

# *Practical Session*

## Prediction Modeling using Random Forest in R

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# Introduction

# Software prerequisites

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For this tutorial, you will need to have installed R and RStudio.

---

```
install.packages(c("randomForest", "tidyverse", "caret",  
"ranger", "pmsampsize", "rms"))  
library(randomForest)  
library(tidyverse)  
library(caret)  
library(ranger)  
library(pmsampsize)  
library(rms)
```

---



# Inference vs Prediction

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$$\hat{Y} = x_1\hat{\beta}_1 + x_2\hat{\beta}_2 + \dots + x_p\hat{\beta}_p$$

- **Inference:** Estimating the effect of a variable on the outcome while adjusting for confounding.
- **Prediction:** Predicting the outcome based on a set of covariate values.

# Supervised learning

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- Training data set  $\mathcal{T}$ :  $\{(y_i, \mathbf{x}_i)\}$
- Using these data, we build a prediction model or *learner*, denoted  $\phi(\mathbf{x}, \mathcal{T})$  (e.g., decision tree, linear regression model, neural network)
- Given an input  $\mathbf{x}^*$ , a prediction is given by

$$\hat{Y}^* = \phi(\mathbf{x}^*, \mathcal{T}).$$

# Terminology

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## Basics

- Supervised learning
- Outcome
- Predictors
- Unsupervised learning

## Tree-based learning

- Classification/regression
- Decision node
- Leaf node

## Development and validation

- Predictive accuracy
- Hyperparameter tuning
- Cross-validation
- Bootstrap resampling
- Out-of-bag
- Generalization error
- Training/test sets

# Decision tree

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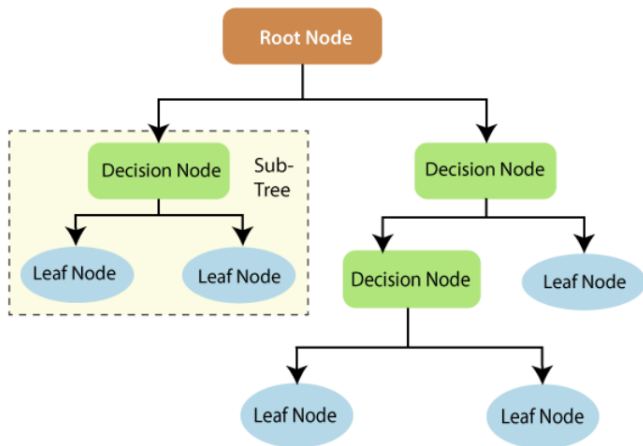
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Source: <https://www.tutorialandexample.com/decision-trees/>

# Bias, variance and model complexity

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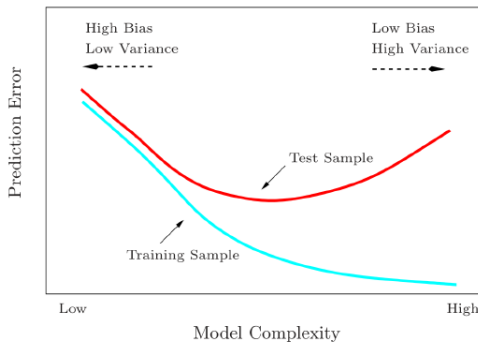
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**FIGURE 2.11.** *Test and training error as a function of model complexity.*

Source: Hastie et al. (2009)



# Goal

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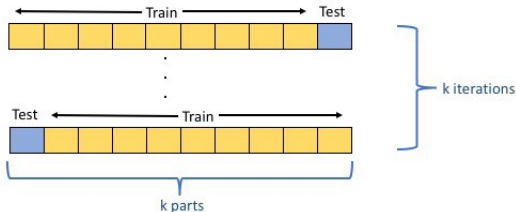
- Minimize the prediction error, i.e.,  $\mathbb{E}[(\hat{Y} - Y)^2]$
- Control for over-fitting

