{Laplace}(w^T X, b)$
 - Member of exponential family
- Equivalent to minimizing sum of absolute deviations
- Properties
 - Robust to outliers
 - Sensitive to changes in data
 - Multiple solutions possible
- R: package **L1pack**



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Probabilistic models

- Why it is beneficial to assume a **probabilistic** model?
- A common approach to modelling in CS and engineering:
 $y = f(x, w)$
- f is known, w is unknown
- Fit model to data with least squares, optimization or ad hoc → find w

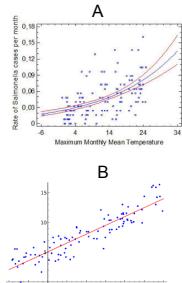
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8

Probabilistic models

Arguments against deterministic models:

- The model does not really describe actual data (error is not explained)
 - No difference between modelling data A (Poisson) and B (Normal)
 - Estimation strategy for A is not good for B
- The model typically gives a **deterministic answer**, no information about uncertainty
 - "...The exchange rate tomorrow will be 8.22 ..." 😊



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Probabilistic models

Probabilistic model

$$Y \sim \text{Distribution}(f(x, w), \theta)$$

- Data is fully explained (error as well)
- Automatic principle for finding parameters: MLE, MAP or Bayes theorem
- Automatic principle for finding uncertainty (conf. limits)
 - Bootstrap**
 - Posterior probability
- Possibility to generate new data of the same type
 - Further testing of the model

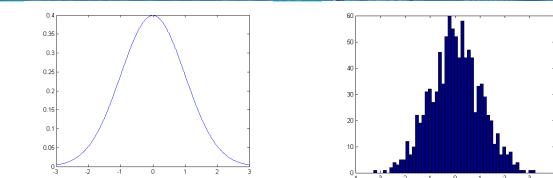
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Uncertainty estimation

- Given estimator $\hat{f} = \hat{f}(x, D)$ (or $\hat{\alpha} = \delta(D)$), how to estimate the uncertainty?
- Answer 1:** if the distribution for data D is given, compute analytically the distribution for the estimator → derive confidence limits
 - Often difficult
 - Example:** In simple linear regression, $\hat{\alpha}$ follows t distribution
- Answer 2:** Use **bootstrap**

The bootstrap: general principle



We want to determine uncertainty of $\hat{f}(D, X)$

- Generate many different D_i from their distribution
- Use histogram of $\hat{f}(D_i, X)$ to determine confidence limits → unfortunately can not be done (distr of D is often unknown)

Instead: Generate many different D_i^* from the empirical distribution (histogram)

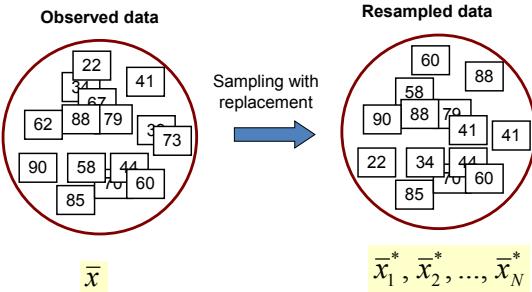
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11

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12

Nonparametric bootstrap



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13

Nonparametric bootstrap

Given estimator $\hat{w} = \hat{f}(D)$

Assume $X \sim F(X, w)$, F and w are unknown

1. Estimate \hat{w} from data $D = (X_1, \dots, X_n)$
2. Generate $D_1 = (X_1^*, \dots, X_n^*)$ by sampling with replacement
3. Repeat step 2 B times
4. The distribution of w is given by $\hat{f}(D_1), \dots, \hat{f}(D_B)$

Nonparametric bootstrap can be applied to any deterministic estimator, distribution-free

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14

Parametric bootstrap

Given estimator $\hat{w} = \hat{f}(D)$

Assume $X \sim F(X, w)$, F is known and w is unknown

1. Estimate \hat{w} from data $D = (X_1, \dots, X_n)$
2. Generate $D_1 = (X_1^*, \dots, X_n^*)$ by generating from $F(X, \hat{w})$
3. Repeat step 2 B times
4. The distribution of w is given by $\hat{f}(D_1), \dots, \hat{f}(D_B)$

Parametric bootstrap is more precise if the distribution form is correct

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Uncertainty estimation

1. Get D_1, \dots, D_B by bootstrap
2. Use $\hat{f}(D_1), \dots, \hat{f}(D_B)$ to estimate the uncertainty
 - Bootstrap percentile
 - Bootstrap Bca
 - ...
- Bootstrap works for all distribution types
- Can be bad accuracy for small data sets $n < 40$ (empirical is far from true)
- Parametric bootstrap works even for small samples

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16

Bootstrap confidence intervals

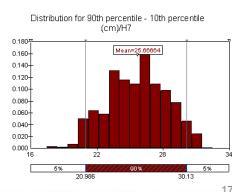
- To estimate $100(1-\alpha)$ confidence interval for w

Bootstrap percentile method

1. Using bootstrap, compute $\hat{f}(D_1), \dots, \hat{f}(D_B)$, sort in ascending order, get w_1, \dots, w_B
2. Define $A_1 = \text{ceil}(B\alpha/2)$, $A_2 = \text{floor}(B-B\alpha/2)$
3. Confidence interval is given by

$$(w_{A_1}, w_{A_2})$$

Look at the plot...



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Bootstrap: regression context

- Model $Y \sim F(X, w)$
- Data $D = \{(Y_i, X_i), i = 1, \dots, n\}$
- Idea: produce several bootstrap sets that are similar to D

Nonparametric bootstrap:

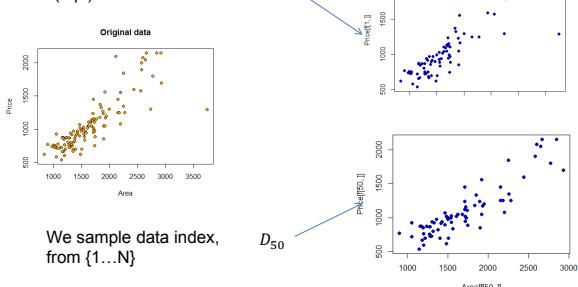
1. Using observation set D , sample pairs (X_i, Y_i) with replacement and get bootstrap sample D_1
2. Repeat step 1 B times → get D_1, \dots, D_B

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Uncertainty estimation

Example: Albuquerque dataset:
 $Y = \text{Price of House}$
 $X = \text{Area (sqft)}$



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19

Bootstrap: regression context

Parametric bootstrap

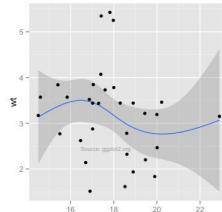
1. Fit a model to $D \rightarrow$ get $\hat{w}(D)$.
2. Set $X_i^* = X_i$, generate $Y_i^* \sim F(X_i, \hat{w})$.
3. $D_i = \{(X_i^*, Y_i^*), i = 1, \dots, n\}$
4. Repeat step 2 B times

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Confidence intervals in regression

- Given $Y \sim \text{Distribution}(y|x, w)$, $EY|X = \mu|x = f(x, w)$
 - Example: $Y \sim N(w^T x, \sigma^2)$, $\mu|x = f(x, w) = w^T x$
- Estimate intervals for $\mu|x = f(x, w)$ for many X , combine in a **confidence band**
- What is estimator?
 - $\mu|x = f(x, w)$



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Confidence intervals in regression

Estimation

1. Compute D_1, \dots, D_B using a bootstrap
2. Fit model to $D_1, \dots, D_B \rightarrow$ estimate $\hat{w}_1, \dots, \hat{w}_B$
3. For a given X , compute $f(X, \hat{w}_1), \dots, f(X, \hat{w}_B)$ and estimate confidence interval by (percentile method)
4. Combine confidence intervals in a band

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Bootstrap: R

- Package **boot**
 - **Functions:**
 - `boot()`
 - `boot.ci()` – 1 parameter
 - `envelope()` – many parameters
- Random random generation for parametric bootstrap:
 - `Rnorm()`
 - `Runif()`
 - ...

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Bootstrap: R

Nonparametric bootstrap:

- Write a function `statistic` that depends on `dataframe` and `index` and returns the estimator

```
library(boot)
data2=data[order(data$Area),]#reordering data according to Area

# computing bootstrap samples
f=function(data, ind){
  data1=data[ind,]# extract bootstrap sample
  res=lm(Price~Area, data=data1) #fit linear model
  #predict values for all Area values from the original data
  priceP=predict(res,newdata=data2)
  return(priceP)
}
res=boot(data2, f, R=1000) #make bootstrap
```

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Bootstrap: R

Parametric bootstrap:

- Compute value mle that estimates model parameters from the data
- Write function $ran.gen$ that depends on $data$ and mle and which generates new data
- Write function $statistic$ that depend on $data$ which will be generated by $ran.gen$ and should return the estimator

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Bootstrap

```

mle=lm(Price~Area, data=data2)

rng=function(data, mle) {
  data1=data.frame(Price=data$Price, Area=data$Area)
  n=length(data$Price)
  #generate new Price
  data1$Price=rnorm(n,predict(mle, newdata=data1),sd(mle$residuals))
  return(data1)
}

f1=function(data1){
  res=lm(Price~Area, data=data1) #fit linear model
  #predict values for all Area values from the original data
  priceP=predict(res,newdata=data2)
  return(priceP)
}

res=boot(data2, statistic=f1, R=1000, mle=mle, ran.gen=rng, sim="parametric")

```

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26

Uncertainty estimation: R

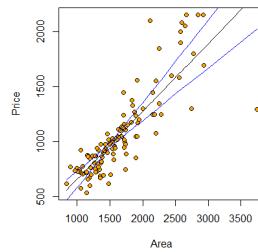
- Bootstrap confidence bands for linear model

```

e=envelope(res) #compute confidence bands
fit=lm(Price~Area, data=data2)
priceP=predict(fit)

plot(Area, Price, pch=21, bg="orange")
points(data2$Area,priceP,type="l", col="blue") #plot fitted line
#plot confidence bands
points(data2$Area,e$point[2,], type="l", col="blue")
points(data2$Area,e$point[1,], type="l", col="blue")

```



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Prediction bands

- Confidence interval for $Y|X=x$ = interval for mean $EY|X$
- Prediction interval for $Y|X=x$ = interval for $Y|X$

$$Y \sim Distribution(x, w)$$

Prediction band for parametric bootstrap

1. Run parametric bootstrap and get D_1, \dots, D_B
2. Fit the model to the data and get $\hat{w}(D_1), \dots, \hat{w}(D_B)$
3. For each X , generate from $Distribution(X, \hat{w}(D_1)), \dots, Distribution(X, \hat{w}(D_B))$ and apply percentile method
4. Connect the intervals → get the band

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28

Estimation of the model quality

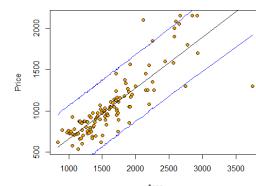
Example: parametric bootstrap

```

mle=lm(Price~Area, data=data2)

f1=function(data1){
  res=lm(Price~Area, data=data1) #fit linear model
  #predict values for all Area values from the original data
  priceP=predict(res,newdata=data2)
  predictedP=rnorm(n,priceP,
  sd(mle$residuals))
  return(predictedP)
}
res=boot(data2, statistic=f1, R=10000,
mle=mle, ran.gen=rng, sim="parametric")

```



Why wider band?

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29

Lecture 2d

Latent variable models

Overview

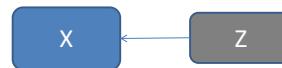
- Principal Component Analysis (PCA)
- Probabilistic PCA
- Independent component analysis (ICA)

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Latent variables

- Sometimes data depends on the variables we can not measure (hard to measure)
 - Answers on the test depend on Intelligence
 - Brain activity in the brain is measured by sensors
 - Stock prices depend on market confidence



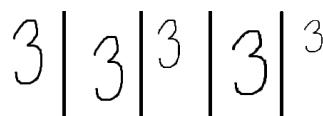
Source: loadbalance.com

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3

Latent variables

- Latent factor discovered → data storage may decrease a lot
- Latent factors
 - Center
 - Scaling
- Original vs compressed
 - $100 \times 100 \times 5 = 50000$
 - $100 \times 100 + 2 \times 5 + 2 \times 5 = 10020$



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Principal Component Analysis (PCA)

- PCA is a technique for reducing the complexity of high dimensional data
- It can be used to approximate high dimensional data with a few dimensions (latent features) → much less data to store
- New variables might have a special interpretation

Applications

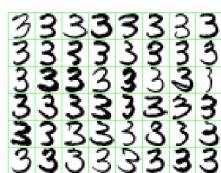
- Image recognition
- Information compression
- Subspace clustering
- ...

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5

Principal Component Analysis (PCA)

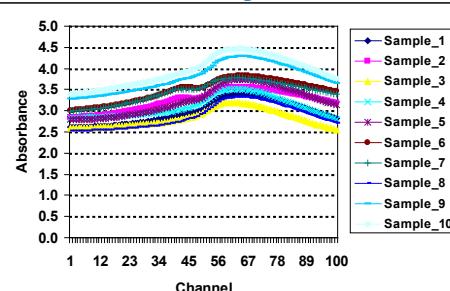
- Example 1: Handwritten digits
 - Can we get a more compact summary?



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Absorbance records for ten samples of chopped meat

Parallel coordinate plot for "FAT"



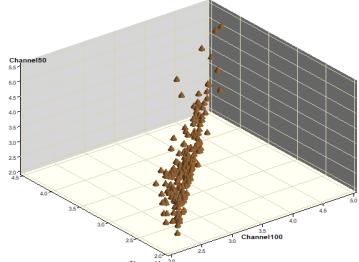
1 target (fat)
100 features
(absorbance at 100 wavelengths or
channels)
The features are
strongly correlated
to each other

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3-D plots of absorbance records for samples of meat - channels 1, 50 and 100

Scatterplot for three components



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Principal components analysis

Idea: Introduce a new coordinate system (PC1, PC2, ...) where

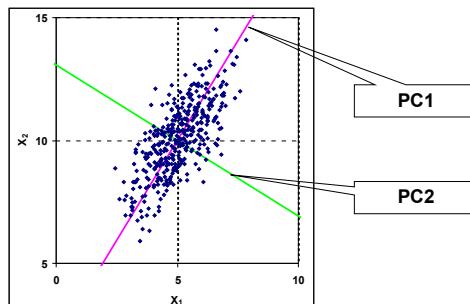
- The first principal component (PC1) is the direction that maximizes the variance of the projected data
- The second principal component (PC2) is the direction that maximizes the variance of the projected data after the variation along PC1 has been removed
- The third principal component (PC3) is the direction that maximizes the variance of the projected data after the variation along PC1 and PC2 has been removed
-

In the new coordinate system, coordinates corresponding to the last principal components are very small → can take away these columns

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9

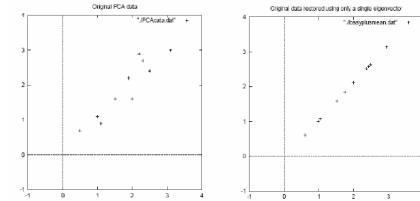
Principal Component Analysis - two inputs



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PCA- after reducing dimensionality



- Data became approximate (but less data to store)
- PC_1, \dots, PC_M are actually eigenvectors of sample covariance (first largest eigenvalue,...,Mth largest eigenvalue)

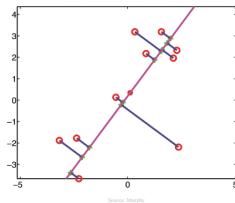
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11

PCA: another view

- Aim: minimize the distance between the original and projected data

$$\min_{\tilde{\mathbf{x}}} \sum_{i=1}^N \|x_i - \tilde{x}_i\|^2$$



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12

PCA: computations

Data $D = \|\mathbf{x}_1 \ \mathbf{x}_2 \ \dots \ \mathbf{x}_p\|, \ \mathbf{x}_i = (x_{i1}, \dots, x_{in})$

