

# The Design and Analysis of Benchmark Experiments – Part II: Analysis

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## Benchmark Experiments

A comparison of algorithms with respect to certain performance measures is of special interest in the following problems

- select the best out of a set of candidates,
- identify groups of algorithms with the same performance,
- test whether any useful structure is inherent in the data or
- demonstrate equivalence of two algorithms.

## Illustrating Example

Stabilization of a Linear Discriminant Analysis (LDA) by using low-dimensional Principal Component (PC- $q$ ) scores (Läuter, 1992; Läuter et al., 1998; Kropf, 2000) for Glaucoma diagnosis (Hothorn et al., 2003; Mardin et al., 2003).

Laser-scanning images from 98 patients and 98 controls ( $n = 196$ ),  $p = 62$  numeric input variables.

Data generating process: The empirical distribution function  $\hat{Z}_n$ .

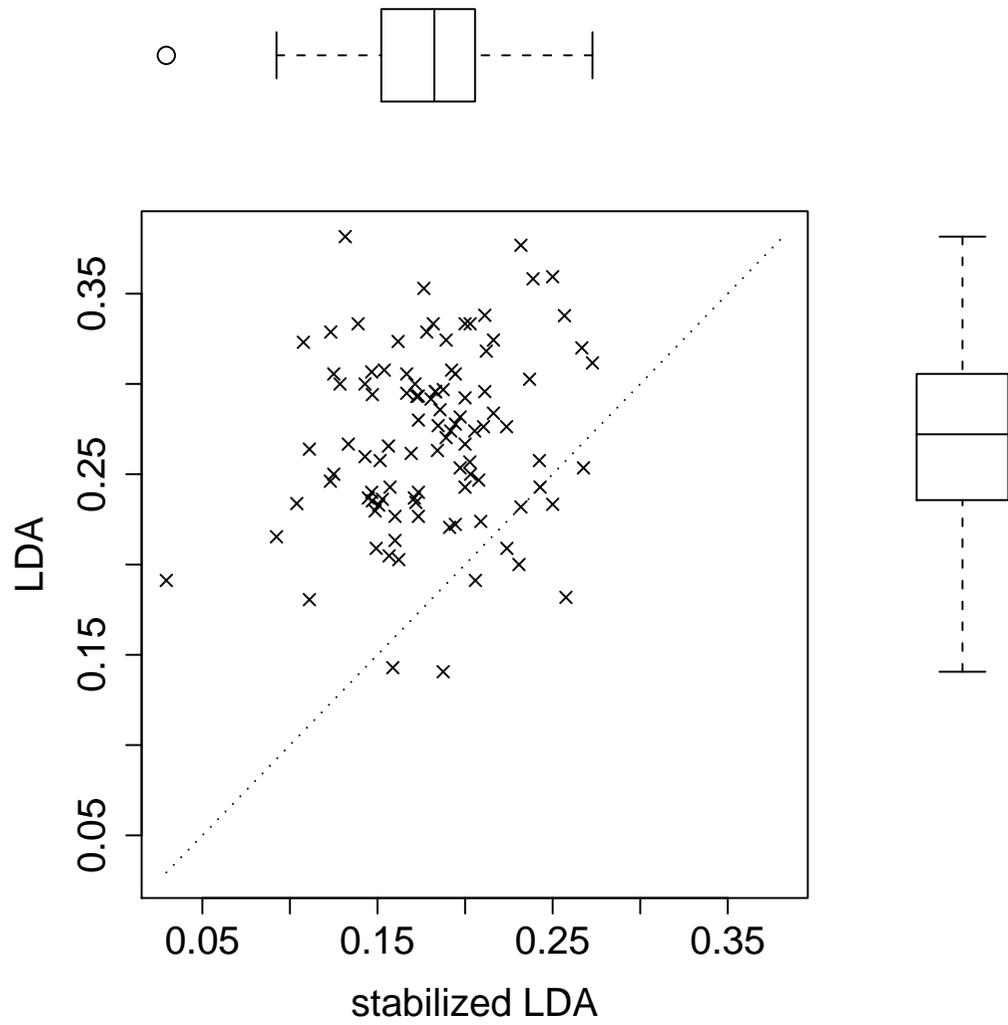
Performance measure: Out-of-bootstrap misclassification error.

## Experiment

**Question:** Does the performance distribution  $\hat{P}_{\text{LDA}}(\hat{Z}_n)$  of a LDA using the original  $p$  input variables differ from the performance distribution  $\hat{P}_{\text{sLDA}}(\hat{Z}_n)$  of a stabilized LDA?

**Experiment:** Draw  $B$  samples  $\mathcal{L}^b$  from the data generating process  $\hat{Z}_n$  and compute  $\hat{p}_{\text{LDA},b}$  and  $\hat{p}_{\text{sLDA},b}$ , the misclassification errors evaluated on the out-of-bootstrap observations.

