

# 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))
```

```

R> ### risk score
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> ### 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)
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 <- ctree_control(teststyp = "Teststatistic",
                        teststat = "maximum", mincriterion = .1, minsplit = 5)
R> ### was: cforest_control(mincriterion = 0.1, mtry = 5, minsplit = 5, ntree = 250)
R>
R> ### fit random forest for censored data (warnings are OK here)
R> AMLrf <- cforest(log(time) ~ ., data = AMLlearn, control = ctrl,
                    weights = AMLw, mtry = 5, ntree = 250,
                    perturb = list(replace = TRUE, fraction = 0.632))

```

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> ### restrict number of boosting iterations and inspect selected variables
R> AMLl2b <- AMLl2b[mstop(aic)]
R> cAML <- coef(AMLl2b)
R> cAML[abs(cAML) > 0]

```

<i>(Intercept)</i>	<i>Age</i>	<i>WBC</i>
0.56429	0.00598	-0.00562
<i>MLL.PTDyes</i>	<i>Tx.Group.AUTO</i>	<i>Tx.Group.Ind</i>
-0.31539	0.45430	-2.12161
<i>`IMAGE:145643`</i>	<i>`IMAGE:345601`</i>	<i>`IMAGE:377560`</i>
0.10626	0.00430	0.02757
<i>`IMAGE:2043415`</i>	<i>`IMAGE:1584563`</i>	<i>`IMAGE:347035`</i>
0.05509	-0.00259	-0.00848
<i>`IMAGE:262695`</i>	<i>`IMAGE:26418`</i>	<i>`IMAGE:950479`</i>
0.02696	0.00802	0.03717