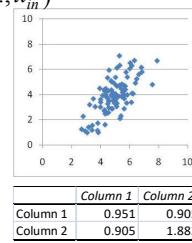
- Centred data

$$X = \|\mathbf{x}_1 - \bar{\mathbf{x}}_1 \ \mathbf{x}_2 - \bar{\mathbf{x}}_2 \ \dots \ \mathbf{x}_p - \bar{\mathbf{x}}_p\|$$

- Covariance matrix

$$\mathbf{S} = \frac{1}{N} X^T X$$

- Search for eigenvectors and eigenvalues of \mathbf{S}



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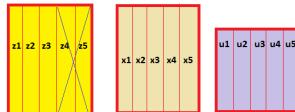
13

PCA: computations

4. Coordinates of any data point

$x = (x_1 \dots x_p)$ in the new coordinate system:

$$z = (z_1, \dots z_n), z_i = x^T u_i$$



Matrix form: $Z = X U$

5. Discard principle components after some M

Store: $N \times M + p \times M$ instead $N \times p$

6. New data will have dimensions $N \times M$ instead of $N \times p$

100*50 vs
100*4+50*4

Getting approximate original data:

$$X' = Z U_M^T$$

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14

Principal Component Analysis

Eigenanalysis of the Covariance Matrix

Eigenvalue 2.8162 0.3835

Proportion 0.880 0.120

Cumulative 0.880 1.000

Variable PC1 PC2

X1 0.523 0.852

X2 0.852 -0.523

Loadings (U)

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15

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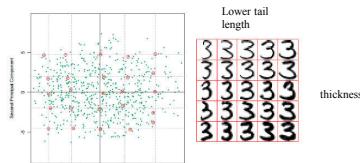
14

Principal Component Analysis

- Digits: two eigenvectors extracted

$$x = \boxed{3} + z_1 \cdot \boxed{3} + z_2 \cdot \boxed{3}$$

- Interptetation of eigenvectors



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16

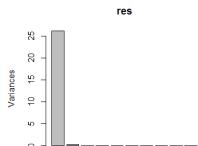
PCA in R

- Prcomp(), biplot(), screeplot()

```
mydata=read.csv2("tecator.csv")
data1=mydata
data1$Fat=c()
res=prcomp(data1)
lambda=res$sdev^2
#eigenvalues
lambda
#proportion of variation
sprintf("%2.3f",lambda/sum(lambda)*100)
screeplot(res)

> lambda
[1] 2.612713e+01 2.385369e-01 7.844883e-02 3.018501e-01
[7] 2.052212e-04 1.084213e-04 2.077326e-05 1.150359e-01

> sprintf("%2.3f",lambda/sum(lambda)*100)
[1] "98.679" "0.901" "0.296" "0.114" "0.006"
[9] "0.000" "0.000" "0.000" "0.000"
```



Only 1 component captures the 99% of variation!

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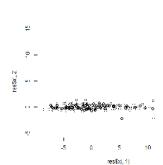
17

PCA in R

- Principal component loadings (U)

```
U=res$rotation
head(U)

> head(U)
PC1      PC2      PC3
Channel1 0.07938192 0.1156228 0.08073156 -0.0927
Channel2 0.07987445 0.1170972 0.0784533 -0.0881
Channel3 0.08036498 0.1185571 0.07702127 -0.1031
Channel4 0.08085611 0.1200006 0.07515015 -0.1077
Channel5 0.08135022 0.1214075 0.07323819 -0.1119
Channel6 0.08184804 0.1227461 0.07135368 -0.1156
```



Do we need second dimension?

- Data in (PC1, PC2) – scores (Z)

plot(res\$x[,1], res\$x[,2], ylim=c(-5,15))

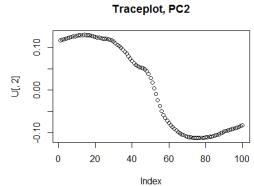
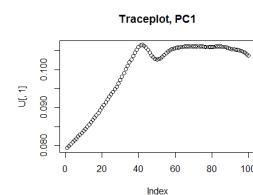
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18

PCA in R

- Trace plots

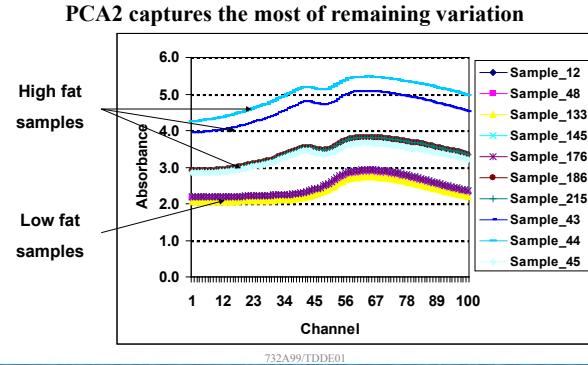
```
U=loadings(res)
plot(U[,1], main="Traceplot, PC1")
plot(U[,2],main="Traceplot, PC2")
```



Which components contribute to PC1-2?

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19



PCA for high-dimensional data

- Standard PCA for $p \gg N$
 - At most N eigenvalues are nonzero
 - Running time is $O(p^3)$

High-dimensional PCA

1. Use $S' = \frac{1}{N} XX^T$ (instead of $S = \frac{1}{N} X^T X$)
2. Eigenvalues do not change
3. Eigenvectors of S are $X^T v_i$

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21

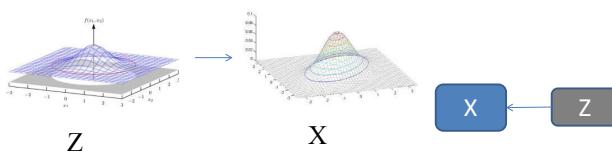


- z_i -latent variables, x_i - observed variables

$$z \sim N(0, I)$$

$$x|z \sim N(x|Wz + \mu, \sigma^2 I)$$
- Alternatively

$$z \sim N(0, I), x = \mu + Wz + \epsilon, \epsilon \sim N(0, \sigma^2 I)$$
- Interpretation: Observed data (X) is obtained by rotation, scaling and translation of standard normal distribution (Z) and adding some noise.



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22



- Aim: extract Z from X

- Distribution of x :

$$x \sim N(\mu, C)$$

$$C = WW^T + \sigma^2 I$$

- Rotation invariance

- Assume that x was generated from $z' = Rz, RR^T = I$, $p(x)$ does not change!

$$x|z' \sim N(x|Wz' + \mu, \sigma^2 I)$$

- Model will not be able find latent factors uniquely! \otimes

- It does not distinguish z from z'

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23



- Estimation of parameters: ML

Theorem. ML estimates are given by

$$\mu_{ML} = \bar{x}$$

$$W_{ML} = U_M(L_M - \sigma_{ML}^2 I)^{\frac{1}{2}} R$$

$$\sigma_{ML}^2 = \frac{1}{p-M} \sum_{i=M+1}^p \lambda_i$$

- U_M matrix of M eigenvectors
- L_M diagonal matrix of M eigenvalues
- R any orthogonal matrix

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24



- Estimation of Z

- Use mean of posterior

$$\hat{z} = (W_{ML}^T W_{ML} + \sigma_{ML}^2 I)^{-1} W_{ML}^T (x - \mu)$$

- Connection to standard PCA

- Assume $R = I, \sigma^2 = 0 \rightarrow$ get standard PCA components scaled by inverse root of eigenvalues

$$Z = XUL^{-\frac{1}{2}}$$

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25

Advantages of probabilistic PCA

- More settings to specify → more flexible
- Can be faster when $M \ll p$
- Missing values can be handled
- M can be derived if a Bayesian version is used
- Probabilistic PCA can be applied to classification problems directly
- Probabilistic PCA can generate new data

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26

Probabilistic PCA in R

- Use **pcaMethods** from Bioconductor
 - Install
 - source("https://bioconductor.org/biocLite.R")
 - biocLite("pcaMethods")
- Ppca(data, nPcs,...)
- Results:** scores, loadings...

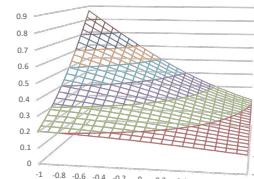
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27

Independent component analysis (ICA)

- Probabilistic PCA does not capture latent factors
 - Rotation invariance
- Let's choose distribution which is not rotation invariant → will get unique latent factors
- Choose non-Gaussian $p_i(z) = p(z)$
- Assuming latent features are **independent**

$$p(z) = \prod_{i=1}^M p_i(z_i)$$



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28

ICA

- Model**
- $$x = \mu + Wz + \epsilon, \quad \epsilon \sim N(0, \Sigma)$$
- Estimation A: Maximum likelihood** ($V = W^{-1}$)
 - Assuming noise-free x
- $$\max_V \sum_{i=1}^n \sum_{j=1}^p \log(p_j(v_j^T x_i))$$
- Subject to $\|v_i\| = 1$

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29

ICA

- Setting $G_j(z) = -\log(p_j(z))$, $z_j = v_i^T x$ and assuming large sample

$$\min_V \sum_{j=1}^p E(G_j(z_j))$$

Subject to $\|v_i\| = 1$

Prewhitening

- Use PCA: $X' = XU$
- Computing z_i s for given V : $Z = X'V$

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30

ICA

- Estimation B: maximize negentropy**
 - ICA looks for model which is as much non-Gaussian as possible
 - Entropy** $H(z) = -\int p(z) \log p(z) dz = E(-\log p(z))$
 - Negentropy** $J(z_i) = H(z'_i) - H(z_i)$
 - $z'_i \sim N(Ez_i, var(z_i))$
 - Negentropy maximization**
- $$\max_V \sum_{j=1}^p J(z_j) = \min_V \sum_{j=1}^p H(z_j) = \min_V \sum_{j=1}^p E(-\log p(z_j))$$

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31

ICA

- Example

Source Signals Measured Signals

Source: This of course by Burt

732A99/TDDE01 32

Independent component analysis: R

```
S <- cbind(sin((1:1000)/20), rep(((1:200)-100)/100), 5)) #Generate data
A <- matrix(c(0.291, 0.6557, -0.5439, 0.5572), 2, 2)
X <- S %*% A
a <- fastICA(X, 2, alg.typ = "parallel", fun = "logcosh", alpha = 1,
method = "R", row.norm = FALSE, maxit = 200, tol = 0.0001, verbose = TRUE) #ICA
```

Original Signals Mixed Signals ICA source estimates

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Lecture 3a Block 1: Kernel Methods

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1/10

Histogram Classification

- Consider binary classification with input space \mathbb{R}^D .
- The best classifier under the 0-1 loss function is $y^*(\mathbf{x}) = \arg \max_y p(y|\mathbf{x})$.
- Since \mathbf{x} may not appear in the finite training set $\{(\mathbf{x}_n, t_n)\}$ available, then
 - divide the input space into D -dimensional cubes of side h , and
 - classify according to majority vote in the cube $C(\mathbf{x}, h)$ that contains \mathbf{x} .

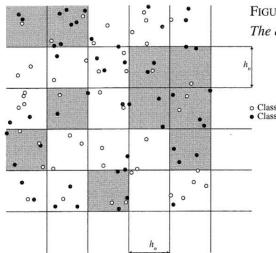


FIGURE 6.1. A cubic histogram rule:
The decision is 1 in the shaded area.

- In other words,

$$y_C(\mathbf{x}) = \begin{cases} 0 & \text{if } \sum_n \mathbf{1}_{\{t_n=1, \mathbf{x}_n \in C(\mathbf{x}, h)\}} \leq \sum_n \mathbf{1}_{\{t_n=0, \mathbf{x}_n \in C(\mathbf{x}, h)\}} \\ 1 & \text{otherwise} \end{cases}$$

4/10

Literature

- Main source
 - Bishop, C. M. *Pattern Recognition and Machine Learning*. Springer, 2006. Sections 2.5 and 6.1-6.2.
- Additional source
 - Devroye, L., Györfi, L. and Lugosi, G. *A Probabilistic Theory of Pattern Recognition*. Springer, 1996. Sections 6.4 and 10.0.
 - Hastie, T., Tibshirani, R. and Friedman, J. *The Elements of Statistical Learning*. Springer, 2009. Chapter 6.

3/10

Moving Window Classification

- The histogram rule is less accurate at the borders of the cube, because those points are not as well represented by the cube as the ones near the center. Then,
 - consider the points within a certain distance to the point to classify, and
 - classify the point according to majority vote.

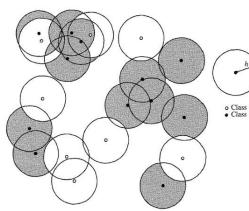


FIGURE 10.1. The moving window rule in \mathbb{R}^2 . The decision is 1 in the shaded area.

- In other words,

$$y_S(\mathbf{x}) = \begin{cases} 0 & \text{if } \sum_n \mathbf{1}_{\{t_n=1, \mathbf{x}_n \in S(\mathbf{x}, h)\}} \leq \sum_n \mathbf{1}_{\{t_n=0, \mathbf{x}_n \in S(\mathbf{x}, h)\}} \\ 1 & \text{otherwise} \end{cases}$$

where $S(\mathbf{x}, h)$ is a D -dimensional closed ball of radius h centered at \mathbf{x} .

5/10

Kernel Classification

- The moving window rule gives equal weight to all the points in the ball, which may be counterintuitive. Then,

$$y_k(\mathbf{x}) = \begin{cases} 0 & \text{if } \sum_n \mathbf{1}_{\{t_n=1\}} k\left(\frac{\mathbf{x}-\mathbf{x}_n}{h}\right) \leq \sum_n \mathbf{1}_{\{t_n=0\}} k\left(\frac{\mathbf{x}-\mathbf{x}_n}{h}\right) \\ 1 & \text{otherwise} \end{cases}$$

where $k : \mathbb{R}^D \rightarrow \mathbb{R}$ is a kernel function, which is usually non-negative and monotone decreasing along rays starting from the origin. The parameter h is called smoothing factor or width.

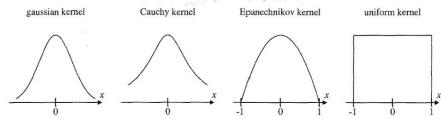


FIGURE 10.3. Various kernels on \mathcal{R} .

- Gaussian kernel: $k(u) = \exp(-\|u\|^2)$ where $\|\cdot\|$ is the Euclidean norm.
- Cauchy kernel: $k(u) = 1/(1 + \|u\|^{p+1})$
- Epanechnikov kernel: $k(u) = (1 - \|u\|^2)\mathbf{1}_{\{|u| \leq 1\}}$
- Moving window kernel: $k(u) = \mathbf{1}_{\{u \in S(0,1)\}}$

6/10

Kernel Classification

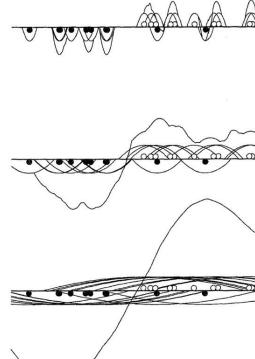


FIGURE 10.2. Kernel rule on the real line. The figure shows $\sum_{i=1}^n (2Y_i - 1)K((x - X_i)/h)$ for $n = 20$, $K(u) = (1 - u^2)I_{\{|u| \leq 1\}}$ (the Epanechnikov kernel), and three smoothing factors h . One definitely undersmooths and one oversmooths. We took $p = 1/2$, and the class-conditional densities are $f_0(x) = 2(1 - x)$ and $f_1(x) = 2x$ on $[0, 1]$.