# Benchmark Experiments



## Inference

$$H_0 : \hat{P}_{\text{LDA}}(\hat{Z}_n) = \hat{P}_{\text{sLDA}}(\hat{Z}_n)$$

**Problem:** We do not know anything about the performances, except that parametric assumptions are surely not appropriate.

**Solution:** Dispose the performance distributions by conditioning on all permutations of the labels for each bootstrap sample.

## Inference

$$T = \sum_{b=1}^B \hat{p}_{\text{LDA},b} - \hat{p}_{\text{sLDA},b} = B(\bar{p}_{\text{LDA},\cdot} - \bar{p}_{\text{sLDA},\cdot})$$

The conditional distribution of the test statistic  $T$  under the conditions described by  $H_0$  can be used to construct a permutation test.

In our case, the  $P$ -value based on the asymptotic conditional distribution is  $p < 0.001$  and therefore  $H_0$  can be rejected.

## A Regression Example

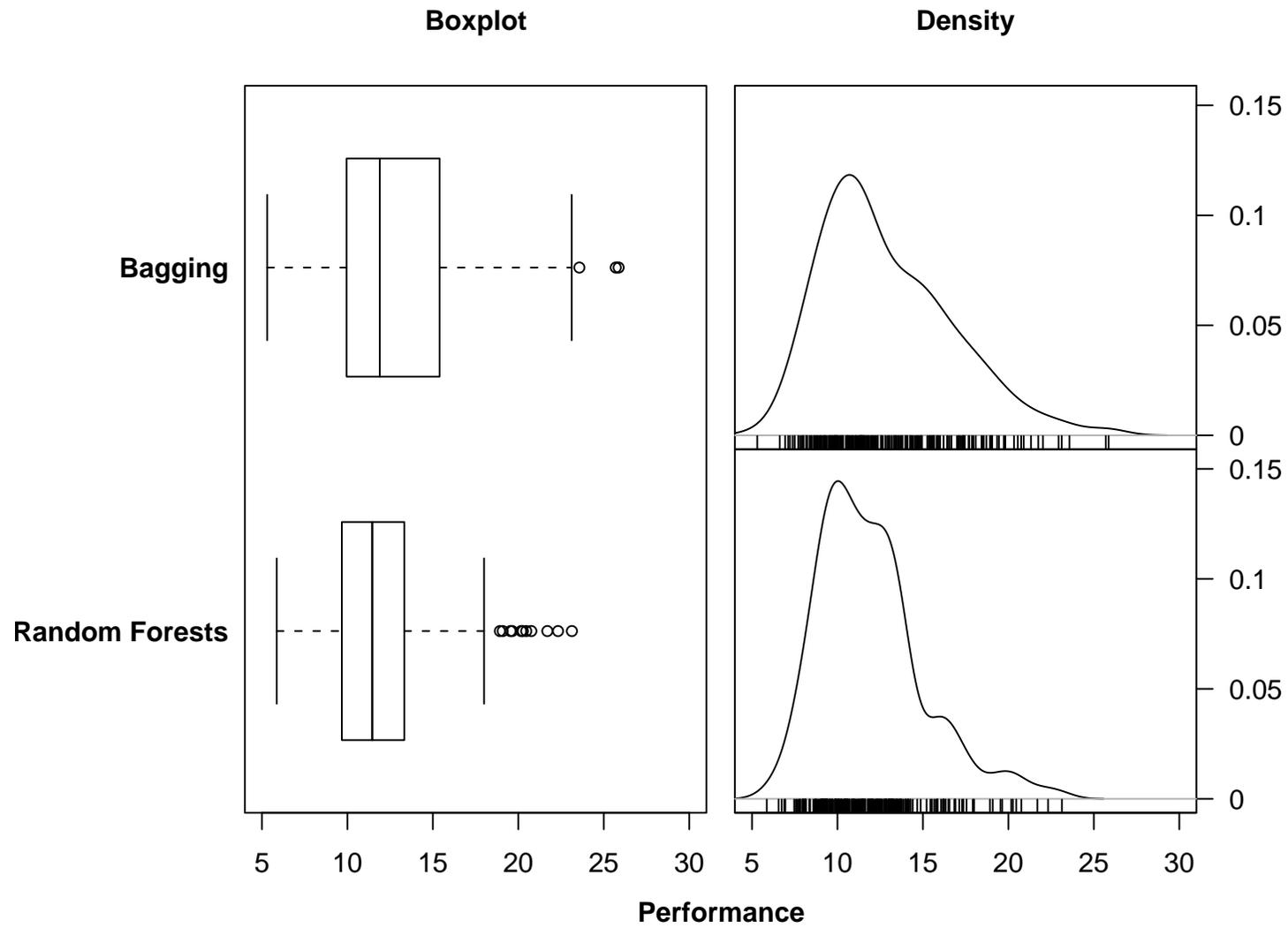
Exactly the same methodology can be applied to regression problems with univariate numeric responses. Example: Can additional randomness via Random Forests improve Bagging for the Boston Housing data?

