ENSEMBLE METHODS

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INTRODUCTION TO ENSEMBLES

SOME PROBLEMS OF WEAK LEARNERS.

- Decision trees have many good properties but some important drawbacks:
 - Smaller accuracy than competing alternatives
 - Very sensitive to small changes in data
 - Overall it makes the highly variable predictors
- Tree are not the only classifers to suffer from such problems.

ENSEMBLES

- A common strategy to deal with these issues is to build repeated (weak learners) models on the same data and combine them to form a single result.
- These are called *ensemble* or consensus estimators/predictors.
- As a general rule, ensemble learners tend to improve the results obtained with the weak learners they are made of.

ENSEMBLE METHODS

- Ensemble can be built on different learners but we will focus on those built on trees:
 - Bagging,
 - Random Forests,
 - Boosting,
 - Bayesian Trees.

BAGGING: AGGREGATING PREDICTORS

BAGGING: BOOTSTRAP AGGREGATION

- Decision trees suffer from high variance when compared with other methods such as linear regression, especially when n/p is moderately large.
 - NOTE: Write a small script to check this assertion
- Given that high variance is intrinsec to the trees a possibility, suggested by Breimann (**Breiman 1996**), is to build multiple trees derived from the same dataset and, somehow, average them.

AVERAGING DECREASES VARIANCE

- Bagging relies, informally, on the idea that:
 - $lacksquare given \ X \sim F()$, s.t. $Var_F(X) = \sigma^2$,
 - given a s.r.s. X_1, \ldots, X_n from F then
 - $lacksquare ext{if } \overline{X} = rac{1}{N} \sum_{i=1}^n X_i ext{ then } var_F(\overline{X}) = \sigma^2/n.$
- That is, relying on the sample mean instead of on simple observations decreases variance by a factor of n.

AVERAGING TREES ...

Two questions arise here:

- 1. How to go from X to X_1, \ldots, X_n ?
- This will be done using *bootstrap resampling*.
- 2. What means "averaging" in this context.
- Depending on the type of tree:
 - Average predictions for regression trees.
 - Majority voting for classification trees.

THE BOOTSTRAP

- *Bootstrap* methods were introduced by Bradley Efron in 1979 (**Efron 1979**) to estimate the standard error of a statistic.
- The success of the idea lied in that the procedure was presented as "automatic", that is:
 - instead of having to do complex calculations,
 - it allowed to approximate them using computer simulation.
- Some people called it ``the end of mathematical statistics".

BOOTSTRAP APPLICATIONS

- The bootstrap has been applied to almost any problem in Statistics.
 - Computing standard errors,
 - Bias estimation and adjustment,
 - Confidence intervals,
 - Significance tests, ...
- We begin with the easiest and best known case: estimating the standard error (that is the square root of the variance) of an estimator.

PRECISION OF AN ESTIMATE (1)

- Assume we want to estimate some parameter θ , that can be expressed as $\theta(F)$, where F is the distribution function of each X_i in (X_1, X_2, \dots, X_n) .
- For example:

$$egin{aligned} heta &= E_F(X) = heta(F) \ heta &= Med(X) = \{m: P_F(X \leq m) = 1/2\} = heta(F). \end{aligned}$$

PLUG-IN ESTIMATES

• To estimate $\theta(F)$ we usually rely on *plug-in estimators*: $\hat{\theta} = \theta(F_n)$:

$$egin{aligned} \hat{ heta} &= \overline{X} = \int X dF_n(x) = rac{1}{n} \sum_{i=1}^n x_i = heta(F_n) \ \hat{ heta} &= \widehat{Med}(X) = \{m: rac{\#x_i \leq m}{n} = 1/2\} = heta(F_n) \end{aligned}$$

PRECISION OF AN ESTIMATE (1)