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

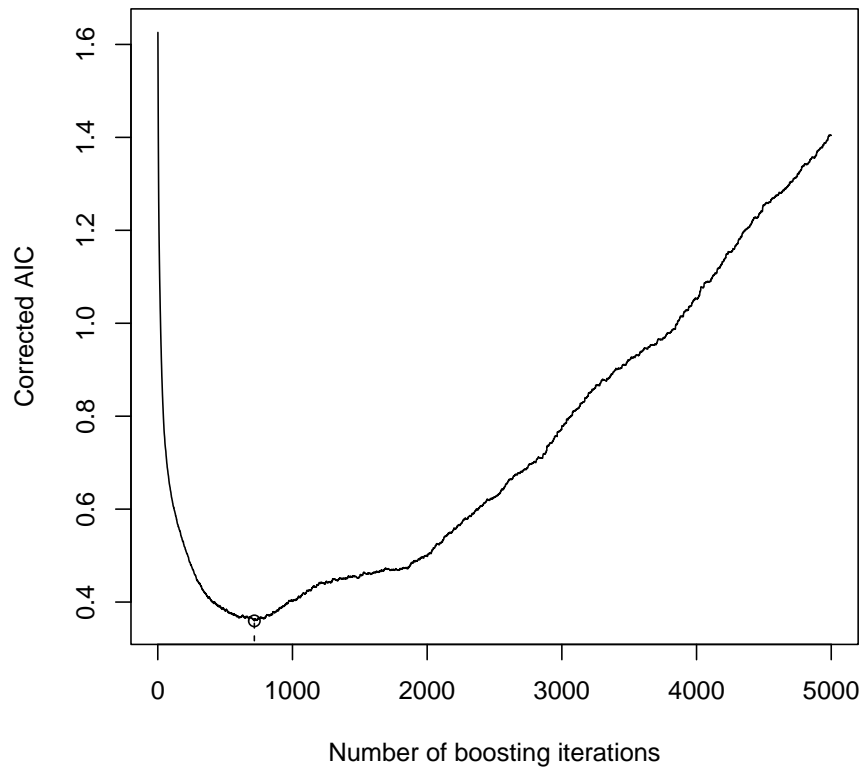


Figure 1: AIC criterion for AML data.

```

`IMAGE:1534700` `IMAGE:1472689` `IMAGE:1526826`
  0.02836      0.02256      -0.02784
`IMAGE:786302` `IMAGE:243614` `IMAGE:417884`
  0.04493      -0.05667      -0.02489
`IMAGE:1592006` `IMAGE:884333` `IMAGE:133273`
 -0.03551      0.01281      0.02579
`IMAGE:950888` `IMAGE:809533` `IMAGE:49389`
  0.03485      -0.05835      0.12105
`IMAGE:856174` `IMAGE:435036` `IMAGE:491751`
  0.02054      0.06202      0.11555
`IMAGE:782835` `IMAGE:52930` `IMAGE:2545705`
 -0.11085      -0.02452      -0.07884
`IMAGE:756405` `IMAGE:129032` `IMAGE:1610168`
  0.00853      -0.11582      0.01380
`IMAGE:69002` `IMAGE:2019101` `IMAGE:1456160`
 -0.27933      -0.09666      -0.10415
`IMAGE:2566064` `IMAGE:565083` `IMAGE:843028`
  0.01547      0.18756      0.06983
`IMAGE:68794` `IMAGE:488505` `IMAGE:291756`
  0.07614      0.27846      0.09949
`IMAGE:810801` `IMAGE:1702742` `IMAGE:380462`
  0.04659      -0.01045      -0.09573
`IMAGE:154472` `IMAGE:302540` `IMAGE:135221`
 -0.14547      0.01888      -0.03668
`IMAGE:1567220`
  0.04851

```

```

R> ### fitted values
R> AMLprf <- predict(AMLrf, 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> ### 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> GBSG2learn <- cbind(GBSG2[,-which(names(GBSG2) %in% c("time", "cens"))],
  ltime = log(GBSG2$time))
R> n <- nrow(GBSG2learn)

```

### Model fitting

```

R> ### linear model
R> LMmod <- lm(ltime ~ ., data = GBSG2learn, weights = GBSG2w)
R> LMerisk <- sum((GBSG2learn$ltime - predict(LMmod))^2*GBSG2w) / n
R> ### regression tree
R> pos <- GBSG2w > 0

