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> AMLw <- IPCweights(Surv(clinical$time, clinical$event))
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"
R> risk[clinical[, "Cytogenetic.group"] %in% rlev[c(5,
         9)]] <- "intermediate"
R> risk[clinical[, "Cytogenetic.group"] %in% rlev[-c(4,
         5, 7, 8, 9)]] <- "high"
R> risk <- as.factor(risk)</pre>
R> AMLlearn <- cbind(clinical[, c("time", "Sex",</pre>
         "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> ctrl <- cforest_control(mincriterion = 0.1, mtry = 5,
         minsplit = 5, ntree = 250)
R> AMLrf <- cforest(I(log(time)) ~ ., data = AMLlearn,</pre>
         control = ctrl, weights = AMLw)
and L_2Boosting for censored data
R> AML12b <- glmboost(I(log(time)) ~ ., data = AMLlearn,</pre>
         weights = AMLw, control = boost_control(mstop = 5000))
   Compute fitted values
R> AML12b <- AML12b[mstop(aic)]</pre>
R> cAML <- coef(AML12b)
R> cAML[abs(cAML) > 0]
     (Intercept)
                            Age
                                             WBC
                                   -0.00364371
     0.03094981
                    0.00854937
     MLL.PTDyes Tx.Group.AUTO Tx.Group.IC
                   0.90185340
    -0.50709786
                                    0.04037578
   Tx.Group.Ind riskintermediate `IMAGE:145643`
    -1.86134842 0.11825619
                                   0.19788355
 `IMAGE:2542486` `IMAGE:345601` `IMAGE:377560`
     0.00442375
                    0.02935101
                                     0.11000322
  `IMAGE:428782` `IMAGE:2043415` `IMAGE:1584563`
     0.01010658
                     0.05911671
                                    -0.17883619
  `IMAGE:347035` `IMAGE:262695`
                                 `IMAGE:950479`
    -0.03307600
                    0.00080156
                                    0.09049309
  `IMAGE:898305` `IMAGE:1472689`
                                  `IMAGE:150702`
     0.00523016
                    0.03498572
                                    0.01367553
                                  `IMAGE:786302`
 `IMAGE:1526826`
                   `IMAGE:66507`
    -0.01805326
                    0.00399127
                                   0.08941300
  `IMAGE:243614` `IMAGE:417884` `IMAGE:1592006`
```

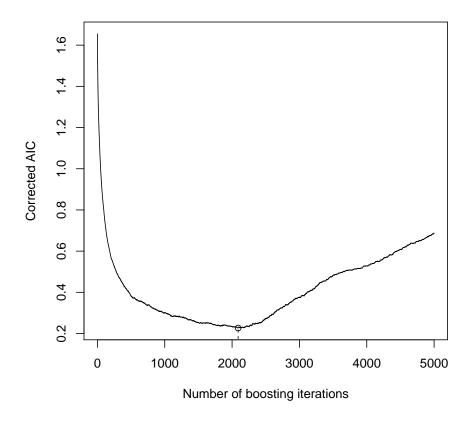


Figure 1: AIC criterion for AML data.

```
-0.05776062
                -0.04890054
                              -0.02269622
`IMAGE:1917063` `IMAGE:884333` `IMAGE:133273`
  -0.06536720
               0.04189990
                             0.06594787
 `IMAGE:950888` `IMAGE:809533`
                            `IMAGE:49389`
0.01115234
                0.06861766
                               0.06094620
              `IMAGE:782835`
                             `IMAGE:52930`
 `IMAGE:491751`
   0.04336285
               -0.17924185
                              -0.03503330
`IMAGE:2545705` `IMAGE:756405` `IMAGE:502664`
               0.07713650
   -0.09886616
                              0.03620466
 `IMAGE:129032` `IMAGE:1610168` `IMAGE:327676`
 -0.31322459 0.01260374 -0.02117310

`IMAGE:69002` `IMAGE:121551` `IMAGE:2019101`
                              -0.02117310
   -0.41671336
                -0.08107446
                              -0.06531175
`IMAGE:1456160` `IMAGE:430318` `IMAGE:2566064`
               -0.07297586
 -0.10208684 -0.07297586
`IMAGE:74537` `IMAGE:1606557`
                              0.06126683
               0.03504441
 0.23722775
                               0.04973319
 `IMAGE:810801` `IMAGE:1702742` `IMAGE:380462`
   0.08725523
               -0.04428190
                              -0.13182519
 `IMAGE:154472` `IMAGE:302540` `IMAGE:135221`
   -0.24723347
                0.17175129
                              -0.01972168
`IMAGE:1567220`
              `IMAGE:594630`
    0.02473376
                -0.07396882
```

