Week3

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Predicting with trees

Pro:

- facile da interpretare
- funziona bene con nonlinear settings

con:

- difficile stimare incertezza

Basic algorithm

1. start con un unico gruppo
2. trovo la variabile che separa meglio glo outcomes
3. divide in leaves attraverso un node

Measure of impurity

1.misclassification error se per esempio c'è una leaf in cui quasi tutti gli stati votano per barak obama il misclassification error è 1-la probabilità che tu voti per barack obama

errori/totale

- 0 perfect purity
- 0.5 no purity

2.gini index 1 - sum(Pkˆ2) dove k è la classe

- 0 perfect purity
- 0.5 no purity

3. deviance/information gain è la probabilità di essee assegnato a una classe k e leaf m, per lgo2 la proabilità di essee assegnato a una classe k e leaf m

- 0 perfect purity
- 1 no purity

al minuto 6.16,esempio

Esempio : iris data

```
data(iris); library(ggplot2)
names(iris)
```

```
## [1] "Sepal.Length" "Sepal.Width"  "Petal.Length" "Petal.Width"  "Species"
```

```
table(iris$Species)
```

```
##
##     setosa versicolor  virginica
##         50         50         50
```

```
library(caret); library(kernlab);
```

```
## Loading required package: lattice
```

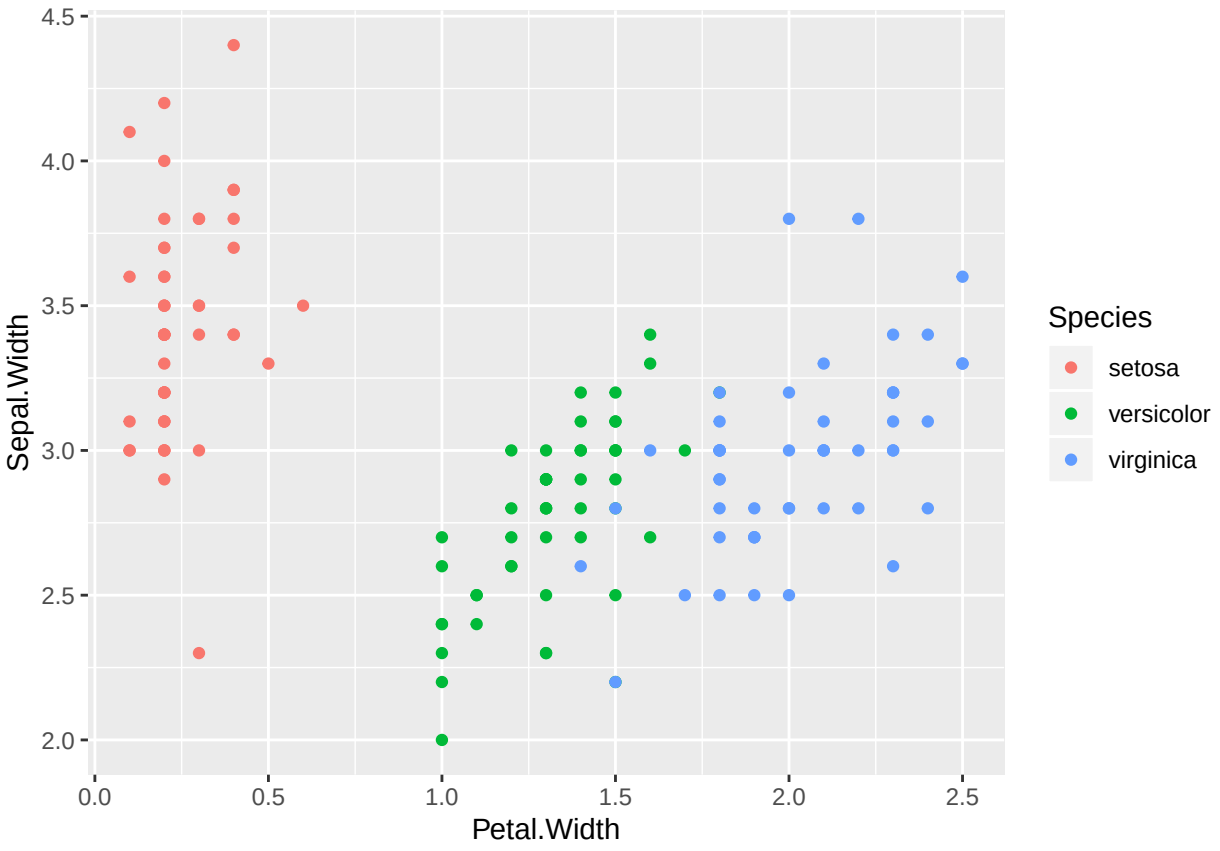
```
##
## Attaching package: 'kernlab'
```

```
## The following object is masked from 'package:ggplot2':
##
##     alpha
```

```
inTrain <- createDataPartition(y = iris$Species, p = 0.8 , list = FALSE)
training <- iris[inTrain,]
testing <- iris[-inTrain,]
dim(training)
```

```
## [1] 120   5
```

```
qplot(Petal.Width, Sepal.Width, colour = Species, data = iris)
```

