Introduction to classification and regression trees, random forests and model-based recursive partitioning in R

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Ensemble methods (bagging, random forests)

have become a popular and widely used tool in many scientific fields, e.g., in genetics and bioinformatics, because they are applicable in high dimensional problems with complex interactions

(cf.,e.g., Furlanello et al., 2003, Gunther et al., 2003, Svetnik et al., 2003, Cummings and Myers, 2004, Cummings and Segal, 2004, Guha and Jurs, 2003, Lunetta et al., 2004, Segal et al., 2004, Arun and Langmead, 2006, Bureau et al., 2005, Huang et al., 2005, Shih, 2005, Diaz-Uriarte and de Andrés, 2006, Qi et al., 2006, Ward et al., 2006)

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- ► small changes in the training sample ⇒ different splitting variable and value selected for a node ⇒ different tree from there on
 - different kinds of instability: two trees may look very different, but identify very similar subgroups and generate very similar predictions for new observations
 - extent of instability depends on characteristics of the data (e.g., signal/noise ratio, correlations between predictor variables)

Solution I: Evaluating stability

- Draw random samples from the training data and refit tree
- Assess stability of variables and values selected for splitting
- ▶ Philipp et al. (2016): Stability assessment of tree-based learners
- Implemented in function stabletree in package stablelearner

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- ► E.g., bagging (Breiman, 1996a, 1998), random forests (Breiman, 2001), boosted tree ensembles (e.g., Breiman, 1997)

Ensemble learning

Motivation:

Can we improve the accuracy of a set of simple trees (weak learners) by combining them into an ensemble (a strong learner)?

Yes, we can!

- ► A weak learner is a method that does better than random guessing
- The predictive accuracy of the ensemble is better than any of its constituent members
- Can be applied to other learners than trees
- Works best for unstable methods

Decorrelating trees I: Bagging

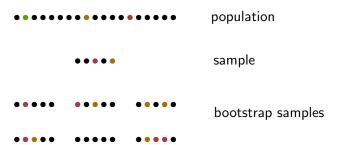
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take bootstrap samples from the original data average over trees bootstrap aggregating (alternatively, we may use subsample aggregating)
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Bootstrap sampling

from the original sample of size N draw a bootstrap sample of size N with replacement

⇒ some observations appear twice or more, some not at all

Bootstrap sampling



Bootstrap sampling

probability for one observation not to be drawn in one draw

$$1-\frac{1}{n}$$

probability for one observation $\underline{\mathsf{not}}$ to be drawn in any one of the n bootstrap draws

$$\lim_{n \to \infty} \left(1 - \frac{1}{n} \right)^n = e^{-1} \approx 0.368 = 1 - 0.632$$

- \Rightarrow approx. 63.2% of all observations are in the bootstrap sample
- ⇒ approx. 36.8% of all observations are "out of bag"

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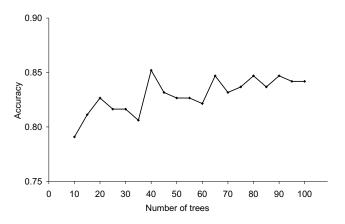
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- use large, unpruned trees (each tree has low bias but high variance)
- reduce variance by ensembling predictions
- ⇒ averaging increases prediction accuracy (Breiman, 1996a, 1998)

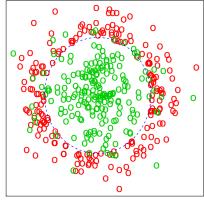
prediction accuracy increases with the number of trees



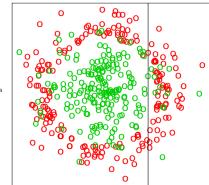
decision boundaries are smoothed

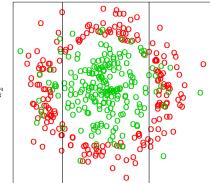
(thanks to Ji Zhu, University of Michigan, for the following graphical illustration)

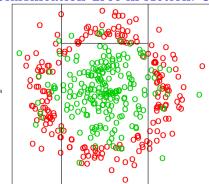
Example: Nested Spheres

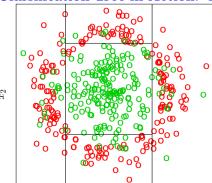


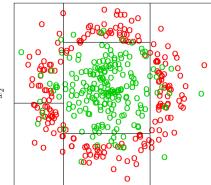
- x_1
- Green class: two independent standard normal inputs X₁, X₂
- Red class: conditioned on $X_1^2 + X_2^2 \ge 4.6$