7/10

Histogram, Moving Window, and Kernel Regression

- Consider regressing an unidimensional continuous random variable on a D -dimensional continuous random variable.
- The best regression function under the squared error loss function is $y^*(\mathbf{x}) = \mathbb{E}_Y[y|\mathbf{x}]$.
- Since \mathbf{x} may not appear in the finite training set $\{(\mathbf{x}_n, t_n)\}$ available, then we average over the points in $C(\mathbf{x}, h)$ or $S(\mathbf{x}, h)$, or kernel-weighted average over all the points.
- In other words,

$$y_C(\mathbf{x}) = \frac{\sum_{\mathbf{x}_n \in C(\mathbf{x}, h)} t_n}{|\{\mathbf{x}_n \in C(\mathbf{x}, h)\}|}$$

or

$$y_S(\mathbf{x}) = \frac{\sum_{\mathbf{x}_n \in S(\mathbf{x}, h)} t_n}{|\{\mathbf{x}_n \in S(\mathbf{x}, h)\}|}$$

or

$$y_k(\mathbf{x}) = \frac{\sum_n k\left(\frac{\mathbf{x}-\mathbf{x}_n}{h}\right) t_n}{\sum_n k\left(\frac{\mathbf{x}-\mathbf{x}_n}{h}\right)}$$

8/10

Histogram, Moving Window, and Kernel Density Estimation

- Consider density estimation for a D -dimensional continuous random variable.
- Let $R \subseteq \mathbb{R}^D$ and $\mathbf{x} \in R$. Then,

$$P = \int_R p(\mathbf{x}) d\mathbf{x} \approx p(\mathbf{x}) \text{Volume}(R)$$

and the number of the N training points $\{\mathbf{x}_n\}$ that fall inside R is

$$|\{\mathbf{x}_n \in R\}| \approx P N$$

and thus

$$p(\mathbf{x}) \approx \frac{|\{\mathbf{x}_n \in R\}|}{N \text{Volume}(R)}$$

- Then,

$$p_C(\mathbf{x}) = \frac{|\{\mathbf{x}_n \in C(\mathbf{x}, h)\}|}{N \text{Volume}(C(\mathbf{x}, h))}$$

or

$$p_S(\mathbf{x}) = \frac{|\{\mathbf{x}_n \in S(\mathbf{x}, h)\}|}{N \text{Volume}(S(\mathbf{x}, h))}$$

or

$$p_k(\mathbf{x}) = \frac{1}{N} \sum_n k\left(\frac{\mathbf{x}-\mathbf{x}_n}{h}\right)$$

assuming that $k(u) \geq 0$ for all u and $\int k(u) du = 1$.

9/10

Histogram, Moving Window, and Kernel Density Estimation

Figure 2.24 An illustration of the histogram approach to density estimation, in which a data set of 50 data points is generated from the distribution shown in the green curve. Histogram density estimates, based on (2.241), with a common bin width Δ are shown for various values of Δ .

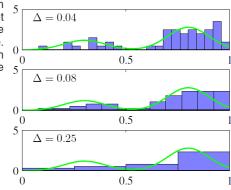
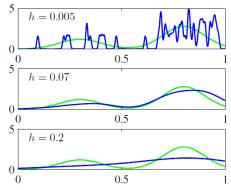


Figure 2.25 Illustration of the kernel density model (2.250) applied to the same dataset used to generate the histogram approach in Figure 2.24. We see that h , acts as a smoothing parameter and that if it is set too small (top panel), the result is a very noisy density model, whereas if it is set too large (bottom panel), then the bimodal nature of the underlying distribution from which the data is generated (shown by the green curve) is washed out. The best density model is obtained for some intermediate value of h (middle panel).



Histogram, Moving Window, and Kernel Density Estimation

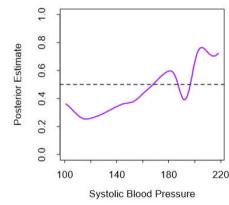
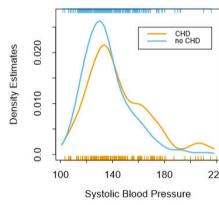


FIGURE 6.14. The left panel shows the two separate density estimates for systolic blood pressure in the CHD versus no-CHD groups, using a Gaussian kernel density estimate in each. The right panel shows the estimated posterior probabilities for CHD, using (6.25).

10/10

Histogram, Moving Window, and Kernel Density Estimation

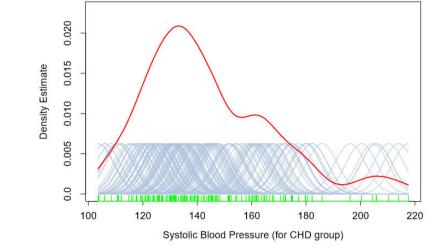


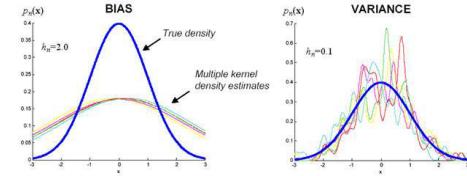
FIGURE 6.13. A kernel density estimate for systolic blood pressure (for the CHD group). The density estimate at each point is the average contribution from each of the kernels at that point. We have scaled the kernels down by a factor of 10 to make the graph readable.

- ▶ From kernel density estimation to kernel classification:
 1. Estimate $p(\mathbf{x}|y=0)$ and $p(\mathbf{x}|y=1)$ using the methods just seen.
 2. Estimate $p(y)$ as class proportions.
 3. Compute $p(y|\mathbf{x}) \propto p(\mathbf{x}|y)p(y)$ by Bayes theorem.

11/10

Kernel Selection

- ▶ How to choose the right kernel and width ? E.g., by cross-validation.
- ▶ What does "right" mean ? E.g., minimize loss function.
- ▶ Note that the width of the kernel corresponds to a bias-variance trade-off.



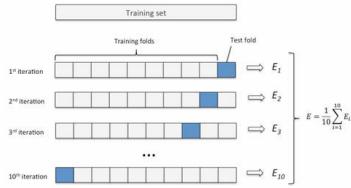
- ▶ Small width implies considering few points. So, the variance will be large (similar to the variance of a single point). The bias will be small since the points considered are close to \mathbf{x} .
- ▶ Large width implies considering many points. So, the variance will be small and the bias will be large.

12/10

13/10

Kernel Selection

- Recall the following from previous lectures.
- Cross-validation is a technique to estimate the prediction error of a model.

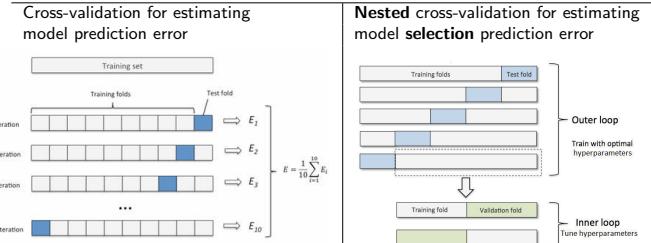


- If the training set contains N points, note that cross-validation estimates the prediction error when the model is trained on $N - N/K$ points.
- Note that the model returned is trained on N points. So, cross-validation overestimates the prediction error of the model returned.
- This seems to suggest that a large K should be preferred. However, this typically implies a large variance of the error estimate, since there are only N/K test points.
- Typically, $K = 5, 10$ works well.

14/15

Kernel Selection

- Model:** For example, ridge regression with a given value for the penalty factor λ . Only the parameters (weights) need to be determined (closed-form solution).
- Model selection:** For example, determine the value for the penalty factor λ . Another example, determine the kernel and width for kernel classification, regression or density estimation. In either case, we do not have a continuous criterion to optimize. Solution: **Nested** cross-validation.



- Error overestimation may not be a concern for model selection. So, $K = 2$ may suffice in the inner loop.
- Which is the fitted model returned by nested cross-validation ?

15/15

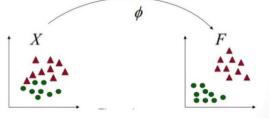
Kernel Trick

- The kernel function $k\left(\frac{\mathbf{x}-\mathbf{x}'}{h}\right)$ is invariant to translations, and it can be generalized as $k(\mathbf{x}, \mathbf{x}')$. For instance,
 - Polynomial kernel: $k(\mathbf{x}, \mathbf{x}') = (\mathbf{x}^T \mathbf{x}' + c)^M$
 - Gaussian kernel: $k(\mathbf{x}, \mathbf{x}') = \exp(-\|\mathbf{x} - \mathbf{x}'\|^2 / 2\sigma^2)$

- If the matrix

$$\begin{pmatrix} k(\mathbf{x}_1, \mathbf{x}_1) & \dots & k(\mathbf{x}_1, \mathbf{x}_N) \\ \vdots & \dots & \vdots \\ k(\mathbf{x}_N, \mathbf{x}_1) & \dots & k(\mathbf{x}_N, \mathbf{x}_N) \end{pmatrix}$$

is symmetric and positive semi-definite for all choices of $\{\mathbf{x}_n\}$, then $k(\mathbf{x}, \mathbf{x}') = \phi(\mathbf{x})^T \phi(\mathbf{x}')$ where $\phi(\cdot)$ is a mapping from the input space to the feature space.



- The feature space may be non-linear and even infinite dimensional. For instance,

$$\phi(\mathbf{x}) = (x_1^2, x_2^2, \sqrt{2}x_1x_2, \sqrt{2}cx_1, \sqrt{2}cx_2, c)$$

for the polynomial kernel with $M = D = 2$.

16/15

Kernel Trick

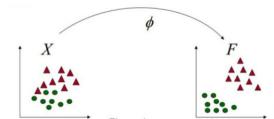
- Consider again moving window classification, regression, and density estimation.
- Note that $\mathbf{x}_n \in S(\mathbf{x}, h)$ if and only if $\|\mathbf{x} - \mathbf{x}_n\| \leq h$.
- Note that

$$\|\mathbf{x} - \mathbf{x}_n\| = \sqrt{(\mathbf{x} - \mathbf{x}_n)^T (\mathbf{x} - \mathbf{x}_n)} = \sqrt{\mathbf{x}^T \mathbf{x} + \mathbf{x}_n^T \mathbf{x}_n - 2\mathbf{x}^T \mathbf{x}_n}$$

- Then,

$$\begin{aligned} \|\phi(\mathbf{x}) - \phi(\mathbf{x}_n)\| &= \sqrt{\phi(\mathbf{x})^T \phi(\mathbf{x}) + \phi(\mathbf{x}_n)^T \phi(\mathbf{x}_n) - 2\phi(\mathbf{x})^T \phi(\mathbf{x}_n)} \\ &= \sqrt{k(\mathbf{x}, \mathbf{x}) + k(\mathbf{x}_n, \mathbf{x}_n) - 2k(\mathbf{x}, \mathbf{x}_n)} \end{aligned}$$

- So, the distance is now computed in a (hopefully) more convenient space.



- Note that we do not need to compute $\phi(\mathbf{x})$ and $\phi(\mathbf{x}_n)$.

17/15

Kernel Trick

- Two alternatives for building $k(\mathbf{x}, \mathbf{x}')$:
 - Choose a convenient $\phi(\mathbf{x})$ and let $k(\mathbf{x}, \mathbf{x}') = \phi(\mathbf{x})^T \phi(\mathbf{x}')$.
 - Build it from existing kernel functions as follows.

Techniques for Constructing New Kernels.

Given valid kernels $k_1(\mathbf{x}, \mathbf{x}')$ and $k_2(\mathbf{x}, \mathbf{x}')$, the following new kernels will also be valid:

$$k(\mathbf{x}, \mathbf{x}') = ck_1(\mathbf{x}, \mathbf{x}') \quad (6.13)$$

$$k(\mathbf{x}, \mathbf{x}') = f(\mathbf{x})k_1(\mathbf{x}, \mathbf{x}')f(\mathbf{x}') \quad (6.14)$$

$$k(\mathbf{x}, \mathbf{x}') = q(k_1(\mathbf{x}, \mathbf{x}')) \quad (6.15)$$

$$k(\mathbf{x}, \mathbf{x}') = \exp(k_1(\mathbf{x}, \mathbf{x}')) \quad (6.16)$$

$$k(\mathbf{x}, \mathbf{x}') = k_1(\mathbf{x}, \mathbf{x}') + k_2(\mathbf{x}, \mathbf{x}') \quad (6.17)$$

$$k(\mathbf{x}, \mathbf{x}') = k_1(\mathbf{x}, \mathbf{x}')k_2(\mathbf{x}, \mathbf{x}') \quad (6.18)$$

$$k(\mathbf{x}, \mathbf{x}') = k_3(\phi(\mathbf{x}), \phi(\mathbf{x}')) \quad (6.19)$$

$$k(\mathbf{x}, \mathbf{x}') = \mathbf{x}^T \mathbf{A} \mathbf{x}' \quad (6.20)$$

$$k(\mathbf{x}, \mathbf{x}') = k_a(\mathbf{x}_a, \mathbf{x}'_a) + k_b(\mathbf{x}_b, \mathbf{x}'_b) \quad (6.21)$$

$$k(\mathbf{x}, \mathbf{x}') = k_a(\mathbf{x}_a, \mathbf{x}'_a)k_b(\mathbf{x}_b, \mathbf{x}'_b) \quad (6.22)$$

where $c > 0$ is a constant, $f(\cdot)$ is any function, $q(\cdot)$ is a polynomial with nonnegative coefficients, $\phi(\mathbf{x})$ is a function from \mathbf{x} to \mathbb{R}^M , $k_3(\cdot, \cdot)$ is a valid kernel in \mathbb{R}^M , \mathbf{A} is a symmetric positive semidefinite matrix, \mathbf{x}_a and \mathbf{x}_b are variables (not necessarily disjoint) with $\mathbf{x} = (\mathbf{x}_a, \mathbf{x}_b)$, and k_a and k_b are valid kernel functions over their respective spaces.

Summary

- Kernel methods: Smoothing models.
- Model selection: Nested cross-validation.
- Kernel trick: It allows to work in the feature space without constructing it.

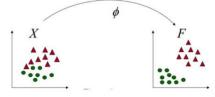
Support Vector Machines for Classification

- Consider binary classification with input space \mathbb{R}^D .
- Consider a training set $\{(\mathbf{x}_n, t_n)\}$ where $t_n \in \{-1, +1\}$.
- Consider using the linear model

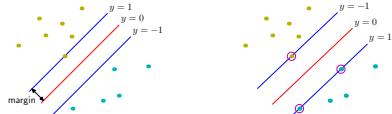
$$y(\mathbf{x}) = \mathbf{w}^T \phi(\mathbf{x}) + b$$

so that a new point \mathbf{x} is classified according to the sign of $y(\mathbf{x})$.

- Assume that the training set is linearly separable in the feature space (but not necessarily in the input space), i.e. $t_n y(\mathbf{x}_n) > 0$ for all n .

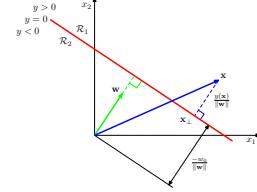


- Aim for the separating hyperplane that maximizes the margin (i.e. the smallest perpendicular distance from any point to the hyperplane) so as to minimize the generalization error.



18/18

Support Vector Machines for Classification



- The perpendicular distance from any point to the hyperplane is given by

$$\frac{t_n y(\mathbf{x}_n)}{\|\mathbf{w}\|} = \frac{t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b)}{\|\mathbf{w}\|}$$

- Then, the maximum margin separating hyperplane is given by

$$\arg \max_{\mathbf{w}, b} \left(\min_n \frac{t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b)}{\|\mathbf{w}\|} \right)$$

- Multiply \mathbf{w} and b by κ so that $t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b) = 1$ for the point closest to the hyperplane. Note that $t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b) / \|\mathbf{w}\|$ does not change.

4/18

18/18

5/18

Support Vector Machines for Classification

- Then, the maximum margin separating hyperplane is given by

$$\arg \min_{\mathbf{w}, b} \frac{1}{2} \|\mathbf{w}\|^2$$

subject to $t_n(\mathbf{w}^T \phi(\mathbf{x}_n) + b) \geq 1$ for all n .

- To minimize the previous expression, we minimize

$$\frac{1}{2} \|\mathbf{w}\|^2 - \sum_n a_n (t_n(\mathbf{w}^T \phi(\mathbf{x}_n) + b) - 1)$$

where $a_n \geq 0$ are called Lagrange multipliers.