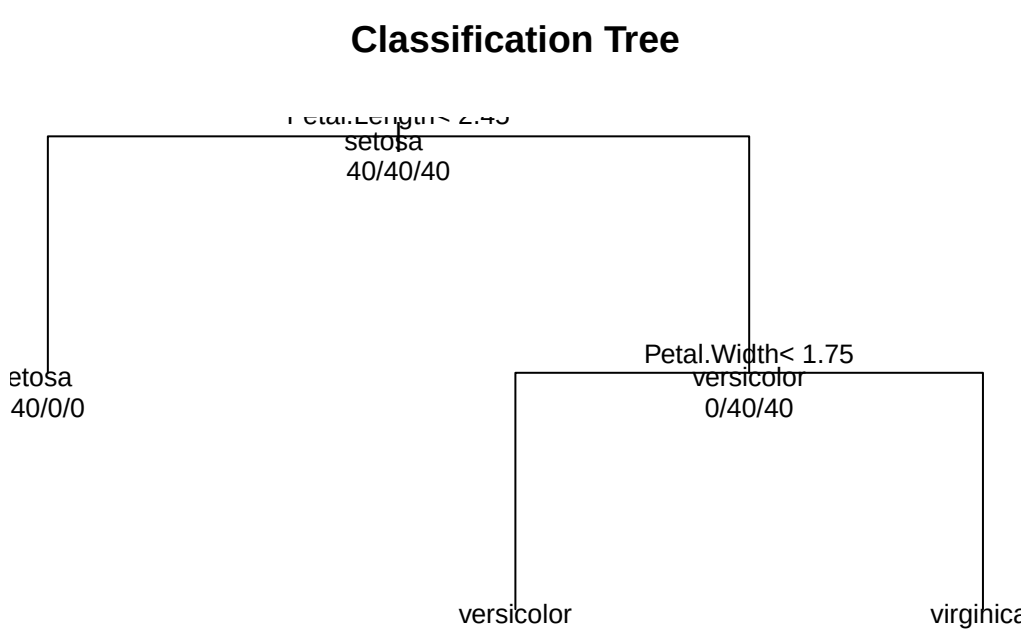



```
## rpart package per regression and classification trees
modFit <- train(Species ~ . , method = "rpart" , data = training)
print(modFit$finalModel)
```

```
## n= 120
##
## node), split, n, loss, yval, (yprob)
##       * denotes terminal node
##
## 1) root 120 80 setosa (0.33333333 0.33333333 0.33333333)
##   2) Petal.Length< 2.45 40  0 setosa (1.00000000 0.00000000 0.00000000) *
##   3) Petal.Length>=2.45 80 40 versicolor (0.00000000 0.50000000 0.50000000)
##     6) Petal.Width< 1.75 43  4 versicolor (0.00000000 0.90697674 0.09302326) *
##     7) Petal.Width>=1.75 37  1 virginica (0.00000000 0.02702703 0.97297297) *
```

n = n°di nodi 2. se la lunghezza dei petali < 2.45 ho il 100% di setosa 3. se maggiore di 2,45 50% versicolor 50% virginica ecc... si può fare un plot

```
plot(modFit$finalModel, uniform = TRUE,
     main = "Classification Tree")
text(modFit$finalModel, use.n = TRUE, all = TRUE, cex = .8)
```