House prices for  $n = 506$  houses near Boston,  $p = 13$  input variables.

Data generating process: The empirical distribution function  $\hat{Z}_n$ .

Performance measure: Out-of-bootstrap mean squared error.

# Benchmark Experiments



## Inference

The null-hypothesis of equal performance distributions can be rejected ( $P$ -value  $< 0.001$ ).

The estimated difference of the mean square error of Bagging compared to Random Forests is 0.969 with confidence limits (0.633, 1.305).

## Comparison of Multiple Algorithms

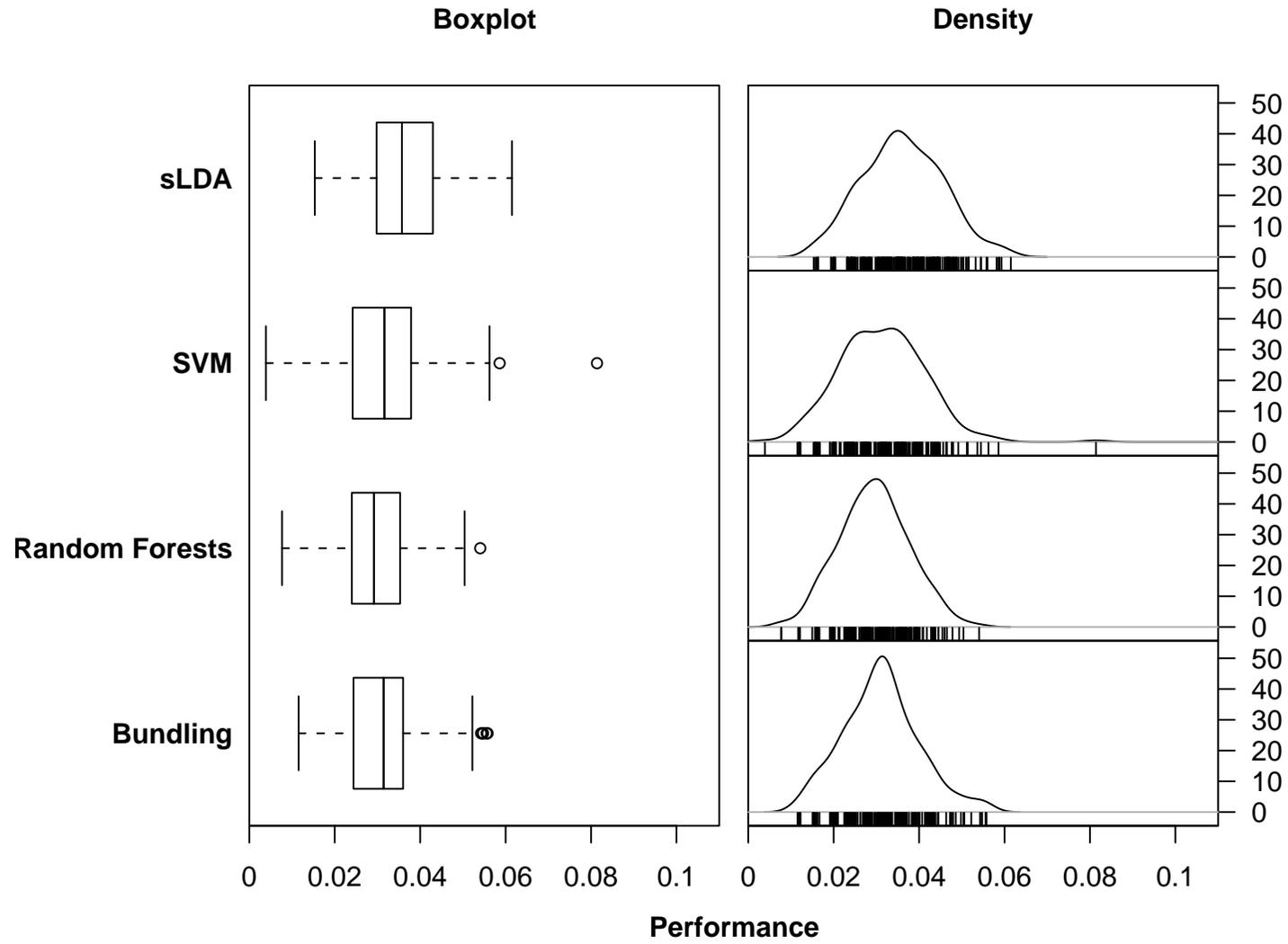
When multiple algorithms are under test, we are interested in both a global test and a multiple test procedure showing where the differences, if any, come from. Example: Breast Cancer data with tumor classification from  $n = 699$  observations with  $p = 9$  inputs.

Comparison of sLDA, Support Vector Machine, Random Forests and Bundling ([Hothorn and Lausen, 2003](#)).

Data generating process: The empirical distribution function  $\hat{Z}_n$ .

Performance measure: Out-of-bootstrap misclassification error.

