Testing Variable Importance in Random Forests

Carolin Strobl (LMU München) and Achim Zeileis (WU Wien)

lifestat 2008

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The permutation importance

The suggested test

Summary and outlook

random forests

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random forests

 have become increasingly popular in, e.g., genetics and the neurosciences The permutation importance

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random forests

- have become increasingly popular in, e.g., genetics and the neurosciences [imagine a long list of references here]
- can deal with "small n large p"-problems, high-order interactions, correlated predictor variables

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random forests

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- can deal with "small n large p"-problems, high-order interactions, correlated predictor variables
- are used not only for prediction, but also to assess variable importance and

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- are used not only for prediction, but also to assess variable importance and
- on the official random forest website Breiman and Cutler (2008) even suggest a significance test for the variable importance...

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learn a random forest as a classification/regression model

to predict Y from X_1, \ldots, X_p

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learn a random forest as a classification/regression model

to predict Y from X_1, \ldots, X_p

result: almost a black-box

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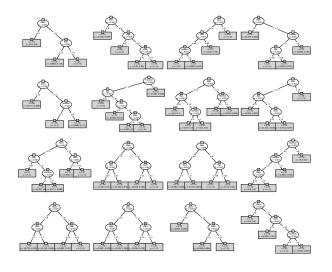
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(Small) random forest



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Measuring variable importance

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Measuring variable importance

Gini importance

mean Gini gain produced by X_j over all trees (can be severely biased due to estimation bias and mutiple testing; Strobl et al., 2007) The permutation importance

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Measuring variable importance

Gini importance

mean Gini gain produced by X_j over all trees (can be severely biased due to estimation bias and mutiple testing; Strobl et al., 2007)

- permutation importance
 mean decrease in classification accuracy after
 permuting X_j 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

(unbiased when subsampling is used; Strobl et al., 2007)

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within each tree t

$$VI^{(t)}(\mathbf{x}_{j}) = \frac{\sum_{i \in \overline{\mathfrak{B}}^{(t)}} I\left(y_{i} = \hat{y}_{i}^{(t)}\right)}{\left|\overline{\mathfrak{B}}^{(t)}\right|} - \frac{\sum_{i \in \overline{\mathfrak{B}}^{(t)}} I\left(y_{i} = \hat{y}_{i,\pi_{j}}^{(t)}\right)}{\left|\overline{\mathfrak{B}}^{(t)}\right|}$$

 $\hat{y}_i^{(t)} = f^{(t)}(\mathbf{x}_i) =$ predicted class before permuting

 $\hat{y}_{i,\pi_j}^{(t)} = f^{(t)}(\mathbf{x}_{i,\pi_j})$ = predicted class after permuting X_j

$$\mathbf{x}_{i,\pi_j} = (x_{i,1}, \ldots, x_{i,j-1}, x_{\pi_j(i),j}, x_{i,j+1}, \ldots, x_{i,p})$$

Note: $VI^{(t)}(\mathbf{x}_j) = 0$ by definition, if X_j is not in tree t

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over all trees:

1. raw importance

$$VI(\mathbf{x}_j) = rac{\sum_{t=1}^{ntree} VI^{(t)}(\mathbf{x}_j)}{ntree}$$

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over all trees:

2. scaled importance (z-score)

$$\frac{VI(\mathbf{x}_j)}{\frac{\hat{\sigma}}{\sqrt{ntree}}} = z_j$$

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• individual $VI^{(t)}(\mathbf{x}_j)$ have standard deviation σ and

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- individual $VI^{(t)}(\mathbf{x}_j)$ have standard deviation σ and
- are computed from *ntree* independent bootstrap samples (where *ntree* is large)

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- individual $VI^{(t)}(\mathbf{x}_j)$ have standard deviation σ and
- are computed from *ntree* independent bootstrap samples (where *ntree* is large)
- central limit theorem for the mean $VI(\mathbf{x}_j)$ \Rightarrow normal with standard error σ/\sqrt{ntree}

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- are computed from *ntree* independent bootstrap samples (where *ntree* is large)
- central limit theorem for the mean $VI(\mathbf{x}_j)$ \Rightarrow normal with standard error σ/\sqrt{ntree}

under the null hypothesis of zero importance:

$$z_j \stackrel{as.}{\sim} N(0,1)$$

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if z_j exceeds the α -quantile of N(0,1) \Rightarrow reject the null hypothesis of zero importance for variable X_j