- An important when computing an estimator $\hat{\theta}$ of a parameter θ is how precise is $\hat{\theta}$ as an estimator of θ ?
 - With the sample mean, \overline{X} , the standard error estimation is immediate because the expression of the variance estimator is known: =
 - So, a natural estimator of the standard error of \overline{X} is: $\hat{\sigma}_{\overline{X}} = \frac{\hat{\sigma}(X)}{\sqrt{n}}$

PRECISION OF AN ESTIMATE (2)

• If, as in this case, the variance of X (and, here, that of \overline{X}) is a functional of F:

$$\sigma_{\overline{X}} = rac{\sigma(X)}{\sqrt{n}} = rac{\sqrt{\int [x-\int x\,dF(x)]ackslash \mathbf{p}2dF(x)}}{\sqrt{n}} = \sigma_{\overline{X}}(F)$$

then, the standard error estimator is the same functional applied on F_n , that is:

$$\hat{\sigma}_{\overline{X}} = rac{\hat{\sigma}(X)}{\sqrt{n}} = rac{\sqrt{1/n\sum_{i=1}^n(x_i-\overline{x})^2}}{\sqrt{n}} = \sigma_{\overline{X}}(F_n).$$

STANDARD ERROR ESTIMATION

- Thus, a way to obtain a standard error estimator $\hat{\sigma}_{\hat{\theta}}$ of an estimator $\hat{\theta}$ consists on replacing F with F_n in the "population" standard error expression of $\hat{\theta}$, $\sigma_{\hat{\theta}} = \sigma_{\hat{\theta}}(F)$, whenever it is known.
- In a schematic form:

$$\sigma_{\hat{ heta}} = \sigma_{\hat{ heta}}(F) \Longrightarrow \sigma_{\hat{ heta}}(F_n) = \widehat{\sigma}_{\hat{ heta}}.$$

That is, the process consists of "plugging-in" F_n in the (known) functional form, $\sigma_{\hat{\theta}}(F)$ that defines $\sigma_{\hat{\theta}}$ }.

THE BOOTSTRAP (1)

- The previous approach, $F \simeq F_n \Longrightarrow \sigma_{\hat{\theta}}(F) \simeq \sigma_{\hat{\theta}}(F_n)$ presents the obvious drawback that, when the functional form $\sigma_{\hat{\theta}}(F)$ is unknown, it is not possible to carry out the substitution of F by F_n .
- This is, for example, the case of standard error of the median or **that of the correlation coefficient**.

THE BOOTSTRAP (2)

- The bootstrap method makes it possible to do the desired approximation: $\hat{\sigma}_{\hat{\theta}} \simeq \sigma_{\hat{\theta}}(F_n)$ without having to to know the form of $\sigma_{\hat{\theta}}(F)$.
- To do this, the bootstrap estimates, or directly approaches $\sigma_{\hat{\theta}}(F_n)$ over the sample.

BOOTSTRAP SAMPLING (RESAMPLING)

- The *bootstrap* allows to estimate the standard error from samples of F_n , that is,
- Substituting F_n by F carried out in the sampling step.

Instead of:

$$F \overset{s.r.s}{\longrightarrow} \mathbf{X} = (X_1, X_2, \dots, X_n) \quad (\hat{\sigma}_{\hat{ heta}} = \underbrace{\sigma_{ heta}(F_n)}_{unknown})$$

It is done:

$$F_n \stackrel{s.r.s}{\longrightarrow} \quad \mathbf{X^*} = (X_1^*, X_2^*, \dots, X_n^*) \quad (\hat{\sigma}_{\hat{ heta}} = \hat{\sigma}_{\hat{ heta}}^* \simeq \sigma_{\hat{ heta}}^*).$$

BOOTSTRAP RESAMPLING (2)

- Here, $\sigma_{\hat{ heta}}^*$ is the bootstrap standard error of $\hat{ heta}$ and
- $\hat{\sigma}^*_{\hat{\theta}}$ the bootstrap estimate of the standard error of $\hat{\theta}$.
- That is, the new (re-)sampling process consists of extracting samples of size n of F_n :
 - $\mathbf{X}^* = (X_1^*, X_2^*, \dots, X_n^*)$ is a random sample of size n obtained with replacement from the original sample (X_1, X_2, \dots, X_n) .
- Samples X^* , obtained through this procedure are called *bootstrap* samples or *re-samples*.