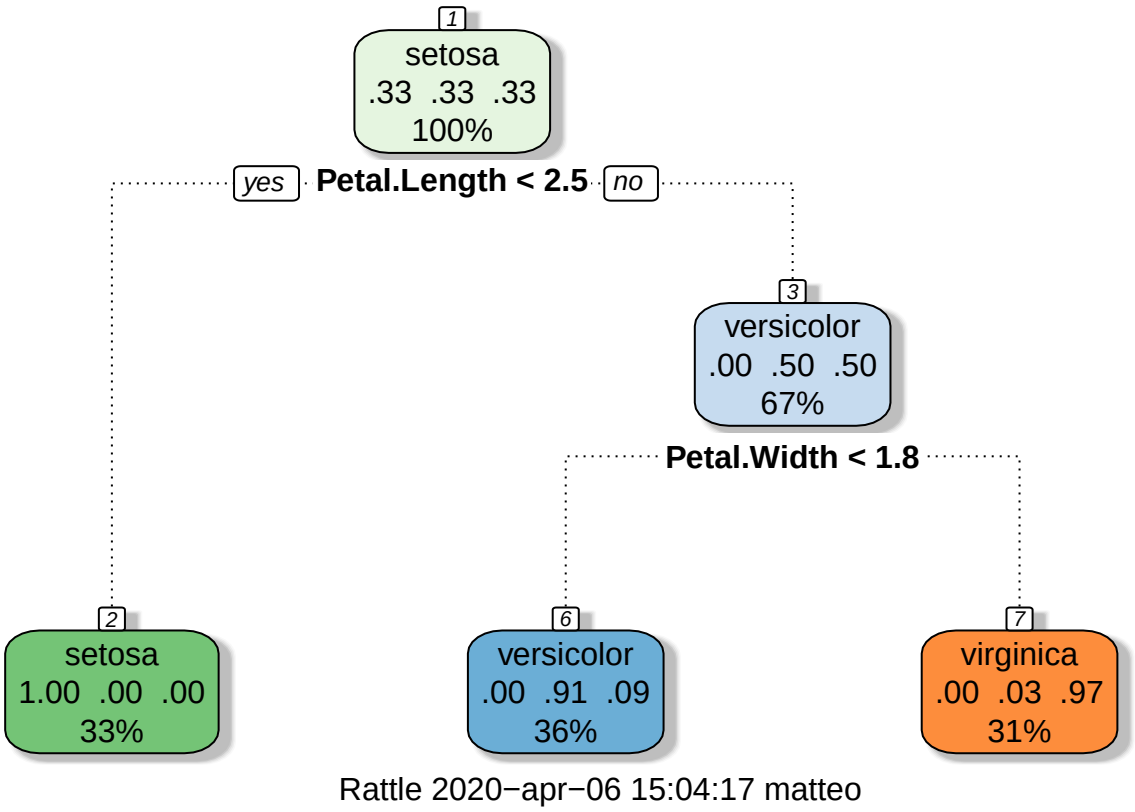


una visualizzazone migliore

```
library(rattle)
```

```
## Rattle: A free graphical interface for data science with R.
## Version 5.3.0 Copyright (c) 2006-2018 Togaware Pty Ltd.
## Type 'rattle()' to shake, rattle, and roll your data.
```

```
fancyRpartPlot(modFit$finalModel)
```



Predict new values utiliziammo il test set e facciamo delle previsioni

```
library(caret); library(kernlab);
pred <- predict(modFit, newdata = testing)
confusionMatrix(testing$Species, pred)
```

```
## Confusion Matrix and Statistics
##
##             Reference
## Prediction   setosa versicolor virginica
##   setosa         10          0         0
##   versicolor      0         10         0
##   virginica       0          1         9
##
## Overall Statistics
##
##                Accuracy : 0.9667
##                  95% CI : (0.8278, 0.9992)
##     No Information Rate : 0.3667
##     P-Value [Acc > NIR] : 4.476e-12
##
##                   Kappa : 0.95
##
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
```

```
##
##                      Class: setosa Class: versicolor Class: virginica
## Sensitivity                 1.0000            0.9091           1.0000
## Specificity                 1.0000            1.0000           0.9524
## Pos Pred Value              1.0000            1.0000           0.9000
## Neg Pred Value              1.0000            0.9500           1.0000
## Prevalence                  0.3333            0.3667           0.3000
## Detection Rate              0.3333            0.3333           0.3000
## Detection Prevalence        0.3333            0.3333           0.3333
## Balanced Accuracy           1.0000            0.9545           0.9762
```

Bagging

bootstrap aggregation Quando si fittano modelli complicati, se si mediano questi insieme per ottenere un miglior bilanciamento dei bias e delle varianze l'idea è:

- Fare resample del dataset e ricalcolo la funzione di previsione
- si ha lo stesso bias che si avrebbe fittando ogni modello singolarmente ma si riduce la variabilità
- utile per non linear

ozone data

```
install.packages("https://cran.r-project.org/src/contrib/Archive/ElemStatLearn/ElemStatLearn_2012.04-0.
```

```
## Installing package into '/home/matteo/R/x86_64-pc-linux-gnu-library/3.6'
## (as 'lib' is unspecified)
```

```
library(ElemStatLearn)
data(ozone, package = "ElemStatLearn")
ozone <- ozone[order(ozone$ozone),]
head(ozone)
```

```
##     ozone radiation temperature wind
## 17      1         8          59  9.7
## 19      4        25          61  9.7
## 14      6        78          57 18.4
## 45      7        48          80 14.3
## 106     7        49          69 10.3
## 7       8        19          61 20.1
```