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Simulation study

- generate data sets of sample size n = 100, 200 and 500
- ► five predictor variables of which only X_1 is relevant with ► $y \sim \begin{cases} B(n, 0.5 - \rho) & \text{for } X_1 = 0 \\ B(n, 0.5 + \rho) & \text{for } X_1 = 1 \end{cases}$ with relevance

$$\rho=0,0.05,\ldots,0.5$$

- fit random forests with ntree = 100, 200 and 500
- for 1000 iterations in each combination:
 count how many times the null hypothesis for X₁
 was rejected

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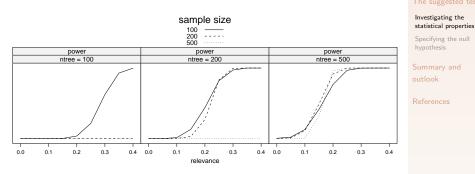
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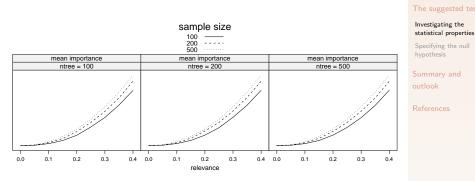
References

The power



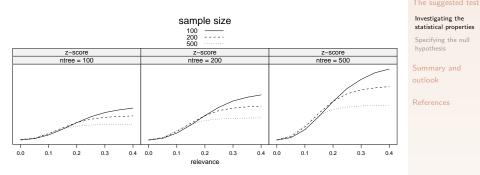
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The average raw importance



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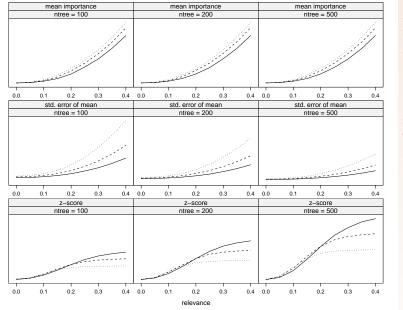
The average z-score



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sample size

100 _____ 200 -----500 -----



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importance

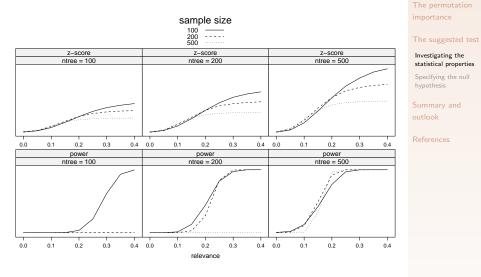
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The average z-score and the power



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Findings

z-score and power

- increase in the number of trees
- decrease in the sample size

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What null hypothesis were we testing in the first place?

obs	Y	X:	7
1	<i>y</i> ₁	$x_{\pi_j(1),j}$	z_1
:	:	: <i>nj</i> (1),j	:
•	:	:	:
i	<i>y</i> ₁	$X_{\pi_j(i),j}$	Zi
÷	÷	÷	:
п	y_1	$X_{\pi_j(n),j}$	Zn

 $H_0: X_i \perp Y, Z \text{ or } X_i \perp Y \land X_i \perp Z$ $P(Y, X_i, Z) \stackrel{H_0}{=} P(Y, Z) \cdot P(X_i)$

Investigating the

ne null

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What null hypothesis were we testing in the first place?

the current null hypothesis reflects independence of X_j from both Y and the remaining predictor variables Z The permutation importance

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the current null hypothesis reflects independence of X_j from both Y and the remaining predictor variables Z

 \Rightarrow a high variable importance can result from violation of either one

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Conditional permutation scheme

 $\begin{array}{rcl} P(Y,X_j|Z) & \stackrel{H_0}{=} & P(Y|Z) \cdot P(X_j|Z) \\ \\ \text{or} & P(Y|X_j,Z) & \stackrel{H_0}{=} & P(Y|Z) \end{array}$

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to be continued...

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the significance test suggested on the random forest website has strange properties:

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the significance test suggested on the random forest website has strange properties:

- the z-score and power increase in the number of trees and decrease in the sample size
- the null hypothesis may not reflect what you wanted

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 \Rightarrow use conditional permutation scheme

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- \Rightarrow use conditional permutation scheme
- \Rightarrow use distribution over > 1 permutations

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the significance test suggested on the random forest website has strange properties:

- the z-score and power increase in the number of trees and decrease in the sample size
- the null hypothesis may not reflect what you wanted
 - \Rightarrow use conditional permutation scheme
 - \Rightarrow use distribution over > 1 permutations

for now: stick to the unscaled importance

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- Breiman, L. and A. Cutler (2008). Random forests classification manual (website accessed in 1/2008) http://www.math.usu.edu/~adele/forests/.
- Strobl, C., A.-L. Boulesteix, A. Zeileis, and T. Hothorn (2007). Bias in random forest variable importance measures: Illustrations, sources and a solution. BMC Bioinformatics 8:25.

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