- Note that any stationary point of the Lagrangian function is a stationary point of the original function subject to the constraints. Moreover, the Lagrangian function is a quadratic function subject to linear inequality constraints. Then, it is concave, actually concave up because of the $+1/2$ and, thus, "easy" to minimize.
- Note that we are now minimizing with respect to \mathbf{w} and b , and maximizing with respect to a_n .
- Setting its derivatives with respect to \mathbf{w} and b to zero gives

$$\begin{aligned} \mathbf{w} &= \sum_n a_n t_n \phi(\mathbf{x}_n) \\ 0 &= \sum_n a_n t_n \end{aligned}$$

6/18

Support Vector Machines for Classification

- When the Lagrangian function is maximized, the Karush-Kuhn-Tucker condition holds for all n :

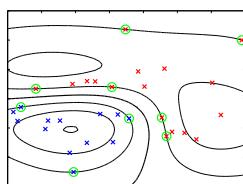
$$a_n(t_n y(\mathbf{x}_n) - 1) = 0$$

- Then, $a_n > 0$ if and only if $t_n y(\mathbf{x}_n) = 1$. The points with $a_n > 0$ are called support vectors and they lie on the margin boundaries.

- A new point \mathbf{x} is classified according to the sign of

$$\begin{aligned} y(\mathbf{x}) &= \mathbf{w}^T \phi(\mathbf{x}) + b = \sum_n a_n t_n \phi(\mathbf{x}_n)^T \phi(\mathbf{x}) + b = \sum_n a_n t_n k(\mathbf{x}, \mathbf{x}_n) + b \\ &= \sum_{m \in S} a_m t_m k(\mathbf{x}, \mathbf{x}_m) + b \end{aligned}$$

where S are the indexes of the support vectors. Sparse solution!



8/18

Support Vector Machines for Classification

- Replacing the previous expressions in the Lagrangian function gives the dual representation of the problem, in which we maximize

$$\sum_n a_n - \frac{1}{2} \sum_n \sum_m a_n a_m t_n t_m \phi(\mathbf{x}_n)^T \phi(\mathbf{x}_m) = \sum_n a_n - \frac{1}{2} \sum_n \sum_m a_n a_m t_n t_m k(\mathbf{x}_n, \mathbf{x}_m)$$

subject to $a_n \geq 0$ for all n , and $\sum_n a_n t_n = 0$.

- Again, this "easy" to maximize.

- Note that the dual representation makes use of the kernel trick, i.e. it allows working in a more convenient feature space without constructing it.

7/18

Support Vector Machines for Classification

- To find b , consider any support vector \mathbf{x}_n . Then,

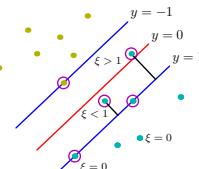
$$1 = t_n y(\mathbf{x}_n) = t_n \left(\sum_{m \in S} a_m t_m k(\mathbf{x}_n, \mathbf{x}_m) + b \right)$$

and multiplying both sides by t_n , we have that

$$b = t_n - \sum_{m \in S} a_m t_m k(\mathbf{x}_n, \mathbf{x}_m)$$

- We now drop the assumption of linear separability in the feature space, e.g. to avoid overfitting. We do so by introducing the slack variables $\xi_n \geq 0$ to penalize (almost-)misclassified points as

$$\xi_n = \begin{cases} 0 & \text{if } t_n y(\mathbf{x}_n) \geq 1 \\ |t_n - y(\mathbf{x}_n)| & \text{otherwise} \end{cases}$$



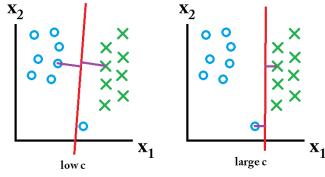
9/18

Support Vector Machines for Classification

- The optimal separating hyperplane is given by

$$\arg \min_{\mathbf{w}, b, \{\xi_n\}} \frac{1}{2} \|\mathbf{w}\|^2 + C \sum_n \xi_n$$

subject to $t_n y(\mathbf{x}_n) \geq 1 - \xi_n$ and $\xi_n \geq 0$ for all n , and where $C > 0$ controls regularization. Its value can be decided by cross-validation. Note that the number of misclassified points is upper bounded by $\sum_n \xi_n$.



- To minimize the previous expression, we minimize

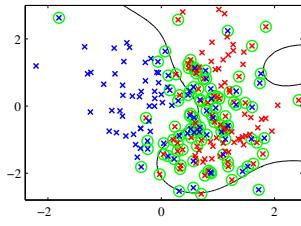
$$\frac{1}{2} \|\mathbf{w}\|^2 + C \sum_n \xi_n - \sum_n a_n (t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b) - 1 + \xi_n) - \sum_n \mu_n \xi_n$$

where $a_n \geq 0$ and $\mu_n \geq 0$ are Lagrange multipliers.

10/18

Support Vector Machines for Classification

- Since the optimal \mathbf{w} takes the same form as in the linearly separable case, classifying a new point is done the same as before. Finding b is done the same as before by considering any support vector \mathbf{x}_n with $0 < a_n < C$.



- Not covered topics:

- Classifying into more than two classes.
- Returning class posterior probabilities.

12/18

Support Vector Machines for Classification

- Setting its derivatives with respect to \mathbf{w} , b and ξ_n to zero gives

$$\begin{aligned} \mathbf{w} &= \sum_n a_n t_n \phi(\mathbf{x}_n) \\ 0 &= \sum_n a_n t_n \\ a_n &= C - \mu_n \end{aligned}$$

- Replacing these in the Lagrangian function gives the dual representation of the problem, in which we maximize

$$\sum_n a_n - \frac{1}{2} \sum_n \sum_m a_n a_m t_n t_m k(\mathbf{x}_n, \mathbf{x}_m)$$

subject to $a_n \geq 0$ and $a_n \leq C$ for all n , because $\mu_n \geq 0$.

- When the Lagrangian function is maximized, the Karush-Kuhn-Tucker conditions hold for all n :

$$\begin{aligned} a_n(t_n y(\mathbf{x}_n) - 1 + \xi_n) &= 0 \\ \mu_n \xi_n &= 0 \end{aligned}$$

- Then, $a_n > 0$ if and only if $t_n y(\mathbf{x}_n) = 1 - \xi_n$ for all n . The points with $a_n > 0$ are called support vectors and they lie

- on the margin if $a_n < C$, because then $\mu_n > 0$ and thus $\xi_n = 0$, or
- inside the margin (even on the wrong side of the decision boundary) if $a_n = C$, because then $\mu_n = 0$ and thus ξ_n is unconstrained.

11/18

Support Vector Machines for Regression

- Consider regressing an unidimensional continuous random variable on a D -dimensional continuous random variable.

- Consider a training set $\{(\mathbf{x}_n, t_n)\}$. Consider using the linear model

$$y(\mathbf{x}) = \mathbf{w}^T \phi(\mathbf{x}) + b$$

- To get a sparse solution, instead of minimizing the classical regularized error function

$$\frac{1}{2} \sum_n (y(\mathbf{x}_n) - t_n)^2 + \frac{\lambda}{2} \|\mathbf{w}\|^2$$

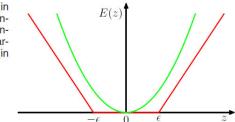
consider minimizing the ϵ -insensitive regularized error function

$$C \sum_n E_\epsilon(y(\mathbf{x}_n) - t_n) + \frac{1}{2} \|\mathbf{w}\|^2$$

where $C > 0$ controls regularization and

$$E_\epsilon(y(\mathbf{x}) - t) = \begin{cases} 0 & \text{if } |y(\mathbf{x}) - t| < \epsilon \\ |y(\mathbf{x}) - t| - \epsilon & \text{otherwise} \end{cases}$$

Figure 7.6 Plot of an ϵ -insensitive error function (in red) in which the error increases linearly with distance beyond the insensitive region. Also shown for comparison is the quadratic error function (in green).



13/18

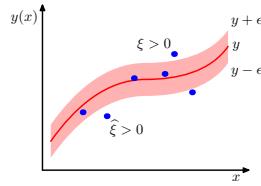
Support Vector Machines for Regression

- The values of C and ϵ can be decided by cross-validation.
- Consider the slack variables $\xi_n \geq 0$ and $\widehat{\xi}_n \geq 0$ such that

$$\xi_n = \begin{cases} t_n - y(\mathbf{x}_n) - \epsilon & \text{if } t_n > y(\mathbf{x}_n) + \epsilon \\ 0 & \text{otherwise} \end{cases}$$

and

$$\widehat{\xi}_n = \begin{cases} y(\mathbf{x}_n) + \epsilon - t_n & \text{if } t_n < y(\mathbf{x}_n) + \epsilon \\ 0 & \text{otherwise} \end{cases}$$



14/18

Support Vector Machines for Regression

- Replacing these in the Lagrangian function gives the dual representation of the problem, in which we maximize

$$\frac{1}{2} \sum_n \sum_m (a_n - \widehat{a}_m)(a_m - \widehat{a}_m) k(\mathbf{x}_n, \mathbf{x}_m) - \epsilon \sum_n (a_n + \widehat{a}_n) + \sum_n (a_n - \widehat{a}_n) t_n$$

subject to $a_n \geq 0$ and $a_n \leq C$ for all n , because $\mu_n \geq 0$. Similarly for \widehat{a}_n .

- When the Lagrangian function is maximized, the Karush-Kuhn-Tucker conditions hold for all n :

$$\begin{aligned} a_n(y(\mathbf{x}_n) + \epsilon + \xi_n - t_n) &= 0 \\ \widehat{a}_n(t_n - y(\mathbf{x}_n) + \epsilon + \widehat{\xi}_n) &= 0 \\ \mu_n \xi_n &= 0 \\ \widehat{\mu}_n \widehat{\xi}_n &= 0 \end{aligned}$$

- Then, $a_n > 0$ if and only if $y(\mathbf{x}_n) + \epsilon + \xi_n - t_n = 0$, which implies that \mathbf{x}_n lies on or above the upper margin of the ϵ -tube. Similarly for $\widehat{a}_n > 0$.

16/18

Support Vector Machines for Regression

- The optimal regression curve is given by

$$\arg \min_{\mathbf{w}, b, \{\xi_n\}, \{\widehat{\xi}_n\}} C \sum_n (\xi_n + \widehat{\xi}_n) + \frac{1}{2} \|\mathbf{w}\|^2$$

subject to $\xi \geq 0$, $\widehat{\xi}_n \geq 0$, $t_n \leq y(\mathbf{x}_n) + \epsilon + \xi_n$ and $t_n \geq y(\mathbf{x}_n) - \epsilon - \widehat{\xi}_n$.

- To minimize the previous expression, we minimize

$$\begin{aligned} & C \sum_n (\xi_n + \widehat{\xi}_n) + \frac{1}{2} \|\mathbf{w}\|^2 - \sum_n (\mu_n \xi_n + \widehat{\mu}_n \widehat{\xi}_n) \\ & - \sum_n a_n (y(\mathbf{x}_n) + \epsilon + \xi_n - t_n) - \sum_n \widehat{a}_n (t_n - y(\mathbf{x}_n) + \epsilon + \widehat{\xi}_n) \end{aligned}$$

where $\mu_n \geq 0$, $\widehat{\mu}_n \geq 0$, $a_n \geq 0$ and $\widehat{a}_n \geq 0$ are Lagrange multipliers.

- Setting its derivatives with respect to \mathbf{w} , b , ξ_n and $\widehat{\xi}_n$ to zero gives

$$\mathbf{w} = \sum_n (a_n - \widehat{a}_n) \phi(\mathbf{x}_n)$$

$$0 = \sum_n (a_n - \widehat{a}_n)$$

$$C = a_n + \mu_n$$

$$C = \widehat{a}_n + \widehat{\mu}_n$$

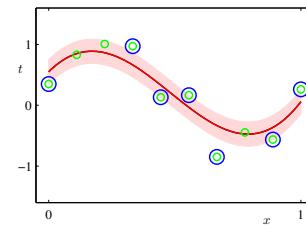
15/18

Support Vector Machines for Regression

- The prediction for a new point \mathbf{x} is made according to

$$y(\mathbf{x}) = \sum_{m \in S} (a_m - \widehat{a}_m) k(\mathbf{x}, \mathbf{x}_m) + b$$

where S are the indexes of the support vectors. Sparse solution!



- To find b , consider any support vector \mathbf{x}_n with $0 < a_n < C$. Then, $\mu_n > 0$ and thus $\xi_n = 0$ and thus $0 = t_n - \epsilon - y(\mathbf{x}_n)$. Then,

$$b = t_n - \epsilon - \sum_{m \in S} (a_m - \widehat{a}_m) k(\mathbf{x}_n, \mathbf{x}_m)$$

17/18

Summary

- Kernel trick: It allows to work in the feature space without constructing it.
- Quadratic objective function: It allows to obtain the global optimum for a given kernel and C/ϵ (which are obtained by cross-validation).
- Sparse model: Only the support vectors are needed for classification/regression (compare with kernel models).

18/18

Neural Networks

- Consider binary classification with input space \mathbb{R}^D . Consider a training set $\{(\mathbf{x}_n, t_n)\}$ where $t_n \in \{-1, +1\}$.
- SVMs classify a new point \mathbf{x} according to

$$y(\mathbf{x}) = \text{sgn} \left(\sum_{m \in S} a_m t_m k(\mathbf{x}, \mathbf{x}_m) + b \right)$$

- Consider regressing an unidimensional continuous random variable on a D -dimensional continuous random variable. Consider a training set $\{(\mathbf{x}_n, t_n)\}$
- For a new point \mathbf{x} , SVMs predict

$$y(\mathbf{x}) = \sum_{m \in S} (a_n - \hat{a}_n) k(\mathbf{x}, \mathbf{x}_m) + b$$

- SVMs imply **data-selected user-defined** basis functions.
- NNs imply a **user-defined** number of **data-selected** basis functions.

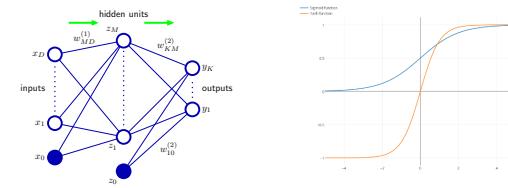
4/16

732A99/TDDE01 Machine Learning
Lecture 3c Block 1: Neural Networks

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1/10

Neural Networks



- Activations: $a_j = \sum_i w_{ji}^{(1)} x_i + w_{j0}^{(1)}$
- Hidden units and activation function: $z_j = h(a_j)$
- Output activations: $a_k = \sum_j w_{kj}^{(2)} z_j + w_{k0}^{(2)}$
- Output activation function for regression: $y_k(\mathbf{x}) = a_k$
- Output activation function for classification: $y_k(\mathbf{x}) = \sigma(a_k)$
- Sigmoid function: $\sigma(a) = \frac{1}{1+\exp(-a)}$
- Two-layer NN:

$$y_k(\mathbf{x}) = \sigma \left(\sum_j w_{kj}^{(2)} h \left(\sum_i w_{ji}^{(1)} x_i + w_{j0}^{(1)} \right) + w_{k0}^{(2)} \right)$$

- Evaluating the previous expression is known as forward propagation. The NN is said to have a feed-forward architecture.
- All the previous is, of course, generalizable to more layers.

5/16

Neural Networks

- For a large variety of activation functions, the two-layer NN can uniformly approximate any continuous function to arbitrary accuracy provided enough hidden units. Easy to fit the parameters ? Overfitting ?!