Cerco di predirre la temperatura in funzione di ozone

Bagged Loess

```
## creo una matrice
ll <- matrix(NA, nrow = 10, ncol = 155)
## faccio un resample dei dati 10 volte
```

```
for(i in 1:10){
    ss <- sample(1:dim(ozone)[1], replace = T)
    ## creo un nuvo set per ogni loop

}
```

Lungo e sbatti usiamo le fun di caret leggi bene la doc per usarlo l'idea è:

- prendere il predittore e metterlo in un data frame
- la variabile da predire metterla in un vettore
- li passo alla funzione bag, B è il numero di resample
- bagcontrol da le caratterstiche per il fit
- fit richiama train fun
- predict predice i valori basandosi sul fit
- aggregate mette insieme i B modelli previsionali fatti da fit e predict e trova la media

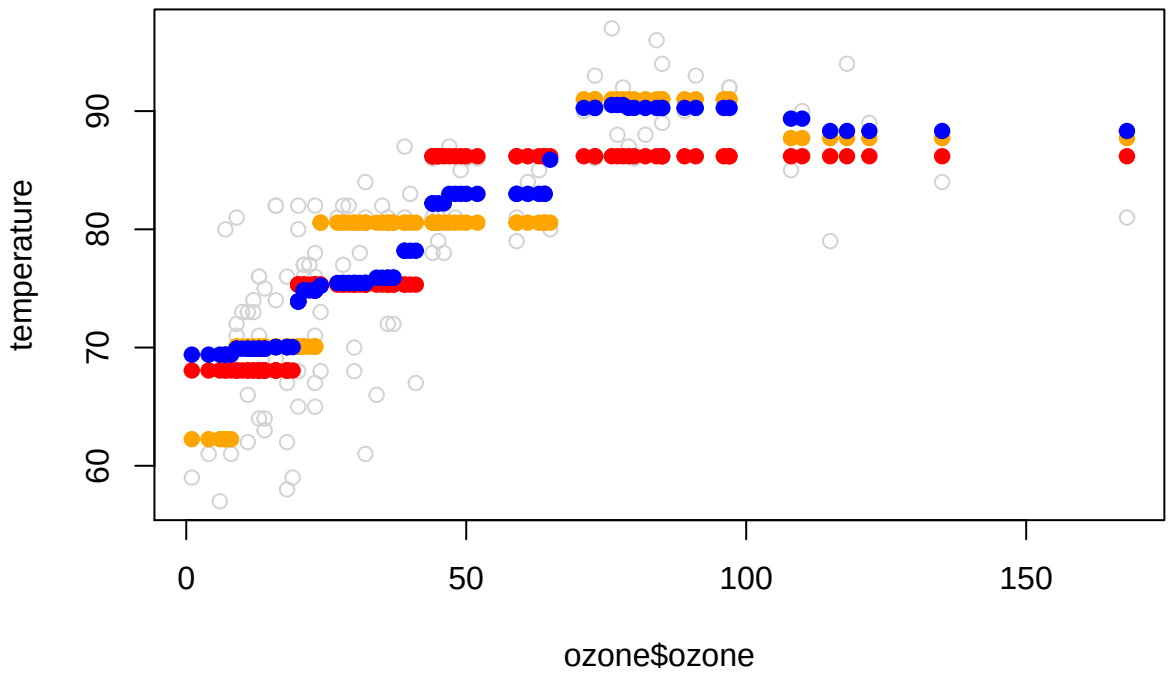
```
predictors <- data.frame(ozone = ozone$ozone)
temperature <- ozone$temperature

treebag <- bag(predictors, temperature , B = 10,
               bagControl = bagControl(fit = ctreeBag$fit,
                                       predict = ctreeBag$pred,
                                       aggregate = ctreeBag$aggregate))
```

```
## Warning: executing %dopar% sequentially: no parallel backend registered
```

plottiamo i risultati

```
plot(ozone$ozone, temperature, col = "lightgrey")
points(ozone$ozone, predict(treebag$fits[[1]]$fit, predictors),pch =19 , col = "red")
points(ozone$ozone, predict(treebag$fits[[2]]$fit, predictors),pch =19 , col = "orange")
points(ozone$ozone, predict(treebag, predictors),pch =19 , col = "blue")
```



I rossi sono il fit di una singol conditional regression tree la media dei 10 regression tree è quella blu

Random Forest

è un estensione del bagging per i regression tree l'idea è:

- Bootstrap samples, quindi faccio resample dei dati
- ad ogni split, bootstrap variables
- faccio diversi alberi e faccio la media

Pro:

- Accuracy

Con:

- speed
- interpretabilità, molti alberi con molti bootstrap tra sample and nodes
- overfitting

esempio

```
data(iris); library(ggplot2);
inTrain <- createDataPartition( y = iris$Species, p=0.7 , list = FALSE)
training <- iris[inTrain, ]
testing <- iris[-inTrain,]
```

```
library(caret)
## prox da più info
modFit <- train( Species ~ . , data = training , method = "rf",
                 prox = TRUE)
modFit
```

```
## Random Forest
##
## 105 samples
##   4 predictor
##   3 classes: 'setosa', 'versicolor', 'virginica'
##
## No pre-processing
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 105, 105, 105, 105, 105, 105, ...
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##   2     0.9372542  0.9047053
##   3     0.9371106  0.9044622
##   4     0.9351691  0.9014606
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 2.
```

getting a single tree

```
library(randomForest)
```

```
## randomForest 4.6-14
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
##
## Attaching package: 'randomForest'
```

```
## The following object is masked from 'package:rattle':
##
##     importance
```

```
## The following object is masked from 'package:ggplot2':
##
##     margin
```

```
## k è  quale albero
getTree(modFit$finalModel, k = 2);
```

```
##    left daughter right daughter split var split point status prediction
## 1              2              3         3        2.60      1          0
## 2              0              0         0        0.00     -1          1
## 3              4              5         3        4.95      1          0
## 4              6              7         3        4.85      1          0
## 5              8              9         1        6.05      1          0
## 6             10             11         1        5.05      1          0
## 7             12             13         4        1.75      1          0
## 8             14             15         2        2.75      1          0
## 9              0              0         0        0.00     -1          3
## 10            16             17         3        3.90      1          0
## 11             0              0         0        0.00     -1          2
## 12             0              0         0        0.00     -1          2
## 13             0              0         0        0.00     -1          3
## 14            18             19         2        2.45      1          0
## 15             0              0         0        0.00     -1          3
## 16             0              0         0        0.00     -1          2
## 17             0              0         0        0.00     -1          3
## 18             0              0         0        0.00     -1          3
## 19             0              0         0        0.00     -1          2
```

