

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.

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))  
R> rlev <- levels(clinical[, "Cytogenetic.group"])
```

```

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)
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)
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,
  control = ctrl, weights = AMLw)

```

and L_2 Boosting for censored data

```

R> AMLl2b <- glmboost(I(log(time)) ~ ., data = AMLlearn,
  weights = AMLw, control = boost_control(mstop = 5000))

```

Compute fitted values

```

R> AMLl2b <- AMLl2b[mstop(aic)]
R> cAML <- coef(AMLl2b)
R> cAML[abs(cAML) > 0]

```

(Intercept)	Age	WBC
0.03094981	0.00854937	-0.00364371
MLL.PTDyes	Tx.Group.AUTO	Tx.Group.IC
-0.50709786	0.90185340	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:1526826`	`IMAGE:66507`	`IMAGE:786302`
-0.01805326	0.00399127	0.08941300
`IMAGE:243614`	`IMAGE:417884`	`IMAGE:1592006`
-0.05776062	-0.04890054	-0.02269622
`IMAGE:1917063`	`IMAGE:884333`	`IMAGE:133273`

```
R> plot(aic <- AIC(AML12b))
```

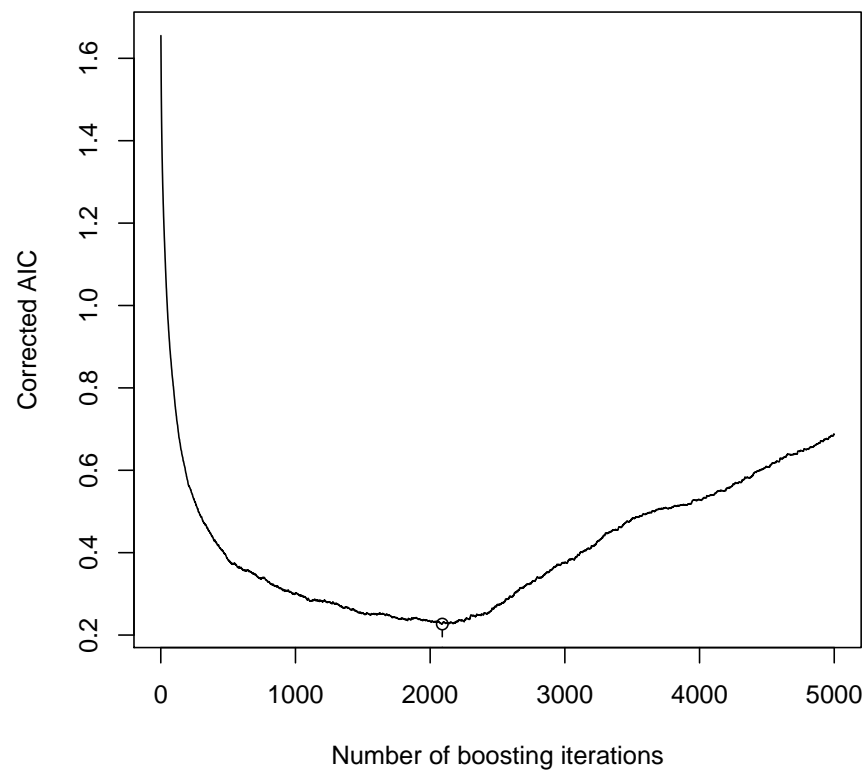


Figure 1: AIC criterion for AML data.

```

-0.06536720      0.04189990      0.06594787
`IMAGE:950888`    `IMAGE:809533`    `IMAGE:49389`
0.02027810      -0.15986981      0.06352703
`IMAGE:789357`    `IMAGE:142139`    `IMAGE:1558053`
-0.01252187      0.00089307      0.07795515
`IMAGE:856174`    `IMAGE:504421`    `IMAGE:435036`
0.01115234      0.06861766      0.06094620
`IMAGE:491751`    `IMAGE:782835`    `IMAGE:52930`
0.04336285      -0.17924185      -0.03503330
`IMAGE:2545705`    `IMAGE:756405`    `IMAGE:502664`
-0.09886616      0.07713650      0.03620466
`IMAGE:129032`    `IMAGE:1610168`    `IMAGE:327676`
-0.31322459      0.01260374      -0.02117310
`IMAGE:69002`    `IMAGE:121551`    `IMAGE:2019101`
-0.41671336      -0.08107446      -0.06531175
`IMAGE:1456160`    `IMAGE:430318`    `IMAGE:2566064`
-0.10208684      -0.07297586      0.06126683
`IMAGE:74537`    `IMAGE:1606557`    `IMAGE:306812`
0.04523784      0.14243526      0.03504441
`IMAGE:565083`    `IMAGE:843028`    `IMAGE:68794`
0.29555347      0.05619983      0.23722775
`IMAGE:488505`    `IMAGE:167205`    `IMAGE:291756`
0.33464829      0.00217136      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(AMLrfr, newdata = AMLlearn)
R> AMLpb <- predict(AMLl2b, newdata = AMLlearn)

```

1.2 Node-positive breast cancer

Data preprocessing Compute IPC weights and set up learning sample:

```

R> data("GBSG2", package = "ipred")
R> GBSG2w <- IPCweights(Surv(GBSG2$time, GBSG2$cens))
R> GBSG2learn <- cbind(GBSG2[, -which(names(GBSG2) %in%
c("time", "cens"))], ltime = log(GBSG2$time))
R> n <- nrow(GBSG2learn)

```

Model fitting

```

R> LMmod <- lm(ltime ~ ., data = GBSG2learn, weights = GBSG2w)
R> LMerisk <- sum((GBSG2learn$ltime - predict(LMmod))^2 *
GBSG2w)/n
R> TRmod <- rpart(ltime ~ ., data = GBSG2learn, weights = GBSG2w)
R> TRerisk <- sum((GBSG2learn$ltime - predict(TRmod))^2 *
GBSG2w)/n
R> ctrl <- cforest_control(mincriterion = qnorm(0.95),

```

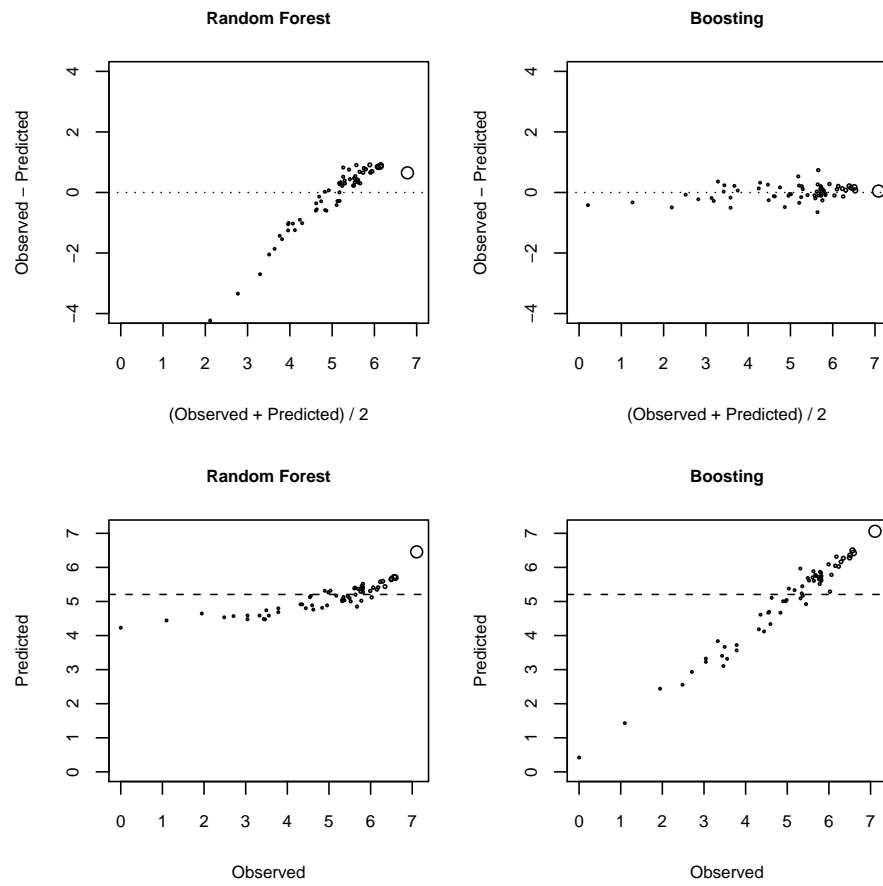


Figure 2: AML data: Reproduction of Figure 1.

