Survival Ensembles

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1 Illustrations and Applications

This document reproduces the data analyses presented in Hothorn et~al. (2006). For a description of the theory behind applications shown here we refer to the original manuscript. The results differ slightly due to technical changes or bug-fixes in **mboost** that have been implemented after the paper was printed.

1.1 Acute myeloid leukemia

Data preprocessing Compute IPC weights, define risk score and set up learning sample:

R> ### compute IPC weights
R> AMLw <- IPCweights(Surv(clinical\$time, clinical\$event))</pre>

```
R> ### risk score
R> risk <- rep(0, nrow(clinical))</pre>
R> rlev <- levels(clinical[, "Cytogenetic.group"])</pre>
R> risk[clinical[, "Cytogenetic.group"] %in% rlev[c(7,8,4)]] <- "low"</pre>
R> risk[clinical[, "Cytogenetic.group"] %in% rlev[c(5, 9)]] <- "intermediate"</pre>
R> risk[clinical[, "Cytogenetic.group"] %in% rlev[-c(4,5, 7,8,9)]] <- "high"
R> risk <- as.factor(risk)</pre>
R> ### set-up learning sample
R> AMLlearn <- cbind(clinical[, c("time", "Sex", "Age", "LDH", "WBC",
                             "FLT3.aberration.", "MLL.PTD", "Tx.Group.")],
                    risk = risk,
                    iexpressions[, colnames(iexpressions) %in% selgenes[["Clone.ID"]]])
R> cc <- complete.cases(AMLlearn)</pre>
R> AMLlearn <- AMLlearn[AMLw > 0 & cc,]
R> AMLw <- AMLw[AMLw > 0 & cc]
Model fitting Fit random forest for censored data
R> ### controls for tree growing
R> ctrl <- cforest_control(mincriterion = 0.1, mtry = 5, minsplit = 5, ntree = 250)
R> ### fit random forest for censored data (warnings are OK here)
R> AMLrf <- cforest(I(log(time)) ~ ., data = AMLlearn, control = ctrl,</pre>
                      weights = AMLw)
and L_2Boosting for censored data
R> AML12b <- glmboost(I(log(time)) ~ ., data = AMLlearn, weights = AMLw,
                         control = boost_control(mstop = 5000))
   Compute fitted values
R> ### restrict number of boosting iterations and inspect selected variables
R> AML12b <- AML12b[mstop(aic)]</pre>
R> cAML <- coef(AML12b)
R> cAML[abs(cAML) > 0]
   (Intercept)
                         Age
                 Age WBC
0.0059785 -0.0056200
     0.5642932
    MLL.PTDyes Tx.Group.AUTO Tx.Group.Ind
 -2.1216104
     0.1062577
                0.0043043
                               0.0275653
`IMAGE:2043415` `IMAGE:1584563` `IMAGE:347035`
     0.0550938
                -0.0025929
                                -0.0084766
               `IMAGE:26418` `IMAGE:950479`
 `IMAGE:262695`
                   0.0080214
     0.0269555
                                  0.0371741
`IMAGE:1534700` `IMAGE:1472689` `IMAGE:1526826`
    0.0283645 0.0225640
                                -0.0278373
 `IMAGE:786302` `IMAGE:243614` `IMAGE:417884`
     0.0449326
                 -0.0566722
                                -0.0248869
`IMAGE:1592006` `IMAGE:884333` `IMAGE:133273`
```