THE BOOTSTRAP DISTRIBUTION

• The distribution of a statistic computed from re-samples is called the *bootstrap* distribution,

$$\mathcal{L}(\hat{ heta}) \simeq P_F(\hat{ heta} \leq t) : ext{Sampling distribution of } \hat{ heta}, \ \mathcal{L}(\hat{ heta}^*) \simeq P_{F_n}(\hat{ heta}^* \leq t) : ext{Bootstrap distribution of } \hat{ heta},$$

- This distribution is usually not known.
- However the sampling process and the calculation of the statistics can be approximated using a Monte Carlo Algorithm.

BOOTSTRAP MONTE CARLO ALGORITHM

- 1. Draw a bootstrap sample, \mathbf{x}_1^* from F_n and compute $\hat{\theta}(\mathbf{x}_1^*)$.
- 2. Repeat (1) B times yielding $\hat{\theta}(\mathbf{x}_2^*), \ldots, \hat{\theta}(\mathbf{x}_B^*)$ estimates.
- 3. Compute:

$$\hat{\sigma}_B(\hat{ heta}) = \sqrt{rac{\sum_{b=1}^B \left(\hat{ heta}(\mathbf{x_i^*}) - \overline{\hat{ heta}^*}
ight)^2}{(B-1)}}, \quad \overline{\hat{ heta}^*} \equiv rac{1}{B} \sum_{b=1}^B \hat{ heta}\left(\mathbf{x_b^*}
ight)$$

BOOTSTRAP ESTIMATES OF SE

• Main idea is that the *bootstrap* standard error of $\hat{\theta}$, $\sigma_B(\hat{\theta})$ can be *approximated* by $\hat{\sigma}_B(\hat{\theta})$.

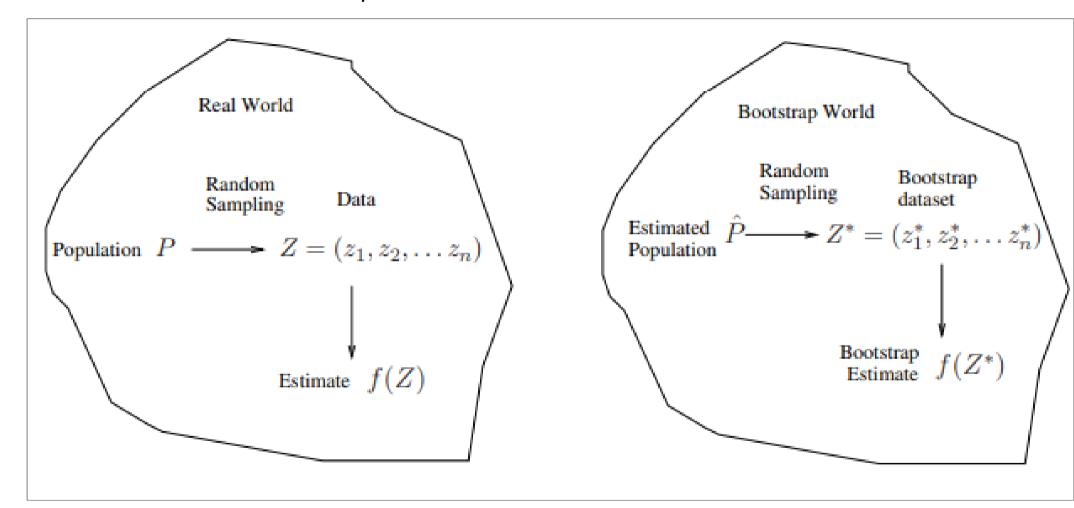
$$\text{if } B \to \infty \text{ then } \hat{\sigma}_B(\hat{\theta}) \to \hat{\sigma}_\infty(\hat{\theta}) = \sigma_B(\hat{\theta}) = \sigma_{\hat{\theta}}(F_n).$$