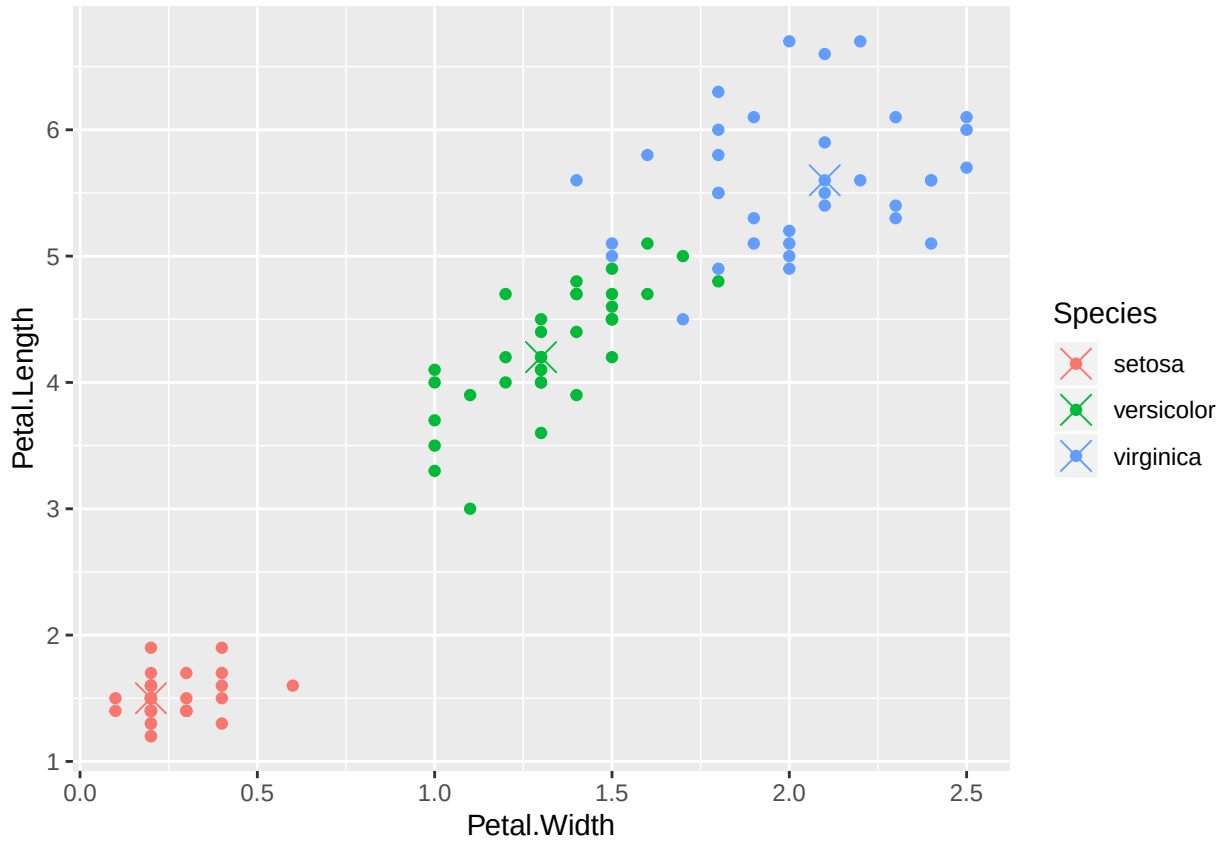
Ogni riga è uno split

Class centers

si usa per vedere quale è il centro della class prediction

```
## vado a vedere il confronto tra length e width
irisP <- classCenter(training[,c(3,4)], training$Species,
                     modFit$finalModel$prox)
## lo converto in dataframe
irisP <- as.data.frame(irisP)
## aggiungo la colonna specie a cui appartengono nel dataframe
irisP$Species <- rownames(irisP)

p <- qplot(Petal.Width, Petal.Length , col = Species , data = training)
p + geom_point(aes(x = Petal.Width, y = Petal.Length, col = Species),
                   size = 5 , shape = 4 ,  data = irisP)
```



Predict new values

)

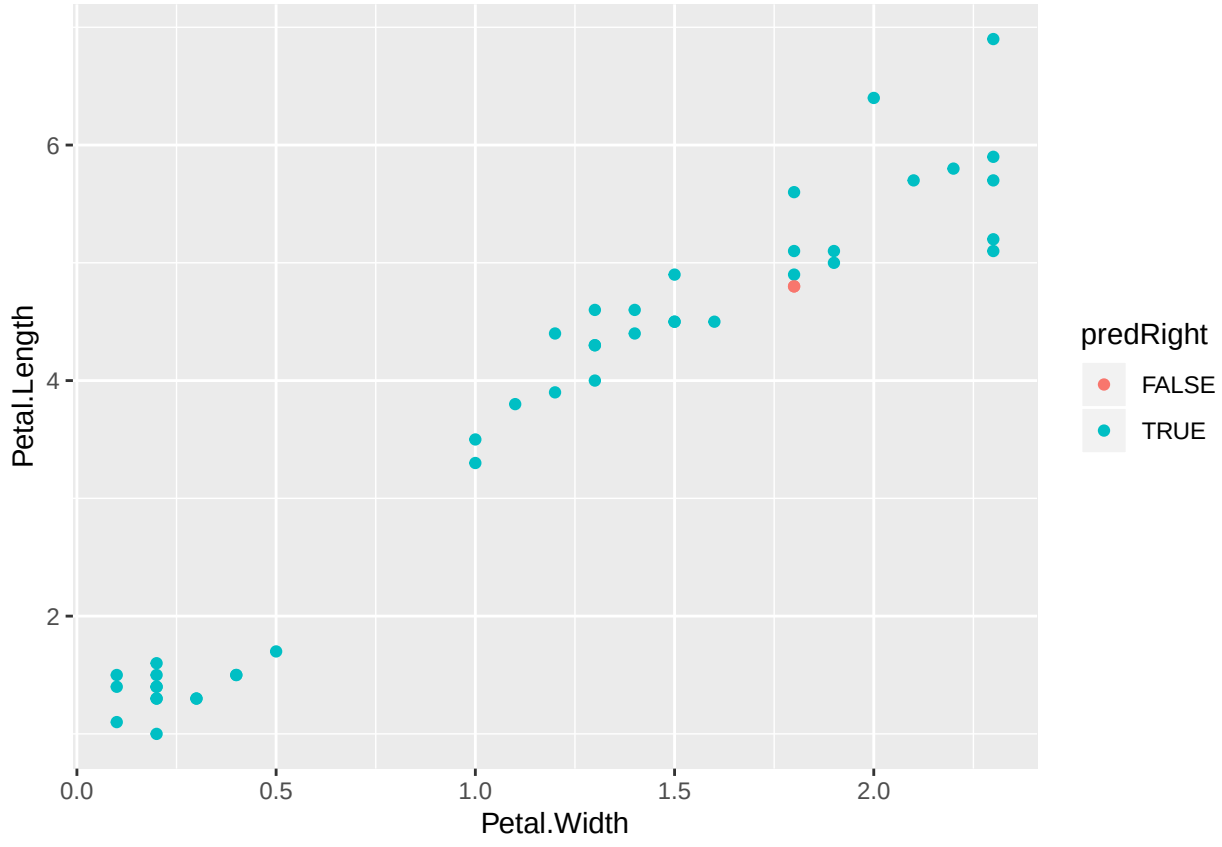
```
pred <- predict(modFit, testing)
## crea variabile true o false per dopo
testing$predRight <- pred == testing$Species
confusionMatrix(pred, testing$Species)
```

```
## Confusion Matrix and Statistics
##
##             Reference
## Prediction   setosa versicolor virginica
##   setosa         15          0         0
##   versicolor      0         15         2
##   virginica       0          0        13
##
## Overall Statistics
##
##                Accuracy : 0.9556
##                  95% CI : (0.8485, 0.9946)
##     No Information Rate : 0.3333
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.9333
```

```
##
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##                      Class: setosa Class: versicolor Class: virginica
## Sensitivity                 1.0000            1.0000           0.8667
## Specificity                 1.0000            0.9333           1.0000
## Pos Pred Value              1.0000            0.8824           1.0000
## Neg Pred Value              1.0000            1.0000           0.9375
## Prevalence                  0.3333            0.3333           0.3333
## Detection Rate              0.3333            0.3333           0.2889
## Detection Prevalence        0.3333            0.3778           0.2889
## Balanced Accuracy           1.0000            0.9667           0.9333
```