R> ### AIC criterion
R> plot(aic <- AIC(AML12b))</pre>

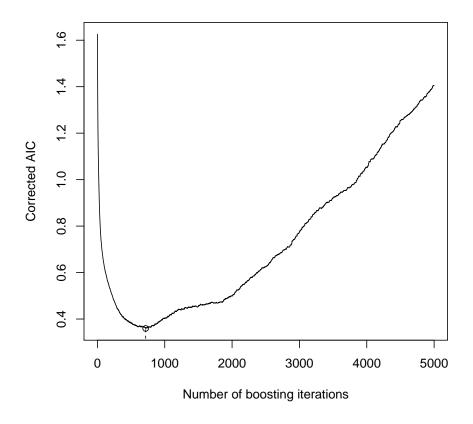


Figure 1: AIC criterion for AML data.

```
-0.0355121 0.0128054 0.0257924

`IMAGE:950888` `IMAGE:809533` `IMAGE:49389`
                                   0.0257924
     0.0348510 -0.0583489 0.1210483
 `IMAGE:856174` `IMAGE:435036` `IMAGE:491751`
 0.0205370 0.0620215 0.1155506

`IMAGE:782835` `IMAGE:52930` `IMAGE:2545705`

-0.1108508 -0.0245246 -0.0788422
                                  0.1155506
                   -0.0245246
                                 -0.0788422
 `IMAGE:756405` `IMAGE:129032` `IMAGE:1610168`
     0.0085293 -0.1158217
                                    0.0137998
  `IMAGE:69002` `IMAGE:2019101` `IMAGE:1456160`
-0.2793326 -0.0966590 -0.1041466
`IMAGE:2566064` `IMAGE:565083` `IMAGE:843028`
                                  -0.1041466
     0.0154665
                  0.1875592
                                  0.0698328
  `IMAGE:68794` `IMAGE:488505` `IMAGE:291756`
                 0.2784632
     0.0761390
                                   0.0994879
 `IMAGE:810801` `IMAGE:1702742` `IMAGE:380462`
     0.0465851 -0.0104549
                                   -0.0957299
 `IMAGE:154472` `IMAGE:302540` `IMAGE:135221`
     -0.1454724 0.0188789
                                   -0.0366827
`IMAGE:1567220`
      0.0485058
R> ### fitted values
R> AMLprf <- predict(AMLrf, newdata = AMLlearn)</pre>
R> AMLpb <- predict(AML12b, newdata = AMLlearn)
      Node-positive breast cancer
Data preprocessing Compute IPC weights and set up learning sample:
R> ### attach data
R> data("GBSG2", package = "TH.data")
R> ### IPC weights
R> GBSG2w <- IPCweights(Surv(GBSG2$time, GBSG2$cens))
R> ### set-up learning sample
R> GBSG21earn <- cbind(GBSG2[,-which(names(GBSG2) %in% c("time", "cens"))],
                      ltime = log(GBSG2$time))
R> n <- nrow(GBSG2learn)</pre>
Model fitting
R> ### linear model
R> LMmod <- lm(ltime \tilde{\ } . , data = GBSG2learn, weights = GBSG2w)
R> LMerisk <- sum((GBSG2learn$ltime - predict(LMmod))^2*GBSG2w) / n
R> ### regression tree
R > pos <- GBSG2w > 0
R> TRmod <- rpart(ltime ~ . , data = GBSG2learn, weights = GBSG2w,</pre>
                      subset = pos)
R> TRerisk <- sum((GBSG2learn$ltime[pos] - predict(TRmod))^2*GBSG2w[pos]) / n</pre>
```

R> ### tree controls

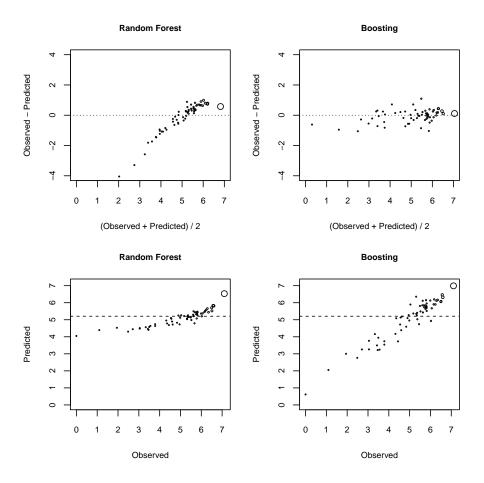


Figure 2: AML data: Reproduction of Figure 1.

R> L2Berisk <- sum((GBSG2learn\$ltime - predict(L2Bmod, newdata = GBSG2learn))^2*GBSG2w) / n
R> RFerisk <- sum((GBSG2learn\$ltime - predict(RFmod, newdata = GBSG2learn))^2*GBSG2w) / n</pre>

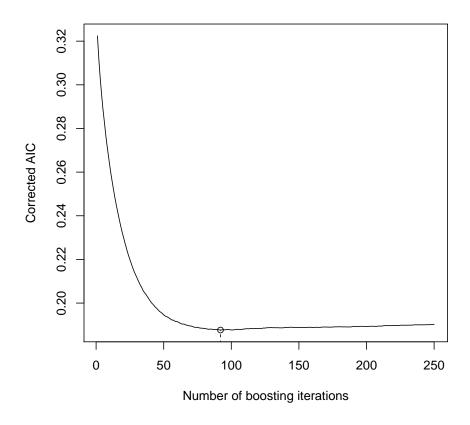


Figure 3: AIC criterion for GBSG2 data.