The bootstrap approximation, $\hat{\sigma}_B(\hat{\theta})$, to the bootstrap SE, $\sigma_B(\hat{\theta})$, provides an estimate of $\sigma_{\hat{\theta}}(F_n)$:

$$\hat{\sigma}_B(\hat{ heta})(\simeq \sigma_B(\hat{ heta}) = \sigma_{\hat{ heta}}(F_n)) \simeq \hat{\sigma}_{\hat{ heta}}(F_n).$$

SUMMARY

From real world to *bootstrap* world:



BACK TO BAGGING

- Breiman (**Breiman 1996**) combined the ideas of:
 - Averaging provides decreased variance estimates,
 - Bootstrap provides multiple (re)samples.
- He suggested: **b**ootstrap **agg**regat**ing**:
 - Take resamples from the original training dataset
 - Learn the model on each bootstrapped training set to get a prediction $\hat{f}^{*b}(x)$.
 - Use the boostrap estimates to obtain improved prediction/classification.

BAGGING PREDICTION/CLASSIFIER

• For regression (trees) the **bagged estimate** is the average prediction at x from these B trees.

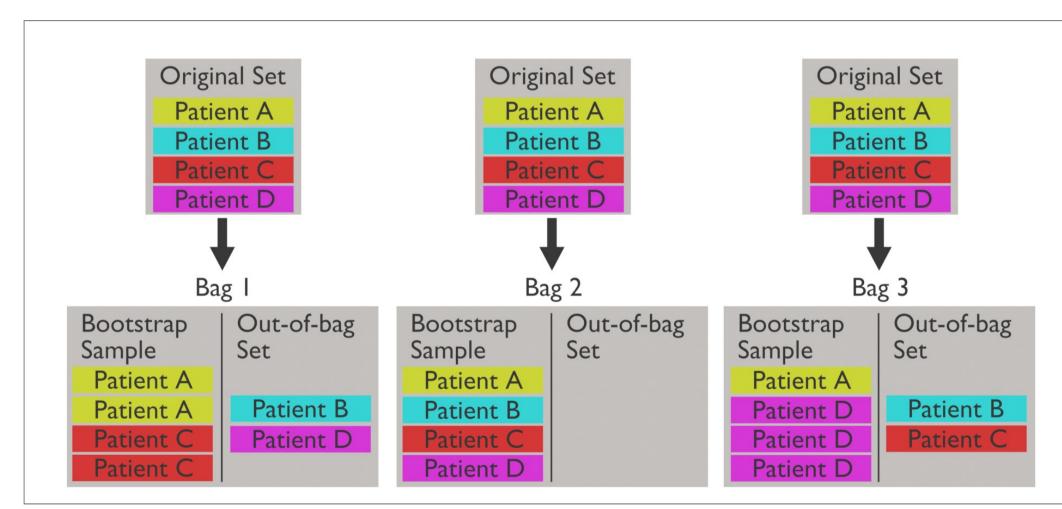
$$\hat{f}_{bag}(x) = rac{1}{B} \sum_{b=1}^{B} \hat{f}^{*b}(x)$$

• For classification (trees) the **bagged classifier** selects the class with the most "votes" from the *B* trees:

$$\hat{G}_{bag}(x) = rg \max_{k} \hat{f}_{\ bag}(x).$$

OUT-OF-BAG OBSERVATIONS

• Every time a resample is taken *with replacement*, some observations are ommitted, due to the multiple occurring of others.