# Benchmark Experiments



## Inference

Again, the global hypothesis

$$H_0 : \hat{P}_1(\hat{Z}_n) = \dots = \hat{P}_K(\hat{Z}_n)$$

can be rejected ( $P$ -value  $< 0.001$ ).

**Problem:** Which differences 'cause' the rejection of  $H_0$ ?

**Solution:** One can avoid complicated closed testing procedures by computing confidence intervals after mapping the  $B$ -block design into a  $K$ -sample problem via alignment ([Hájek et al., 1999](#)).

## Alignment

When we look at the performance measure of algorithm  $k$  in the  $b$ th sample drawn from the data generating process, we might want to write

$$p_{kb} = \mu + \beta_b + \gamma_k + \varepsilon_{kb}$$

where  $\mu$  corresponds to the performance of the Bayes-rule,  $\beta_b$  is the error induced by the  $b$  sample and  $\gamma_k$  is the error of the  $k$ th algorithm, the quantity we are primarily interested in,  $\varepsilon$  indicates an error term.

## Alignment (cont'd)

The aligned performance measures  $p_{kb}^*$  cover the difference of the performance of the  $k$ th algorithm from the average performance of all  $K$  algorithms:

$$p_{kb}^* = p_{kb} - \bar{p}_{\cdot b} = (\gamma_k + \varepsilon_{kb}) - \frac{1}{K} \sum_{k=1}^K (\gamma_k + \varepsilon_{kb})$$

For classification problems,  $p_{k_1 b}^* - p_{k_2 b}^*$  is the difference of the misclassification error.

## Alignment (cont'd)

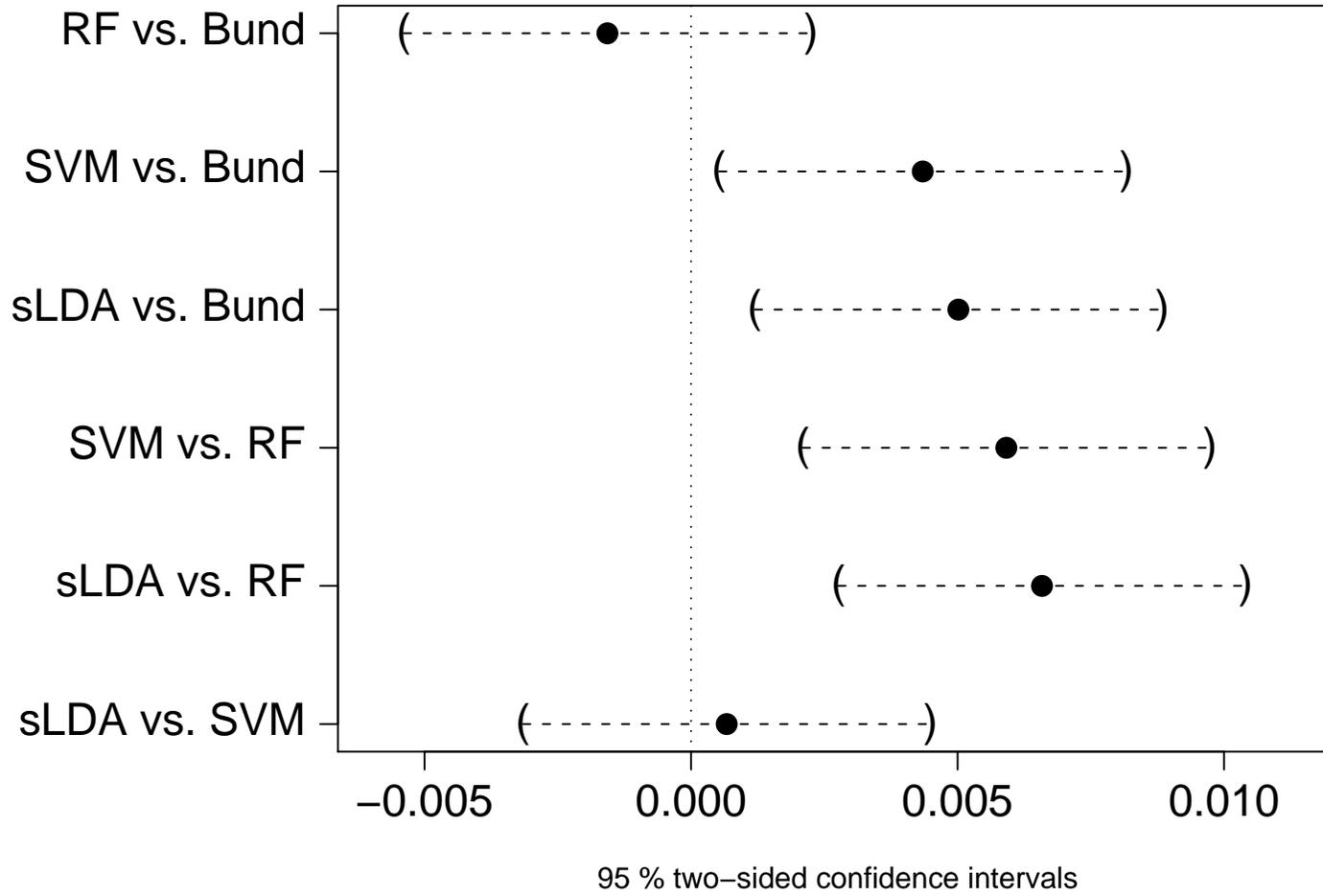
The aligned random variables are not independent but exchangeable for each of the  $b$  samples and are independent between samples.