# Estimation of the generalization/test error

- Cross-validation
- Bootstrap resampling

## K Folds Cross Validation Method

1. Divide the sample data into  $k$  parts.
2. Use  $k-1$  of the parts for training, and 1 for testing.
3. Repeat the procedure  $k$  times, rotating the test set.
4. Determine an expected performance metric (mean square error, misclassification error rate, confidence interval, or other appropriate metric) based on the results across the iterations



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# Tree-based regression and classification

# The CART algorithm

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## Greedy algorithm:

- 1 At the root node: Scan through all inputs to find the best combination of splitting variable  $j$  and split point  $s$ .
  - Criterion for regression: Sum of squared errors
$$\sum (y_i - f(x_i))^2$$
  - Criterion for classification: Measure of node impurity (e.g., Gini index)
- 2 Partition the data into the two resulting regions and repeat the splitting process on each of the two regions, and so on.

**Question:** How large should we grow the tree? The deeper the tree is grown, the lower the bias is !

# Node impurity measures

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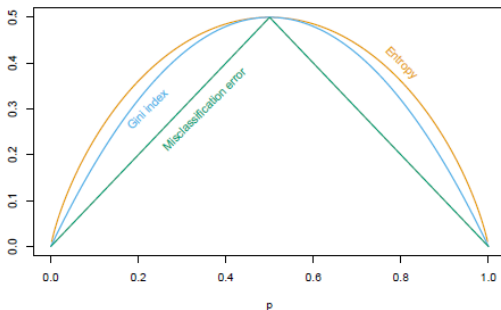
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**FIGURE 9.3.** Node impurity measures for two-class classification, as a function of the proportion  $p$  in class 2. Cross-entropy has been scaled to pass through  $(0.5, 0.5)$ .

Source: Hastie et al. (2009)

# Pros and cons of trees

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## Pros:

- Interpretability
- Requires little effort in data preparation

## Cons:

- Trees tend to be unstable, i.e., they tend to over-fit the data.
- *Bagging* averages many trees to reduce this variance.

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# Random forest

# Bagging and random forest (Breiman, 2001)

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Bagging or *bootstrap aggregation* is a variance reduction method which works well for high-variance, low-bias procedures such as trees.

- Random: random selection of samples and features
- Forest: Ensemble of tree learners



# Random forest

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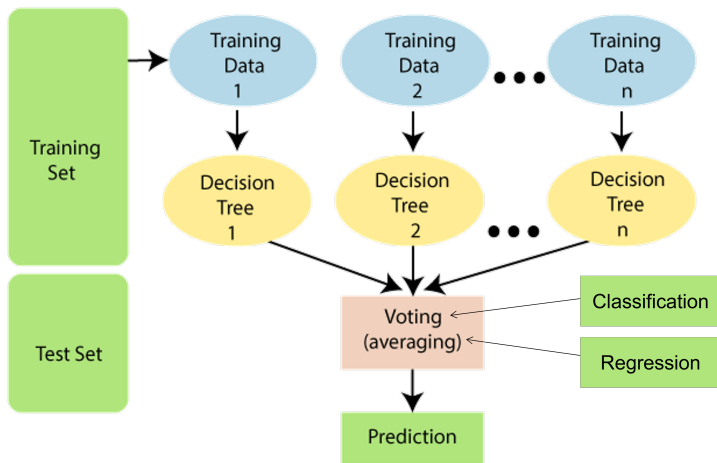
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Source: <https://www.javatpoint.com/machine-learning-random-forest-algorithm>

# Hyperparameter tuning

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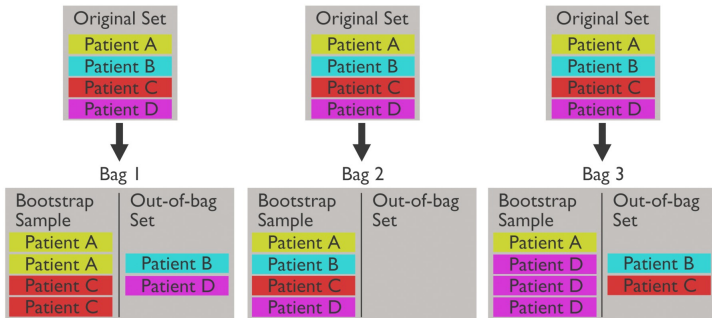
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A **hyperparameter** is a parameter of the model that is set prior to the start of the learning process.