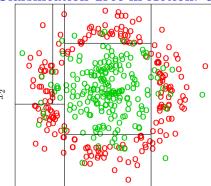




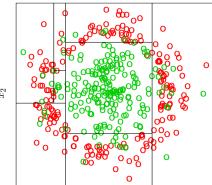




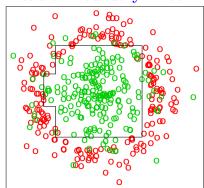




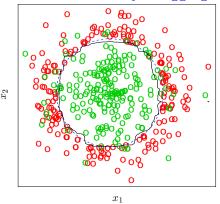
 x_1



Decision Boundary: Tree



Decision Boundary: Bagging



Bagging averages many trees, and produces more flexible decision boundaries.

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- add: sampling "columns" of data set (randomly draw variables)
 - ▶ a random subset of *mtry* variables is used for selecting each split in each tree

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- ⇒ individual trees look even more different

Decorrelating trees II: Random forests

main idea: even more variation in individual trees

- bootstrap sampling observations: vary "rows" of data set
- add: sampling "columns" of data set (randomly draw variables)
 - a random subset of mtry variables is used for selecting each split in each tree
- ⇒ individual trees look even more different
- ⇒ prediction accuracy is even higher (Breiman, 2001)

Advanced reading

- ▶ why bagging works: Bühlmann and Yu (2002) bagging smoothes hard decisions ⇒ reduces variance (ugly asymptotics for trees as base learners)
- why random forests work: Lin and Jeon (2006) random forests can be viewed as adaptively weighted k-NN with terminal node size determining size of neighborhood

Bagging and random forests - tuning parameters

- number of trees argument ntree (default: 500)
 - more is better (does not negatively affect predictive accuracy) especially with many potential predictor variables
- ▶ number of randomly preselected predictors for each split argument mtry (usually \sqrt{p} for classification, for smaller number of predictor variables sometimes p/3 is suggested, in cforest default: 5)
 - ▶ mtry = p is bagging
 - different values for mtry can affect performance and estimates of variable importance

Random forests - tuning parameters

- ▶ tree depth
 - in bagging and random forests trees are usually grown large without pruning
 - only the minimum number of observations per node is fixed
 - results of Lin and Jeon (2006) indicate that the depth / number of observations per node do affect performance
- ▶ sampling size and method: for bootstrap sampling (default: N) and subsampling (default: .632 · N)
 - subsampling gives better estimates of variable importance, see below

Decorrelating trees III: Boosting

main idea: fit trees on modified versions of the outcome variable Y

- can be used in addition to random sampling of rows and columns of X
- boosting is performed sequentially (in bagging and random forests, trees can be fit simultaneously)

Boosting

- ▶ At each stage $1 \le m \le M$ we have an imperfect model $F_{\ell}(m-1)$
- we aim to improve the model with an estimator h_m , such that $F_m(X) = F_{m-1}(X) + h(X)$ provides a better model
 - ▶ How to find h(X)?
 - ▶ the perfect model would be $F_m(X) = F_{m-1}(X) + h(X) = y$
 - or, equivalently, $h(X) = y F_{m-1}(X)$
- ▶ Therefore, we fit the model (the tree) at stage m to the residual $(y F_{m-1}(X))$ instead of y
- ▶ Generally, a learning rate $0 < \nu < 1$ is applied in updating the ensemble:
 - $F_m(X) = F_{m-1}(X) + \nu \cdot h_m(X)$

Boosting

Requires more parameter tuning than bagging and random forests.

In noisy data, bagging and random forests are often more robust than boosting (Kotsiantis, 2011, e.g.,).

In R: function gbm() from package gbm

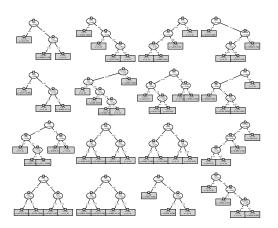
Boosting - tuning parameters

- n.trees = Increasing the number of trees may overfit the data with boosting. Optimal number of trees depends on learning rate and best determined by k-fold CV.
- interaction.depth = Typically, 4 through 8 terminal nodes work well, results are fairly insensitive to the exact choice (e.g., Hastie et al., 2009).
- ▶ shrinkage = a.k.a. learning rate ν . Typically, small values (e.g., .001 $\leq \nu <$.01) perform well (e.g., Efron et al., 2004, Bühlmann and Yu, 2003). Like number of trees, best determined by CV.

Note: list is non-exhaustive.