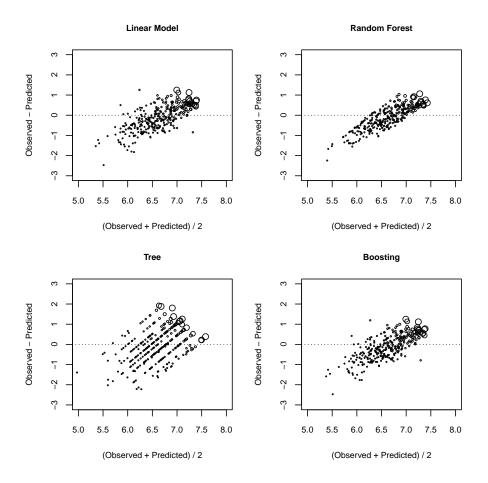


Figure 4: GBSG-2 data: Reproduction of Figure 3.

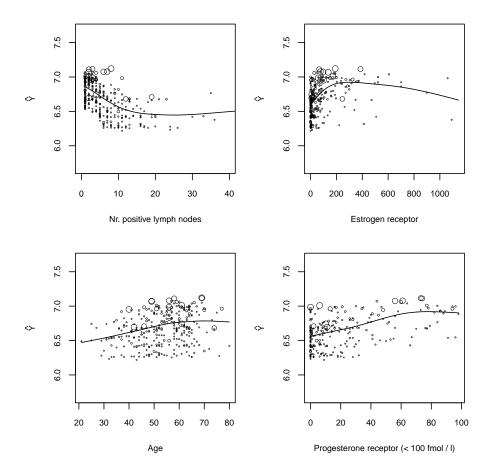


Figure 5: GBSG-2 data: Reproduction of Figure 5.

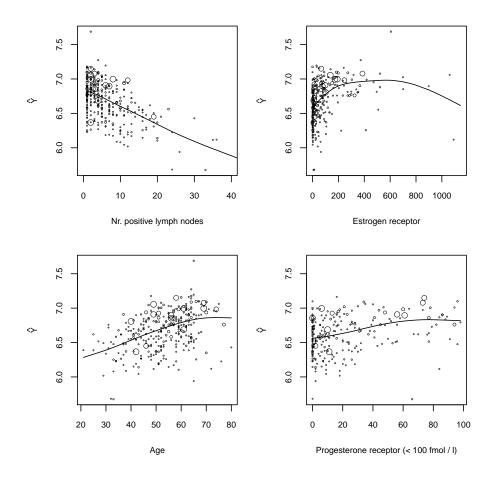


Figure 6: GBSG-2 data: Reproduction of Figure 6.

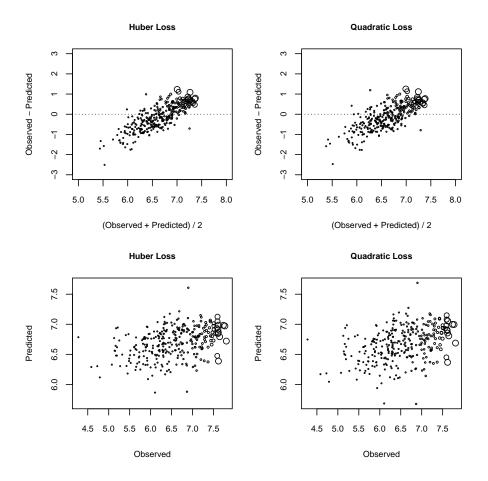


Figure 7: GBSG-2 data: Reproduction of Figure 7.

References

T. Hothorn, P. Bühlmann, S. Dudoit, A. Molinaro, and M. van der Laan. Survival ensembles. *Biostatistics*, 7:355–373, 2006.