Therefore, (asymptotic) permutation test procedures can be used to assess the deviations from the global null-hypothesis.

For example, asymptotic simultaneous confidence intervals for Tukey-contrasts can be used for an all-pair comparison of the  $K$  algorithms under test.

Benchmark Experiments

Asymptotic Tukey Confidence Sets



## Classical Tests?

We advocate usage of permutation tests, but what about more classical tests?

Consider a paired comparison of sLDA vs. SVM for the Breast Cancer data:

- Permutation test:  $T = 1.488$ ,  $p = 0.776$
- $t$  test:  $t = 0.284$ ,  $p = 0.777$
- Wilcoxon signed rank test:  $W = 18216$ ,  $p < 0.001$

## Rank Tests: A Warning

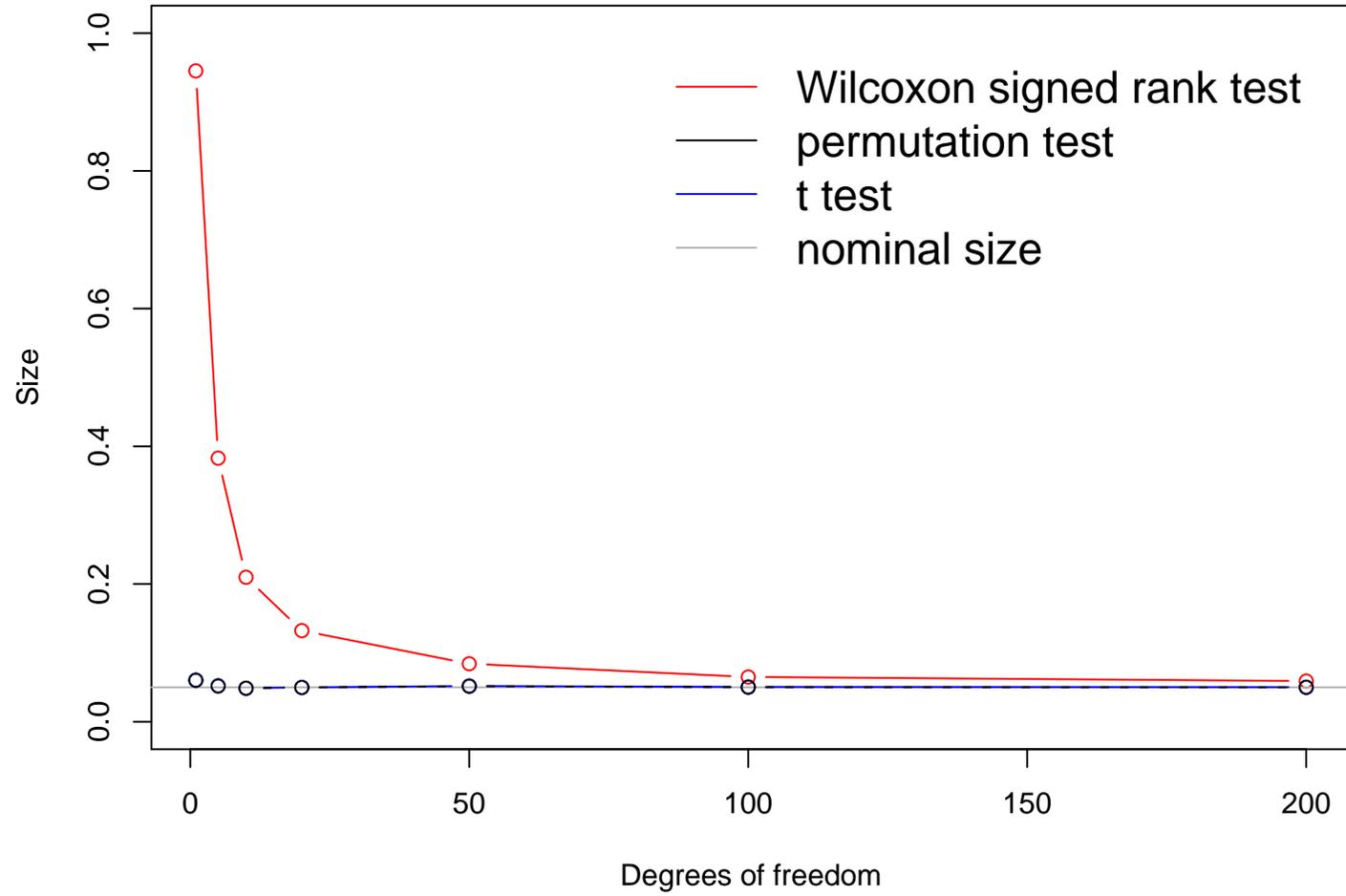
Tests like the Wilcoxon signed rank test are constructed for the null-hypothesis 'the difference of the performance measures is **symmetrically** distributed around zero'. For non-symmetric distributions this leads to a complete disaster.