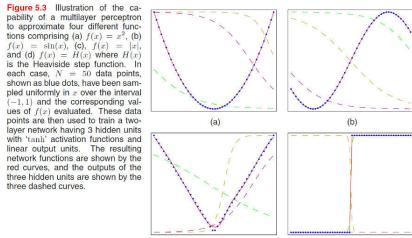
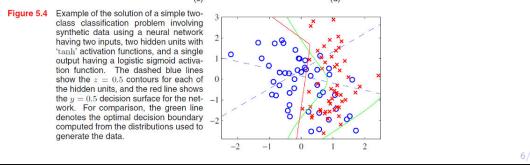


Figure 5.3 Illustration of the capability of a multilayer perceptron to approximate four different functions comprising (a) $f(x) = x^2$, (b) $f(x) = \sin(x)$, (c) $f(x) = \exp(-x^2)$, and (d) $f(x) = H(x)$ where $H(x)$ is the Heaviside step function. In each plot, blue dots represent data points shown as blue dots. These data points are then used to train a two-layer neural network with three hidden units with ‘tanh’ activation functions and linear output units. The resulting hidden units are shown by the red curves, and the outputs of the three hidden units are shown by the three dashed curves.



Backpropagation Algorithm

- Consider regressing an K -dimensional continuous random variable on a D -dimensional continuous random variable.
- Consider a training set $\{(\mathbf{x}_n, \mathbf{t}_n)\}$. Consider minimizing the sum-of-squares error function

$$E(\mathbf{w}) = \sum_n E_n(\mathbf{w}) = \sum_n \frac{1}{2} \|\mathbf{y}(\mathbf{x}_n) - \mathbf{t}_n\|^2 = \sum_n \sum_k \frac{1}{2} (y_k(\mathbf{x}_n) - t_{nk})^2$$

- This error function can be justified from a maximum likelihood approach to learning \mathbf{w} . To see it, assume that

$$p(t_k | \mathbf{x}, \mathbf{w}, \sigma) = \mathcal{N}(t_k | y_k(\mathbf{x}), \sigma)$$

- Then, the likelihood function is

$$p(\{\mathbf{t}_n\} | \{\mathbf{x}_n\}, \mathbf{w}, \sigma) = \prod_n \prod_k \mathcal{N}(t_{nk} | y_k(\mathbf{x}_n), \sigma) = \prod_n \prod_k \frac{1}{(2\pi\sigma^2)^{1/2}} e^{-\frac{1}{2\sigma^2}(t_{nk} - y_k(\mathbf{x}_n))^2}$$

and thus

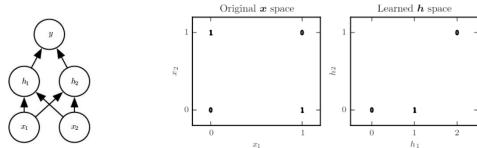
$$-\ln p(\{\mathbf{t}_n\} | \{\mathbf{x}_n\}, \mathbf{w}, \sigma) = \sum_n \sum_k \frac{1}{2\sigma^2} (t_{nk} - y_k(\mathbf{x}_n))^2 + \frac{N}{2} \ln \sigma^2 + \frac{N}{2} \ln 2\pi$$

which is equivalent to the sum-of-squares error function for a given σ .

- If σ is not given, then we can find the ML estimates of \mathbf{w} , plug them into the log likelihood function, and maximize it with respect to σ .

Neural Networks

- Solving the XOR problem with NNs.
- No line shatters the points in the original space.
- The NN represents a mapping of the input space to an alternative space where a line can shatter the points. Note that the points $(0,1)$ and $(1,0)$ are mapped both to the point $(1,0)$.
- It resembles SVMs.



$$\begin{aligned} w_{11}^{(1)} &= w_{12}^{(1)} = w_{21}^{(1)} = w_{22}^{(1)} = 1 \\ w_{10}^{(1)} &= 0, w_{20}^{(1)} = -1 \\ h_j &= z_j = h(a_j) = \max\{0, a_j\} \\ w_{11}^{(2)} &= 1, w_{12}^{(2)} = -2 \\ w_{10}^{(2)} &= 0 \\ y &= y_k = a_k \end{aligned}$$

6/16

7/16

Backpropagation Algorithm

- The weight space is highly multimodal and, thus, we have to resort to approximate iterative methods to minimize the previous expression.

- Batch gradient descent

$$\mathbf{w}^{t+1} = \mathbf{w}^t - \eta_t \nabla E(\mathbf{w}^t)$$

where $\eta_t > 0$ is the learning rate ($\sum_t \eta_t = \infty$ and $\sum_t \eta_t^2 < \infty$ to ensure convergence, e.g. $\eta_t = 1/t$).

- Sequential, stochastic or online gradient descent

$$\mathbf{w}^{t+1} = \mathbf{w}^t - \eta_t \nabla E_n(\mathbf{w}^t)$$

where n is chosen randomly or sequentially.

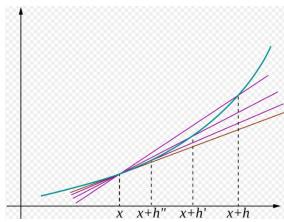
- Sequential gradient descent is less affected by the multimodality problem, as a local minimum of the whole data will not be generally a local minimum of each individual point.

8/16

9/16

Backpropagation Algorithm

- Recall that $f'(x) = \lim_{h \rightarrow 0} \frac{f(x+h) - f(x)}{h}$



- Recall that $\nabla E_n(\mathbf{w}^t)$ is a vector whose components are the partial derivatives of $E_n(\mathbf{w}^t)$.

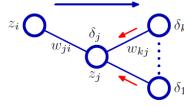
10/10

Backpropagation Algorithm

- Backpropagation algorithm:

- Forward propagate to compute activations, and hidden and output units.
- Compute δ_k for the output units.
- Backpropagate the δ 's, i.e. evaluate δ_j for the hidden units recursively.
- Compute the required derivatives.

Figure 5.7 Illustration of the calculation of δ_j for hidden unit j by backpropagation of the δ 's from those units k to which unit j sends connections. The blue arrow denotes the direction of information flow during forward propagation, and the red arrows indicate the backward propagation of error information.



- For classification, we minimize the negative log likelihood function, a.k.a. cross-entropy error function:

$$E_n(\mathbf{w}) = - \sum_k [t_{nk} \ln y_k(\mathbf{x}_n) + (1 - t_{nk}) \ln(1 - y_k(\mathbf{x}_n))]$$

with $t_{nk} \in \{0, 1\}$ and $y_k(\mathbf{x}_n) = \sigma(a_k)$. Then, again

$$\frac{\partial E_n}{\partial w_{kj}} = \delta_k z_j \text{ and } \delta_k = \frac{\partial E_n}{\partial a_k} = y_k - t_k$$

- This is an example of embarrassingly parallel algorithm.

12/16

Backpropagation Algorithm

- Since E_n depends on w_{ji} only via a_j , and $a_j = \sum_i w_{ji} x_i$, then

$$\frac{\partial E_n}{\partial w_{ji}} = \frac{\partial E_n}{\partial a_j} \frac{\partial a_j}{\partial w_{ji}} = \frac{\partial E_n}{\partial a_j} x_i = \delta_j x_i$$

- Since E_n depends on a_j only via a_k , then

$$\delta_j = \frac{\partial E_n}{\partial a_j} = \sum_k \frac{\partial E_n}{\partial a_k} \frac{\partial a_k}{\partial a_j} = \sum_k \delta_k \frac{\partial a_k}{\partial a_j}$$

- Since $a_k = \sum_j w_{kj} z_j$ and $z_j = h(a_j)$, then

$$\frac{\partial a_k}{\partial a_j} = h'(a_j) w_{kj}$$

- Putting all together, we have that

$$\delta_j = h'(a_j) \sum_k \delta_k w_{kj}$$

- Since $y_k = a_k$ for regression and $a_k = \sum_j w_{kj} z_j$, then

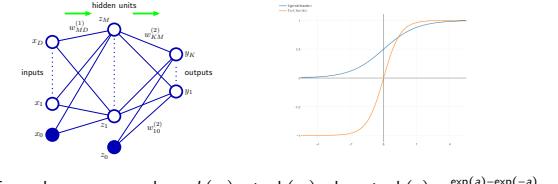
$$\frac{\partial E_n}{\partial w_{kj}} = \frac{\partial E_n}{\partial a_k} \frac{\partial a_k}{\partial w_{kj}} = \delta_k z_j \text{ and } \delta_k = \frac{\partial E_n}{\partial a_k} = y_k - t_k$$

- Backpropagation algorithm:

- Forward propagate to compute activations, and hidden and output units.
- Compute δ_k for the output units.
- Backpropagate the δ 's, i.e. evaluate δ_j for the hidden units recursively.
- Compute the required derivatives.

11/10

Backpropagation Algorithm



- Example: $y_k = a_k$, and $z_j = h(a_j) = \tanh(a_j)$ where $\tanh(a) = \frac{\exp(a) - \exp(-a)}{\exp(a) + \exp(-a)}$.
- Note that $h'(a) = 1 - h(a)^2$.

- Backpropagation:

- Forward propagation, i.e. compute

$$a_j = \sum_i w_{ji} x_i \text{ and } z_j = h(a_j) \text{ and } y_k = \sum_j w_{kj} z_j$$

- Compute

$$\delta_k = y_k - t_k$$

- Backpropagate, i.e. compute

$$\delta_j = (1 - z_j^2) \sum_k w_{kj} \delta_k$$

- Compute

$$\frac{\partial E_n}{\partial w_{kj}} = \delta_k z_j \text{ and } \frac{\partial E_n}{\partial w_{ji}} = \delta_j x_i$$

13/16

Backpropagation Algorithm

- The weight space is non-convex and has many symmetries, plateaus and local minima. So, the initialization of the weights in the backpropagation algorithm is crucial.
- Hints based on experimental rather than theoretical analysis:
 - Initialize the weights to different values, otherwise they would be updated in the same way because the algorithm is deterministic, and so creating redundant hidden units.
 - Initialize the weights at random, but
 - too small magnitude values may cause losing signal in the forward or backward passes, and
 - too big magnitude values may cause the activation function to saturate and lose gradient.
 - Initialize the weights according to prior knowledge: Almost-zero for hidden units that are unlikely to interact, and bigger magnitude values for the rest.
 - Initialize the weights to almost-zero values so that the initial model is almost-linear, i.e. the sigmoid function is almost-linear around the zero. Let the algorithm to introduce non-linearities where needed.
 - Note however that this initialization makes the sigmoid function take a value around half its saturation level. That is why the hyperbolic tangent function is sometimes preferred in practice.

14/16

Summary

- NNs: Nonlinear mapping from input to output.
- Extremely expressive.
- Training: Backpropagation algorithm, and regularization.

16/16

Regularization

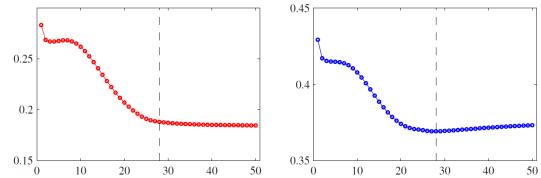


Figure 5.12 An illustration of the behaviour of training set error (left) and validation set error (right) during a typical training session, as a function of the iteration step, for the sinusoidal data set. The goal of achieving the best generalization performance suggests that training should be stopped at the point shown by the vertical dashed lines, corresponding to the minimum of the validation set error.

- Regularization when learning the parameters: Early stopping the backpropagation algorithm according to the error on some validation data.
- Regularization when learning the structure:
 - Cross-validation.
 - Penalizing complexity according to

$$E(\mathbf{w}) + \frac{\lambda}{2} \|\mathbf{w}\|^2 \text{ or } E(\mathbf{w}) + \frac{\lambda_1}{2} \|\mathbf{w}^{(1)}\|^2 + \frac{\lambda_2}{2} \|\mathbf{w}^{(2)}\|^2$$

and choose λ , or λ_1 and λ_2 by cross-validation. Note that the effect of the penalty is simply to add λw_{ji} and λw_{kj} , or $\lambda_1 w_{ji}$ and $\lambda_2 w_{kj}$ to the appropriate derivatives.

15/16

Limitations of Neural Networks

Theorem (Universal approximation theorem)

For every continuous function $f : [a, b]^D \rightarrow \mathbb{R}$ and for every $\epsilon > 0$, there exists a NN with one hidden layer such that

$$\sup_{\mathbf{x} \in [a, b]^D} |f(\mathbf{x}) - y(\mathbf{x})| < \epsilon$$

Theorem (Universal classification theorem)

Let $\mathcal{C}^{(k)}$ contain all classifiers defined by NNs of one hidden layer with k hidden units and the sigmoid activation function. Then, for any distribution $p(\mathbf{x}, t)$,

$$\lim_{k \rightarrow \infty} \inf_{y \in \mathcal{C}^{(k)}} E_X[y(\mathbf{x})] - E_X[p(t|\mathbf{x})] = 0$$

- How many hidden units has such a NN ?
- How much data do we need to learn such a NN (and avoid overfitting) via the backpropagation algorithm ?
- How fast does the backpropagation algorithm converge to such a NN ? Assuming that it does not get trapped in a local minimum...
- The answer to the last two questions depends on the first: More hidden units implies more training time and higher generalization error.

16/16

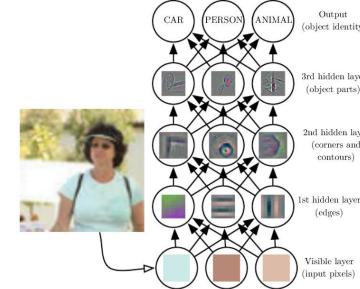
Limitations of Neural Networks

- ▶ How many hidden units does the NN need ?
- ▶ Any Boolean function can be written in disjunctive normal form (OR of ANDs) or conjunctive normal form (AND of ORs). This is a depth-two logical circuit.
- ▶ For most Boolean functions, the size of the circuit is exponential in the size of the input.
- ▶ However, there are Boolean functions that have a polynomial-size circuit of depth k and an exponential-size circuit of depth $k - 1$.
- ▶ Then, there is no universally right depth. Ideally, we should let the data determine the right depth.

Theorem (No free lunch theorem)

For any algorithm, good performance on some problems comes at the expense of bad performance on some others.

Deep Neural Networks



- ▶ A deep NN is a function that maps input to output.
- ▶ The mapping is formed by composing many simpler functions.
- ▶ Each layer provides a new representation of the input, i.e. complex concepts are built from simpler ones.
- ▶ The representation is learned automatically from data.

Deep Neural Networks

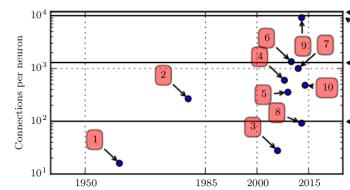


Figure 1.10: Initially, the number of connections between neurons in artificial neural networks was limited by hardware capabilities. Today, the number of connections between neurons is mostly a design consideration. Some artificial neural networks have nearly as many connections per neuron as a cat, and it is quite common for other neural networks to have as many connections per neuron as smaller mammals like mice. Even the human brain does not have an exorbitant amount of connections per neuron. Biological neural network sizes from Wikipedia (2015).

1. Adaptive linear element (Widrow and Hoff, 1960)
2. Neocognitron (Fukushima, 1980)
3. GPU-accelerated convolutional network (Chenapilla et al., 2006)
4. Deep Boltzmann machine (Salakhutdinov and Hinton, 2009a)
5. Unsupervised convolutional network (Jarrett et al., 2009)
6. GPU-accelerated multilayer perceptron (Ciresan et al., 2010)
7. Distributed autoencoder (Le et al., 2012)
8. Multi-GPU convolutional network (Krizhevsky et al., 2012)
9. COTS HPC unsupervised convolutional network (Coates et al., 2013)
10. GoogleNet (Szegedy et al., 2014a)

Deep Neural Networks

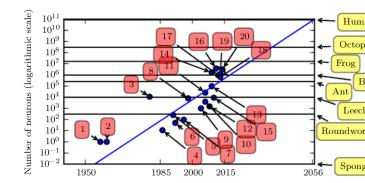


Figure 1.11: Since the introduction of hidden units, artificial neural networks have doubled in size roughly every 2.4 years. Biological neural network sizes from Wikipedia (2015).