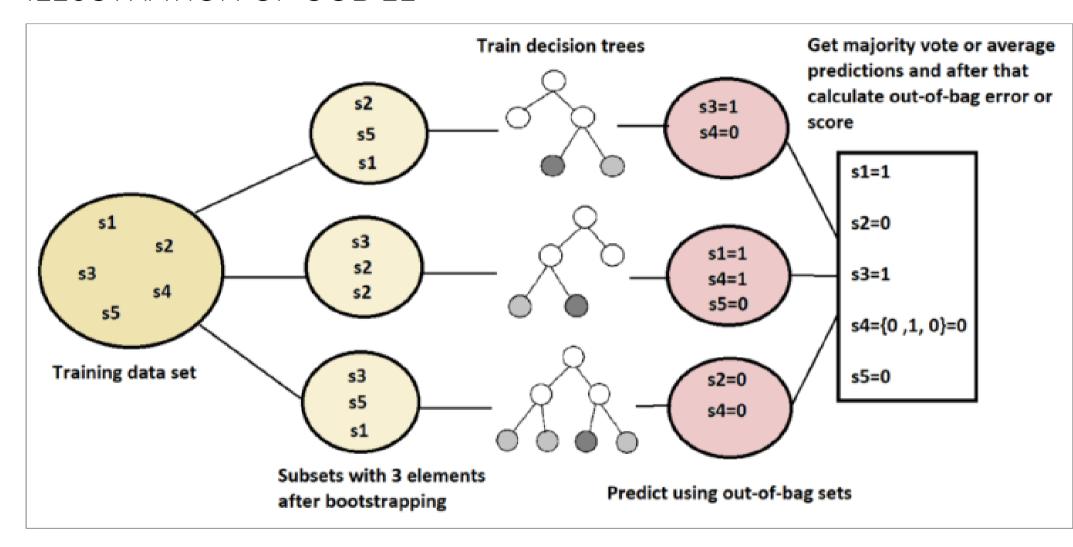
• These out-of-bag (OOB) observations can be used to build an estimate of prediction error.

OUT-OF-BAG ERROR ESTIMATES

Since each out-of-bag set is not used to train the model, it can be used to evaluate performance.

- 1. Find all trees that are not trained by the OOB instance.
- 2. Take the majority vote of these trees for the OOB instance, compared to the true value of the OOB instance.
- 3. Compile OOB error for all instances in the OOB dataset.

ILLUSTRATION OF OOB EE



Source: https://www.baeldung.com/cs/random-forests-out-of-bag-error

BAGGING IN R (1.1)

- This exampe relies on the well-known AmesHousing dataset on house prices in Ames, IA.
- We use libraries:
 - rpart for stratified resampling
 - ipred for bagging.

BAGGING IN R (1.2)

```
1 system.time(
2 ames_bag1 <- ipred::bagging(
3   formula = Sale_Price ~ .,
4   data = ames_train,
5   nbagg = 100,   coob = TRUE,
6   control = rpart::rpart.control(minsplit = 2, cp = 0)
7 )
8 )
9 # user system elapsed
10 # 40.16  0.15  40.34</pre>
```

```
1 show(ames_bag1)
2 # Bagging regression trees with 100 bootstrap replications
3 #
4 # Call: bagging.data.frame(formula = Sale_Price ~ ., data = ames_train,
5 # nbagg = 100, coob = TRUE, control = rpart.control(minsplit = 2,
6 # cp = 0))
```

7 #

8 # Out-of-bag estimate of root mean squared error: 26350.91

.

INTERPETABILITY: THE "ACHILES HEEL"

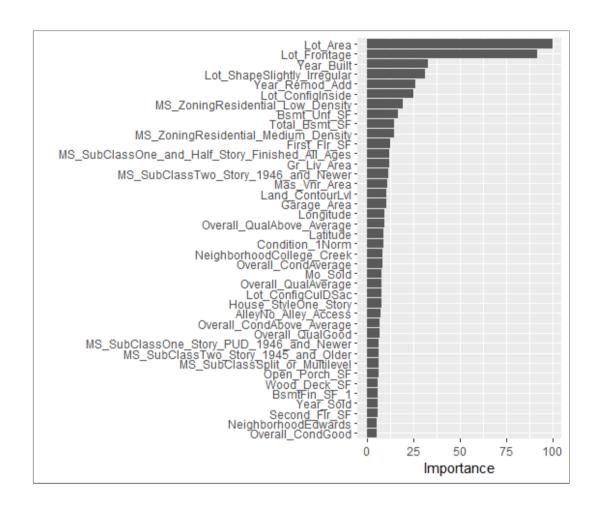
- Trees may have a straightforward interpretation,
 - Plotting the tree provides information about
 - which variables are important
 - how they act on the prediction
- Ensembles are less intuitive because
 - there is no consensus tree.
 - not clear which variables are most important