```

      mtry = 5, minsplit = 5, ntree = 100)
R> RFmod <- cforest(ltime ~ ., data = GBSG2learn,
  weights = GBSG2w, control = ctrl)
R> L2Bmod <- glmboost(ltime ~ ., data = GBSG2learn,
  weights = GBSG2w, control = boost_control(mstop = 250))
R> L2BHubermod <- glmboost(ltime ~ ., data = GBSG2learn,
  weights = GBSG2w, family = Huber(d = log(2)))

```

Compute fitted values:

```

R> GBSG2Hp <- predict(L2BHubermod, newdata = GBSG2learn)
R> L2Berisk <- sum((GBSG2learn$ltime - predict(L2Bmod,
  newdata = GBSG2learn))^2 * GBSG2w)/n
R> RFerisk <- sum((GBSG2learn$ltime - predict(RFmod,
  newdata = GBSG2learn))^2 * GBSG2w)/n

```

```
R> plot(aic <- AIC(L2Bmod))
```

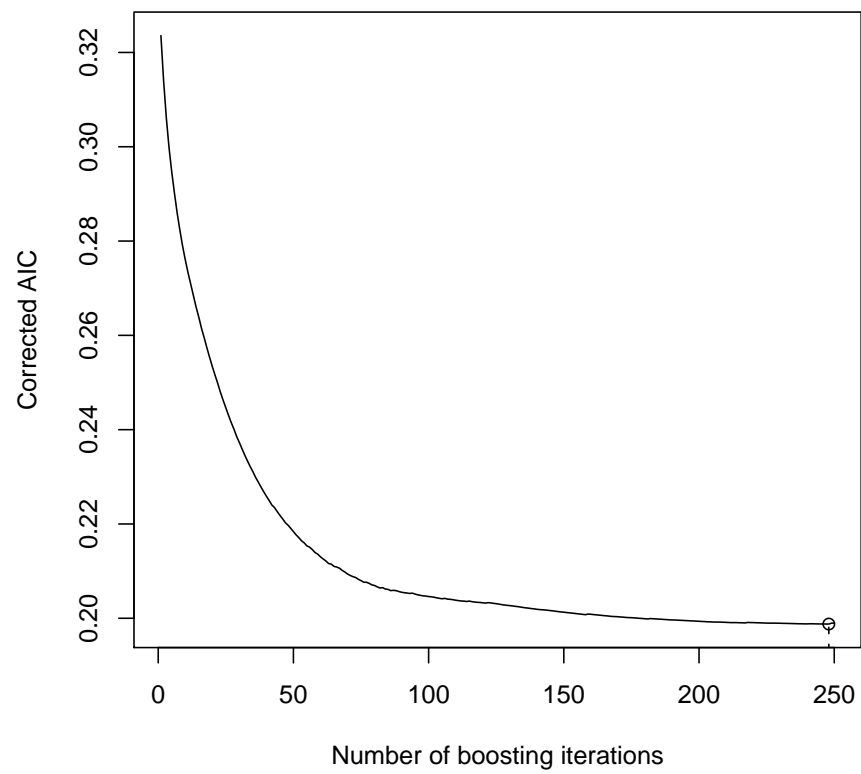


Figure 3: AIC criterion for GBSG2 data.

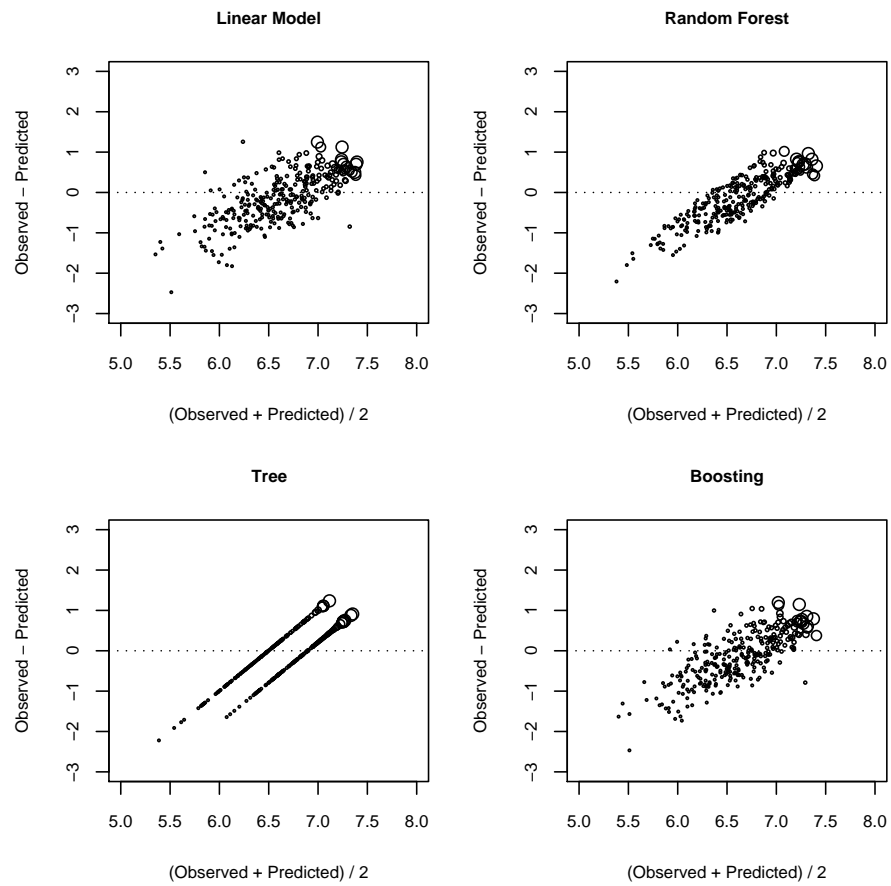