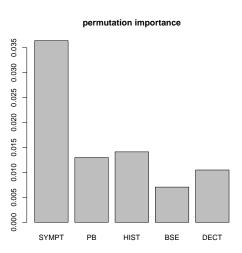
Interpretation

interpretation of predictor variables?



► Gini importance mean Gini gain produced by X_i over all trees

- Gini importance
 mean Gini gain produced by X_i over all trees
- permutation importance mean decrease in classification accuracy after permuting X_i over all trees
 - informative variables produce a systematic decrease in accuracy when permuted
 - uninformative variables produce a random decrease or increase in accuracy when permuted



Problems:

▶ Gini importance biased estimation of Gini gain in each tree ⇒ Gini importance is biased in favor of continuous variables and variables with many categories

Strobl et al. (2007)

Problems:

- ▶ Gini importance biased estimation of Gini gain in each tree ⇒ Gini importance is biased in favor of continuous variables and variables with many categories
- permutation importance even if individual trees are unbiased, as in function cforest
 - bootstrap sampling affects variance of variable importance
 - variable importance of variables with many categories may be over/underestimated
 - \Rightarrow subsampling without replacement is used by default

Strobl et al. (2007)



Conditional permutation importance

spurious correlation between shoe size and reading skills in school-children

```
> mycf <- cforest(score ~ ., data = readingSkills,
                 control = cforest_unbiased(mtry = 2))
+
> varimp(mycf)
nativeSpeaker
                                shoeSize
                       age
     12.62926
                  74.89542
                                20.01108
> varimp(mycf, conditional = TRUE)
nativeSpeaker
                                shoeSize
                       age
    11.808192 46.995336
                                2.092454
```

Strobl et al. (2008)

Choice of hyperparameters:

- results are more stable when ntree is high
- results can vary for different mtry, especially in the case of correlated predictors
- ► subsampling size down to .5 · N (Buja and Stuetzle, 2006)

pros	cons
nonparametric approach	heuristic
easy to grasp	

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applicable when predictors are correlated	
applicable to predictors of different types	selection can be biased

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few hyperparameters work well "off-the-shelve"

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variable importance

merely descriptive importance can be biased

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merely descriptive

out of bag error estimates

each tree is grown on a training (bootstrap or sub-) sample each tree brings its own test (out of bag; OOB) sample \Rightarrow OOB error estimates are not overly optimistic (e.g., Breiman, 1996b)



Highly recommended

- Friedman, J., Hastie, T., & Tibshirani, R. (2009). The elements of statistical learning. Second edition. Springer, Berlin.
 - ► Especially chapters 1, 2, 9, 10, 15
 - ► Yay, free! http://statweb.stanford.edu/~tibs/ElemStatLearn/download.html
- ▶ James, G., Witten, D., Hastie, T., & Tibshirani, R. (2013). *An introduction to statistical learning*. New York: Springer.
 - ▶ More introductory version of Friedman et al. (2009)
 - ► Yay, free! http://www-bcf.usc.edu/~gareth/ISL/getbook.html
- Strobl, C., Malley, J., & Tutz, G. (2009). An introduction to recursive partitioning: rationale, application, and characteristics of classification and regression trees, bagging, and random forests. *Psychological Methods*, 14(4), 323.
 - ▶ Note of first author: please do not interpret negative importances as a measure of statistical significance

References I

- K. Arun and C. J. Langmead. Structure based chemical shift prediction using random forests non-linear regression. In T. Jiang, U.-C. Yang, Y.-P. P. Chen, and L. Wong, editors, Proceedings of the Fourth Asia-Pacific Bioinformatics Conference, Taipei, Taiwan, pages 317–326, 2006.
- L. Breiman. Bagging predictors. Machine Learning, 24(2):123-140, 1996a.
- L. Breiman. Out-of-bag estimation. Unpublished Technical Report, Statistics Department, University of California at Berkeley, CA, USA, 1996b.
- L. Breiman. Arcing the edge. Technical report, Technical Report 486, Statistics Department, University of California at Berkeley, 1997.
- L. Breiman. Arcing classifiers. The Annals of Statistics, 26(3):801–849, 1998.
- L. Breiman. Random forests. Machine Learning, 45(1):5-32, 2001.
- P. Bühlmann and B. Yu. Analyzing bagging. The Annals of Statistics, 30:927-961, 2002.
- P. Bühlmann and B. Yu. Boosting with the L2 loss: Regression and classification. Journal of the American Statistical Association, 98:324–339, 2003.
- A. Buja and W. Stuetzle. Observations on bagging. Statistica Sinica, 16:323-351, 2006.
- A. Bureau, J. Dupuis, K. Falls, K. L. Lunetta, B. Hayward, T. P. Keith, and P. Van Eerdewegh. Identifying SNPs predictive of phenotype using random forests. *Genetic Epidemiology*, 28(2):171–182, 2005.
- M. P. Cummings and D. S. Myers. Simple statistical models predict C-to-U edited sites in plant mitochondrial RNA. BMC Bioinformatics, 5:132, 2004.
- M. P. Cummings and M. R. Segal. Few amino acid positions in rpoB are associated with most of the rifampin resistance in Mycobacterium tuberculosis. BMC Bioinformatics, 5:137, 2004.
- R. Diaz-Uriarte and S. Alvarez de Andrés. Gene selection and classification of microarray data using random forest. BMC Bioinformatics, 7:3, 2006.
- B. Efron, T. Hastie, I. Johnstone, and R. Tibshirani. Least angle regression. The Annals of statistics, 32(2): 407–499, 2004.

