

# 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,
minsplitt = 5, ntree = 250)
R> AMLrfr <- 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))
```

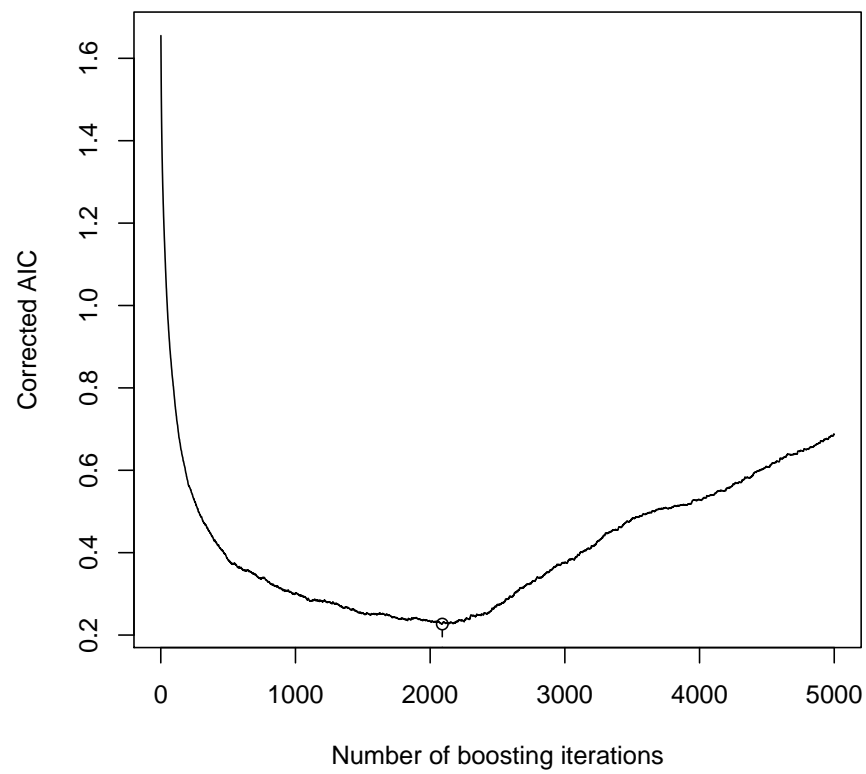


Figure 1: AIC criterion for AML data.

```

-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),

```

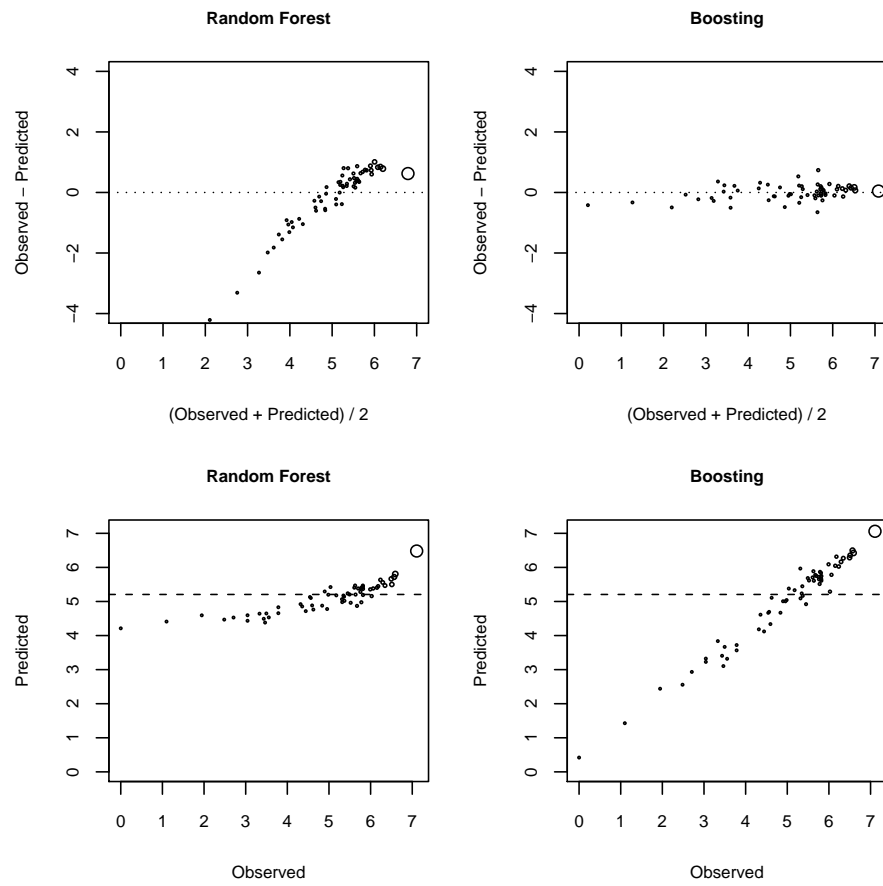


Figure 2: AML data: Reproduction of Figure 1.