Figure 4: GBSG-2 data: Reproduction of Figure 3.

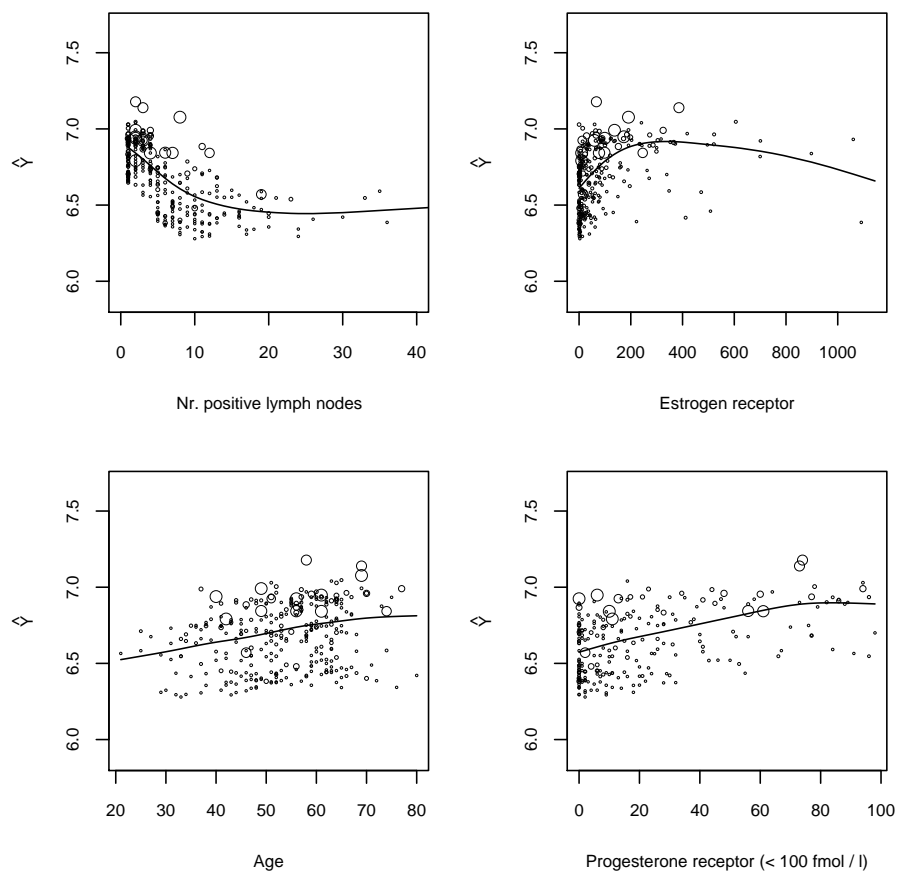


Figure 5: GBSG-2 data: Reproduction of Figure 5.

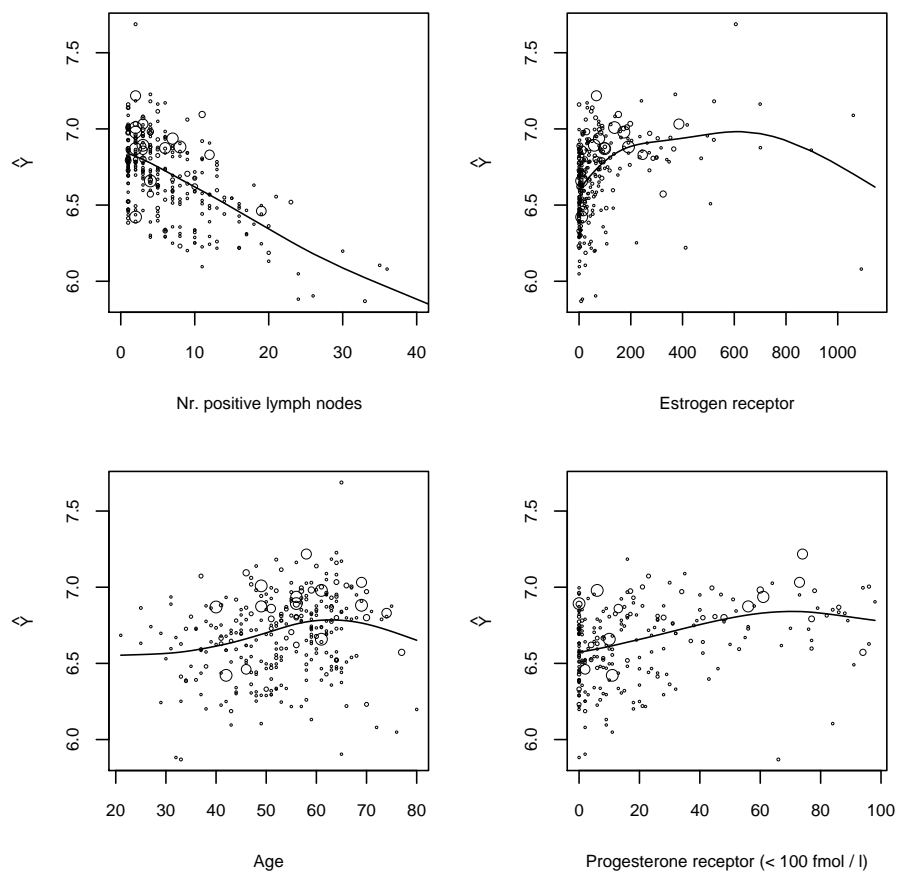


Figure 6: GBSG-2 data: Reproduction of Figure 6.

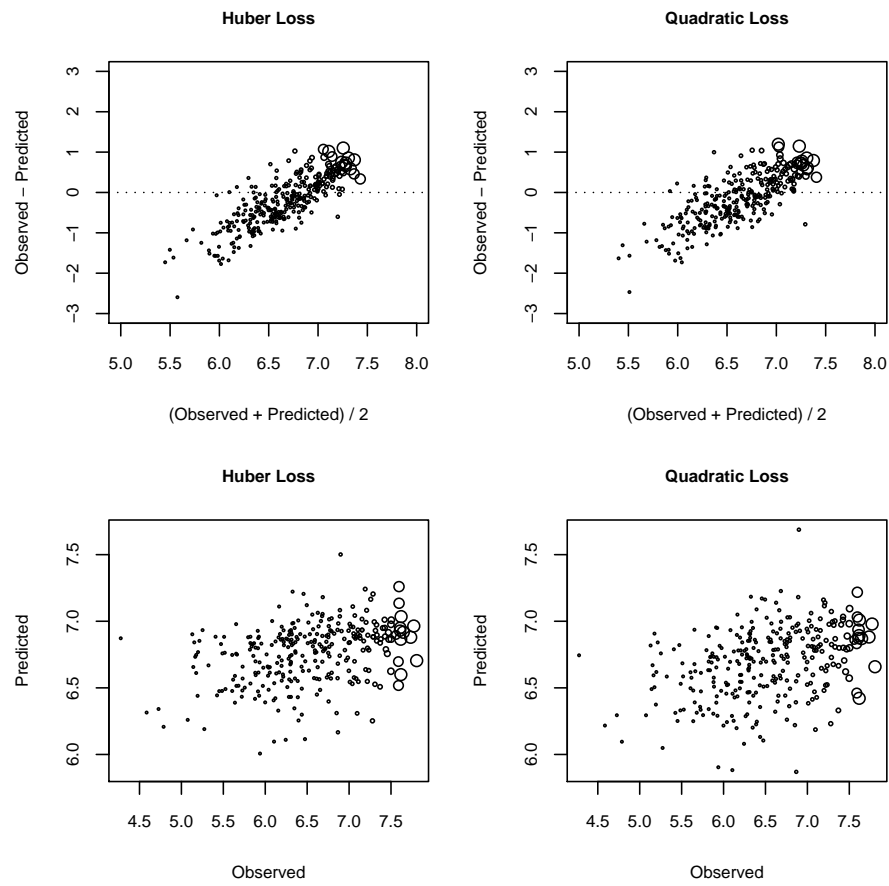


Figure 7: GBSG-2 data: Reproduction of Figure 7.

References

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