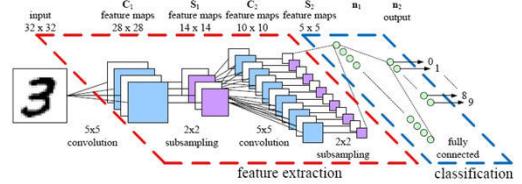
1. Perceptron (Rosenblatt, 1958, 1962)
2. Adaptive linear element (Widrow and Hoff, 1960)
3. Neocognitron (Fukushima, 1980)
4. Early back-propagation network (Rumelhart et al., 1986b)
5. Recurrent neural network for speech recognition (Rabiner and Fallside, 1991)
6. Multilayer perceptron for speech recognition (Bengio et al., 1991)
7. Mean field sigmoid belief network (Saul et al., 1996)
8. LeNet-5 (Le et al., 2004)
9. Edge-state networks (Jang et al., 2004)
10. Deep belief network (Hinton et al., 2006)
11. GPU-accelerated convolutional network (Chenapilla et al., 2006)
12. Deep Boltzmann machine (Salakhutdinov and Hinton, 2009a)
13. GPU-accelerated deep belief network (Ranzato et al., 2009)
14. Unsupervised convolutional network (Jarrett et al., 2009)
15. GPU-accelerated multilayer perceptron (Ciresan et al., 2010)
16. OMNeT++ networks (Coates and Ng, 2011)
17. GPU-accelerated convolutional network (Krizhevsky et al., 2012)
18. Multi-GPU convolutional network (Krizhevsky et al., 2012)
19. COTS HPC unsupervised convolutional network (Coates et al., 2013)
20. GoogleNet (Szegedy et al., 2014a)
21. 22 layers DNN, but 12 times fewer weights than DNN 19

Deep Neural Networks

- ▶ Training DNNs is difficult:
 - ▶ Typically, poorer generalization than (shallow) NNs.
 - ▶ The gradient may vanish/explode as we move away from the output layer, due to multiplying small/big quantities. E.g. the gradient of σ and \tanh is in $[0, 1]$. So, they may only suffer the gradient vanishing problem. Other activation functions may suffer the gradient exploding problem.
 - ▶ There may be larger plateaus and many more local minima than with NNs.
- ▶ Training DNNs is doable:
 - ▶ Convolutional networks, particularly suitable for image processing.
 - ▶ Rectifier activation function, a new activation function.
 - ▶ Layer-wise pre-training, to find a good starting point for training.
- ▶ In addition to performance, the computational demands of the training must be considered, e.g. CPU, GPU, memory, parallelism, etc.
 - ▶ The authors state that GoogleNet was trained "using modest amount of model and data-parallelism. Although we used a CPU based implementation only, a rough estimate suggests that the GoogleNet network could be trained to convergence using few high-end GPUs within a week, the main limitation being the memory usage".

8/10

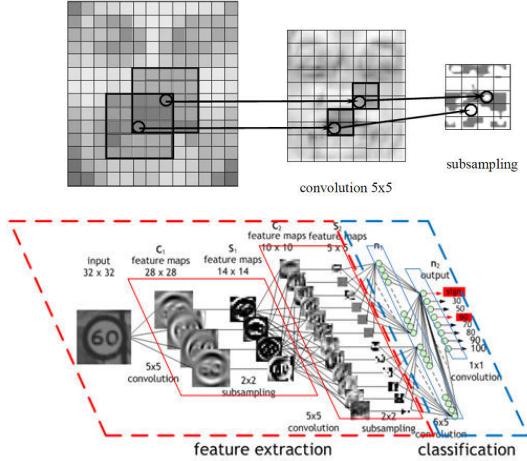
Convolutional Networks



- ▶ DNNs suitable for image recognition, since they exhibit invariance to translation, scaling, rotations, and warping.
- ▶ Convolution: Detection of local features, e.g. a_j is computed from a 5×5 pixel patch of the image.
- ▶ To achieve invariance, the units in the convolution layer share the same activation function and weights.
- ▶ Subsampling: Combination of local features into higher-order features, e.g. a_k is compute from a 2×2 pixel patch of the convoluted image.
- ▶ There are several feature maps in each layer, to compensate the reduction in resolution by increasing in the number of features being detected.
- ▶ The final layer is a regular NN for classification.

10/10

Convolutional Networks



11/10

Convolutional Networks

- ▶ DNNs allow increased depth because
 - ▶ they are sparse, which allows the gradient to propagate further, and
 - ▶ they have relatively few weights to fit due to feature locality and weight sharing.
- ▶ The backpropagation algorithm needs to be adapted, by modifying the derivatives with respect to the weights in each convolution layer m .
- ▶ Since E_n depends on $w_i^{(m)}$ only via $a_j^{(m)}$, and $a_j^{(m)} = \sum_{i \in L_j^{(m)}} w_i^{(m)} z_i^{(m-1)}$ where $L_j^{(m)}$ is the set of indexes of the input units, then

$$\frac{\partial E_n}{\partial w_i^{(m)}} = \sum_j \frac{\partial E_n}{\partial a_j^{(m)}} \frac{\partial a_j^{(m)}}{\partial w_i^{(m)}} = \sum_j \delta_j^{(m)} z_i^{(m-1)}$$

- ▶ Note that $w_i^{(m)}$ does not depend on j by weight sharing, whereas $i \in L_j^{(m)}$ by feature locality.

12/10

Rectifier Activation Function

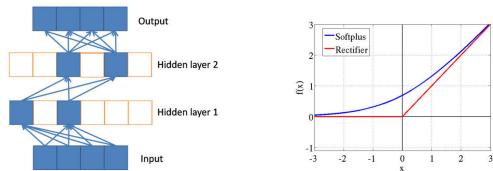


Figure 2: *Left:* Sparse propagation of activations and gradients in a network of rectifier units. The input selects a subset of active neurons and computation is linear in this subset. *Right:* Rectifier and softplus activation functions. The second one is a smooth version of the first.

- ▶ $\text{rectifier}(x) = \max\{0, x\}$, i.e. hidden units are off or operating in a linear regime.
- ▶ The most popular choice nowadays.
- ▶ Sparsity promoting: Uniform initialization of the weights implies that around 50 % of the hidden units are off.
- ▶ Piece-wise linear mapping: The input selects which hidden units are active, and the output is a liner function of the input in the selected hidden units.

13/18

Layer-Wise Pre-Training

- ▶ The pre-training aims to find a good starting point for the subsequent run of the backpropagation algorithm.
- ▶ Supervised version:
 1. Train each layer of the DNN as if it was the hidden layer in a depth-two NN. As input, use the output of the last of the previously trained layers. As output, use the original classification or regression function.
 2. Run the backpropagation algorithm to fine-tune the weights.
- ▶ Unsupervised version: Similar to the supervised one but the hidden layers (except the last one) are trained to learn an encoding of the output of the previous layer, instead of the original classification or regression function.

15/18

Rectifier Activation Function

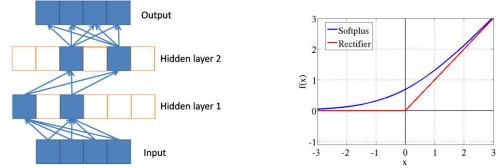


Figure 2: *Left:* Sparse propagation of activations and gradients in a network of rectifier units. The input selects a subset of active neurons and computation is linear in this subset. *Right:* Rectifier and softplus activation functions. The second one is a smooth version of the first.

- ▶ It simplifies the backpropagation algorithm as $h'(a_j) = 1$ for the selected units. So, there is no gradient vanishing on the paths of selected units. Compare with the sigmoid or hyperbolic tangent, for which
 - ▶ the gradient is smaller than one, or
 - ▶ even zero due to saturation.
- ▶ Note that $h'(0)$ does not exist since $h'_+(0) \neq h'_-(0)$. We can get around this problem by simply returning one of two one-sided derivatives. Or using a generalization of the rectifier function.
- ▶ Regularization is typically added to prevent numerical problems due to the activation being unbounded, e.g. when forward propagating.

14/18

Summary

- ▶ Direct application of the backpropagation algorithm to DNNs produces poor results.
- ▶ Convolutional networks: It makes the backpropagation algorithm more efficient by using local features and weight sharing. This also achieves invariance, which is particularly important for image processing.
- ▶ Rectifier activation function: Free of gradient vanishing problem and it simplifies the backpropagation algorithm.
- ▶ Layer-wise pre-training: Heuristic weight initialization to alleviate the local optima problem.

16/18

R Markdown

Cheat Sheet

learn more at rmarkdown.rstudio.com

rmarkdown 0.2.50 Updated: 8/14



1. Workflow R Markdown is a format for writing reproducible, dynamic reports with R. Use it to embed R code and results into slideshows, pdfs, html documents, Word files and more. To make a report:

i. Open - Open a file that uses the .Rmd extension.



ii. Write - Write content with the easy to use R Markdown syntax



iii. Embed - Embed R code that creates output to include in the report

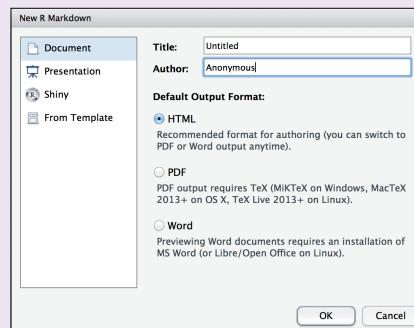


iv. Render - Replace R code with its output and transform the report into a slideshow, pdf, html or ms Word file.



2. Open File Start by saving a text file with the extension .Rmd, or open an RStudio Rmd template

- In the menu bar, click **File ► New File ► R Markdown...**
- A window will open. Select the class of output you would like to make with your .Rmd file
- Select the specific type of output to make with the radio buttons (you can change this later)
- Click OK



4. Choose Output Write a YAML header that explains what type of document to build from your R Markdown file.

YAML

A YAML header is a set of key-value pairs at the start of your file. Begin and end the header with a line of three dashes (---)

```
---  
title: "Untitled"  
author: "Anonymous"  
output: html_document  
---
```

The RStudio template writes the YAML header for you

The output value determines which type of file R will build from your .Rmd file (in Step 6)

output: html_document html file (web page)

output: pdf_document pdf document

output: word_document Microsoft Word .docx

output: beamer_presentation beamer slideshow (pdf)

output: ioslides_presentation ioslides slideshow (html)



3. Markdown Next, write your report in plain text. Use markdown syntax to describe how to format text in the final report.

syntax

Plain text

End a line with two spaces to start a new paragraph.

italics and _italics_

bold and __bold__

superscript^2^

~~strikethrough~~

[link] (www.rstudio.com)

Header 1

Header 2

Header 3

Header 4

Header 5

Header 6

endash: --

emdash: ---

ellipsis: ...

inline equation: \$A = \pi r^2\$

image:

horizontal rule (or slide break):

> block quote

* unordered list

* item 2

+ sub-item 1

+ sub-item 2

1. ordered list

2. item 2

+ sub-item 1

+ sub-item 2

Table Header | Second Header

-----|-----

Table Cell | Cell 2

Cell 3 | Cell 4

becomes

Plain text

End a line with two spaces to start a new paragraph.

italics and italics

bold and bold

superscript²

strikethrough

link

Header 1

Header 2

Header 3

Header 4

Header 5

Header 6

endash: –

emdash: —

ellipsis: ...

inline equation: $A = \pi * r^2$



horizontal rule (or slide break):

block quote

- unordered list

- item 2

- sub-item 1

- sub-item 2

1. ordered list

2. item 2

- sub-item 1

- sub-item 2

Table Header	Second Header
--------------	---------------

Table Cell	Cell 2
------------	--------

Cell 3	Cell 4
--------	--------

5. Embed Code

Use knitr syntax to embed R code into your report. R will run the code and include the results when you render your report.

inline code

Surround code with back ticks and r.
R replaces inline code with its results.

```
Two plus two equals `r 2 + 2`.
```

Two plus two equals 4.

Start a chunk with ``{r}.
End a chunk with ```.

```
Here's some code
``{r}
dim(iris)
```

Here's some code

```
dim(iris)
```

```
## [1] 150 5
```

display options

Use knitr options to style the output of a chunk.
Place options in brackets above the chunk.

```
Here's some code
``{r eval=FALSE}
dim(iris)
```

Here's some code
dim(iris)

```
Here's some code
``{r echo=FALSE}
dim(iris)
```

Here's some code
[1] 150 5

option default effect

eval	TRUE	Whether to evaluate the code and include its results
echo	TRUE	Whether to display code along with its results
warning	TRUE	Whether to display warnings
error	FALSE	Whether to display errors
message	TRUE	Whether to display messages
tidy	FALSE	Whether to reformat code in a tidy way when displaying it
results	"markup"	"markup", "asis", "hold", or "hide"
cache	FALSE	Whether to cache results for future renders
comment	"##"	Comment character to preface results with
fig.width	7	Width in inches for plots created in chunk
fig.height	7	Height in inches for plots created in chunk

For more details visit yihui.name/knitr/

8. Publish

Share your report where users can visit it online

Rpubs.com

Share non-interactive documents on RStudio's free R Markdown publishing site
www.rpubs.com

ShinyApps.io

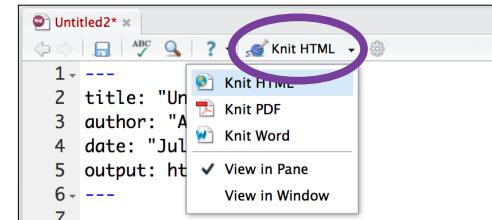
Host an interactive document on RStudio's server. Free and paid options
www.shinyapps.io

6. Render

Use your .Rmd file as a blueprint to build a finished report.

Render your report in one of two ways

- Run `rmarkdown::render("<file path>")`
- Click the **knit HTML** button at the top of the RStudio scripts pane



When you render, R will

- execute each embedded code chunk and insert the results into your report
- build a new version of your report in the output file type
- open a preview of the output file in the viewer pane
- save the output file in your working directory

7. Interactive Docs

Turn your report into an interactive Shiny document in 3 steps

1 Add `runtime: shiny` to the YAML header

```
---
title: "Line graph"
output: html_document
runtime: shiny
---
```

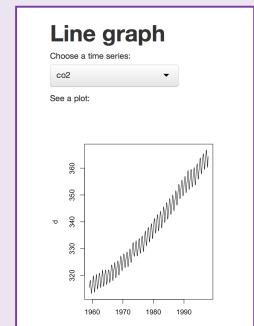
2 In the code chunks, add Shiny `input` functions to embed widgets. Add Shiny `render` functions to embed reactive output

```
---
title: "Line graph"
output: html_document
runtime: shiny
---

Choose a time series:
``{r echo = FALSE}
selectInput("data", "", 
           c("co2", "lh"))
``

See a plot:
``{r echo = FALSE}
renderPlot({
  d <- get(input$data)
  plot(d)
})``
```

3 Render with `rmarkdown::run` or click Run Document in RStudio



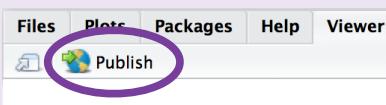
* Note: your report will be a Shiny app, which means you must choose an html output format, like `html_document` (for an interactive report) or `ioslides_presentation` (for an interactive slideshow).