- How many tree learners should we train? (`ntree` in `randomForest`, default is 500)
- How many features should be considered for splitting a node? (`mtry` in `randomForest`, default is  $\sqrt{p}$  for classification)
- How deep should we grow each tree? (controlled by `maxnode` and `nodesize`)

# Out-of-bag (OOB) error

Under the OOB method, the model is tested as it is being trained.



Source: [https://en.wikipedia.org/wiki/Out-of-bag\\_error](https://en.wikipedia.org/wiki/Out-of-bag_error)

# Comparison of OOB and test errors

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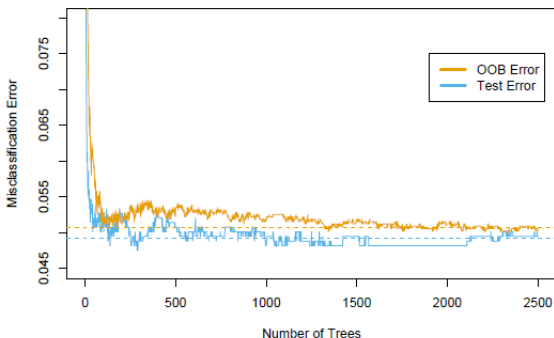
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**FIGURE 15.4.** OOB error computed on the `spam` training data, compared to the test error computed on the test set.

Source: Hastie et al. (2009)

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# Data analysis showcase

# Cardiotocography data set (Dua and Graff, 2017)

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See the markdown file.

- 2126 fetal cardiotocograms (CTGs) were automatically processed and assessed by three expert obstetricians.
- **Outcome:** Fetal state (N, S, P)
  - Normal
  - Suspect
  - Pathologic
- **Potential predictors:** 21 features, including measurements of fetal heart rate (FHR) and uterine contraction (UC)

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# Best practices for health research

# Sample size considerations

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RESEARCH ARTICLE

Open Access

## Modern modelling techniques are data hungry: a simulation study for predicting dichotomous endpoints

Tjeerd van der Ploeg<sup>1,3\*</sup>, Peter C Austin<sup>2</sup> and Ewout W Steyerberg<sup>3</sup>

“Modern modelling techniques such as [support vector machine], [neural network] and [random forest] may need over 10 times as many events per variable to achieve a stable AUC and a small optimism than classical modelling techniques such as [logistic regression].”



# Sample size considerations

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- Sample size required for classification is driven by the **number of events per predictor parameters/variables**.
- Each tree learner in the random forest incorporates complex interactions between features → Number of predictor parameters?
- Given a data set, a good practice is to first determine the budget of predictor parameters for conventional methods (regression).
- Package `pmsampsize` (Riley et al., 2020)

# Sample size considerations

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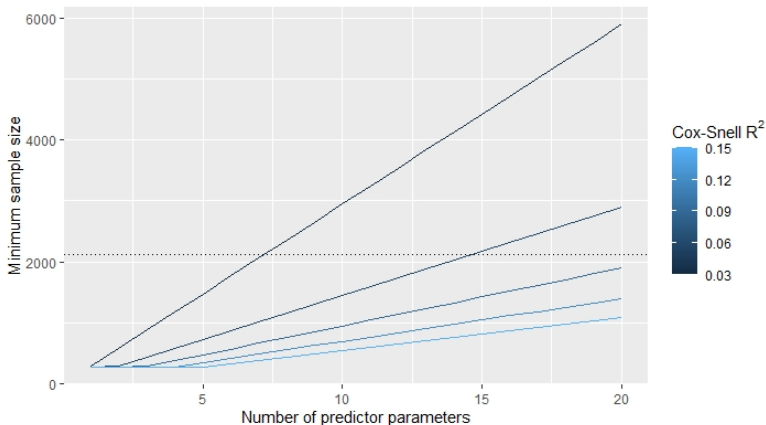
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# Selection of predictors