Look at the false prediction

```
qplot(Petal.Width, Petal.Length , colour = predRight ,
      data = testing)
```



Boosting

è il miglior classificatore che si possa usare l'idea è:

- prendere la maggior parte possibile di predittori deboli
- pesarli e sommarli
- ottenendo un miglior predittore

boosting:

- inizio con un set di classificatori, tutti i possibili tree, tutti i possibili regression model eccc *creare un classificatore che li combina tutti
- l'idea è minimizzare l'errore nel training set ad ogni iterata
- calcola i pesi basandsi sull'errore
- aumenta i pesi di quelli che ho sbagliato

Adaboost è il più famoso esempio

Wage esempio

```
library(ISLR); data(Wage); library(ggplot2); library(caret)
Wage <- subset(Wage , select = -c(logwage))
inTrain <- createDataPartition( y = Wage$wage, p = 0.7, list = FALSE)
training <- Wage[inTrain, ]
testing <- Wage[-inTrain,]
```

Fit the model

```
modFit <- train(wage ~ . , method = "gbm", data = training,
                verbose = FALSE)
```

```
## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 14: region2. Middle Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 15: region3. East North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 16: region4. West North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 17: region5. South Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 18: region6. East South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 19: region7. West South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 20: region8. Mountain has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 21: region9. Pacific has no variation.
```

```
## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 14: region2. Middle Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 15: region3. East North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 16: region4. West North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 17: region5. South Atlantic has no variation.

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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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```

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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 14: region2. Middle Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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```

```
## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 16: region4. West North Central has no variation.
```

```
## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 17: region5. South Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 20: region8. Mountain has no variation.

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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 17: region5. South Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 18: region6. East South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 19: region7. West South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 20: region8. Mountain has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 21: region9. Pacific has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 14: region2. Middle Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 15: region3. East North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 16: region4. West North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 17: region5. South Atlantic has no variation.
```

```
## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 18: region6. East South Central has no variation.

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## "bernoulli", : variable 19: region7. West South Central has no variation.

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## "bernoulli", : variable 20: region8. Mountain has no variation.

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## "bernoulli", : variable 17: region5. South Atlantic has no variation.

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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 21: region9. Pacific has no variation.

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## "bernoulli", : variable 14: region2. Middle Atlantic has no variation.
```

```
## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 15: region3. East North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 16: region4. West North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 17: region5. South Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 18: region6. East South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 19: region7. West South Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 20: region8. Mountain has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 21: region9. Pacific has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 14: region2. Middle Atlantic has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 15: region3. East North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 16: region4. West North Central has no variation.

## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
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## "bernoulli", : variable 15: region3. East North Central has no variation.
```

```
## Warning in (function (x, y, offset = NULL, misc = NULL, distribution =
## "bernoulli", : variable 16: region4. West North Central has no variation.

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## "bernoulli", : variable 18: region6. East South Central has no variation.