9. Learn More

Documentation and examples - rmarkdown.rstudio.com
Further Articles - shiny.rstudio.com/articles

blog.rstudio.com

@rstudio



SUPervised Learning	ALGORITHM	DESCRIPTION	R PACKAGE::FUNCTION	SAMPLE CODE
	NBC	A classification technique based on Bayes' Theorem with an assumption of independence among predictors. In simple terms, a Naive Bayes classifier assumes that the presence of a particular feature in a class is unrelated to the presence of any other feature.	e1071::naiveBayes	naiveBayes(class ~ ., data = x)
	kNN	A non-parametric method used for classification and regression. In both cases, the input consists of the k closest training examples in the feature space. The output depends on whether k-NN is used for classification or regression	class::knn	knn(train, test, cl, k = 1, l = 0, prob = FALSE, use.all = TRUE)
	REG	Model the linear relationship between a scalar dependant variable Y and one or more explanatory variables (or independent variables) denoted X	stats::lm	lm(dist ~ speed, data=cars)
	LREG	Used to predict a binary outcome (1 / 0, Yes / No, True / False) given a set of independent variables.	stats::glm	glm(Y ~ ., family = binomial(link = 'logit'), data = X)
	TM	The idea is to consecutively divide (branch) the training dataset based on the input features until an assignment criterion with respect to the target variable into a "data bucket" (leaf) is reached	rpart::rpart	rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
	ANN	Neural networks are built from units called perceptrons. Perceptrons have one or more inputs, an activation function and an output. An ANN model is built up by combining perceptrons in structured layers.	neuralnet::neuralnet	neuralnet(f,data=train_hidden=c(5,3),linear.output=T)
	SVM	A data classification method that separates data using hyperplanes	e1071::svm	svm(formula, data = NULL, ..., subset, na.action = na.omit, scale = TRUE)
	PCA	A procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components.	stats::prcomp stats::princomp FactoMineR::PCA ade4::dudi.pca amap::acp	stats : prcomp(formula, data = NULL, subset, na.action, ...) stats : princomp(formula, data = NULL, subset, na.action, ...) FactoMineR : PCA(decathlon, quanti.sup = 11:12, quall.sup=13) ade4 : dudi.pca(deugStab, center = deug\$cent, scale = FALSE, scan = FALSE) amap : acp(lubisch)
UNSupervised Learning	KMC	Aims at partitioning n observations into k clusters in which each observation belongs to the cluster with the nearest mean	stats::kmeans	kmeans(x, centers, iter.max = 10, nstart = 1, algorithm = c("Hartigan-Wong", "Lloyd", "Forgy", "MacQueen"), trace=FALSE)
	HCL	An approach which builds a hierarchy from the bottom-up, and doesn't require the number of clusters to be specified beforehand.	stats::hclust	hclust(d, method = "complete", members = NULL)

	ALGORITHM	DESCRIPTION	R PACKAGE::FUNCTION	SAMPLE CODE
META ALGORITHM	REGU Regularisation L1 (Lasso) L2 (Ridge)	Regularization adds a penalty on the different parameters of a model to reduce the freedom of the model. Hence, the model will be less likely to fit the noise of the training data and will improve the generalization abilities of the model	glmnet::glmnet	L1 : glmnet(myMatrixA, myMatrixB, family = "gaussian", alpha = 1) L2 : glmnet(myMatrixA, myMatrixB, family = "gaussian", alpha = 0)
	BAG Boosting	A process of iteratively refining, e.g. by reweighting, of estimated regression and classification functions (though it has primarily been applied to the latter), in order to improve predictive ability.	Parametric model - mboost::gbmboost	gbmboost(Yen ~ ., data = curr1[trnidxs,])
	BAG Bagging	Bagging is a way to increase the power of a predictive statistical model by taking multiple random samples (with replacement) of the training data set, and using each of them to construct a separate model and separate predictions for the original test set	All models: foreach Tree models: ipred::bagging	foreach : d <- data.frame(x=1:10, y=rnorm(10)) s <- foreach(d=iter(d, by='row'), .combine=rbind) %dopar% identical(s, d) ipred : bagging(formula, data, subset, na.action=na.rpart, .dots)
	PRUN Pruning	Pruning is a technique that reduces the size of decision tree by removing sections of the tree that provide little power to classify instances. Pruning reduces the complexity of the final classifier and hence improves predictive accuracy by reducing overfitting	rpart::prune	prune(x, cp = 0.1)
	RF Random Forrest	An ensemble learning method for classification, regression and other tasks, that operate by constructing a multitude of decision trees at training time and outputting the class that is the mode of the classes (classification) or mean prediction (regression)	randomForest::randomForest	randomForest(X ~ ., data = Y, subset = mySub)
	TSA Lead-lag analysis, Auto-correlation, Spectral analysis, Time series clustering, Seasonality, Trend....	Random sampling of observations for training and testing a model can be an issue when faced with a times dimension. Random sampling may either destroy serial correlation properties in the data which we would like to exploit	stats xts forecast spectral TTR	Auto-correlation: acf(x, lag.max = NULL, type = c("correlation", "covariance", "partial")) Spectral Analysis: spec.pgram(myTs, spans = NULL) Seasonal Decomposition of Time Series - stl(x, s.window = 7, t.window = 50, t.jump = 1)
MODEL VALIDATION	PM Performance metrics	Depends on the problem: • Regression: squared errors, outliers, error rate... • Classification: Accuracy, precision, recall, F-score...	Regression-stats::outlierTest, stats:: qqPlot ... Classification-ROCR:: Tree: caret:: confusionMatrix	Regression: fit <- lm(Y~X,data=myData) outlierTest(fit) qqPlot(fit, main="QQ Plot")
	BVT Bias-Variance Tradeoff	Simple models with few parameters are easier to compute but may lead to poorer fits (high bias). Complex models may provide more accurate fits but may over-fit the data (high variance)	Tailored to the analysis	Tailored to the analysis
	CV Cross validation	Cross validation compares the test performances of different model realisations with different sets or values of parameters	caret::createDataPartition caret::createFolds	createDataPartition(classes, p = 0.8, list = FALSE)
	LC Learning Curves	Learning curves plot a model's training and test errors, or the chosen performance metric, depending on the training set size	caret:: learning_curve_dat	learning_curve_dat(dat, outcome = NULL, proportion = (1:10)/10, test_prop = 0, verbose = TRUE, ...)

R Reference Card

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Getting help

Most R functions have online documentation.

help(topic) documentation on topic
?topic id.

help.search("topic") search the help system

apropos("topic") the names of all objects in the search list matching the regular expression "topic"

help.start() start the HTML version of help

str(a) display the internal "str"ucture of an R object

summary(a) gives a "summary" of a, usually a statistical summary but it is generic meaning it has different operations for different classes of a

ls() show objects in the search path; specify pat="pat" to search on a pattern

ls.str() str() for each variable in the search path

dir() show files in the current directory

methods(a) shows S3 methods of a

methods(class=class(a)) lists all the methods to handle objects of class a

Input and output

load() load the datasets written with save

data(x) loads specified data sets

library(x) load add-on packages

read.table(file) reads a file in table format and creates a data frame from it; the default separator sep="" is any whitespace; use header=TRUE to read the first line as a header of column names; use as.is=TRUE to prevent character vectors from being converted to factors; use comment.char="" to prevent "#" from being interpreted as a comment; use skip= to skip n lines before reading data; see the help for options on row naming, NA treatment, and others

read.csv("filename",header=TRUE) id. but with defaults set for reading comma-delimited files

read.delim("filename",header=TRUE) id. but with defaults set for reading tab-delimited files

read.fwf(file,widths,header=FALSE,sep=" ",as.is=FALSE) read a table of fixed width formatted data into a 'data.frame'; widths is an integer vector, giving the widths of the fixed-width fields

save(file,...) saves the specified objects (...) in the XDR platform-independent binary format

save.image(file) saves all objects

cat(..., file="", sep=" ") prints the arguments after coercing to character; sep is the character separator between arguments

print(a, ...) prints its arguments; generic, meaning it can have different methods for different objects

format(x,...) format an R object for pretty printing

write.table(x,file="",row.names=TRUE,col.names=TRUE,sep=" ") prints x after converting to a data frame; if quote is TRUE,

character or factor columns are surrounded by quotes (""); sep is the field separator; eol is the end-of-line separator; na is the string for missing values; use col.names=NA to add a blank column header to get the column headers aligned correctly for spreadsheet input

sink(file) output to file, until sink()

Most of the I/O functions have a file argument. This can often be a character string naming a file or a connection. file="" means the standard input or output. Connections can include files, pipes, zipped files, and R variables. On windows, the file connection can also be used with description = "clipboard". To read a table copied from Excel, use

x <- read.delim("clipboard")

To write a table to the clipboard for Excel, use

write.table(x,"clipboard",sep="\t",col.names=NA)

For database interaction, see packages RODBC, DBI, RMySQL, RPostgreSQL, and ROracl. See packages XML, hdf5, netCDF for reading other file formats.

Data creation

c(...) generic function to combine arguments with the default forming a vector; with recursive=TRUE descends through lists combining all elements into one vector

from:to generates a sequence; ":" has operator priority; 1:4 + 1 is "2,3,4,5"
seq(from,to) generates a sequence by= specifies increment; length= specifies desired length

seq(along=x) generates 1, 2, ..., length(along); useful for for loops

rep(x,times) replicate x times; use each= to repeat "each" element of x each times; rep(c(1,2,3),2) is 1 2 3 1 2 3; rep(c(1,2,3),each=2) is 1 1 2 2 3 3

data.frame(...) create a data frame of the named or unnamed arguments; data.frame(v=1:4,ch=c("a","B","c","d"),n=10); shorter vectors are recycled to the length of the longest

list(...) create a list of the named or unnamed arguments; list(a=c(1,2),b="hi",c=3);

array(x,dim=) array with data x; specify dimensions like dim=c(3,4,2); elements of x recycle if x is not long enough

matrix(x,nrow=,ncol=) matrix; elements of x recycle

factor(x,levels=) encodes a vector x as a factor

gl(n,k,length=n*k,labels=1:n) generate levels (factors) by specifying the pattern of their levels; k is the number of levels, and n is the number of replications

expand.grid() a data frame from all combinations of the supplied vectors or factors

rbind(...) combine arguments by rows for matrices, data frames, and others

cbind(...) id. by columns

Slicing and extracting data

Indexing vectors

x[n]	n th element
x[-n]	all but the n th element
x[1:n]	first n elements
x[-(1:n)]	elements from n+1 to the end
x[c(1,4,2)]	specific elements
x["name"]	element named "name"
x[x > 3]	all elements greater than 3
x[x > 3 & x < 5]	all elements between 3 and 5
x[x %in% c("a","and","the")]	elements in the given set

Indexing lists

x[n]	list with elements n
x[[n]]	n th element of the list
x[["name"]]	element of the list named "name"
x\$name	id.

Indexing matrices

x[i,j]	element at row i, column j
x[i,]	row i
x[,j]	column j
x[,c(1,3)]	columns 1 and 3
x[["name",]]	row named "name"
x[["name"]]	column named "name"
x\$name	id.

Variable conversion

as.array(x), as.data.frame(x), as.numeric(x), as.logical(x), as.complex(x), as.character(x), ... convert type; for a complete list, use methods(as)

Variable information

is.na(x), is.null(x), is.array(x), is.data.frame(x), is.numeric(x), is.complex(x), is.character(x), ... test for type; for a complete list, use methods(is)

length(x) number of elements in x

dim(x) Retrieve or set the dimension of an object; dim(x) <- c(3,2)

dimnames(x) Retrieve or set the dimension names of an object

nrow(x) number of rows; NROW(x) is the same but treats a vector as a one-row matrix

ncol(x) and **NCOL(x)** id. for columns

class(x) get or set the class of x; class(x) <- "myclass"

unclass(x) remove the class attribute of x

attr(x,which) get or set the attribute which of x

attributes(obj) get or set the list of attributes of obj

Data selection and manipulation

which.max(x) returns the index of the greatest element of x

which.min(x) returns the index of the smallest element of x

rev(x) reverses the elements of x

sort(x) sorts the elements of x in increasing order; to sort in decreasing order: rev(sort(x))

cut(x,breaks) divides x into intervals (factors); breaks is the number of cut intervals or a vector of cut points

match(x, y) returns a vector of the same length than x with the elements of x which are in y (NA otherwise)

which(x == a) returns a vector of the indices of x if the comparison operation is true (TRUE), in this example the values of i for which x[i] == a (the argument of this function must be a variable of mode logical)

choose(n, k) computes the combinations of k events among n repetitions = $n! / [(n-k)!k!]$

na.omit(x) suppresses the observations with missing data (NA) (suppresses the corresponding line if x is a matrix or a data frame)

na.fail(x) returns an error message if x contains at least one NA

unique(x) if x is a vector or a data frame, returns a similar object but with the duplicate elements suppressed

table(x) returns a table with the numbers of the different values of x (typically for integers or factors)

subset(x, ...) returns a selection of x with respect to criteria (...), typically comparisons: $x\$V1 < 10$; if x is a data frame, the option `select` gives the variables to be kept or dropped using a minus sign

sample(x, size) resample randomly and without replacement size elements in the vector x, the option `replace = TRUE` allows to resample with replacement

prop.table(x, margin=) table entries as fraction of marginal table

Math

sin, cos, tan, asin, acos, atan, atan2, log, log10, exp

max(x) maximum of the elements of x

min(x) minimum of the elements of x

range(x) id. then $c(\min(x), \max(x))$

sum(x) sum of the elements of x

diff(x) lagged and iterated differences of vector x

prod(x) product of the elements of x

mean(x) mean of the elements of x

median(x) median of the elements of x

quantile(x, probs=) sample quantiles corresponding to the given probabilities (defaults to 0.25,.5,.75,.1)

weighted.mean(x, w) mean of x with weights w

rank(x) ranks of the elements of x

var(x) or cov(x) variance of the elements of x (calculated on $n - 1$); if x is a matrix or a data frame, the variance-covariance matrix is calculated

sd(x) standard deviation of x

cor(x) correlation matrix of x if it is a matrix or a data frame (1 if x is a vector)

var(x, y) or cov(x, y) covariance between x and y, or between the columns of x and those of y if they are matrices or data frames

cor(x, y) linear correlation between x and y, or correlation matrix if they are matrices or data frames

round(x, n) rounds the elements of x to n decimals

log(x, base) computes the logarithm of x with base base

scale(x) if x is a matrix, centers and reduces the data; to center only use the option `center=FALSE`, to reduce only `scale=FALSE` (by default `center=TRUE, scale=TRUE`)

pmin(x, y, ...) a vector which i th element is the minimum of $x[i], y[i], \dots$

pmax(x, y, ...) id. for the maximum

cumsum(x) a vector which i th element is the sum from $x[1]$ to $x[i]$

cumprod(x) id. for the product

cummin(x) id. for the minimum

cummax(x) id. for the maximum

union(x, y), intersect(x, y), setdiff(x, y), setequal(x, y), is.element(el, set) "set" functions

Re(x) real part of a complex number

Im(x) imaginary part

Mod(x) modulus; `abs(x)` is the same

Arg(x) angle in radians of the complex number

Conj(x) complex conjugate

convolve(x, y) compute the several kinds of convolutions of two sequences

fft(x) Fast Fourier Transform of an array

mvfft(x) FFT of each column of a matrix

filter(x, filter) applies linear filtering to a univariate time series or to each series separately of a multivariate time series

Many math functions have a logical parameter `na.rm=FALSE` to specify missing data (NA) removal.