```

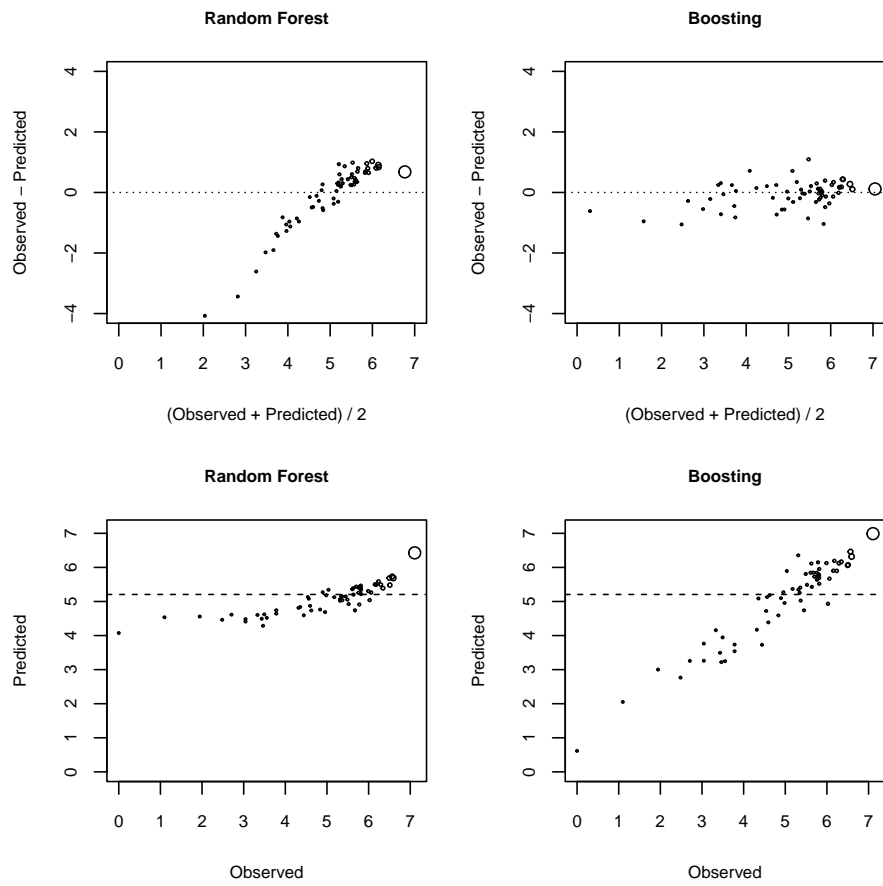


Figure 2: AML data: Reproduction of Figure 1.

```

R> TRmod <- rpart(ltime ~ . , data = GBSG2learn, weights = GBSG2w,
                 subset = pos)
R> TRerisk <- sum((GBSG2learn$ltime[pos] - predict(TRmod))^2*GBSG2w[pos]) / n
R> ### tree controls
R> ctrl <- ctree_control(testtype = "Teststatistic",
                        teststat = "maximum", mincriterion = qnorm(.95),
                        minsplit = 5)
R> ### was: cforest_control(mincriterion = qnorm(0.95), mtry = 5,
R> ###                                minsplit = 5, ntree = 100)
R>
R>
R> ### fit random forest for censored data (warnings are OK here)
R> RFmod <- cforest(ltime ~ . , data = GBSG2learn, weights = GBSG2w,
                  control = ctrl, mtry = 5, ntree = 100,
                  perturb = list(replace = TRUE,
                                fraction = 0.632 * sum(GBSG2w > 0)))
R> ### fit L2 boosting for censored data
R> L2Bmod <- glmboost(ltime ~ . , data = GBSG2learn, weights = GBSG2w,
                   control = boost_control(mstop = 250))
R> ### with Huber loss function
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))
```

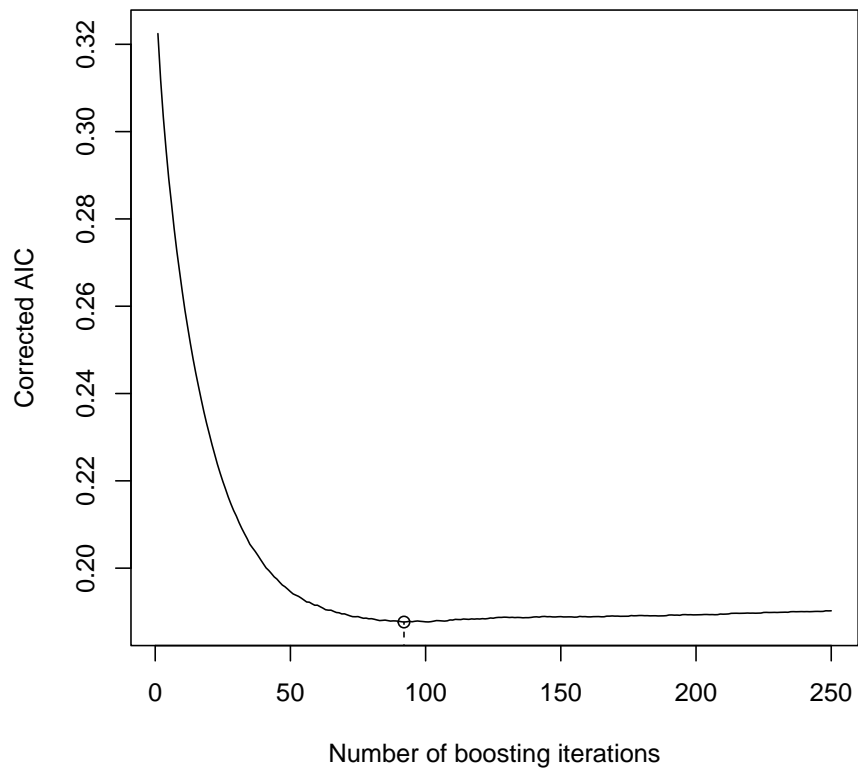


Figure 3: AIC criterion for GBSG2 data.