Look at  $n = 500$  realizations of a skewed random variable

$$\frac{X - d}{\sqrt{2d}}$$

with expectation zero and unit variance with  $X \sim \chi_d^2$ .

# Benchmark Experiments

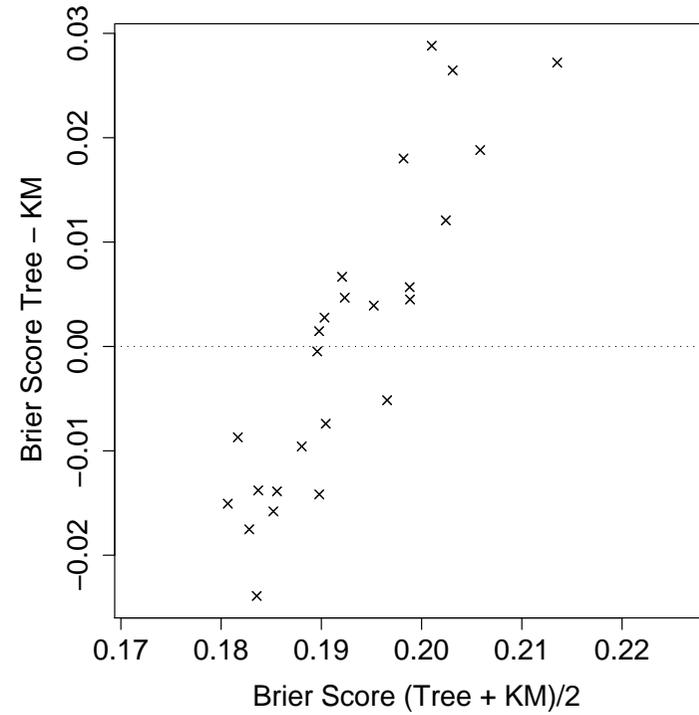
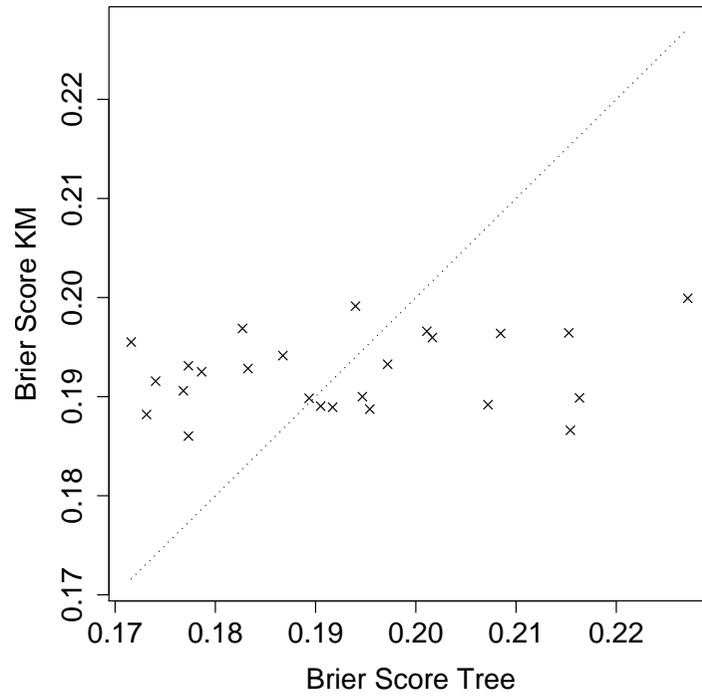