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“[Automated solutions] allow us not to think about the problem ” - FE Harrell

- To guard against over-fitting, avoid data-driven decisions.
  - Excluding a variable on the basis that it is non-significant.
  - “Exploratory” analyses.
- Prespecify predictor variables and use variables regardless of what the data tell you.
- Correlations between predictors may be examined for selection, but avoid looking at associations with the outcome.

# Model validation

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- **Apparent performance:** Predictive ability of a model on the same data from which the model was developed.
- Studies developing prediction models for diagnosis or prognosis should include some form of interval validation to quantify **optimism**.
- Randomly splitting a single data set into model training and model test/validation → Weak and **inefficient** approach to internal validation (Collins et al., 2015)
- **Solution:** Perform internal validation through bootstrap resampling

# Model validation through the rms package

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**Table:** Output of `rms::validate()` for a logistic regression model fitted on the CTG dataset

	index.orig	training	test	optimism	index.corrected
Dxy	0.92	0.92	0.91	0.00	0.91
R2	0.72	0.72	0.71	0.01	0.71
Intercept	0.00	0.00	-0.01	0.01	-0.01
<b>Slope</b>	1.00	1.00	0.97	0.03	0.97
Emax	0.00	0.00	0.01	0.01	0.01
D	0.63	0.64	0.63	0.01	0.62
U	-0.00	-0.00	0.00	-0.00	0.00
Q	0.63	0.64	0.63	0.01	0.62
B	0.07	0.07	0.07	-0.00	0.07
g	4.61	4.72	4.56	0.15	4.46
gp	0.32	0.32	0.32	0.00	0.31

# Take-away message

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- Given its nice variance reduction properties, random forest is a popular algorithm that can be used for classification or regression.
- More studies are warranted to understand the minimal sample size required for Random Forest or other out-of-the-box prediction methods. Should they be restricted to very large data sets?
- During the development phase of a model, data-driven decisions should be minimized to reduce the chance of over-fitting and ensure generalizability of the model.

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Leo Breiman. Random forests. *Machine learning*, 45(1):5–32, 2001.

Gary S Collins, Johannes B Reitsma, Douglas G Altman, and Karel GM Moons. Transparent reporting of a multivariable prediction model for individual prognosis or diagnosis (TRIPOD): the TRIPOD statement. *Journal of British Surgery*, 102(3):148–158, 2015.

Dheeru Dua and Casey Graff. UCI machine learning repository, 2017. URL <http://archive.ics.uci.edu/ml>.

Frank E Harrell et al. *Regression modeling strategies: with applications to linear models, logistic regression, and survival analysis*. Springer, New York, 2001.

Frank E Harrell Jr. *rms: Regression Modeling Strategies*, 2021. URL <https://CRAN.R-project.org/package=rms>. R package version 6.2-0.

Trevor Hastie, Robert Tibshirani, and Jerome Friedman. *The elements of statistical learning*. Springer, 2009.

Richard D Riley, Joie Ensor, Kym IE Snell, Frank E Harrell, Glen P Martin, Johannes B Reitsma, Karel GM Moons, Gary Collins, and Maarten Van Smeden. Calculating the sample size required for developing a clinical prediction model. *British Medical Journal*, 368, 2020.

Mark J Van der Laan, Eric C Polley, and Alan E Hubbard. Super Learner. *Statistical Applications in Genetics and Molecular Biology*, 6(1), 2007.

Tjeerd van der Ploeg, Peter C Austin, and Ewout W Steyerberg. Modern modelling techniques are data hungry: a simulation study for predicting dichotomous endpoints. *BMC medical research methodology*, 14(1):1–13, 2014.