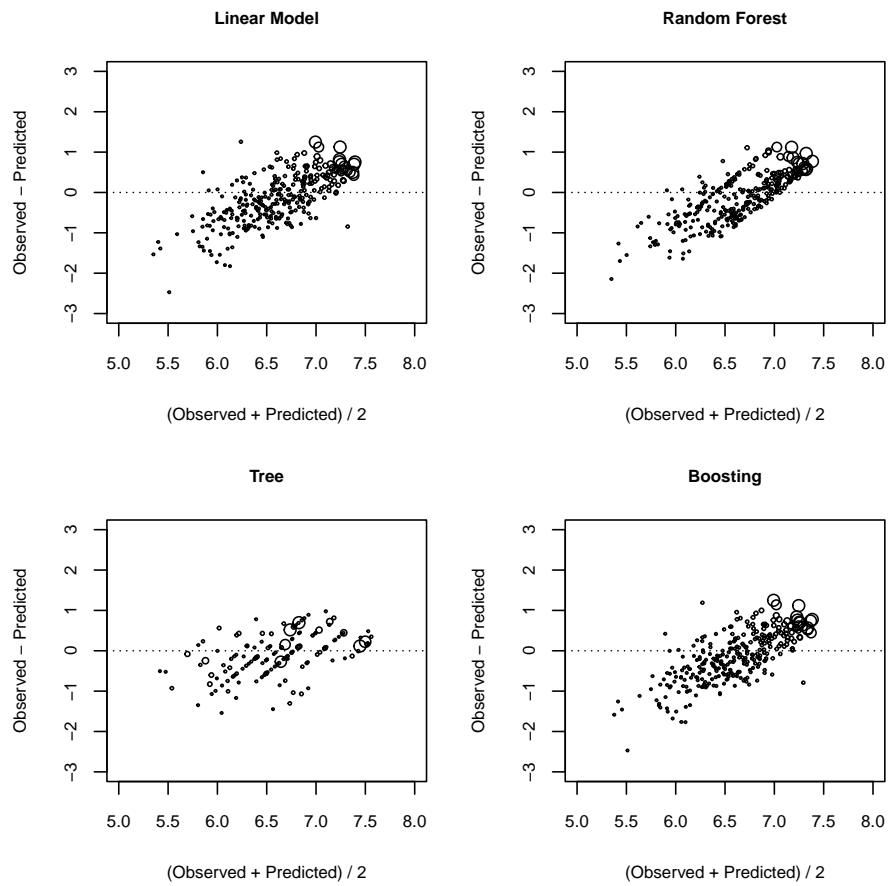


Figure 4: GBSG-2 data: Reproduction of Figure 3.



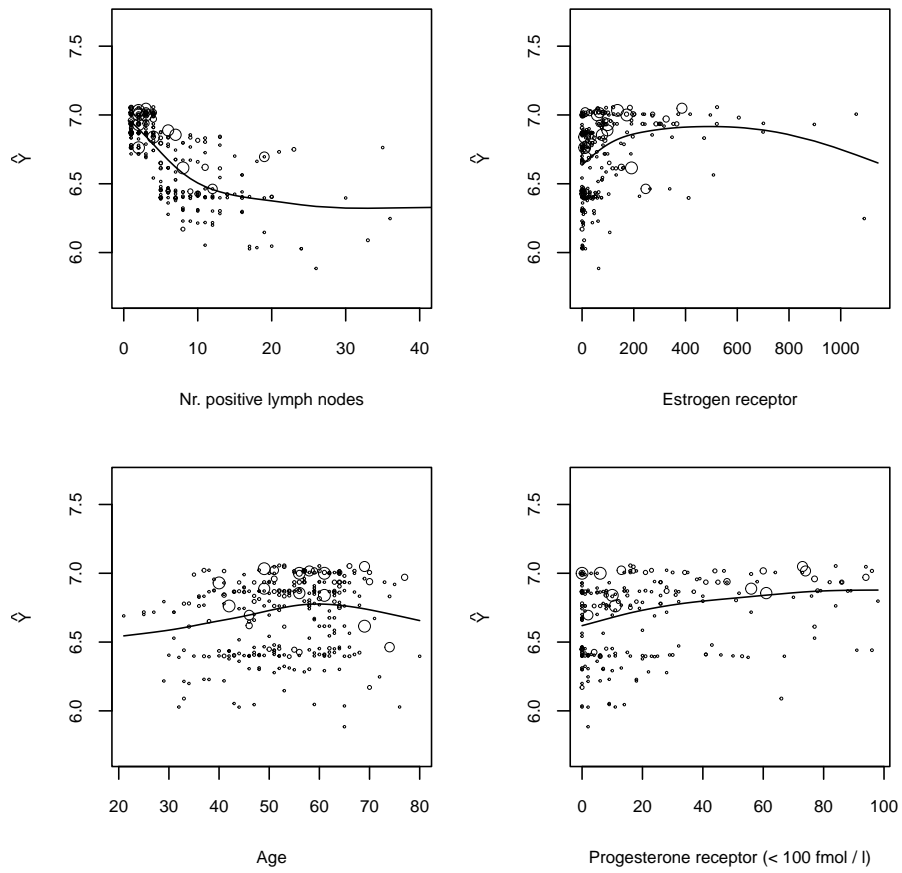


Figure 5: GBSG-2 data: Reproduction of Figure 5.