## Lifetime Analysis Problems

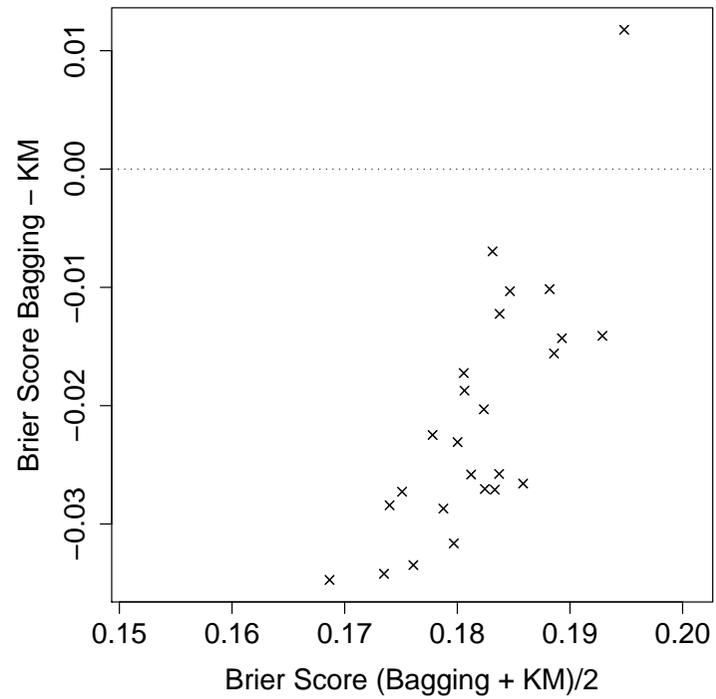
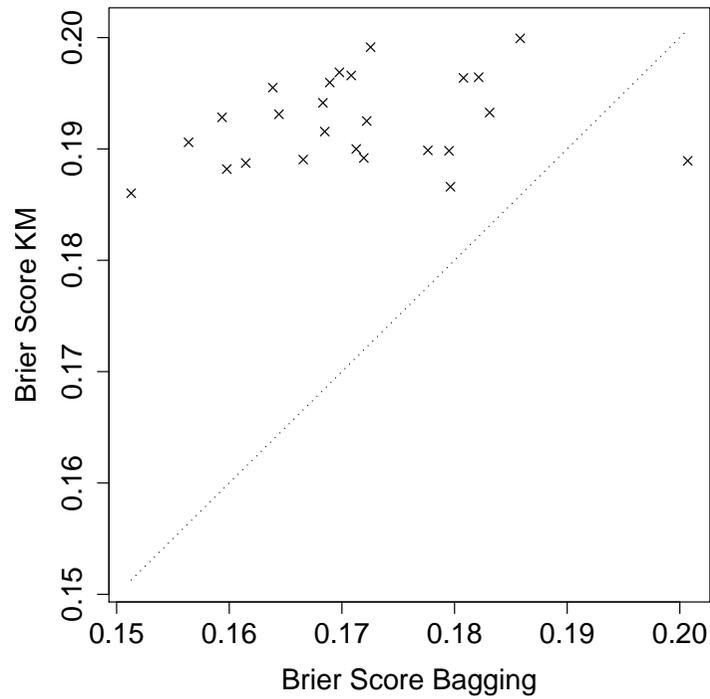
Appropriate performance measures for censored responses are by no means obvious and still a matter of debate ([Henderson, 1995](#); [Graf et al., 1999](#); [Molinaro et al., 2004](#)). We use the Brier score for censored data suggested by [Graf et al. \(1999\)](#).

Example: Predictive performance of the Kaplan-Meier estimator, a single survival tree and Bagging of survival trees ([Hothorn et al., 2004](#)) measured for  $n = 686$  women enrolled in the German Breast Cancer Study (Group 2).