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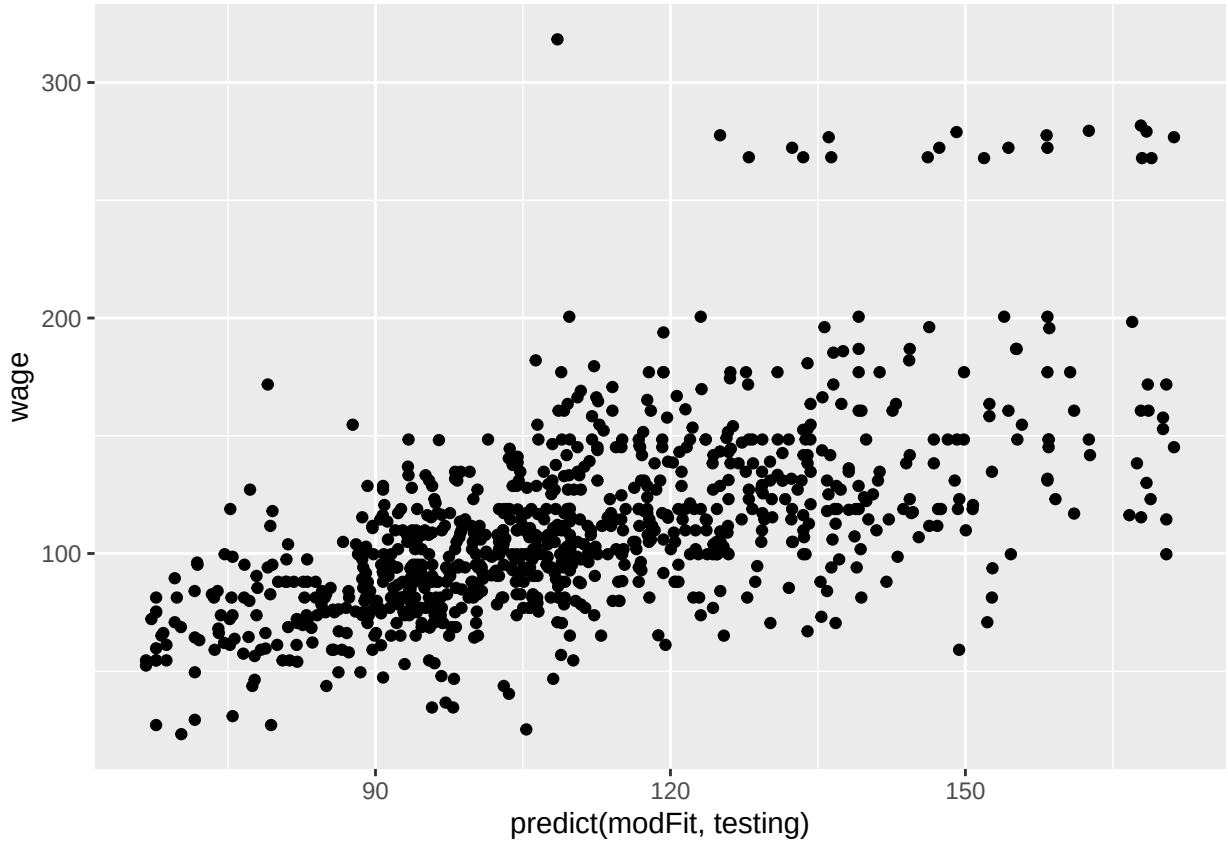
```

```
print(modFit)
```

```
## Stochastic Gradient Boosting
##
## 2102 samples
##    9 predictor
##
## No pre-processing
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 2102, 2102, 2102, 2102, 2102, 2102, ...
## Resampling results across tuning parameters:
##
##   interaction.depth  n.trees  RMSE      Rsquared   MAE
##   1                   50      35.61238  0.3014476  24.02677
##   1                  100      35.07016  0.3115005  23.59275
##   1                  150      35.00702  0.3129259  23.55384
##   2                   50      35.06088  0.3128979  23.53472
##   2                  100      34.93813  0.3157573  23.50469
##   2                  150      35.02264  0.3131879  23.61197
##   3                   50      34.91984  0.3173147  23.44587
##   3                  100      35.06291  0.3114734  23.64062
##   3                  150      35.25680  0.3057206  23.83800
##
## Tuning parameter 'shrinkage' was held constant at a value of 0.1
##
## Tuning parameter 'n.minobsinnode' was held constant at a value of 10
## RMSE was used to select the optimal model using the smallest value.
## The final values used for the model were n.trees = 50, interaction.depth =
##  3, shrinkage = 0.1 and n.minobsinnode = 10.
```

plot the result

```
qplot(predict(modFit, testing), wage, data = testing)
```



Model based prediction

l'idea è:

- assumo che i dati seguano un modello probabilistico
- uso bayes's theorem to identify optimal classifiers

... un sacco di roba da imparare

esempio

```
library(caret); library(kernlab);
inTrain <- createDataPartition(y = iris$Species, p = 0.7 , list = FALSE)
training <- iris[inTrain,]
testing <- iris[-inTrain,]
dim(training)
```

```
## [1] 105   5
```

build predictions

```r
modlba = train(Species ~ . , method = "lda", data = training)
## naive base
modnb = train(Species ~ . , method = "nb" ,data = training)
plda = predict(modlba, testing)
pnb = predict(modnb, testing)
table(plda, pnb)
```

```
##             pnb
## plda         setosa versicolor virginica
##   setosa         15          0         0
##   versicolor      0         15         0
##   virginica       0          2        13
```