```
R> AMLprf <- predict(AMLrf, newdata = AMLlearn)
R> AMLpb <- predict(AMLl2b, newdata = AMLlearn)</pre>
```

1.2 Node-positive breast cancer

Data preprocessing Compute IPC weights and set up learning sample:

Model fitting

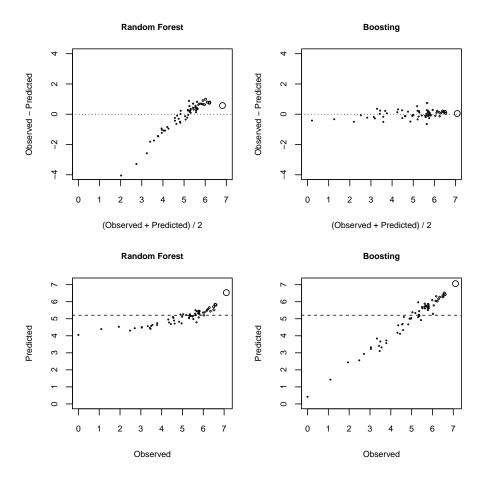


Figure 2: AML data: Reproduction of Figure 1.

GBSG2w)/n

Compute fitted values:

- R> GBSG2Hp <- predict(L2BHubermod, newdata = GBSG2learn)

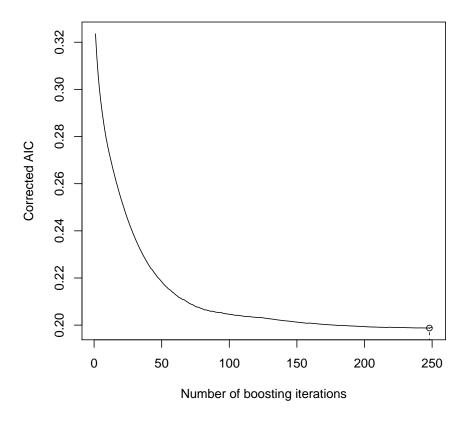


Figure 3: AIC criterion for GBSG2 data.

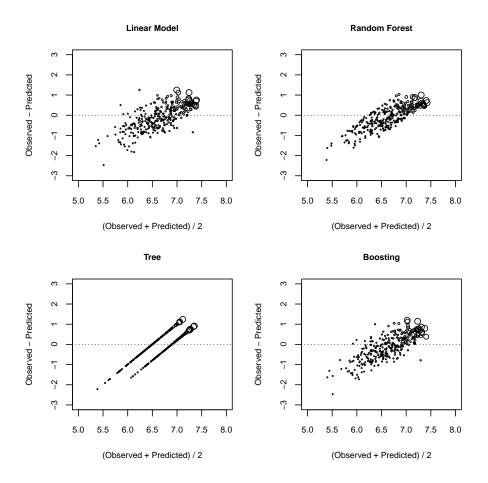


Figure 4: GBSG-2 data: Reproduction of Figure 3.

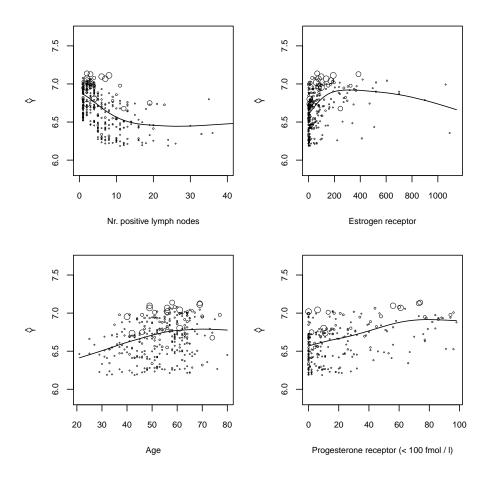


Figure 5: GBSG-2 data: Reproduction of Figure 5.

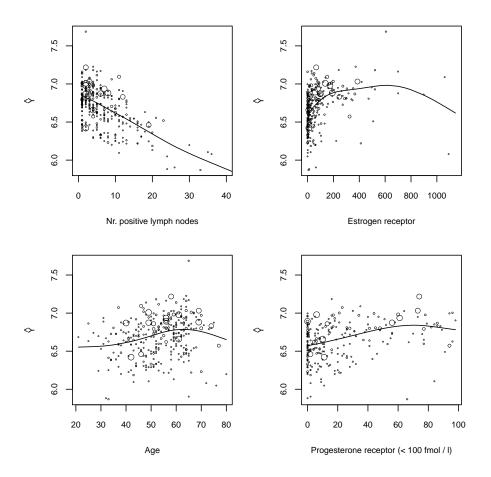


Figure 6: GBSG-2 data: Reproduction of Figure 6.

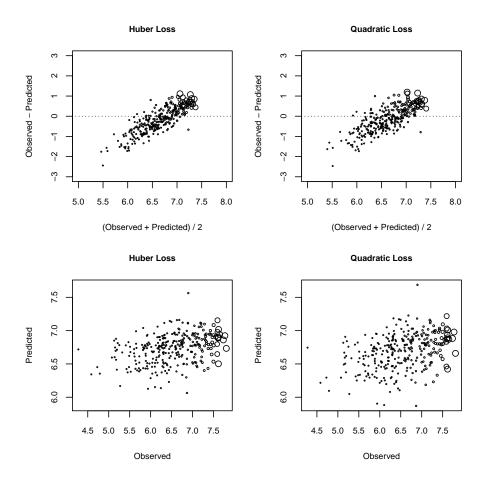


Figure 7: GBSG-2 data: Reproduction of Figure 7.

References

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