```

      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))
```

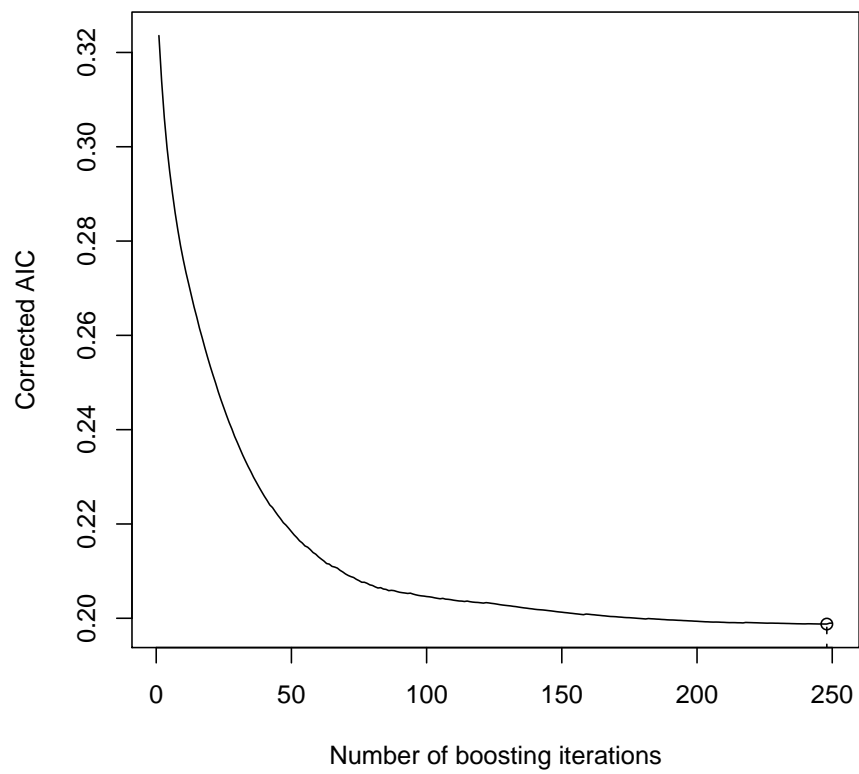


Figure 3: AIC criterion for GBSG2 data.

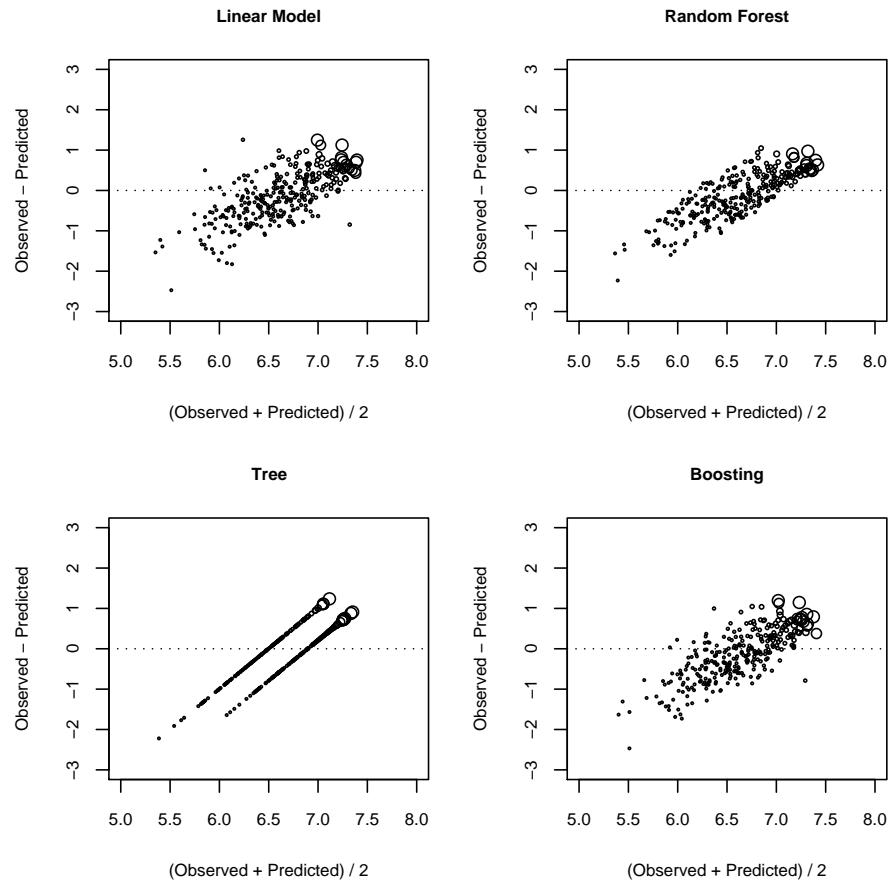


Figure 4: GBSG-2 data: Reproduction of Figure 3.