References II

- C. Furlanello, M. Neteler, S. Merler, S. Menegon, S. Fontanari, D. Donini, A. Rizzoli, and C. Chemini. GIS and the random forest predictor: Integration in R for Tick-Borne desease risk assessment. In F. Leisch K. Hornik and A. Zeileis, editors, Proceedings of the 3rd international workshop on distributed statistical computing DSC, 2003.
- R. Guha and P. C. Jurs. Development of linear, ensemble, and nonlinear models for the prediction and interpretation of the biological activity of a set of PDGFR inhibitors. *Journal of Chemical Information and Computer Sciences*, 44(6):2179–2189, 2003.
- E. C. Gunther, D. J. Stone, R. W. Gerwien, P. Bento, and M. P. Heyes. Prediction of clinical drug efficacy by classification of drug-induced genomic expression profiles in vitro. Proceedings of the National Academy of Sciences, 100(16):9608–9613, 2003.
- T. Hastie, R. Tibshirani, and J. H. Friedman. The Elements of Statistical Learning. Springer, New York, 2nd edition, 2009.
- X. Huang, W. Pan, S. Grindle, X. Han, Y. Chen, S. J. Park, L. W. Miller, and J. Hall. A comparative study of discriminating human heart failure etiology using gene expression profiles. BMC Bioinformatics, 6:205, 2005.
- S. Kotsiantis. Combining bagging, boosting, rotation forest and random subspace methods. Artificial Intelligence Review, 35(3):223–240, 2011.
- Y. Lin and Y. Jeon. Random forests and adaptive nearest neighbors. Journal of the American Statistical Association, 101(474):578–590, 2006.
- K. L. Lunetta, L. B. Hayward, J. Segal, and P. Van Eerdewegh. Screening large-scale association study data: Exploiting interactions using random forests. BMC Genetics, 5:32, 2004.
- M. Philipp, A. Zeileis, and C Strobl. A toolkit for stability assessment of tree-based learners. Technical report, Working Papers in Economics and Statistics, 2016.
- Y. Qi, Z. Bar-Joseph, and J. Klein-Seetharaman. Evaluation of different biological data and computational classification methods for use in protein interaction prediction. *Proteins*, 63(3):490–500, 2006.
- M. R. Segal, J. D. Barbour, and R. M. Grant. Relating HIV-1 sequence variation to replication capacity via trees and forests. Statistical Applications in Genetics and Molecular Biology, 3(1):2, 2004.
- Y.-S. Shih. Tumor classification by tissue microarray profiling: Random forest clustering applied to renal cell carcinoma. Modern Pathology, 18:547–557, 2005.



References III

- C. Strobl, A.-L. Boulesteix, A. Zeileis, and T. Hothorn. Bias in random forest variable importance measures: Illustrations, sources and a solution. BMC Bioinformatics, 8:25, 2007.
- C. Strobl, A.-L. Boulesteix, T. Kneib, T. Augustin, and A. Zeileis. Conditional variable importance for random forests. BMC Bioinformatics. 9:307, 2008.
- V. Svetnik, A. Liaw, C. Tong, J. C. Culberson, R. P. Sheridan, and B. P. Feuston. Random Forest: A classification and regression tool for compound classification and QSAR modeling. *Journal of Chemical Information and Computer Sciences*, 43(6):1947–1958, 2003.
- M. M. Ward, S. Pajevic, J. Dreyfuss, and J. D. Malley. Short-term prediction of mortality in patients with systemic lupus erythematosus: Classification of outcomes using random forests. Arthritis and Rheumatism, 55(1):74–80, 2006.