Matrices

t(x) transpose

diag(x) diagonal

%*% matrix multiplication

solve(a, b) solves a $\%*% x = b$ for x

solve(a) matrix inverse of a

rowsum(x) sum of rows for a matrix-like object; **rowSums(x)** is a faster version

colsum(x), colSums(x) id. for columns

rowMeans(x) fast version of row means

colMeans(x) id. for columns

Advanced data processing

apply(X, INDEX, FUN=) a vector or array or list of values obtained by applying a function FUN to margins (INDEX) of X

lapply(X, FUN) apply FUN to each element of the list X

tapply(X, INDEX, FUN=) apply FUN to each cell of a ragged array given by X with indexes INDEX

by(data, INDEX, FUN) apply FUN to data frame data subsetted by INDEX

merge(a, b) merge two data frames by common columns or row names

xtabs(b, data=x) a contingency table from cross-classifying factors

aggregate(x, by, FUN) splits the data frame x into subsets, computes summary statistics for each, and returns the result in a convenient form; by is a list of grouping elements, each as long as the variables in x

stack(x, ...) transform data available as separate columns in a data frame or list into a single column

unstack(x, ...) inverse of stack()

reshape(x, ...) reshapes a data frame between 'wide' format with repeated measurements in separate columns of the same record and 'long' format with the repeated measurements in separate records; use (direction="wide") or (direction="long")

Strings

paste(...) concatenate vectors after converting to character; `sep=` is the string to separate terms (a single space is the default); `collapse=` is an optional string to separate "collapsed" results

substr(x, start, stop) substrings in a character vector; can also assign, as `substr(x, start, stop) <- value`

strsplit(x, split) split x according to the substring split

grep(pattern, x) searches for matches to pattern within x; see ?regex

gsub(pattern, replacement, x) replacement of matches determined by regular expression matching `sub()` is the same but only replaces the first occurrence.

tolower(x) convert to lowercase

toupper(x) convert to uppercase

match(x, table) a vector of the positions of first matches for the elements of x among table

x %in% table id. but returns a logical vector

pmatch(x, table) partial matches for the elements of x among table

nchar(x) number of characters

Dates and Times

The class Date has dates without times. POSIXct has dates and times, including time zones. Comparisons (e.g. `>`, `seq()`, and `difftime()`) are useful. Date also allows `+` and `-`. `?DateTimeClasses` gives more information. See also package `chron`.

as.Date(s) and **as.POSIXct(s)** convert to the respective class; `format(dt)` converts to a string representation. The default string format is "2001-02-21". These accept a second argument to specify a format for conversion. Some common formats are:

`%a, %A` Abbreviated and full weekday name.
`%b, %B` Abbreviated and full month name.
`%d` Day of the month (01–31).
`%H` Hours (00–23).
`%I` Hours (01–12).
`%j` Day of year (001–366).
`%m` Month (01–12).
`%M` Minute (00–59).
`%p` AM/PM indicator.
`%S` Second as decimal number (00–61).
`%U` Week (00–53); the first Sunday as day 1 of week 1.
`%w` Weekday (0–6, Sunday is 0).
`%W` Week (00–53); the first Monday as day 1 of week 1.
`%y` Year without century (00–99). Don't use.
`%Y` Year with century.
`%z` (output only.) Offset from Greenwich; -0800 is 8 hours west of.
`%Z` (output only.) Time zone as a character string (empty if not available).

Where leading zeros are shown they will be used on output but are optional on input. See `?strftime`.

Plotting

plot(x) plot of the values of x (on the y-axis) ordered on the x-axis

plot(x, y) bivariate plot of x (on the x-axis) and y (on the y-axis)

hist(x) histogram of the frequencies of x

barplot(x) histogram of the values of x; use `horiz=FALSE` for horizontal bars

dotchart(x) if x is a data frame, plots a Cleveland dot plot (stacked plots line-by-line and column-by-column)

pie(x) circular pie-chart

boxplot(x) "box-and-whiskers" plot

sunflowerplot(x, y) id. than `plot()` but the points with similar coordinates are drawn as flowers which petal number represents the number of points

stripplot(x) plot of the values of x on a line (an alternative to `boxplot()` for small sample sizes)

coplot(x~y | z) bivariate plot of x and y for each value or interval of values of z

interaction.plot(f1, f2, y) if f1 and f2 are factors, plots the means of y (on the y-axis) with respect to the values of f1 (on the x-axis) and of f2 (different curves); the option `fun` allows to choose the summary statistic of y (by default `fun=mean`)

matplot(x,y) bivariate plot of the first column of x vs. the first one of y, the second one of x vs. the second one of y, etc.

fourfoldplot(x) visualizes, with quarters of circles, the association between two dichotomous variables for different populations (x must be an array with `dim=c(2, 2, k)`, or a matrix with `dim=c(2, 2)` if `k = 1`)

assocplot(x) Cohen-Friendly graph showing the deviations from independence of rows and columns in a two dimensional contingency table

mosaicplot(x) ‘mosaic’ graph of the residuals from a log-linear regression of a contingency table

pairs(x) if x is a matrix or a data frame, draws all possible bivariate plots between the columns of x

plot.ts(x) if x is an object of class "ts", plot of x with respect to time, x may be multivariate but the series must have the same frequency and dates

ts.plot(x) id. but if x is multivariate the series may have different dates and must have the same frequency

qqnorm(x) quantiles of x with respect to the values expected under a normal law

qqplot(x, y) quantiles of y with respect to the quantiles of x

contour(x, y, z) contour plot (data are interpolated to draw the curves), x and y must be vectors and z must be a matrix so that `dim(z)=c(length(x), length(y))` (x and y may be omitted)

filled.contour(x, y, z) id. but the areas between the contours are coloured, and a legend of the colours is drawn as well

image(x, y, z) id. but with colours (actual data are plotted)

persp(x, y, z) id. but in perspective (actual data are plotted)

stars(x) if x is a matrix or a data frame, draws a graph with segments or a star where each row of x is represented by a star and the columns are the lengths of the segments

symbols(x, y, ...) draws, at the coordinates given by x and y, symbols (circles, squares, rectangles, stars, thermometres or “boxplots”) which sizes, colours ... are specified by supplementary arguments

termpplot(mod.obj) plot of the (partial) effects of a regression model (`mod.obj`)

The following parameters are common to many plotting functions:

add=FALSE if TRUE superposes the plot on the previous one (if it exists)

axes=TRUE if FALSE does not draw the axes and the box

type="p" specifies the type of plot, "p": points, "l": lines, "b": points connected by lines, "o": id. but the lines are over the points, "h": vertical lines, "s": steps, the data are represented by the top of the vertical lines, "S": id. but the data are represented by the bottom of the vertical lines

xlim=, **ylim=** specifies the lower and upper limits of the axes, for example with `xlim=c(1, 10)` or `xlim=range(x)`

xlab=, **ylab=** annotates the axes, must be variables of mode character

main= main title, must be a variable of mode character

sub= sub-title (written in a smaller font)

Low-level plotting commands

points(x, y) adds points (the option `type=` can be used)

lines(x, y) id. but with lines

text(x, y, labels, ...) adds text given by labels at coordinates (x,y); a typical use is: `plot(x, y, type="n"); text(x, y, names)`

mtext(text, side=3, line=0, ...) adds text given by text in the margin specified by side (see `axis()` below); line specifies the line from the plotting area

segments(x0, y0, x1, y1) draws lines from points (x0,y0) to points (x1,y1)

arrows(x0, y0, x1, y1, angle= 30, code=2) id. with arrows at points (x0,y0) if code=2, at points (x1,y1) if code=1, or both if code=3; angle controls the angle from the shaft of the arrow to the edge of the arrow head

abline(a,b) draws a line of slope b and intercept a

abline(h=y) draws a horizontal line at ordinate y

abline(v=x) draws a vertical line at abcissa x

abline(lm.obj) draws the regression line given by lm.obj

rect(x1, y1, x2, y2) draws a rectangle which left, right, bottom, and top limits are x1,x2,y1, and y2, respectively

polygon(x, y) draws a polygon linking the points with coordinates given by x and y

legend(x, y, legend) adds the legend at the point (x,y) with the symbols given by legend

title() adds a title and optionally a sub-title

axis(side, vect) adds an axis at the bottom (side=1), on the left (2), at the top (3), or on the right (4); vect (optional) gives the abcissa (or ordinates) where tick-marks are drawn

rug(x) draws the data x on the x-axis as small vertical lines

locator(n, type="n", ...) returns the coordinates (x,y) after the user has clicked n times on the plot with the mouse; also draws symbols (type="p") or lines (type="l") with respect to optional graphic parameters (...); by default nothing is drawn (type="n")

Graphical parameters

These can be set globally with `par(...)`; many can be passed as parameters to plotting commands.

adj controls text justification (0 left-justified, 0.5 centred, 1 right-justified)

bg specifies the colour of the background (ex. : `bg="red", bg="blue", ...` the list of the 657 available colours is displayed with `colors()`)

bty controls the type of box drawn around the plot, allowed values are: "o", "l", "7", "c", "u" ou "] "(the box looks like the corresponding character); if `bty="n"` the box is not drawn

cex a value controlling the size of texts and symbols with respect to the default; the following parameters have the same control for numbers on the axes, `cex.axis`, the axis labels, `cex.lab`, the title, `cex.main`, and the sub-title, `cex.sub`

col controls the color of symbols and lines; use color names: "red", "blue" see `colors()` or as "#RRGGBB"; see `rgb()`, `hsv()`, `gray()`, and `rainbow()`; as for cex there are: `col.axis`, `col.lab`, `col.main`, `col.sub`

font an integer which controls the style of text (1: normal, 2: italics, 3: bold, 4: bold italics); as for cex there are: `font.axis`, `font.lab`, `font.main`, `font.sub`

las an integer which controls the orientation of the axis labels (0: parallel to the axes, 1: horizontal, 2: perpendicular to the axes, 3: vertical)

lty controls the type of lines, can be an integer or string (1: "solid", 2: "dashed", 3: "dotted", 4: "dotdash", 5: "longdash", 6: "twodash", or a string of up to eight characters (between "0" and "9") which specifies alternatively the length, in points or pixels, of the drawn elements and the blanks, for example `lty="44"` will have the same effect than `lty=2`

lwd a numeric which controls the width of lines, default 1

mar a vector of 4 numeric values which control the space between the axes and the border of the graph of the form `c(bottom, left, top, right)`, the default values are `c(5.1, 4.1, 4.1, 2.1)`

mfcol a vector of the form `c(nr,nc)` which partitions the graphic window as a matrix of nr lines and nc columns, the plots are then drawn in columns

mfrow id. but the plots are drawn by row

pch controls the type of symbol, either an integer between 1 and 25, or any single character within "

1○ 2△ 3+ 4× 5◊ 6▽ 7⊗ 8* 9⊕ 10⊖ 11⊗ 12⊖ 13⊗ 14⊖ 15■

16● 17▲ 18◆ 19● 20● 21○ 22□ 23◊ 24△ 25▽ * . · X X a a ? ?

ps an integer which controls the size in points of texts and symbols

pty a character which specifies the type of the plotting region, "s": square, "m": maximal

tck a value which specifies the length of tick-marks on the axes as a fraction of the smallest of the width or height of the plot; if `tck=1` a grid is drawn

tcl a value which specifies the length of tick-marks on the axes as a fraction of the height of a line of text (by default `tcl=-0.5`)

xaxt if `xaxt="n"` the x-axis is set but not drawn (useful in conjunction with `axis(side=1, ...)`)

yaxt if `yaxt="n"` the y-axis is set but not drawn (useful in conjunction with `axis(side=2, ...)`)

Lattice (Trellis) graphics

xyplot(~x) bivariate plots (with many functionalities)

barchart(y~x) histogram of the values of y with respect to those of x

dotplot(y~x) Cleveland dot plot (stacked plots line-by-line and column-by-column)

densityplot(~x) density functions plot

histogram(~x) histogram of the frequencies of x

bwplot(y~x) “box-and-whiskers” plot

qqmath(~x) quantiles of x with respect to the values expected under a theoretical distribution

stripplot(y~x) single dimension plot, x must be numeric, y may be a factor

qq(y~x) quantiles to compare two distributions, x must be numeric, y may be numeric, character, or factor but must have two ‘levels’

spplot(~x) matrix of bivariate plots

parallel(~x) parallel coordinates plot

levelplot(z~x*y|g1*g2) coloured plot of the values of z at the coordinates given by x and y (x, y and z are all of the same length)

wireframe(z~x*y|g1*g2) 3d surface plot

cloud(z~x*y|g1*g2) 3d scatter plot

1 Sannolikhetslära

1.1 Några diskreta fördelningar

- Binomialfördelning

$$X \sim \text{Bin}(n, p)$$

$$p_X(k) = \binom{n}{k} p^k (1-p)^{n-k}, \quad k = 0, 1, \dots, n$$

$$\text{E}[X] = np, \quad \text{var}(X) = np(1-p), \quad G_X(s) = (1 + p(s-1))^n$$

- Poissonfördelning

$$X \sim \text{Po}(\mu)$$

$$p_X(k) = \frac{\mu^k}{k!} e^{-\mu}, \quad k = 0, 1, 2, \dots$$

$$\text{E}[X] = \mu, \quad \text{var}(X) = \mu, \quad G_X(s) = e^{(s-1)\mu}$$

- Hypergeometriskfördelning

$$X \sim \text{Hyp}(N, n, p)$$

$$p_X(k) = \frac{\binom{Np}{k} \binom{N(1-p)}{n-k}}{\binom{N}{n}}, \quad k = 0, 1, \dots, n$$

$$\text{E}[X] = np, \quad \text{var}(X) = \frac{N-n}{N-1} np(1-p)$$

- Geometrisk fördelning

$$X \sim \text{Ge}(p)$$

$$p_X(k) = (1-p)^k p, \quad k = 0, 1, 2, \dots$$

$$\text{E}[X] = \frac{1-p}{p}, \quad \text{var}(X) = \frac{1-p}{p^2}, \quad G_X(s) = \frac{p}{1-(1-p)s}$$

- För första-gången-fördelning

$$X \sim Ffg(p)$$

$$p_X(k) = (1-p)^{k-1} p, \quad k = 1, 2, 3, \dots$$

$$\text{E}[X] = \frac{1}{p}, \quad \text{var}(X) = \frac{1-p}{p^2}, \quad G_X(s) = \frac{sp}{1-(1-p)s}$$

- Negativ Binomialfördelning

$$X \sim \text{NB}(r, p)$$

$$p_X(k) = \binom{k+r-1}{r-1} p^r (1-p)^{k-r} \quad k = 0, 1, 2, \dots$$

$$\text{E}[X] = \frac{r(1-p)}{p}, \quad \text{var}(X) = \frac{r(1-p)}{p}, \quad G_X(s) = \left(\frac{p}{1-(1-p)s} \right)^r$$

1.2 Några kontinuerliga fördelningar

- Likformig (rektangulär) fördelning på intervallet (a,b)

$$X \sim U(a, b)$$

$$f_X(x) = \frac{1}{b-a}, \quad a \leq x \leq b$$

$$\text{E}[X] = \frac{a+b}{2}, \quad \text{var}(X) = \frac{(b-a)^2}{12}, \quad M_X(p) = \frac{e^{pb} - e^{pa}}{p(b-a)}$$

- Exponentialfördelning

$$X \sim \text{Exp}(\lambda),$$

där λ betecknar intensiteten. Ibland används väntevärdet $\mu = \frac{1}{\lambda}$ som parameter.

$$f_X(x) = \lambda e^{-\lambda x}, \quad x \geq 0$$

$$\text{E}[X] = \frac{1}{\lambda}, \quad \text{var}(X) = \frac{1}{\lambda^2}, \quad M_X(p) = \frac{\lambda}{\lambda - p}, \quad \lambda > p.$$

- Normalfördelning

$$X \sim N(\mu, \sigma)$$

$$f_X(x) = \frac{1}{\sqrt{2\pi}\sigma} \exp \left\{ -\frac{(x-\mu)^2}{2\sigma^2} \right\}, \quad -\infty < x < +\infty$$

- χ^2 -fördelning

$$Y \sim \chi^2(n)$$

Uppkomst: Om X_1, \dots, X_n är oberoende, var och en $N(0, 1)$, gäller att $Y = X_1^2 + \dots + X_n^2$ får en χ^2 fördelning med n frihetsgrader.

$$f_Y(x) = \frac{x^{(n/2)-1} e^{-x/2}}{2^{(n/2)} \Gamma(n/2)}, \quad x \geq 0,$$

där $\Gamma(\cdot)$ är gammafunktionen

$$\Gamma(c) = \int_0^\infty x^{c-1} e^{-x} dx, \quad \text{där } c > 0.$$

$$\text{E}[Y] = n, \quad \text{var}(Y) = 2n, \quad M_Y(p) = \frac{1}{(1-p)^{n/2}}, \quad p < 1$$