VARIABLE IMPORTANCE

- A complementary way to interpret a tree is by quantifying how *important* is each feature.
- Done measuring the total reduction in loss function associated with each variable across all splits.
- This measure can be extended to an ensemble simply by adding up variable importance over all trees built.

VARIABLE IMPORTANCE EXAMPLE

- If bagging is performed with caret
- the vip function from the vip package can be used (see lab examples).



RANDOM FORESTS

RANDOM FORESTS: DECORRELATING PREDICTORS

- Bagged trees, based on re-samples (of the same sample) tend to be highly correlated.
- To get away from this Breimann introduced Random forests, that use a "clever trick" that decorrelates trees:
 - When growing a tree from one bootstrap sample,
 - At each split use only a randomly selected subset of predictors.

RANDOM FORESTS

HOW MANY VARIABLES PER SPLIT?

- The usual recommendation for random selection of variables at each split has been studied by simulation:
 - For regression default value is m=p/3
 - For classification default value is $m = \sqrt{p}$.
- ullet Alternatively the number m can be chosen using cross-validation.

RANDOM FOREST ALGORITHM

Random Forests Algorithm, from chapter 17 in (Hastie and Efron 2016)

OUT-OF-THE BOX PERFORMANCE

- Random forests have become popular because they tend to provide very good out-of-the-box performance, that is:
 - Although they have several hyperparameters that can be tuned,
 - the default values tend to produce good results.
- Moreover, among the more popular machine learning algorithms, random forests have the least variability in their prediction accuracy when tuning (<u>Probst, Wright, and Boulesteix 2019</u>).

OUT OF THE BOX PERFORMANCE

- Training a random forest model with all hyperparameters set to their default values, we get an OOB RMSE that is better than many other classifiers, with or without tuning.
- This combined with good stability and ease-of-use has made it the option of choice for many problems

OUT OF THE BOX PERFORMANCE EXAMPLE

```
1 # number of features
 2 n features <- length(setdiff(names(ames train), "Sale Price"))</pre>
 4 # train a default random forest model
   ames rf1 <- ranger(</pre>
 6 Sale_Price ~ .,
 7 data = ames_train,
     mtry = floor(n_features / 3),
    respect.unordered.factors = "order",
10
   seed = 123
11 )
12
13 # get OOB RMSE
14 (default_rmse <- sqrt(ames_rf1$prediction.error))</pre>
15 ## [1] 24859.27
```

TUNING HYPERPARAMETERS

There are several parametres that, appropriately tuned, can improve RF performance.

- 1. The number of trees in the forest.
- 2. The number of features to consider at any given split (m_{try}).
- 3. The complexity of each tree.
- 4. The sampling scheme.
- 5. The splitting rule to use during tree construction.
 - 1 and 2 tend to have the largest impact on predictive accuracy.

RANDOM FORESTS IN BIOINFORMATICS

- Random forests have been thoroughly used in Bioinformatics. See (<u>Boulesteix</u> et al. 2012).
- Bioinformatics data are often high dimensional with
 - dozens or (less often) hundreds of samples/individuals
 - thousands (or hundreds of thousands) of variables.

APPLICATION OF RANDOM FORESTS

- Random forests provide robust classifers for instance for
 - Distinguishing cancer from non cancer
 - Predicting tumor type in cancer of unknown origin
 - Selecting variables (SNPs) in Genome Wide Association Studies
- Some variation of Random forests are used only for variable selection

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