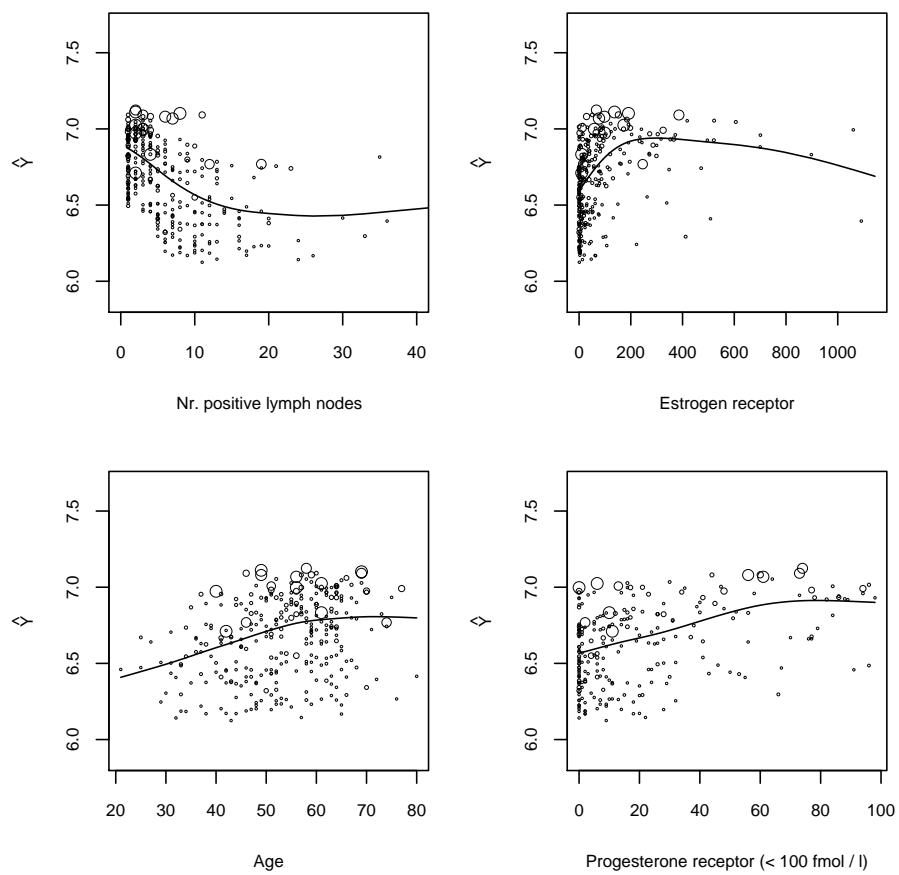


Figure 5: GBSG-2 data: Reproduction of Figure 5.