# Kaplan-Meier vs. Single Tree

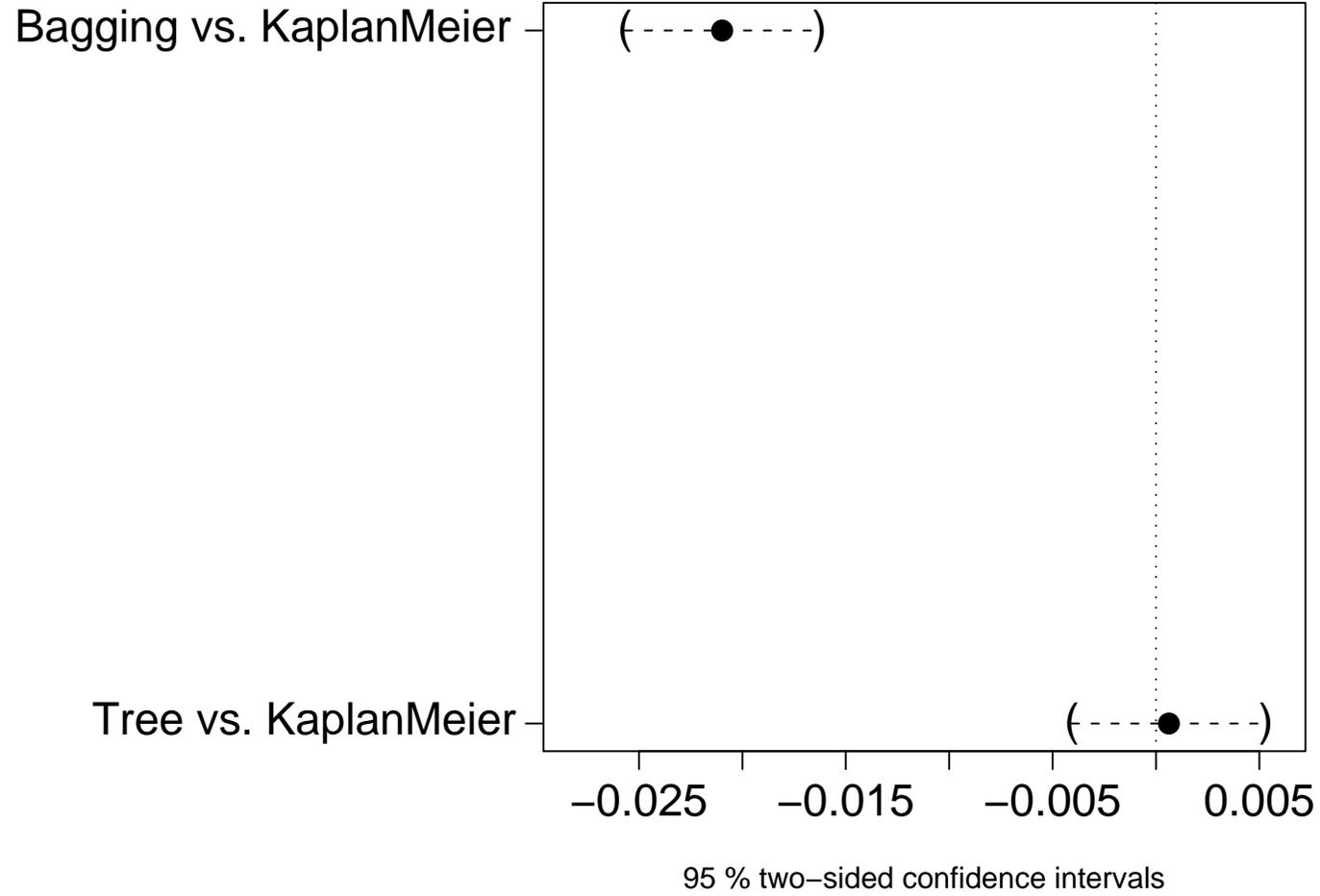


# Kaplan-Meier vs. Bagging



Benchmark Experiments

Asymptotic Dunnett Confidence Sets



## Interpretation

Predictions derived from the estimated Kaplan-Meier curve don't take any information covered by the input variables into account. A test for the hypothesis

*there is no (detectable) relationship between the input variables and the response*

can therefore be performed by comparing the performance of the simple Kaplan-Meier curve with the performance of the best tools available for predicting survival times.

## Conclusion

When comparing the performance of  $K$  algorithms it is appropriate to treat the  $B$  samples from the data generating process as blocks.

Standard statistical test procedures can be used to compare arbitrary performance measures for multiple algorithms.

Some classical parametric and non-parametric procedures are only sub-optimal, we advocate procedures based on the conditional distribution of test statistics for inference.

## References

- Graf, E., Schmoor, C., Sauerbrei, W., and Schumacher, M. (1999), "Assessment and comparison of prognostic classification schemes for survival data," *Statistics in Medicine*, 18, 2529–2545.
- Hájek, J., Šidák, Z., and Sen, P. K. (1999), *Theory of Rank Tests*, London: Academic Press, 2nd edition.
- Henderson, R. (1995), "Problems and prediction in survival-data analysis," *Statistics in Medicine*, 14, 161–184.
- Hothorn, T. and Lausen, B. (2003), "Bundling classifiers by bagging trees," *Preprint, Friedrich-Alexander-University Erlangen-Nuremberg*, URL <http://www.mathpreprints.com/>.
- Hothorn, T., Lausen, B., Benner, A., and Radespiel-Tröger, M. (2004), "Bagging survival trees," *Statistics in Medicine*, 23, 77–91.
- Hothorn, T., Pal, I., Gefeller, O., Lausen, B., Michelson, G., and Paulus, D. (2003), "Automated classification of optic nerve head topography images for glaucoma screening," in *Studies in Classification, Data Analysis, and Knowledge Organization: Exploratory Data Analysis in Empirical Research*, eds. M. Schwaiger and O. Opitz, Heidelberg: Springer, pp. 346–356.
- Kropf, S. (2000), *Hochdimensionale multivariate Verfahren in der medizinischen Statistik*, Aachen: Shaker Verlag.
- Läuter, J. (1992), *Stabile multivariate Verfahren: Diskriminanzanalyse - Regressionsanalyse - Faktoranalyse*, Berlin: Akademie Verlag.
- Läuter, J., Glimm, E., and Kropf, S. (1998), "Multivariate tests based on left-spherically distributed linear scores," *The Annals of Statistics*, 26, 1972–1988, correction: 1999, Vol. 27, p. 1441.
- Mardin, C. Y., Hothorn, T., Peters, A., Jünemann, A. G., Nguyen, N. X., and Lausen, B. (2003), "New glaucoma classification method based on standard HRT parameters by bagging classification trees," *Journal of Glaucoma*, 12, 340–346.
- Molinaro, A. M., Dudoit, S., and van der Laan, M. J. (2004), "Tree-based multivariate regression and density estimation with right-censored data," *Journal of Multivariate Analysis*, 90, 154–177.