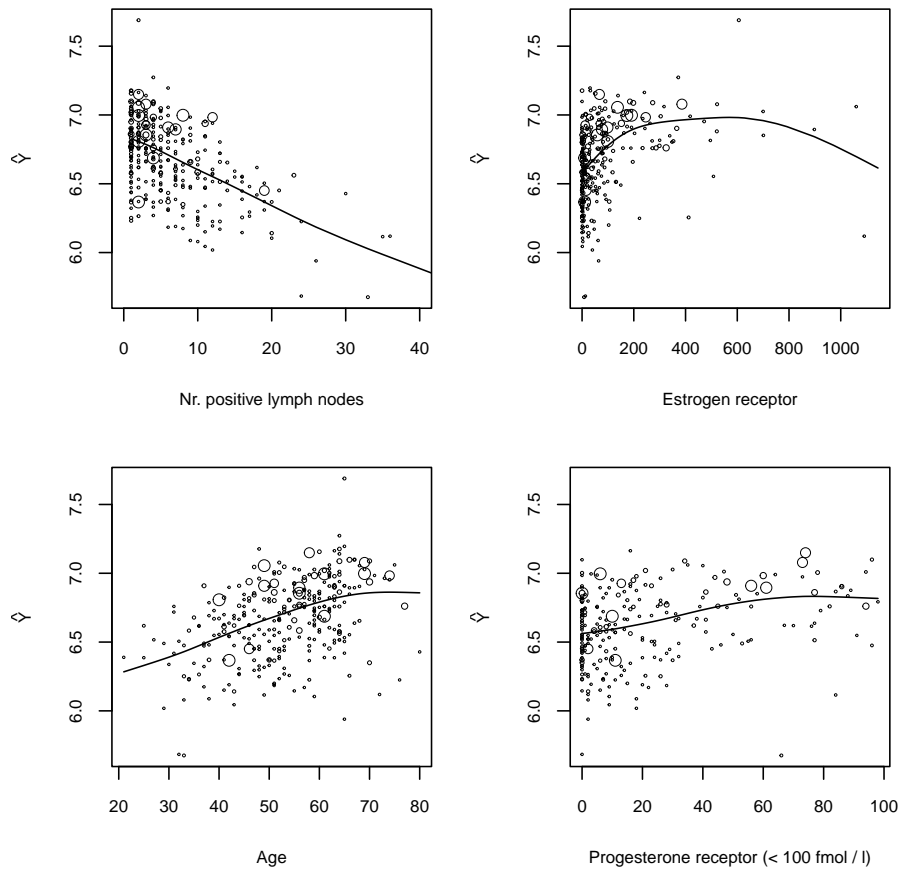


Figure 6: GBSG-2 data: Reproduction of Figure 6.

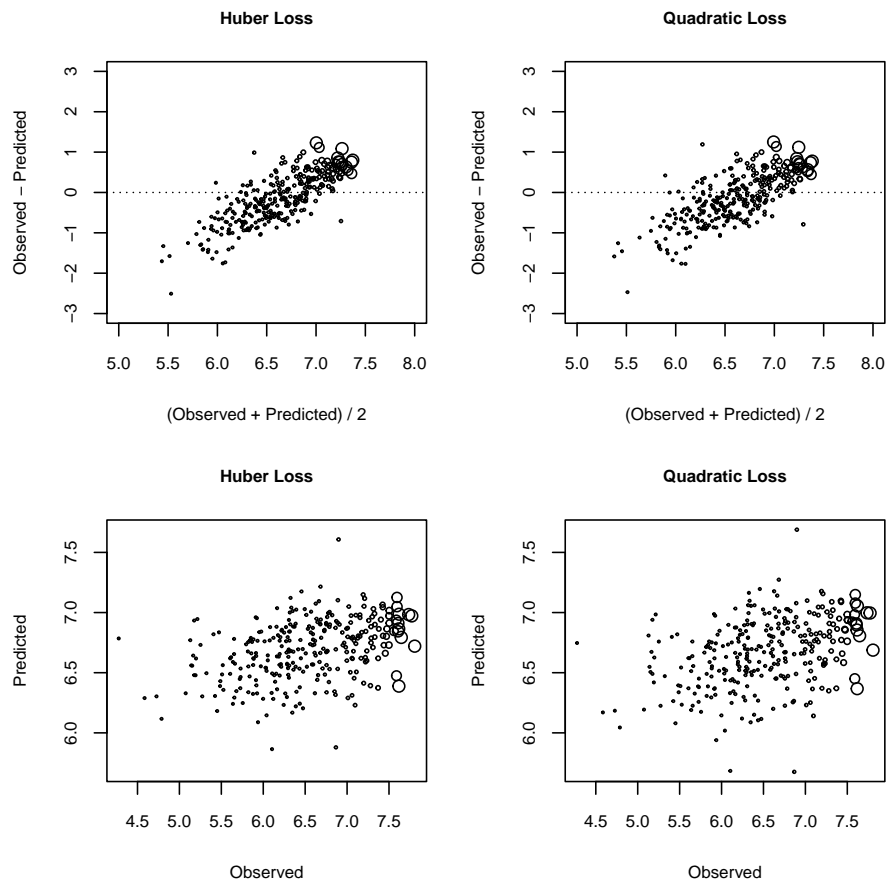


Figure 7: GBSG-2 data: Reproduction of Figure 7.

## References

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