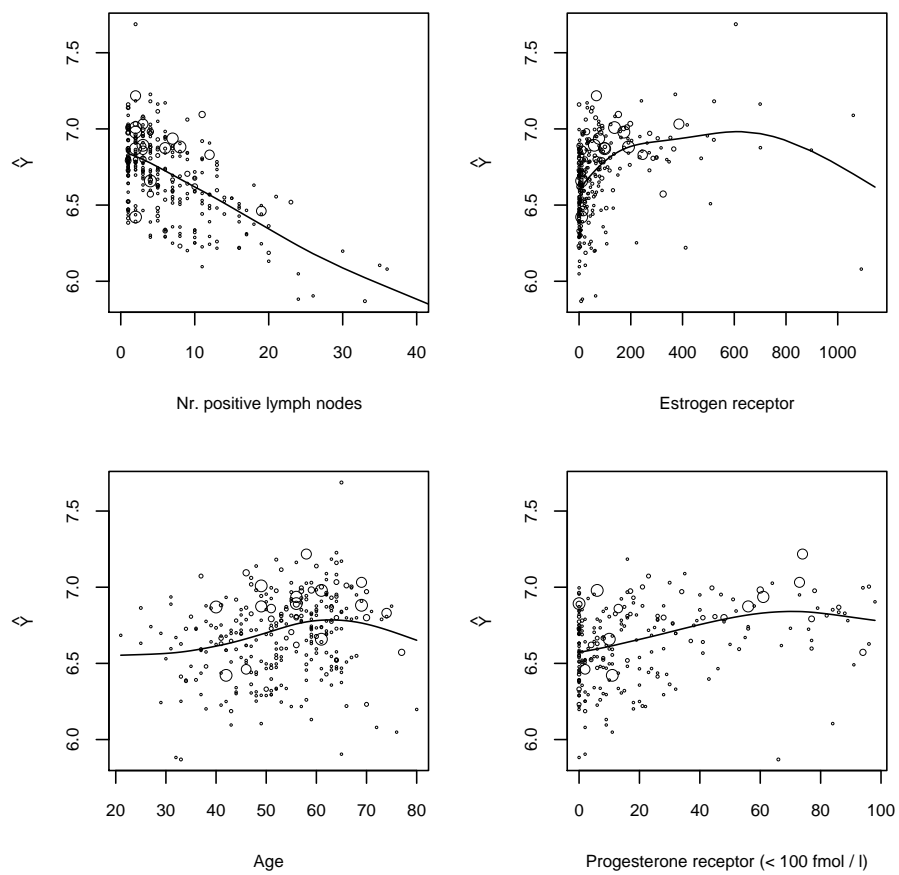


Figure 6: GBSG-2 data: Reproduction of Figure 6.

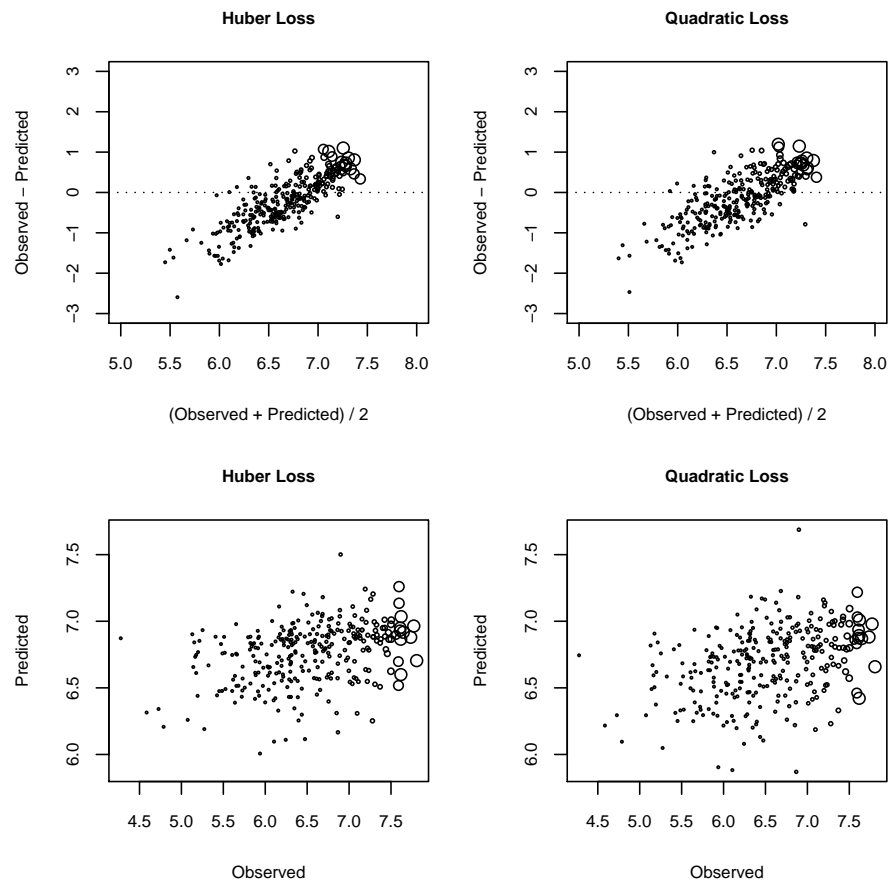


Figure 7: GBSG-2 data: Reproduction of Figure 7.

## References

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